Morphological and Physiological Traits

Note: Levy and Feldman {797} studied the inheritance of more than 20 morphological and biochemical traits in crosses of four *T. dicoccoides* lines and *T. durum*. Similarly, Kuspira *et al.* {744} studied 12 qualitative characters in *T. monococcum*. The symbols applied to the characters examined in these studies are not being reserved and listed in the Catalogue. However, both studies should serve as bases for future work.

1. **Gross Morphology: Spike characteristics**

Major hexaploid wheat types are categorized into groups with respect to three major gene pairs; viz. *Q*, *C* and *S1* {1038}.

1. Common wheat *Q c S1* v: vulgare group.
2. Club wheat *Q C S1* v: compactum group.
3. Shot wheat *Q c s1* v: sphaerococcum group.
4. Spelt wheat *q c S1* and *q C S1* v: spelta group (including vavilovi).

The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups.

Diploid wheat is assumed to be *q*. Durum and carthlicum groups have the genotype *Q* {1049}.

1.1. **Squarehead/spelt**

*Q* {881}. [K (1550)]. 5AL{1293}. **bin**: 5AL-17{10541}. **v**: Common wheats, CS; Iranian spelts{0140}. **tv**: *T. turgidum* ssp. *carthlicum, durum* and *polonicum*{10457}. **ma**: Complete linkage with cDNA clone PtAq22{0127}; *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2), the *Q* allele was more abundantly transcribed than the *q* allele transcription factors{10457}.

1.2. **Club/Compact spike**

*C* {1517}. [Cd{047}]. 2D{1192}. 2DL{1192,1517}.probably 2DL{10578}. **bin**: C-2DS1 - C-2DL3, markers flanking *C* were located on either side of the centromere{10578}. **i**: S-615′/Elgin{1500}. **s**: CS′8/White Spring Spelt 5A{1048}. **tv**: *T. turgidum* ssp. *dicoccum, dicoccoides*{10457}. **ma**: Cent - Xrsq805(Emph)-5A - 4.6 cM - *Q* - 4.3 cM - Xpsr370-5A{419}; *Q* was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23{446}; *Q* - 9.3 cM - Xpsr370-5A{9903}.

The speltoid phenotype of at least some spelts may be caused by genes at other loci {0140}. Fine mapping of the 20 cM region possessing *Q* and delimited by deletions 5AL-7 and -23 is reported in {0324}.

**QTL**: Six QTLs for spike compactness were detected in Courtot/Chinese Spring but only 4 on chromosome arms 1AL, 2BS, 2DS and 4AS were consistent for at least two years{0114}.

Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring {10080} on chromosome arms 5DL (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers Xcfd26-5D and Xcfd38-6D explained 13.6% and 12.2% of the variance in spike compactness, respectively {10080}.

Although gene C may be present in some forms of group *macha* {1447} and *spelta* {0623},...
it is not universally present. Tsunewaki {1500} found that compact spike in one form was controlled by polygenes. 

C may be orthologous to gene Sog for soft glumes on chromosome 2A m {10578}

Tetraploid wheat: A compact spike gene C17648 in mutant line MA 17648 was located in chromosome 5AL {10541}. Xbarc319-5A - 9.7 cM - C17648 - 24.8 cM - Xgwm179-5A {10541}. C17648 was distal to the Q locus {10541}.

1.3. Sphaerococcum

The naturally-occurring sphaerococcum gene in chromosome 3D and various mutant alleles conferring a similar phenotype form a homoeologous series. The sphaerococcoid alleles are either recessive or incompletely dominant. All three mapped loci are closely linked to the respective centromeres {0030}. The "a" alleles are allocated to Chinese Spring or "normal" wheats.

s2. Partially dominant{1286}. [sp2{1286}]. v: Sphaerococcoid wheats. "Sphaerococcum simulator"{1286}.

Sphaerococcum-like tetraploid wheats were reported{122,1282,1286}, but comparisons between them, or with s2, were not made. Whereas Schmidt & Johnson{1281} reported a single recessive controlling the sphaerococcum character in tetraploid wheat, Joppa{621} using the same stock found that two recessive genes were necessary to produce this phenotype.

S-A1{0029}. 3A{0056}. v: CS{0029}.
S-A1a{0029}. v: CS{0029}; common wheats{0029}.
S-A1b{0029}. [S3{0056}]. v: MS 1453 {0056}. ma: Xgwm2-3A(S) - 5.1 cM - S-A1 - 6.6 cM - Xgwm720-3A(L){0030}.
S-B1{0029}. 3B{0030}. v: CS{0029}.
S-B1a{0029}. v: CS{0029}; common wheats{0029}.
S-B1b{0029}. [S2{0030},S1219{10541}]. v: MSK 2452{0056}; MSK 2454{0056}. tv:
MA 16219{10541}. ma: Xgwm685-3B(S) - 4.2 cM - S-B1 - 0.5 cM - Xgwm566/Xgwm845/cent{0030}.
S-D1{0029}. 3D{1292,0030}.3DS{1193,1194}.3DL{692}. v: CS{0029}.
S-D1a{0029}. v: CS{0029}; common wheats{0029}.
S-D1b{0029}. [Sl, spI{1286}]. i: S-615"11/T. sphaerococcum var. rotundatum{1500}.
s: CS"7/T. sphaerococcum rubiginosum 3D{1304}. v: Sphaerococcum wheats{0029}; T. antiquorum K056397 & K56398{10234}.
S-D1c{0029}. [S1{0056}]. v: MS 3287{0056}. ma: Xgdm72-3D(S) - 8.0 cM - S-D1 - 2.9 cM - Xgwm456-3D/cent{0030}.

1.4. Branched spike

Synonyms: branched spike, four-rowed spike, multi-rowed spike, supernumerary spikelet, tetrastichon spikelet.

Branched spike and multi-rowed spike are phenotypes involving the presence of supernumerary spikelets, or the presence of additional spikelets at rachis nodes. A similar condition in rye is known as 'monstrosus ear' (reviewed in {10637}). Genetic studies of branched spike in tetraploid and hexaploid wheats indicate that the phenotype is recessive, involves one or more genes, and is strongly influenced by environmental effects.

Comparative genetic studies suggest an orthologous gene series in homoeologous group 2 {10637}.

bh-A1{10637}. [bh{665}]. 2AS{665}. tv: PI 349056{665}.

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3 MORPHOLOGICAL AND PHYSIOLOGICAL TRAITS

bh-D1{10637}. [mrs{10637}]. bin: 2DS-5 0.47-1.0{10637}. v: Ra1{10637}; Ruc163-1-02 = Ra1 / ZGK242-81{10637}; RUC163167-1-02 = Alana /3/Ra1/ZGK242-82 // Ra1{10637}. ma: Xwmc453-2D / bh-D1 - 7.8 cM - Xgwm988-2D{10637}; Xwmm484-2D - 3.3 cM - Xwmc453-2D/bh-D1 - 3 cM - Xwgm988-2D{10637}. Ra1 is a mutant stock maintained at the NI Vavilov Research Institute of Plant Industry, St Petersburg, Russia.

A chromosome 2B gene of minor effect was identified {9907}. In a monosomic analysis of the hexaploid line LYB with supernumerary spikelets, Peng et al. {9908} located recessive genes in chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene in chromosome 2D that prevents their expression.

bh-R1{10637}. [mo{10637}]. 2R{10637}. al: S. cereale D40{10637}. ma: Xrms056-2R - 15.7 cM - bh-R1 - 10.7 cM - Xcfe209-2R{10637}.

1.5. Elongated glume

Elongated glume is the phenotype associated with the polonicum group of tetraploid wheats. Expression in hexaploid wheat is much reduced compared with tetraploids. Matsumura {911} reported linkage of gene P and a gene for red coleoptiles implicating chromosomes 7A or 7B. A different gene was subsequently located in chromosome 7B {9990}.

P1. [P{911}, Eg{922}, P-A\textsuperscript{pol} /{0254}, P-A\textsuperscript{pet} /{0254}]. 7AL{1546,1547}.7A or 7B (based on linkage of 0.2 with a gene for red coleoptile){922}. i: Saratovskaya29' 8//Nosvibirskaya 67' 2/T. polonicum{922,0066}. itv: P-LD222 = LD222' 11/T. turgidum var polonicum{1546,1547}. tv: T. polonicum{0254}; T. petropavlovskyi{0254}. ma: Xgwm260 - 7A(S) - 2.3 cM - P1 - 5.6 cM - Xgwm1083-7A(L){0254}; Xgwm890 -7A - 2.1 cM - P1{0254}; Xgwm260-7AS - 2.3 cM - P1\textsuperscript{pol} - 5.6 cM - Xgwm1083-7AL {0254}; Xgwm890-7AS - 2.1 cM - P1\textsuperscript{pet} {0254}. Note: The loci determining elongated glumes in T. turanicum and T. durum conv. falcatum are not homoeologous to the P loci in the centromeric region of the group 7 chromosomes{0254}.

P2{9990}. 7BL{9990}. itv: LD222' 7l/T. ispahanicum{9990}. tv: T. ispahanicum{9990}. According to {0254} the loci of T. polonicum, T. petropavlovsky and T. ispahanicum are allelic (homoeoallelic) whereas other workers had claimed genes in the first two forms were not allelic. Wang et al. {0254} however concluded that loci bearing alleles for elongated glumes in T. turanicum and T. durum conv. falcatum were not part of the above series.

1.6. Ear length

QElocs-5A.1{0068}. 5AL{0068}. v: CS(T. spelta 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. ma: Associated with Xbcd9-5A{0068}.

1.7. Multi-gynoecium

Synonym: three pistils (TP).

This trait describes a dominant phenotype consisting of 3 kernels within each wheat floret; that is, the flower consists of 3 separate ovaries, 3 anthers and 2 lodicules.

Pis1{10636}. 2DL{10636}. bin: C-2DL3.0.49{10636}. v: TP Mutant{10636}. ma: Xgwm539-2D - 17.6 cM - Pis1 - 19.5 cM Xgwm349-2D{10636}.

2. Accumulation of Abscisic Acid
A QTL was mapped on 5AL between Xpsr575-5A [proximal] and Xpsr426-5A [distal] [1180].

3. Alkylresocinols Content in Grain
   \( Arf \) [0281]. High alkylresocinols content is dominant [0281]. 5AL [0281]. \( tv: \) Langdon [0281].
   \( arf \) [0281]. \( tv: \) Ardente [0281]; this cultivar has a low content compared to all tested durum and common wheats [0281].

4. Aluminium Tolerance
   \( Alt1 \) [234]. \( v: \) ET3 = Carazinho/4\(^4\)Egret [234].
   \( alt1 \) [234]. \( v: \) ES3 = Carazinho/4\(^4\)Egret [234].
   \( Alt2 \) [848]. \( Alt2_{BH} \) [1213]. 4DL [848]. \( su: \) T. turgidum cv. Langdon 4D(4B) [848].
   \( v: \) BH1146 [1213, 0115]; IAC-24 [0115]; IAC-60 [0115]; 13 induced mutants of Anahuac [0115]. \( ma: \) Alt2 was mapped to a 4 cM interval flanked by Xpsr914-4D and Xpsr1051-4D [848]; on a consensus 4B-4D map of T. aestivum; Alt2 -1.1 cM - Xbcd1230-4D [1213]; Alt2 cosegregated with Xbcd1230-4D and fell within the interval Xgdm125-4D - 4.8 cM - Alt2 -1.1 cM - Xpsr914-4D [0248].

   Malate transporter \( Almt-D1 \) gene (GenBank AB081803) is completely linked to aluminium tolerance in chromosome arm 4DL between SSR markers Xwmc48b and Xwmc331 in a similar region to \( Alt2 \). \( Almt1 \) transgenic expression in barley conferred and Al-activated efflux of malate with properties similar to those of Al-tolerant wheat [10286].

   Allelic variation at the promoter of \( Almt-D1 \) is associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germplasm is derived from several independent sources [10532].

   **QTL**: Atlas 66/Century: A QTL in the region Xgdm125-4DL - Xwmc331-4DL accounted for nearly 50% of the phenotypic variation in root growth rate in hydroponic solution [10265]. An Al-activated malate transporter \( LMT1 \) was earlier mapped to the same location [10266]. Atlas 66 (insensitive)/Chisholm (sensitive) RILs: One QTL, located in chromosome 4DL, corresponded to ALMT1 and accounted for 50% of the phenotypic variation [10483]. A second QTL was located on 3BL (\( R^2 = 0.11 \)) nearest marker Xbarc164-3B [10483]. Both QTLs were verified in Atlas/Century [10483].

   FSW (A1 tolerant) / ND35 (A1 sensitive): 3 QTLs for tolerance, Qalt.pser-4DL cosegregating with Xups4, a marker for the promoter of the ALMT1 gene, Qalt.pser-3BL (Xbarc164-3B - Xbarc344-3B) and Qalt.pser-2A (Xgwm515-2A - Xgwm296-2A) [10605].

   In D genome introgression lines of Chinese Spring a major QTL was located in the interval Xgwm125-4D - Xgwm976-4D, \( R^2 = 0.31 \) [10598], probably coinciding with Alt2. A second QTL from CS, Qalt.ipk-3B, \( R^2 = 0.49 \), occurred in interval Xgwm1029-3BL - Xgwm1005-3BL in a CS / CS (Synthetic 3B) population [10598].

5. Anthocyanin Pigmentation

   The genetic determinants of anthocyanin pigmentation of various tissues are largely located in homoeologous regions in group 7, viz. 7BS (\( Rc-B1, Pc-B1, Plb-B1, Pls-B1 \)) and 7DS (\( Rc-D1, Pc-d1, Plb-D1 \)), and appear to be linked clusters rather than multiple alleles on each chromosome [10700]. Their relationship with genes for purple auricle and purple pericarp are still not clear.

5.1. Purple anthers.
A single, dominant factor was reported \cite{1326}.

### Pan1
\cite{921}. \textit{v}: Ilyitchevka\cite{921}; Mironovskaya 808\cite{921}; Novosibirskaya 67\cite{921}; Pyrothrix 28\cite{921}; Saratovskaya 210\cite{921}; Strela\cite{921}; Ukrainka\cite{921}. \textit{tv}: \textit{T. polonicum}\cite{921}.

### Pan2
\cite{9959}. \textit{tv}: \textit{T. turgidum} ssp. \textit{dicoccoides} acc. MG4343\cite{9959}.

### 5.2. Purple/Red auricles. Purple leaf base/sheath
For review see \cite{1641}.

Melz and Thiele \cite{983} described a "purple leaf base" phenotype where anthocyanin pigmentation extended to the leaf base as well as auricles. Purple leaf base was expressed only when pigmentation occurred in the coleoptiles.

### An5
\cite{983}. \textit{v}: Ilyitchevka; Mironovskaya 808; Novosibirskaya 67; Pyrothrix 28; Saratovskaya 210; Strela; Ukrainka.

### Pc/Pls/Plb
\cite{10692}. \textit{tv}: TRI 15744 (IPK GeneBank, Gatersleben)\cite{10692}.

### 5.3. Red/purple coleoptiles.
There is an orthologous gene series on the short arms of homoeologous group 7. The 'a' alleles confer red coleoptiles.

### Rc-A1
\cite{10451}. \textit{dv}: PAU14087\cite{10451}. \textit{ma}: Xgwm951 - 7B - 6.7 cM - \textit{Pc} - 8.2 cM - \textit{Pp} - 8.9 cM - Xgwm753 - 7B\cite{10451}.

### Rc-A1a
\cite{0250}. \textit{s}: CS\textsuperscript{6}/Hope 7A\cite{1293}.

### Rc-D1a
\cite{0250}. \textit{ma}: Xgwm263 - 7B - 26.1 cM - Rc - 11.0 cM - Xgwm1184 - 7B\cite{0250}.

### 5.4. Purple/red culm/straw/stem
Purple or red colour is dominant.

### Pc1
\cite{743}. \textit{tv}: LD222\textsuperscript{*}11/CS (Hope 7B)\cite{1546}.
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\( \text{Pc}2 \{921\} \). 7DS\{921\}.  v: Illyitchevka\{921\}; Mironovskaya 808\{921\}; Novosibirskaya 67\{921\}; Pyrothrix 28\{921\}; Saratovskaya 210\{921\}; Strela\{921\}; Ukrainka\{921\}.

\( \text{Pc/Pls/Plb} \{10692\}. 7B\{10692\}. \text{tv}: \) TRI 15744 (IPK GeneBank, Gatersleben)\{10692\}. \text{ma}: Xgwm951-7B - 6.7 cM - \text{Pc/Pls/Plb} - 8.2 cM - \text{Pp1} - 8.9 cM - Xgwm753-7B\{10692\}.

5.5. Purple grain/pericarp

Genes for purple pericarp were transferred from tetraploid wheats to the hexaploid level \{112,214,941,1138\}. At the hexaploid level duplicate genes \{112,941\} and complementary genes \{112,939,1138,438\} were reported. At the tetraploid level, duplicate-gene \{941\} and single-gene \{1327\} inheritances were observed. Purple colour is dominant and may be affected by environment and genetic background. Complementary genes were located in chromosomes 3A and 7B \{1138\}. Possible pleiotropic relationships of genes affecting pigmentation of various tissues have not been studied in detail. \( \text{Pc2} \) and \( \text{Rc-B1a} \) may be the same gene \{769\}. Also, complementary genes involved in determination of purple pericarp could be related to culm colour \{112\}. For review, see \{1643\}.

Complementary dominant genes.

\( \text{Pp1} \{041\}. 6A\{041\}.7BL\{10392\}. \text{i}: \) Saratovskaya 29*8/Purple \{Australia\} \( \text{Pp2} \{040\}. \text{v}: \) Novosibirsk 67 (this cultivar has white pericarp)\{10392\}. \text{v2}: Purple K49426 \( \text{Pp3a} \{10392\}; \) Purple Feed \( \text{Pp3b} \{10392\}. \text{ma}: \) Xgwm983-7B - 15.2 cM - \text{Pp1} - 11.3 cM - Xgwm767-7B\{10392\}.

\( \text{Pp2} \{041\}. 7A\{041\}. \text{tv}: \) T. durum Desf. subsp. abyssinicum Vav\{040\}. Piech and Evans\{1138\} located complementary genes on chromosomes 3A and 7B. \( \text{Pp2} \) was renamed \( \text{Pp3b} \).

\( \text{Pp3} \{10392\}. 2A, \text{not} 6A\{0066,10392\}. \text{Pp3a} \{10392\}. \text{v2}: \) Purple K49426 \( \text{PpI} \{10392\}. \text{ma}: \) Xgwm328-2AS - 2.7 cM - \text{Pp3a} - 3.2 cM - Xgwm817-2AL\{10392\}.

\( \text{Pp3b} \{10392\}. \text{Pp2} \{041\}. \text{v2}: \) Purple Feed\{10392,0066\}. \text{ma}: Xgwm328-2AS - 5.2 cM - \text{Pp3b/Xgwm817/Xgwm912-2A - 3.6 cM - Xgwm445-2A} \{10392\}.

\( \text{pp1pp3}. \text{v}: \) Saratovskaya 29 (this cultivar has red pericarp)\{10329\}.

5.6. Purple glume

\( \text{Pg} \{10692\}. 2A\{10692\}. \text{tv}: \) TRI 15744 (IPK GeneBank, Gatersleben)\{10692\}. \text{ma}: Xgwm328-2A - 19.2 cM - \text{Pg} - 1.4 cM - \text{Pp3} - 5.1 cM - Xgwm817-2A\{10692\}.

5.7. Purple leaf blade

\( \text{Plb} \{10692\}. 7B\{10692\}. \text{tv}: \) TRI 15744 (IPK GeneBank, Gatersleben)\{10692\}. \text{ma}: Xgwm951-7B - 6.7 cM - \text{Pc/Pls/Plb} - 8.2 cM - \text{Pp1} - 8.9 cM - Xgwm753-7B\{10692\}.

6. Awnedness

\( \text{hd b1 b2}. \) Bearded or fully awned genotype

6.1. Dominant inhibitors

6.1.1. Hooded
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\[ H_d \{1551\}. \ 4A S\{1195,1293\}. \ i: S-615^*11/CS\{1500\}. \ v: Chinese Spring B2\{1293\}. \ ma: \ Xcdo1387-4A - 8.2 \ cM - H_d - 7.2 \ cM - Xpsr163-4A \{0047\} was mapped as a QTL with a peak on Xfba78-4A\{0309\}.

\[ Ld. \ s: \ CS^*6/Hope 4A; CS^*5/Thatcher 4A; CS^*6/Timstein 4A.

### 6.1.2. Tipped 1

\[ B1 \{1551\}. \ 5A L\{1293,0242\}. \ i: S-615^*11/Jones Fife\{1500\}. \ v: Timstein\{741\}; Redman\{160\}; WAWHT2046\{10040\}. \ tv: LD222\{10541\}. \ ma: \ Xgwm410.2-5A - 8.2 \ cM - B1 - 12.2 \ cM - Yr34\{10040\}; Terminally located\{10189\}; Xgwm291-5A.3 - 5.3 \ cM - B1\{10330\}. \ matv: \ Xgwm291-5A - 8.0 \ cM - B1\{10541\}.

\[ B1 \{1551\}. \ i: S-615^*11/CS\{1500\}. \ v: Chinese Spring B2\{1293\}. \ b2. \ s: \ CS^*6/Hope 6B; CS^*5/Thatcher 6B; CS^*9/Timstein 6B.

### 6.1.3. Tipped 2

\[ B2 \{1551\}. \ 6B L\{1293,1297\}. \ i: S-615^*11/CS\{1500\}. \ v: Chinese Spring H_d\{1293\}.

### 6.1.4. Awnless

Genotypes \( H_d \) \( B2 \) (e.g., Chinese Spring) and \( B1 \) \( B2 \) (e.g., Federation) are awnless. Presumably \( H_d B1 \) is awnless. Watkins & Ellerton \{1551\} noted the probability of a third allele "\( b1a \)" leading to a half-awned condition, and in discussion they consider the possibility of a similar third allele at the \( B2 \) locus. In view of more recent cytogenetic analyses, it seems that the half-awned condition could result from epistatic interactions between the alleles \( B1 \) and/or \( B2 \) and various promotor genes.

Although hooded, half-awned, tip-awned and awnless variants occur among tetraploid wheats, these are relatively infrequent. It has not been established with certainty that the above inhibitors are involved.

The inhibitor alleles have a pleiotropic effect on glume-beak shape \{1348\}. Acuminate beak is associated with full beardedness and occurs only in \( b1 b2 \) types. \( B2 \) reduces beak length producing an acute beak shape. \( B1 \) reduces beak length producing an obtuse beak shape. In this effect \( B1 \) is epistatic to \( B2 \).

### 6.2. Promotors

The effects of (recessive) awn-promoting genes were documented in a number of studies, mainly through monosomic and disomic F1 comparisons, and in tetraploids, whereas Heyne & Livers \{549\} provided genetic evidence of their effects. A series of a" genes was documented, but the evidence for the existence of at least some of these was not well supported. Hence symbols for this gene series are not recognized.
6.3. Smooth awns
Smooth-awned tetraploid wheats were reported \{016,045,690,1259\} and genetic analyses \{016,045,690\} suggested a single recessive factor, with modifiers in most instances, relative to rough awns. The phenotype has not been reported in hexaploid wheats. No gene symbol is applied.

7. Basal Sterility in Speltoids
The presence of gene Q ensures the fertility of the first and subsequent florets in wheat spikelets \{378\}. In speltoids lacking Q, fertility of the second and subsequent florets is ensured by the dominant allele Bs (designated A in \{378\}) located on chromosome 5D \{377\}. In the presence of Bs the fertility of the first floret is under polygenic control. In bs bs speltoids floret development is under polygenic control, and stocks with varying levels of basal fertility were isolated.

All group vulgare genotypes so far studied carry Bs.

The following stocks were described \{378\}:

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Approx. sterile-base score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group vulgare</td>
<td>QQ Bs Bs</td>
</tr>
<tr>
<td>Speltoids</td>
<td></td>
</tr>
<tr>
<td>StFF</td>
<td>qq Bs Bs</td>
</tr>
<tr>
<td>StF</td>
<td>qq Bs Bs</td>
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<td>St1</td>
<td>qq Bs Bs</td>
</tr>
<tr>
<td>St2</td>
<td>qq bs bs</td>
</tr>
</tbody>
</table>

8. Blue Aleurone
The Ba allele in T. monococcum spp. aegilopoides acc. G3116 determines a half-blue seed phenotype and is different from the allele present in Elytrigia pontica that determines a solid blue phenotype \{282\}. They are treated as different genes.

For review see \{1643\}.

Ba1 \{643\} Derived from Elytrigia pontica \(2n=70\). \(Ba\{643\}\). 4B[4BS-4el2]\{643\}. tr: UC66049B\{594\}.

Ba2 \(Ba\{10451\}\). 4A\(^m\)L\{282\}\(^3\). dv: G3116\{282\}; PAU5088 = G2610 = PI 427389\{10451\}.

ma: Ba2 cosegregated with Xcdo1387-4A, Xmwg677-4A and Xbcd1092-4A \{282\}; Xcfd71-4A - 10.3 cM - Ba - 16.5 cM - Xcfa2173-4A\{10451\}\(^3\).

9. Brittle Rachis
Brittle rachis in T. durum was defined as a spike that disarticulated when the tip was bent by 45 degrees relative to the peduncle \{10242\}.


Br-B1 \{10061\}. \(Br3\{0130\}, Br-A3\{10280\}\). 3B\{0130\}.3BS\{10061\}. sutv: LTN(DIC 3B)\{0130\}. itv: ANW10B=LD222*7/LDN-DIC DS 3A\{10242\}. ma: Xbarc218-3B - 22 cM - Br-B1 - 2 cM - Xwmc777-3B\{10280\}. tv: Senatore Cappelle PI 242646\{10242\};
Sammartinara\{10242\}; others\{10242\}.  

The presence of \textit{Br-B1} in some durums apparently does not lead to significant shattering under conditions of Mediterranean agriculture \{10242\}. \textit{Br-D1} \{10061\}. \textit{Br1} \{9970\}. \textit{Br61} \{10362\}. 3DS\{9970\}. \textit{v}: KU510, KU511, KU515\{10061\}; R-61\{10362\}; \textit{T. aestivum var. tibetanum}\{9970\}.  

Evidence for an orthologous series extending to many related species is discussed in \{0130\} and \{10061\}. \textit{Br4} \{10082\}. 2A\{10082\}. tv: \textit{T. dicoccoides}\{10082\}. ma: 33 cM distal to Xgwm294-2A (LOD=6.3, R\(^2\)=14.4\%)\{10082\}.

### 10. Boron Tolerance

Genes controlling tolerance to high concentrations of soil boron act additively. \textit{Bo1}\{1111,1113\}. 7B\{177\}.7BL\{10460\}. v: Carnamah\{10460\}; Frame\{10460\}; Krichauff\{10460\}. \textit{v2}: Halberd \textit{Bo2Bo3}. ma: \textit{Bo1} co-segregated with several STS-PCR markers, including \textit{Xaww11}-7BL, falling within a 1.8 cM interval\{10460\}; The AWW7L7 (\textit{Xaww11}) PCR marker allele was a good predictor of boron tolerance\{10460\}.

\textit{Bo2}\{1111,1113\}. \textit{v2}: (W1\`MMC)/Warigal \textit{Bo3}. Halberd \textit{Bo1 Bo3}.

\textit{Bo3}\{1111,1113\}. 4A\{0012\}. \textit{v2}: Warigal \textit{Bo2}. Halberd \textit{Bo1 Bo2}.

Very sensitive genotype: Kenya Farmer \textit{bo1 bo2 bo3}.

In contrast to tolerance, boron efficiency was studied in \{10135\}. Monogenic segregation occurred in Bonza (B inefficient)/SW41 (moderately B inefficient) and SW41/Fang60 (B efficient). Two genes, designated \textit{Bod1} and \textit{Bod2} segregated in Bonza/Fang60.

### 11. Cadmium Uptake

#### 11.1. Low cadmium uptake

\textit{Cdu1}\{963\}. \textit{Cdu1}\{1128\}. 5BL\{10104\}. itv: Kyle*2/Biodur\{10104\}. tv: Biodur\{1128\}; Hercules\{1128\}; Nile\{1128\}.

\textit{cdu1}\{963\}. \textit{cdu1}\{1128\}. itv: Kofa\{10104\}. tv: Kyle\{1128\}. ma: \textit{Cdu1} - 4.6 cM - \textit{OPC-20}\{1128\}; \textit{Cdu1} - 21.2 cM - \textit{UBC-180}\{1128\}.

### 12. Chlorophyll Abnormalities

#### 12.1. Virescent

\textit{V1}. 3B\{122,1311,1294\}.3BS\{1423\}. v: CS.

\textit{v1a}. [\textit{v1a}\{1294\}]. i: S-615*/Neatby's Virescent\{1500\}. s: CS*9/Neatby's Virescent\{1304\}. v: Neatby's Virescent\{1055\}.

\textit{v1b}. i: CS*/Hermsen's Virescent v2b\{1304\}. v: Hermsen's Virescent v2b\{1311\}.

\textit{V2}. 3A\{1311,1545\}. v: CS.

\textit{v2a}. v: Viridis 508\{1545\}.

\textit{v2b}. Expressed only when combined with \textit{v2b} i: CS*/Hermsen's Virescent \textit{v1a}\{1304\}. v: Hermsen's Virescent \textit{v1a}\{1311\}.

\textit{v1b} and \textit{v2b} are expressed only when both are present. Corresponding normal alleles are designated \textit{V1} \{3B\} and \textit{V2} \{3A\} following Sears' \{1295\} demonstration of their effects on the expression of \textit{v1a}.
12.2. Chlorina

*Cn-AI*. 7A{1132}.7AL{1131,1304,1311}. v: CS.
   *cn-Ala*. [cn1a]. i: Chlorina-1{1311}.
   *cn-Alb*. [cn1b]. i: Cornell Wheat Selection 507aB-2B-21/6’CS{1133}.
   *cn-Alc*. [cn2]. i: Chlorina-448. (CS background){1545}.

*Cn-Adl{665}. tv: CDd6{665,666}.

*Cn-B1*. 7BL{1131}. v: Chinese Spring{1131}.
   *cn-B1a{665}. tv: CDd1{665,666}; CBC-CDd1{665}.
   *cn-B1b{665}. tv: CDd2{665,666}.

*Cn-D1*. [Cn3]. 7D{1545}.7DL{1131}. v: Chinese Spring{1131}.
   *cn-D1a{665}. i: Chlorina-214{1545}. v: CD3{1583}.

12.3. Striato-virescens

A mutant of this type was described {376} but has been lost.

13. Cleistogamous Flowering in Durums

Cleistogamy, a rare flowering habit in durum wheats, is controlled by a single recessive gene relative to chasmogamy {191}.

*Cleistogamous genotypes* clcl. tv: HI8332 {191}; WH880 {191}.

*Chasmogamous genotypes* ClCl. tv: IWP5308 {191}; PWB34 {191}; WH872 {191}.

14. Copper Efficiency

Copper efficiency is a genetic attribute that enhances plant growth in copper deficient soil.

*Ce{1276}. 4BL = T4BL.5RL{1276}. v: Cornell Selection 82a1-2-4-7{462}; Backcross derivatives of Cornell Selection to Oxley, Timgalen, Warigal{464}; Hairy necked Viking{1276}.

5BS = T5BS.5RL. *ad: CS+5R{463}. su: CS 5R{5D}{463}. v: Sears’ stock HN-2{464}; Backcross derivatives to Warigal and Timgalen{464}.

15. Corroded

*co1*. [co{1297}]. 6BS{1293}. v: Sears’ corroded mutant.

*co2*. 6D{1570}. v: Kurrachee{1570}.

A gene(s) in chromosome 6A acts as an inhibitor of corroded {1039,1570}.

16. Crossability with Rye and *Hordeum* and *Aegilops* spp.

16.1. Common wheat

High crossability of some wheats, particularly those of Chinese origin, viz. Chinese 446 {790}, Chinese Spring {1216}, and TH 3929 {939}, with cereal rye, weed rye (*S. segetale* L.) {1646}, and other species, e.g., *Aegilops squarrosa* {691}, *Hordeum bulbosum* {1387,1397,1469} and *H. vulgare* {349,693}, is determined by additive recessive genes. The *kr* genes influence crossability with *H. vulgare*. Allele *kr1* is more potent in suppressing
crossability than Kr2 which is stronger in effect than Kr3 \cite{1387}. According to Zheng et al. \cite{1649}, the effect of Kr4 falls between Kr1 and Kr2.

**Kr1.** 5B\{1216\}.5BL\{762\}.

**Kr2.** 5A\{1216\}.5AL\{1387\}.

**Kr3.** 5D.

**Kr4.** 1A\{1649\}.

**Kr1 Kr2.** \textit{v}: Chinese 446\{790\}; Chinese Spring\{762,1216,1025\}; Martonvarsari 9\'4/CS\{1016\}.

**Kr1 Kr2.** \textit{s}: CS\'6/Hope 5B\{762,1216\}. \textit{v}: Blausamtiger Kolben\{790\}.

**Kr1 Kr2.** \textit{s}: CS\'6/Hope 5A\{1216\}.

**Kr1 Kr2.** \textit{v}: Marquis\{790\}; Peragis\{790\}.

**Kr1 kr2 kr3 kr4.** \textit{v}: J-11\{1649\}.

**Kr1 Kr2/Kr1 kr2.** (heterogeneous). \textit{v}: Martonvarsari 9\{1016\}.

Using the Chinese Spring/Cheyenne chromosome substitution series, Sasaki & Wada \cite{1265} found significant differences in crossability for chromosome 5B, 7D, 1D and 4B. Differences between rye lines also occur \cite{1265,1458}. Allelic variation in the potencies of the dominant suppressor genes was reported \cite{1385,343}. Evidence for allelic variation in dominant suppressors is reported in \cite{1386}. Lists of wheat/rye crossabilities: \cite{1383,1642,850,858}.

**QTL:** 65\% of the variability in a Courtot/CS population was associated with Xfba-367-5A(5AS), Xwg583-5B(5BL) and Xtam51-7A\{0134\}. Only the second QTL appears to coincide with known locations of Kr genes.

16.2. Tetraploid wheat

The Chinese tetraploid, Ailanmai, possesses recessive crossability genes on chromosomes 1A, 6A and 7A with the 6A gene being the least effective \cite{0017}.

17. Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to pre-harvest sprouting (PHS).

17.1. Vivipary

Orthologues of maize viviparous 1 (\textit{Vp-I}) are located in chromosomes 3AL, 3BL and 3DL \cite{9961} approximately 30 cM distal to the \textit{R} loci. Variability at one or more of these loci may be related to germination index and hence to PHS \{10468\}.

Three sequence variants of \textit{Vp-B1} identified in \{10468\} were used to develop STS marker \textit{VpiB3} whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.

Alleles of \textit{Vp-B1} were recognised using STS marker \textit{Vp1B3} \{10615, 10621\}.

**Vp-B1a**\{10615\}. \textit{c}: AJ400713\{10615\}. \textit{v}: Charger\{10616\}; Zhongyou 9507\{10615\}; 271 accessions\{10616\}.

**Vp-B1b**\{10615\}. \textit{c}: 193 bp insertion in third intron relative to \textit{Vp-A1a}. \textit{v}: Altria\{10616\}; Recital\{10616\}; Yongchuanbaimai\{10615\}; 2 accessions\{10616\}.

**Vp-B1c**\{10615\}. \textit{c}: 83 bp deletion relative to \textit{Vp-B1a}. \textit{v}: Scipion\{10616\}; Xinong 979\{10615\}; 101 others\{10616\}.

**Vp-B1d**\{10616\}. \textit{c}: 25 bp deletion relative to \textit{Vp-A1a}.
Vp-B1e\{10621\}. c: 83 bp deletion, 4 bp insertion and 2 SNPs relative to Vp-B1a\{10621\}. v: Hongheshangtou\{10621\}.

There was a suggestion of a relationship between alleles and PHS response \{10615\}. Vp-B1 allelic identifications for Chinese landraces, historical and current wheat cultivars are listed in \{10621\}.

17.2. Pre-harvest sprouting

Phs1\{10500\}. Semi-dominant \{9960\}. 4AL\{9960\}. i: Haruyokoi*6/Leader\{10500\}; Haruyokoi*6/Os21-5\{10500\}; Soleil\{9960\}. v: Leader\{10500\}; Os21-5\{10500\}; Soleil\{9960\}. ma: Associated with Xpsr1327-4A\{10346\}; Xhbe03-4AL - 0.5 cM - Phs1 - 2.1 cM - Xbarc170-4AL\{10500\}.

\textit{phs1}. v: Haruyokoi\{10500\}.

QTL: Several QTL for falling number and alpha-amylase activity, two indicators for pre-harvest sprouting resistance, were identified in \{0169\}. The most significant were associated with Xglk699-2A and Xsfr4(NBS)-2A, Xglk80-3A and Xpsr1054-3A, Xpsr1194-5A and Xpsr918-5A, Xpsr644-5A and Xpsr945-5A, Xpsr8(Cxp3)-6A and Xpsr563-6A, and Xpsr350-7B and Xbzh232(Tha)-7B \{0169\}. In cross AC Domain/Haruyutaka, one major QTL in chromosome 4AL and two lesser possibly homoeologous QTLs for dormancy in 4BL and 4DL \{0226\} were found. Tolerance to preharvest sprouting (PHS) in the cross SPR8198/HD2329 was associated with Xwmc104-6B and Xmst101-7D \{0032\}. In AC Domain (red seeded, PHS resistant) / RL4137 (white seeded, PHS moderately resistant) most measures of PHS occurred as clusters at the R loci. However, QSi.crc-5D for sprouting index, $R^2=0.44$, was independent of seed colour \{10626\}.

QTL for preharvest sprouting were identified on chromosomes 3A (associated with Xfbb293-3A at P=0.01), 3B (associated with Xgwm403-3B and Xbcd131-3B at P=0.001), 3D (associated with Xgwm3-3D at P=0.001) and 5A (associated with Xbcd1871-5A at P=0.001) in the population Renan/Recital \{0347\}. The resistant alleles on the group 3 chromosomes and on 5A were contributed by Renan and Recital, respectively. All QTL for preharvest sprouting co-located with QTL for grain colour \{0347\}. Zenkoujikomugi/CS: Qphs.ocs-3A.1 on chromosome 3AS was associated with Xbcd1380-3A and Xfbb370-3A accounting for 38% of the phenotypic variation \{10195\}. Zenkoujikomugi/Spica: White seeded wheats with the dormancy-related QTL, QPhs-3AS from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica \{10377\}. White seeded wheats with contrasting alleles of QPhs-4AL were not different \{10377\}.

QPhs.ocs.3A-1 was localized to a 4.6 cM interval flanked by Xbarc310-3A and Xbcd907-3A \{10245\}. A weaker QTL, Qphs.ocs-3A.2 in 3AL, was not associated with TaVp1 \{10195\}, the wheat orthologue of the maize transcription factor Viviparous-1.

Qphs.ocs-4A.1 may be the same as a QTL in AC Domain/Haruyutaka due to tight linkage with Xcdo785-4A \{10245\}. QPhs.ocs.4B.1, a CS allele contributing to dormancy, was located in the region of Xgwm495-4B \{10245\}.

In cross SPR 8198 (dormant)/HD2329, QPhs.occсу-3A was located in the Xgwm155-3A - Xwmc153-3A region with $R^2=75\%$ across 6 environments \{10261\}. QTL analyses in several crosses \{10275\} indicated a common region in chromosome 4A associated with dormancy, dormant genotypes included AUS1408, SW95-50213 and Halberd. The location was consistent with Japanese and U.K. work even though different flanking markers were involved.
13 Morphological And Physiological Traits

CN10955 (PHS resistant white seeded) / Annello (PHS susceptible, white seeded) F8 RIL population: *QPhs.dpivic-4A.2* in the *Xgwm637-4AS - Xgwm937/Xgwm894-4AL* region and *QPhs.dpivic-4A.1* in the *Xwmc48-4AS - Xgwm397-4AS* region {10599}.

Rio Blanco (white seeded, PHS resistant) / NW97S186 (white seeded, PHS susceptible) RIL population: *QPhs.pseru-3AS*, R²=0.41, *Xgwm369-3A - Xbarc12-3A*, and one minor QTL {10634}. This major QTL was confirmed in a Blanco / NW98S079 RIL population, R² up to 0.58 {10634}.

RL4452 (red seeded, low PHS tolerance)/AC Domain (red seeded, high PHS tolerance): DH lines: Genes associated with falling number, germinat ion index and sprouting index contributing to PHS were locatged on chromosomes 3A, 4A (locus-2) and 4B in AC Domain and 3D, 4A (locus-1) and 7D in RL4452 {10671}.

SPR8198 (red seeded, PHS tolerance)/HD2329 (white seeded, PHS susceptible): RIL population: 7 QTL located on chromosomes 2AL, 2DL, 3AL and 3BL, the most important on 2AL and 3AL {10670}.

Sun325B (dormant white seeded)/QT7475 (semi-dormant white seeded), both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77 - Xwmc527 - Xwmc527* interval (R²=0.19) in the approximate region of the *R-B1* locus {10669}.

Diploid wheat QTL: *T. monococcum* KT3-5 (non-dormant)/*T. boeoticum* KT1-1 (dormant): RIL population: QTL on chromosome 5A *mL, Xcdo1236c - Xabc3025A*, R²=0.2-0.27. Weaker QTLs were found on 3A^m (TmA18 - Xwmc102-3A and Xrz444-3A - TmA18) and 4A^m (Xrz261-4A - Xrz141-4A) {10417}. The 3A^m QTL co-located with TmA18 and TmA18 {10417}, derived from orthologous ABA signaling genes in *Arabidopsis*. The 5A QTL may be orthologous to the barley dormancy gene *SD1* {10417}.

18. Ear Emergence

*QEt.ocs-4A.1* {0047}. 4AL{0047}. v: CS/CS(Kanto107 4A) mapping population. ma: Associated with Wx-B1{0047}.

*QEt.ocs-5A.1* {0068}. 5AL{0068}. v: CS(T. spelta 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. ma: Associated with Xcdo584-5A and morphological locus Q{0068}.

*QEt.ocs-5A.2* {0026}. 5AL{0026}. ma: Xcdo 412-5A - Xbcd9-5A region{0026}.

*QEt.inra-2B* {10069}. 2B. ma: 2B linked to Xgwm148 (LOD=5.7, R²=11.9%).

*QEt.inra-2D* {10069}. 2D. ma: 2D linked to XksuE3 (LOD=2.7, R²=6.5%).

*QEt.inra-7D* {10069}. 7D. ma: 7D linked to Pch1 (LOD=3.9, R²=7.3%).

*QEt.ipk-2D* {0255}. *QEt.ipk-2D* coincides with a QTL for flowering time, *QFlt.ipk-2D*. Both QTLs may correspond to *Ppd-D1* {0255}. 2DS{0255}. v: Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. ma: Associated with Xfba400-2D and Xcdo1379-2D{0255}.

*QEt.ipk-5D* {0255}. *QEt.ipk-5D* coincides with a QTL for flowering time, *QFlt.ipk-5D*. Both QTLs probably correspond to *Vrn-D1* {0255}. 5DL{0255}. v: Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. ma: Associated with Xbcd450-5D{0255}.
19. Earliness Per Se

Genes for earliness *per se* \{0023\} affect aspects of developmental rate that are independent of responses to vernalization and photoperiod.

**Eps-IA**\textsuperscript{m} \{0364\}. \[Eps-IA\]^1\]. 1AL \{0364\}. **dv:** *T. monococccum* DV92 allele for late flowering, G3116 early flowering. \{0364\}. **ma:** 0.8 cM distal to *Xwg241-1A* \{0364\}; within a 0.9 cM region within the *VAtPC* - *Smp* region \{10246\}.

**Eps-5BL.1** \{10075\}. 5BL \{10075\}. \[Eps-5BL.1\]^1\]. **ma:** QTL mapped on chromosome 5BL, linked to *Xwmc73-5B* (this QTL explained 8\% of the variance in flowering time, \(P<0.03\) \{10075\}).

**Eps-5BL.2** \{10075\}. 5BL \{10075\}. \[Eps-5BL.2\]^1\]. \[Eps-5BL.2\]^1\]. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm499-5B* (this QTL explained 6\% of the variance in flowering time) \{10075\}.

**Eps-A1a** \{0024\}. 3A \{0024\}. **ma:** Chinese Spring \{0024\}.

**Eps-A1b** \{0024\}. \[Eps-A1b\]^1\]. **v:** Timstein \{0024\}.

**EpsCnn** \{0025\}. \[EpsCnn\]^1\]. **v:** Chinese Spring \{0025\}.

**EpsWi** \{0025\}. 3A \{0025\}. **su:** Cheyenne \{0025\} - Wichita 3A \{0025\}. **ma:** Linked to QTLs for plant height, kernel number per spike, and 1,000-kernel weight in SRLs derived from CNN/CNN(WI3A) \{0025\}.

QTL: Analysis in Courtot/CS \{0132\}. Two QTLs for narrow-sense earliness were detected on chromosome 2B in a CS/T. *spelta* var. *duhamelianum* KT19-1 RI population \{10057\}. These QTLs were associated with markers *Xpsr135-2B* and *Xabc451-2B* \{10057\}. For both QTLs, earliness was conferred by the CS allele.

**QEet.fcu.5AL** identified in *Xfcp359-5A* - *Xfcp231-5A* interval (\(R^2=0.38\)), at or near the \(Q\) locus in Grandin/BR34 \{10256\}. Grandin was the earlier parent.

20. Flowering Time

The isolation of wheat genes orthologous to the Arabidopsis *Co* and rice *Hdl* genes was reported in \{10054\}. The genomic clones TaHdl1-1, TaHdl1-2 and TaHdl1-3 originate from the long arms of chromosomes 6A, 6B and 6D, respectively. The orthology of the *TadHdl* genes with *Co/Hdl* was demonstrated by complementation of a rice line deficient in *Hdl* function with the TaHdl1-1 genomic clone. It should be noted that the wheat *TaHdl* and rice *Hdl* genes are located in non-syntenic locations \{10054\}. To date, no variation for flowering time has been identified on the wheat group 6 chromosomes.

Winter wheat cross, Arina (149 days)/Forno (150 days): Six QTL were detected over six environments. The 3 most important, all from Arina, were in chromosomes 6DL (\(R^2=16\%\)), 3DL (\(R^2=14\%\)) and 7BL (\(R^2=13\%\)); 3 others in 2AL, 5BL and 6DL were from Forno \{10172\}.

Winter wheat cross Ernie (early)/MO94-317 (late), days to anthesis (dta):

**Qdta.unc-2D** linked to *Xbarc95-2D*; \(R^2 = 0.74\) \{10456\}.

Spring wheat cross: Nanda 2419 / Wangshuibai: Seven QTLs for flowering time identified with earlier alleles for five coming from Nanda 2419: *QFlt.nau-1B* (closest marker *Xbarc80-1B*; \(R^2=11\%\)), *QFlt.nau-1D* (*Xbarc62-1D*, *Xgwm232-1D*, \(R^2=6.13\%\)), *QFlt.nau-2B* (*Xwmc35-2B*, \(R^2=10\%\)), *XFlt.nau-2D* (*Xwmc601-2D*, \(R^2=10\%\)), *XFlt.nau-4A.1* (*Xcfd2-4A*, *Xmag1353-4A*, \(R^2=10\%\)), *XFlt.nau-4A.2* (*Xmag3386-4A*, *Xwmc161-4A*, \(R^2=18\%\)), *XFlt.nau7B* (*Xmag2110-7B*, *Xmag1231-7B*, *Xgwm537-7B*, *Xwmc218-7B*, \(R^2=18\%\)) \{10566\}.

**QFlt.ikp-3A** \{0255\}. 3AL \{0255\}. **v:** Opata/W-7984 (ITMI) RI mapping population \{0255\}; Lateness was contributed by W-7984 \{0255\}. **ma:** Associated with *Xbcd451-3A* \{0255\}.

**QFlt.cri-3B.1** \{10567\}. Nearest marker *Xbarc164-3B*; identified in crosses of substitution lines of Ceska Presivka and Zlatka or Sandra \{10567\}. 
21. Flour Colour
Loci controlling flour colour were identified and mapped in a recombinant inbred population derived from Schumborg/Yarralinka {9936}. Regions in 3A and 7A accounted for 13% and 60% of the genetic variation, respectively, and Xbcd828-3A, Xcdo347-7A and Xwgc232-7A.L were significantly associated with flour colour. The association was highly significant in all three replicates only for the 7A QTL. Symbols were not assigned to the flour colour loci. See also 29.2. Flour, semolina and pasta colour.

22. Free-threshing Habit

QFt.mgb-5A{0046}. 5AL{0046}. tv: Messapia/T. dicoccoides MG4343 mapping population{0046}. ma: Associated with XksuG44-5A{0046}.

QFt.mgb-6A{0046}. 6A{0046}. tv: Messapia/T. dicoccoides MG4343 mapping population{0046}. ma: Associated with Xpsr312-6A{0046}.

23. Frost Resistance
Fr{1}[1446]. 5AL{1446}. v: Hobbit{1446}. ma: Mapped to the mid-region of 5AL, 2.1 cM distal from Xcdo504-5A and Xwgc644-5A and proximal to Xpsr426-5A{419}; Mapped 2 cM proximal to Xwgc644-5A and Vrn-A1{0291}; and flanked by deletion points 0.67 and 0.68{0292}.

Studies using Vrn-1 induced and natural mutants suggest that differences in frost tolerance previously associated to Fr1 are actually pleiotropic effects of Vrn-1 {10078}.

Fr2{0291}. 5DL{0291}. s: CS"7/Cheyenne 5D{0291}. ma: Fr2 mapped 10 cM proximal to Vrn-D1{0291}.

Fr-A2{10079}. dv: Triticum monococcum. Frost tolerant parent G3116, frost susceptible parent DV92. ma: The QTL mapped on chromosome 5AL had a LOD score of 9 and explained 49% of the variation in frost tolerance. Closest markers: Xbcd508-5A and Xucw90(Cbf3)-5A. These markers are 30 cM proximal to Xwgc644-5A, which is closely linked to frost tolerance locus Fr-1. Eleven different Cbf transcription factors were identified at the Fr-A2 locus {10302}; QTLs for frost tolerance in the Fr-2 region were also identified in wheat chromosome 5B (Fr-B2 {10079}) and in barley chromosome 5H(Fr-H2{10083}).

Fr-B2. [Fr-B1{10075}]. ma: QTL mapped on chromosome 5BL, linked to Xwgc639-5B (this QTL explained 12-31\% of the variance in frost tolerance) {10075}. Xwgc639-5B mapped close to Xmwf914-5B, and to Xbcd508-5B, a marker located at the peak of the Fr-A2 QTL {10075}. This data suggests that this locus is more likely orthologous to Fr-2 than to Fr-1.

QWin.ipk-6A. 6AS{0255}. v: Opata/W-7984 (ITMI) RI mapping population{0255}; Winter hardiness was contributed by W-7984{0255}. ma: Associated with Xfba85-6A and Xpsr10(Gli-2)-6A{0255}.

Responses to cold exposure and their genetics are reviewed in {0020,0274}.

QTL:Norstar(tolerant)/Winter Manitou(non-tolerant): DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the vrn-A1 locus (R²=0.4); its peak co-incident with Xwmc206-5A and Xcfd2-5A,
and expression of C-repeat Binding Factor genes with strong homology to Cfb14 and Cfb15 located at the Fr-2 locus in T. monococcum {10414}.

24. Gametocidal Genes

24.1. Gametocidal activity

Gc1-B1a{1485}. [Gc1a{1490}, Gc1{1487}]. 2B{1490}. i: CS’S/Aegilops speltoides subsp. aucheri{1487}.  
Gc1-B1b{1485}. [Gc1b{1490}]. 2B{1490}. i: S’S/Ae. speltoides subsp. ligustica{1490}.  
Gc1-C1{1286}. 2CL{0189}. ad: CS/2C{0189}. su: CS2C(2A), CS2C(2B), CS2C(2D){0189}.  
Gc1-S1a{1485}. [Gc-S1a{1485}]. 4S2{1548}. ad: CS/Ae. sharonensis{1549}.  
Gc1-S1b{1485}. [Gc-S1b{1485}]. 4S2{1548}. ad: CS/Ae. longissima{1549}.  
Gc3-C1{1485}. [Gc-C1{1485}]. 3C{333}. ad: CS/Ae. triuncialis{338}.  

Gc1-B1a, Gc1-B1b and Gc1-S1, classified in the same functional group, are hypostatic to the genes Gc2-S1a and Gc2-S1b. Gc3-C1 does not interact with the Gc genes in the other two groups.

In addition to these genes, chromosomes carrying gametocidal genes occur in Ae. caudata {337}, Ae. cylindrica {336} and other strains of Ae. longissima and Ae. sharonensis {335,1484}.

Gametocidal genes in chromosomes in the same homoeologous group have the same gametocidal action {0190}. In monosomic additions of chromosomes with gametocidal effects, chromosome deletions and translocations are produced in gametes not having the gametocidal genes. This feature has been exploited to isolate genetic stocks suitable for physical mapping of wheat {0191} chromosomes, and of rye {0192} and barley {0193,0194,0195} chromosomes in a wheat background.

Genes with gametocidal activity (Sd1 {1647} and Sd2 {1161}) in wheat are present in homoeologous group 7 chromosomes of Thinopyrum elongatum {653,1647}. A segment earlier believed to be derived from Thin. distichum {889,892} is probably the same as that from Thin. elongatum {1162}.

In the presence of both Sd1 and Sd2, Lr19 is transmitted preferentially in heterozygotes, the degree of distortion being determined by genetic background. In heterozygotes with the same background, and in the presence of only Sd2, Lr19 shows strong self-elimination. Based on these results, it seems likely that the Sears’ translocation 7D-7Ag#7 does not carry Sd1 {939}.

See also Pollen Killer.

Sd1{1647}. 7D{1647}. v2: Agatha Sd2{1647,1161}. ma: Proximal to Lr19 and distal to Xpsr165-7D{10255}.  
Sd2{1161}. 7BL{1163}. v: 88M22-149{1163,1161}.  
Zhang et al. {10255} question the existence of this gene and alternatively suggest a duplication or deletion event influencing the transmission.

24.2. Suppression of gametocidal genes

Igc1{1489}. Causes suppression of the 3C chromosome gametocidal gene of Ae. triuncialis.

This alien gametocidal factor also promotes chromosome breakage {1486}. 3B{1488}. v: Norin 26{1483,1488}; Nineteen wheats listed in{1483,1488}.

igc1. v: Chinese Spring{1483,1488}; Forty wheats are listed in{1483,1488}.  

25. Gibberellic Acid Response (insensitivity)

\textbf{Gai1.} \([GAI1\{565,1246\}]\). 4B{406}.4BS{980}. \textbf{i:} See{408}. \textbf{v:} Norin 10 Der.{407,565}. \textbf{ma:} Xpsr622-4B (distal) - 1.9 cM - Gai1 - 8.3 cM - Xbcd110-4B (proximal){9959}. \textbf{tv:} Messapia{9959}.

\textbf{Gai2.} \([GAI2\{565,1246\}]\). 4D{411}.4DS{980}. \textbf{i:} See{408}. \textbf{v:} Maris Hobbit{411}; Norin 10 Der.{565}; List in{407}.

\textbf{Gai3.} \([GAI3\{565,1246\}]\). 4B{413}.4BS{980}. \textbf{i:} See{408}. \textbf{v:} Minister Dwarf{413}; Selection D6899{359}; Tom Thumb{405}; Tom Thumb Der.{565,567}.

In wheats with \(Gai3\), the aleurone layer fails to respond to applied GA \(\{405\}\). Two studies involving crosses between Tom Thumb derivatives and tall parents suggested that gibberellic acid insensitivity and reduced height were controlled by one gene, i.e., \(Gai3\) \(\{359,413\}\). In a third study involving a Tom Thumb derivative, recombinants were isolated, indicating separate but linked genes, i.e., \(Gai3\) and \(Rht-B1c\) \(\{565,567\}\). Further evidence was obtained for linkage between genes for gibberellic acid insensitivity and Norin 10 genes for reduced height in hexaploid \(\{568\}\) and durum \(\{720\}\) wheats. Hu & Konzak \(\{567\}\) reported 27\% recombination between \(Gai1\) and \(Rht-B1b\) and 10\% recombination between \(Gai2\) and \(Rht-D1b\) in hexaploid wheats involving Norin 10 and Suwon 92 derivatives. In durum derived from crosses involving Norin 10, 15\% recombination was obtained between one of the genes for reduced height and gibberellic acid insensitivity \(\{1246,1247\}\). Gale & Law \(\{403\}\) considered \(Gai1\) and \(Rht-B1b, Gai2\) and \(Rht-D1b, Gai3\) and \(Rht-B1c\) to be pleiotropic genes.

26. Glaucousness (Waxiness/Glossiness)

Glaucousness refers to the whitish, wax-like deposits that occur on the stem and leaf-sheath surfaces of many graminaceous species. The expression of glaucousness depends on the arrangement of wax deposits rather than the amount of wax \(\{603\}\). Non-glaucous variants also occur and genetic studies indicate that non-glaucousness can be either recessive or dominant. Recessive forms of non-glaucousness are apparently mutants of the genes that produce the wax-like deposits.

Dominant non-glaucous phenotypes (as assessed visually) appear to be due to mutations that affect the molecular structure, and reflectance, of the wax-like substances \(\{10001\}\). The genes involved in wax production and the "inhibitors" are duplicated in chromosomes 2B and 2D. There appear to be independant genes for wax production and "inhibitors" \(\{912,1493,10001\}\). In earlier issues of the gene catalogue the two kinds of genes were treated as multiple alleles \(\{1432\}\). All forms of wild and cultivated einkorn are non-glaucous \(\{10001\}\). Orthologous loci occur in barley chromosome 2HS \((gs1, gs6, gs8)\) \(\{467\}\), rye chromosome 7RL \((wa1)\) \(\{725\}\) and maize \((gl2)\) \(\{211\}\).

A gene for spike glaucousness, \(Ws\), was mapped distally on chromosome 1BS in the cross \(T.\ \text{durum}\ \text{cv.} \text{Langdon} / T.\ \text{dicocoides} \text{acc.} \text{Hermon H52} \{0171\}\).

26.1. Genes for glaucousness

\textbf{W1.} 2BS\(\{267,1493\}\). \textbf{i:} Chinese Spring mono-2D/S615//10*wS615{10001}. \textbf{v:} Chinese Spring{1493}. \textbf{itv:} LD222‘11/T. turgidum var. pyramidale recognitum{1546}. \textbf{v2:} S615 W2\(\{10001\}\).

\textbf{W1.} Recessive allele for reduced glaucousness. 2BS\(\{1432\}\). \textbf{v:} CS mono-4B mutant\(\{1064\}\); Mentana\(\{1432\}\); Salmon\(\{1493\}\).

\textbf{W2.} \textbf{i:} Chinese Spring mono-2B/S615//11*wS615{10001}. \textbf{v:} T. compactum cv. No 44\(\{10001\}\). \textbf{v2:} S615 W1\(\{10001\}\).
W2a. dv: Glaucous forms of Ae. tauschii.

W2b. v: Chinese Spring - weak hypomorph recognized at increased dosage\cite{1432}.

A non-glaucous spike phenotype in line L-592, a 7S(7A) substitution line, is described in \{0113\}.

wIw2\{10001\}. i: w-S615 = S615*11/Salmon\{10001\}. v: Salmon\{10001\}; Mentana\{1432\}; CS mono-4B mutant\{1064\}.

\subsection*{26.2. Epistatic inhibitors of glaucousness}
Each inhibitor inhibits all genes for glaucousness.

\textit{Iw1}\{10001\}. [\textit{W1}\{1493\},\textit{II-W}\{1493\}]. 2BS\{10001\}. i: S615/Cornell 5075//10*S615\{10001\}.

\textit{Iw2}\{10001\}. [\textit{I2-W}\{1493\},\textit{Jw3672}\{10510\}]. 2DS\{10001\}. bin: 2DS5-0.47-1.00\{10578\}. i: S615/Golden Ball Synthetic//10*S615\{10001\}; Synthetic hexaploid line 3672\{10510\}; Vernal Synthetic\{10001\}. dv: Non-glaucous forms of \textit{Ae. tauschii}\{1493\}. ma: In \textit{Ae. tauschii}: \textit{Iw2} - 30.1 cM - \textit{Xgdm35}-2DS\{10227\}; \textit{Xbarc124-2D} - 0.9 cM - \textit{Iw2} - 1.4 cM - \textit{Xwe6(AL731727)}\{10510\}; \textit{Xcfd56-2D} - 6 cM - \textit{Iw2} - 10 cM - \textit{Xcfd51-2D}\{10578\}.

\textit{Iw3}\{277\}. [\textit{IW3}\{277\},\textit{J3-W}\{277\}]. 1BL\{277\}. tv: \textit{T. turgidum} var. \textit{dicoccoides}\{277\}.

A non-glaucous spike phenotype in line L-592. A 7S(7A) substitution line, is described in \{0113\}.

A dominant gene (\textit{Vir}) for non-glaucousness was located in chromosome 2BL of cv. Shamrock, a derivative of \textit{T. dicoccoides}\{10543\}. This gene mapped 2 cM distal to \textit{Xgwm614}-2B \{10543\} whereas the \textit{W1/Iw1} locus was placed distal to \textit{Xgwm614-2B} in \{10189\}. Lines with \textit{Vir} had delayed senescence (‘staygreen’) and an average yield advantage over their glaudous sibs \{10543\}.

\subsection*{26.3. Spike glaucousness}
Spike glaucousness is recessive \{10666\}.

Ws\{10666\}. 1AS\{10666\}. bin: 1AS1 - 0.47 - 1.00\{10666\}. v: Svenno\{10666\}. ma: BJ23702a - 3.5 cM - Tc95235 - 4.8 cM - Bla\{10666\}.

ws\{10666\}. v: Ciccio\{10666\}.

\section*{27. Glume Colour and Awn Colour}
Black glumes are now included in the following homoeologous series with red/brown/bronze glumes.

\subsection*{27.1. Red (brown/bronze/black) glumes}
The majority of studies report a single dominant gene for red glume colour. A few papers report two factors \{1009,1477,1520\}. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes \{1277\} suggesting, because \textit{Hg} is located in chromosome 1A, that a red glume factor different from \textit{Rg1} is involved in the Swedish stocks. Nothing was known of the possible association of such a gene with \textit{Bg}, another glume colour gene on chromosome 1A. See \{1640\} for review. A chromosome 1A gene, \textit{Rg3}, was eventually identified by linkage with \textit{Gli-A1}\{1405\} and shown to cosegregate with \textit{Hg}\{624\}.

\textit{Rg-A1}\{10378\}. [\textit{Rg3}\{562,924,923\}]. 1AS\{562,923,924,9906\}.
**Rg-A1a** [10378].  
- **v**: TRI 542 [10378]; White glumed genotypes.  
- **dv**: DV92 [282]; G2528 [10378].

**Rg-A1b** [10378].  
- **i**: Saratovskaya 29*3//F2 CS mono 1/Strela [924].  
- **v**: CS/Strela Seln [9006]; Iskra [9006]; L’goskaya-47 [1405]; Zhitsa [9006, 10378].  
- **v2**: Milturum 553 Rg-B1b [9006]; Milturum 321 Rg-B1b [9006]; Strela Rg-B1b [9006, 924]; Sobko & Sozinov [1405, 1406]; reported a further group of 30 international wheats which, by inference from their Gli-A1 alleles, probably carry Rg-A1b.  
- **ma**: A linkage order of Glu-A1 - cent - Hg - Rg-A1b [1405]; Xgwm1223-IA / Rg-A1 / Hg - 2.2 cM - Xgwm136-IA - 4.2 cM - Xgwm33-IA [10635].

**Rg-A1c** [10378].  
- **Bg(282,1304),Bg(a)(282)** [1]. A [282, 1304].  
- **i**: ANK-22A [10378]; S29BgHg [10378].  
- **s**: CS*7/Indian 1A [1304].  
- **v**: TRI 14341 [10638].  
- **dv**: Sears Synthetic Rg-D1c [10638].  
- **ma**: Milturum 321 Rg-A1b [9006]; Milturum 553 Rg-A1b [9006]; Strela Rg-A1b [9006].  
- **tv**: Messapia [9959]; Ward [792].  
- **dv**: G3116 [282].  

At the diploid level Rg-A1c (Bga) and Rg-Ald (Bgb) were determinant and caused a solid black and a black line at the margins of the glume, respectively [282]. A single factor for black glumes was reported in diploid, tetraploid and hexaploid wheats [1347]. Linkage with Hg was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; Bg is epistatic to Rg.

**Rg-B1** [10378].  
- **[Rg],Rg**.  
- **1B** [1517].  

**Rg-B1a** [10378].  
- **v**: TRI 542 [10378]; White glumed genotypes.  
- **dv**: T. turgidum ssp. dicocoides acc. MG4343 [9959].

**Rg-B1b** [10378].  
- **[Rg]**.  
- **s**: CS*5/Red Egyptian 1B [1304].  
- **v**: Diamant I [9006]; Federation 41 [1517]; Golubka [10635]; Highbury [1121]; Red Egyptian [1304]; T. petrapavlovsky [9006].  
- **v2**: Milturum 321 Rg-A1b [9006]; Milturum 553 Rg-A1b [9006]; Strela Rg-A1b [9006].  
- **tv**: Messapia [9959]; Ward [792].  
- **ma**: Xutv1518-1B (distal) - 7.7 cM - Rg-B1b - 0.8 cM - Gli-B1 (proximal) [9959]; Xgwm1078-1B - 1.5 cM - Rg-B1b - 3.1 cM - Xgwm0550-B1 [10378]; Xutv1518-1B (distal) - 7.7 cM - Rg-B1b - 0.8 cM - Gli-B1 (proximal) [9959]; Xgwm1078-1B - 4.6 cM - Rg-B1 - 2.0 cM - MW1B002 (Gli-B1) - 4.1 cM - Xgwm550-1B [10635].

**Rg-D1** [10378].  
- **[Rg]**.  
- **1DL** [769, 1241].  

**Rg-D1a** [10378].  
- **v**: Novosibirskaya 67 [10378]; L301 [10378].  
- **White glumed genotypes.**

**Rg-D1b** [10378].  
- **Derived from Ae. tauschii** [Rg2].  
- **i**: Saratovskaya 29*5//T. timopheevii ssp. timopheevii/T. tauschii [9006].  
- **v**: ITMI Synthetic W7984 [10635]; Synthetic Hexaploid-11 [10218]; (Triticum turgidum ssp. dicoccoides/Ae. tauschii) [769]; (Tetra Canthatch/Ae. tauschii var. strahtula RL 5271); RL5404 [1240]; (Tetra Canthatch/Ae. tauschii var. meyeri RL5289); RL5406 [1648, 1240].  
- **v2**: Sears Synthetic Rg-A1c [10638].  
- **dv**: Aegilops squarrosa accessions.  
- **QTL**: QRg.ipk-1D was mapped in the Opata/W-7984 (T) mapping population [0255]; Linkage with Gli-D1 implied Rg2. This QTL coincided with a QTL for awn colour, QRaw.ipk-1D [0255].  
- **ma**: Xpsp2000-1D - 9.3 cM - Rg-D1b - 21.2 cM - Xgwm106-1D [10128]; Xgwm1223-1D - 6.6 cM - Rg-D1 / Xsud14-1D - 13.9 cM - Xgwm33-D1 [10635]; Rg-A1c - 3.9 cM - Xgwm1223-1D [10638].

**Rg-D1c** [10378].  
- **Brown or smokey-grey phenotype** [729].  
- **[Brg] [729]**.  
- **i**: ANK-23 = Novosibirskaya 67*10/K-28535 [729]; G10579 [729]; T. aestivum botanical varieties cinereum, columbina and albiglaucum [10378].  
- **ma**: Xgwm1223-1D - 1.5 cM - Rg-D1c - 13.1 cM - Xbarc152-1D [10378]; Xbarc149-1D - 6.3 cM - Rg-D1c - 26.5 cM - Xbarc152-1D [10378].
27.2. **Pseudo-black chaff**

This is a blackening condition transferred from Yaroslav emmer to Hope wheat by McFadden at the same time as stem-rust resistance was transferred. The association of this condition with mature-plant stem-rust reaction {\( \text{Sr2} \)} has been noted in a number of papers. According to {\cite{742}}, the condition is recessive. Pan {\cite{1102}} considered linkage with stem-rust reaction could be broken, but this seems unlikely.

\[ \text{Pbc} \]: 3B{\cite{742}}.3BS.  \( s \): CS 6/Hope 3B{\cite{742}}; CS\(^*\) 6/Ciano 5B{\cite{939}}.

27.3. **Black-striped glumes**

This phenotype was reported in group \( \text{dicoccon} \). \( v \): E4225 {\cite{1417}}.

27.4. **Inhibitor of glume pigment**

An inhibitor of glume pigment was reported on chromosome 3A {\cite{106}}.

27.5. **Chocolate chaff**

\( cc \){\cite{719}}.  7B{\cite{719}}.7BS{\cite{665}}.  \( tv \): Langdon mutant{\cite{719}}; PI 349056{\cite{665}}.  \( dv \): CBC-CDd1{\cite{665}}.

The chocolate chaff phenotype was suppressed by a gene(s) in chromosome 7D {\cite{719}}.

27.6. **Awn colour**

The literature on awn colour is not clear. In general, awn colour is associated with glume colour {\cite{045}}. Occasionally, however, awn colour and glume colour may be different. According to Panin & Netsvetaev {\cite{1103}}, black awns were determined by three complementary genes designated \( \text{Bla1, Bla2, Bla3} \). \( \text{Bla1} \) was located in chromosome 1A and linked with \( \text{Gld 1A} (\text{= Gli-A1}) \) and \( \text{Hg} \).

\( QRaw.ipk-1A \){\cite{0255}}.  1AS{\cite{0255}}.  \( v \): Opata/W-7984 (ITMI) RI mapping population{\cite{0255}}; The awn colour was contributed by W-7984{\cite{0255}}.  \( ma \): Associated with \( \text{Gli-A1} \){\cite{0255}}.

\textbf{Rg3}{\cite{924,562}}.  1AS{\cite{924,562},906}.  \( i \): Saratovskaya 29{\cite{924}} //F2 CS mono 1A/Strela{\cite{924}}.  \( v \): CS/Strela Seln{\cite{906}}; Iskra{\cite{906}}; L’goskaya-47{\cite{1405}}; L’govskaya-47{\cite{1405}}; Zhnitstra{\cite{906}}.  \( v2 \): Milturum 553 \( \text{Rg1} \){\cite{906}}; Milturum 321 \( \text{Rg1} \){\cite{906}}; Strela \( \text{Rg1} \){\cite{906,924}}; Sobko & Sozinov{\cite{1405}} reported a further group of 30 international wheats which, by inference from their \( \text{Gli-A1} \) alleles, probably carry \( \text{Rg3} \).

\( ma \): A linkage order of \( \text{Glu-A1} - \text{cent} - \text{Hg} - \text{Rg3} \) was reported{\cite{1406}}.

Kovel {\cite{729}} described a brown or smokey-grey glume phenotype in \( \text{T. aestivum var caesium} \) K-28535. This phenotype was also present in accession K-40579 and botanical varieties cincereum, columbina and albiglaucum. Close linkage to \( \text{Gli-D1} \) was shown and a gene designated \( \text{Brg} \) was assumed to be an allele of \( \text{Rg2} \) present in \( \text{Ae. tauschii} \) and synthetic hexaploid wheats. \( v \): K-28535 {\cite{729}}.  \( i \): ANK = Novosibirskaya 67*10/ K-28535 {\cite{729}}.

\( QRg.ipk-1D \){\cite{0255}}.  This QTL coincides with a QTL for awn colour, \( QRaw.ipk-1D \){\cite{0255}}.  1DS{\cite{0255}}.  \( v \): Opata/W-7984 (ITMI) RI mapping population{\cite{0255}}; The glume colour was contributed by W-7984{\cite{0255}}.  \( ma \): Associated with \( \text{Gli-D1} \){\cite{0255}}.
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**QRaw.ipk-1D**{0255}.  **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Awn colour was contributed by W-7984{0255}.  **ma:** Associated with *Gli-D1*{0255}.

**Bla1**{10666}.  **v:** 1AS{10666}.  **ma:** TC95235 - 4.8 cM - *Bla1*{10666}.

**28. Grain Hardness/Endosperm Texture**

Grain hardness or endosperm texture significantly influences flour milling, flour properties and end-use. The difference in particle size index between a hard wheat (Falcon) and a soft wheat (Heron) was reported by Symes {1452} to be due to a single major gene. Symes {1452} also found evidence for "different major genes or alleles" which explained differences amongst the hard wheats Falcon, Gabo and Spica. Using Cheyenne (CNN) substitution lines in CS and a Brabender laboratory mill, Mattern et al. {915} showed that the hard wheat milling and flour properties of Cheyenne were associated with 5D. Using Hope 5D substitution line in CS [CS(Hope 5D)] crossed to CS, and CS(Hope 5D) crossed to CS ditelosomic 5DL, Law et al. {777} showed that grain hardness was controlled by alleles at a single locus on 5DS. The dominant allele, *Ha*, controlling softness was present in Chinese Spring and the allele for hardness, *ha*, was present in the others. A similar study using CS (CNN5D)/CS recombinant inbred lines was reported by Morris et al. {03106}.

A pleiotropic result of hardness is the decreased level of a 15 kD starch granule protein, friabilin, on the surface of water-isolated starch {470}. In endosperm, soft and hard wheats have similar amounts of friabilin, consequently the distinction between the two textural types depends upon the manner in which the friabilin co-purifies with starch. Friabilin is also referred to by the name 'Grain Softness Protein' (GSP) {0384}, and was later shown to be comprised primarily of puroindoline a and puroindoline b {0295}. Grain hardness of reciprocal soft x hard F1 kernels was well correlated with friabilin occurrence on starch in triploid endosperm {0381}. See IV, Proteins: 5.8 Puroindoline. GSP-1 genes, which are closely related to puroindolines, are also listed in section 5.8.

*Ha*{777}.  **Soft phenotype.  5DS**{777}.  **i:** Falcon/7*Heron, Heron/7*Falcon{03109}; Paha*2//Early Blackhull/5*Paha{0203,0298}; Early Blackhull Derived/5*Nugaines{0203,0298}.  **v:** Chinese Spring {777,03106}; Cappelle Desprez {470}; Heron {1452,470}; Paha, Nugaines {0203,0298}; NY6432-18 {0241}.

*ha*{777}.  **Hard phenotype.  i:** Falcon/7*Heron, Heron/7*Falcon{03109}; Paha*2//Early Blackhull/5*Paha{0203,0298}; Early Blackhull Derived/5*Nugaines{0203,0298}.  **s:** CS*6/Cheyenne 5D {915}; CS*6/Hope 5D {777}; Capelle Desprez/7/Besostaya 5D {470}.  **v:** Falcon {1452,470}; Holdfast {470}; Early Blackhull, Early Blackhull Derived{0203,0298}; Cheyenne {03106}; Clark's Cream {0241}.  **ma:** *Ha* was closely linked to Xmta9(Pui1)-5D {1414}.

Single factor effects on hardness were found for chromosomes 2A, 2D, 5B and 6D, and interactive effects were found for chromosomes 5A, 6D and 7A {1414}.

The addition of King II rye chromosome 5R converted Holdfast wheat from hard to soft {470}. A 14.5 kD rye analogue was also isolated from 6x triticales which have soft texture {470}. All ryes are thought to have soft texture.

Two genes for grain hardness were reported in {055}.

Hard and soft NILs are listed in {0298}.

**QTL:** In a DH population of Courtot/CS a major locus in chromosome 5DS coincided with *Ha*; minor QTLs mapped in chromosomes 1A (associated with Xfba92-1A) and 6D (associated with Xgwm55-6D) {0141}.

Ten QTLs for kernel hardness (54 % of the variation) were mapped in 'Forno' 'Oberkulmer' spelt {0280}. Two QTLs were detected for grain hardness in RILs of the ITMI population.
(Synthetic / Opata 85) {10051}. The QTL on the short arm of chromosome 5D was associated with \(Xmta10\)-5D, and increased hardness was contributed by Opata {10051}. The locus located proximally on the long arm of 5D was associated with \(Xbcd450\)-5D and increased hardness was contributed by the Synthetic allele {10051}.

Two QTLs, \(QHa.ksu\)-3B, associated with \(Xksum9\)-3B (\(R^2=0.09\), and \(QHa.ksu\)-5D(Ha), associated with \(Xcfd\)-5D (\(R^2=0.3\)), were identified in Karl*2/TA 4152-4 {10273}.

Two QTLs were detected for grain hardness in RILs of the ITMI population (Synthetic / Opata 85) {10051}. The QTL on the short arm of chromosome 5D was associated with \(Xmta10\)-5D, and increased hardness was contributed by Opata {10051}. The locus located proximally on the long arm of 5D was associated with \(Xbcd450\)-5D and increased hardness was contributed by the Synthetic allele {10051}.

Two QTLs, \(QHa.ksu\)-3B, associated with \(Xksum9\)-3B (\(R^2=0.09\), and \(QHa.ksu\)-5D(Ha), associated with \(Xcfd\)-5D (\(R^2=0.3\)), were identified in Karl*2/TA 4152-4 {10273}.

Using proteomic analysis of 2D-protein gels applied to 101 lines of the Opata/W-7984 (ITMI) RI mapping population, and after a preliminary study of a sub-group of these lines {10086}, 446 amphiphilic protein spots were resolved, 170 specific to either of the two parents and 276 common to both {10087}. An important category of these proteins comprises the puroindolines. Seventy-two loci encoding amphiphilic proteins were conclusively assigned to 15 chromosomes. At least one Protein Quantity Locus (PQL) was associated with each of 96 spots out of the 170 spots segregating; these PQL were distributed throughout the genome. The majority of the amphiphilic proteins were shown to be associated with plant membranes and/or play a role in plant defence against external invasions. Not only the puroindolines were associated with kernel hardness - a number of other amphiphilic proteins were also found to influence this trait.

Neixiang 188 (hard)/Yanshan 1 (medium hard) RIL population: \(QGh.caas\)-1B.1 with hardness allele from Yanshan 1, \(R^2=0.28\), \(Xwms153\) - 1BL - \(Xbarc81\) - 1BL{10640}.

29. Grain Quality Parameters

In the comprehensive study of 46 quality-related traits in a RL4452/AC Domain RIL population, 99 QTLs involving 41 traits were located in 18 chromosomes {10361}; 14 QTLs clustered in the \(Glu\)-1B region (50cM), 20 QTLs occurred in the \(Xwmc617\)-4D - \(Xwmc48\)-4D region (30cM), 10 QTLs mapped to the \(Xgwm130\)-7D - \(Xwmc405\)-7D region (14cM) and 66 QTLs were dispersed {10361}. In a large study of 11 seed quality traits in a AC Karma/87E03-S2B1 DH population, 26 QTLs were detected in 7 chromosomes {10434}; 6 were clustered in the \(Glu\)-D1 region and 5 were clustered in the \(Rht\)-D1 region.

QTL analyses of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California) are reported in {10436}. Neixing 188 / Yanshan 1 RIL population: 75 QTLs for 5 quality-related traits are reported in {10640}.

29.1. Sedimentation value

\(Qsev.mgb\)-6A{9920}. 6AL{9920}. \(tv:\) Nessapia/\(T. dicoccoides\) MG4343 mapping population{9920}. \(ma:\) Associated with \(Xrsq805\)-6A{9920}.

\(Qsev.mgb\)-7A{9920}. 7BS{9920}. \(tv:\) Messapia/\(T. dicoccoides\) MG4343 mapping population{9920}. \(ma:\) Associated with \(Xpsr103\)-7A{9920}. \(QTL:\) QTLs Associated with \(Glu\)-1 on chromosome arms 1AL and 1DL and \(Gli\)-1/\(Glu\)-3 on 1BS in RSLs from the
29. **Flour, semolina and pasta colour**

**QTL:** A QTL was detected on chromosome 7A {9936}. Cultivar Schomburgk contributed the yellow colour allele in a cross Schomburgk/Yarralinka {9936}. Markers Xcdo347-7A and Xwg232-7A accounted for 60% of the genetic variation {9936}. A Sequence Tagged Site PCR marker is available {0180}.

A major QTL was detected in the distal region of chromosome 7BL in the cross Omrabi 5/ T. dicoccoides 600545. The QTL explained 53% of the variation and was completely linked to microsatellite marker Xgwm344-7B. Omrabi 5 contributed the allele for high yellow pigment level. Two additional small QTLs were detected on 7AL {0365}. Other references to flour colour are given under Flour Colour, Lr19, and Sr25.

W9262-260D3 (low yellow colour)/Kofa (high colour): Four QTLs identified on chromosomes 2A (Xgwm425-2A), 4B (Xgwm495-4B), 6B (Xgwm193-6B) and Psy-B1 (chromosome 7BL) {10230}. See also Enzymes Phytoene synthase.

Analysis of yellow flour pigment in a RIL population of PH82-2 (low)/Neixiang (high) revealed major QTL on chromosomes 7A co-segregating with marker YP7A (R² = 0.2 - 0.28) (see Phytoene synthase 1), and 1B (R² = 0.31 - 0.54) probably contributed by 1RS {10501}. Huapei 3/Yumai 57: DH lines: 18 additive QTLs and 24 pairs of epistatic QTLs affected flour colour parameters; qa-1B, closely linked with Xbarc372-1B was associated with variation of a*, R²=0.256 {10625}.

A further study confirmed major QTL on chromosome 1RS (R²=0.319) and 7A (R²=0.339), minor QTL occurred on 1A and 4A {10716}.

29.3. **Amylose content**

Amylose content has a significant effect on industrial quality; for example, reduced amylose wheats perform better in some types of noodles. The waxy protein genes have an important influence, but other genes are also involved.

**QAmc.ocs-4A.I**{0047}. 4AS{0047}. v: CS/CS(Kanto107 4A) mapping population{0047}.

**ma:** Associated with Xbcd1738-4A and Xcdo1387-4A{0047}.

29.4. **Milling yield**

**QTL:** A QTL was detected on chromosome 3A {0181}. Cultivar Schomburgk contributed an allele for the higher milling yield in cross Schomburgk/Yarralinka {0181}. RFLP markers Xbcd115-3A and Xpsr754-3A were associated with this QTL at LOD>3 {0181}.

A QTL associated with Pinb on chromosome arm 5DS was detected in RILs from the cross NY6432-18/Clark's Cream {0241}. Cultivar Clark's Cream contributed the higher flour yield allele {0241}. This QTL coincided with QTL for hardness, hydration traits (dough water absorption, damaged starch and alkaline water retention capacity (AWRC)), and baked product traits (cookie diameter and cookie top grain) {0241}.
29.5. Alveograph dough strength W

**QTL:** QTLs for W were detected on chromosome arms 5DS (associated with *Xmta10-5D*), 1AS (associated with *Xfba92-1A*), and 3B (associated with *XksuE3-3B*) in cross Courtot/Chinese Spring \{0141\}. The first two QTLs coincided with those for hardness. Ten QTL for W (39% of the variation), nine QTL for P (48% of the variation) and seven QTL for P:L (38% of the variation) were mapped in Forno/Oberkulmer spelt \{0280\}.

29.6. Mixograph peak time

**QTL:** A QTL associated with *Glu-Dy1* on chromosome arm 1DL was detected in RILs from the cross NY6432-18/Clark’s Cream \{0241\}. Clark’s Cream contributed the higher mixograph peak time allele \{0241\}. This QTL coincided with a QTL for bread mixing time \{0241\}.

29.7. Starch characteristics

The Isoamylase-1 gene from *Ae. tauschii (Iso-1)* complements the deficient rice sugary-1 mutant line \{10295\}.

**QTL:** QTLs for starch viscosity and swelling were associated with the *Wx-B1* locus in Cranbrook (*Wx-B1a*)/Halberd (null *Wx-B1b*). An additional QTL for starch viscosity was found on 7BL between markers *Xgwm344-7B* and *Xw420-7B* in the first cross. This QTL disappeared when amylase activity was inhibited indicating that it was determined by the late maturing a-amylase activity contributed by Cranbrook. A QTL for starch viscosity was associated with the *Wx-A1* locus in the cross CD87/Katepwa \{0362\}.

29.8. Loaf volume

**LvII** \{10312\}. \*[LvI \{10312\}]. 3A \{10312\}. \*v:* Cappelle Desprez*7/Bezostaya 1 3A \{10312\}. ma: *Xgwm720-3A-LvII* appeared to be located in the *Xgwm2-3A - Xgwm720-3A* region \{10312\}.

**QTL:** Loaf volume score consistent across three environments was scored in a RIL population Renan/Recital and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A, Xgwm666-3A*, positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A, Xbcd1930-7A*, positive effect from Recital) \{10536\}. A total of 30 QTLs were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTLs of largest effect were located on chromosomes 6B and 6D \{10659\}.

29.9. Dough rheological properties

**QTL:** In a Cranbrook/Halberd DH population, environmental factors were a major determinant of dough extensibility whereas additive effects of alleles at the hight and low molecular weight glutenin loci determined dough strength \{10247\}.

29.10. Grain fructan content

Fructans are non-digestible carbohydrates considered to have health benefits to consumers.

**QTL:** Berkut (high fructan concentration) / Krickauff (low fructan concentration): QTL detected on chromosomes 2B, 3B, 5A, 6D, and 7A of which *QGfc.aww-6D.2* (\(R^2=0.17\), nearest marker, *Xbarc54-6D*) and *QGfc.aww-7A.1* (\(R^2=0.27, Xgwm681-7A\) ) had the largest effects \{10631\}. 
29.11. Water absorption
Neixiang 188 / Yanshan 1 RIL population: XAbs.caas-5D.I with positive effects from Yanshan 1, $R^2=0.3$, XcfdI8-5DS - XcfdI89-5DS {10640}

29.12. Chinese dry noodle quality
Chuan 35050 / Shannong 483 RIL populations: 3 QTLs for noodle palate, elasticity and smoothness clustered near Glu-D1 with beneficial effects associated with subunits 5+10 coming from Chuan 35050. A very significant taste QTL, QStas.sdau-4A.1 and positive QTLs for stickiness and total score also on chromosome 4A came from Shannong 483 {10647}

30. Grass-Clump Dwarfness/Grass Dwarfness
Complementary dominant genes. Genotypes producing dwarfness: D1-D2-D3-, D1-D2D2, D1-D4-D3-, D1-D2-D4 and D1-D4D4.

D1{534}. [G{972}]. 2D{534,939,1595}.2DS{942}. s: CS’7/Kenya Farmer 2D{1000}; CS’6/Timstein 2D{534}. v: Big Club{534}; Burt{1000}; Federation{942}; Mus{534}; Ramona 50{358}; Selection 1403{1000}. v2: Hermsen’s pure-breeding dwarf D2{1000}; Falcon D3{1172}; Gabo D3{944}; Timstein D3{534}; Metzger’s pure-breeding dwarf D2 D3{1000}.

D2{534}. [Bi{972}]. 2B{536,574}.2BL{944}. s: CS’7/Cheyenne 2B{1000}; CS’4/Red Egyptian 2B{1000}. v: Bezostaya 1{1595}; Crete-367{1029}; Desprez 80{1595}; Florence{1000}; Kenya W744{944}; Loro{1172}; Mara{1595}; Marquis{1000}; Poros{1595}; Redman{534,1001}; Riebesel{534}; Tobari 66{358}. v2: Hermsen’s pure-breeding dwarf D1{534,1000}; Amby D2{358}; Cedar D3{1000}; Mendel D3{534}; Plantahof D3{534}; Spica D3{944}; Cappelle-Desprez D4{1595}; Brevor D4{1000}; Cheyenne D4{1000}; Metzger’s pure-breeding dwarf D1D3{1000}.

D3{534}. [A{972}]. 4A{534,1595}.4AL{939}. s: CS’6/Timstein 4A{534,1000}; CS’7/Kenya Farmer 4A{534,1000}. v2: Amby D1{358}; Falcon D1{1172}; Gabo D1{944}; Kenya Farmer D1{1000}; Timstein D1{534}; Metzger’s pure-breeding dwarf D1 D2{1000}.

D4{1000}. 2D{1000,1595}.2DL{1598}. s: CS’7/Cheyenne 2D{1000}. v2: Cappelle-Desprez D2{1595}; Cheyenne D2{1000}; Brevor D2{1000}.

d1d2d3d4. v: Chinese Spring{534,1000}.

Genotype lists in can be found in {358,534,972}. The effects of multiple allelism at D2, and possibly at D1, and modifying genes were demonstrated {1595}. Knott {683} described a lethal dwarf condition controlled by a dominant gene closely linked with Sr30 (chromosome 5D) in Webster and a complementary recessive gene in LMPG. Phenotypes resembling grass clump dwarfs in hybrids carrying a 2BL.2RS translocation were reported in {916}. The complementary gene[s] in wheat was not D1, D2 or D3. The effect was suppressed at high temperature.

31. Grain Weight
QTL : Variation at locus QGw1.ccsu-1A, associated with Xwmc333-1A, accounted for 15% of the variation in a RIL population from RS111/CS {0143}.
Rye Selection 111 (high GW)/CS (low GW) RIL: two definitive QTLs QGw.ccsu-2B.1 and
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$QGw.ccsu-7A.1$ and one tentative QTL, $QGw.ccsu-1A.1$, were detected by CIM analysis (10363). The chromosome 7A QTL co-located with a QTL for early heading (10363).

$QGw1.inra-2B\{10071\}$. v: Renan/Recital; favourable allele from Renan \{10071\}. ($R^2=10.7-19.7\%\{10071\}$). ma: Xgwm374-2B-Xgwm388-2B\{10071\}.

$QGw1.inra-5B\{10071\}$. v: Renan/Recital; favourable allele from Recital \{10071\}. ($R^2=4.9-10.4\%\{10071\}$). ma: Xgwm639-5B - Xgwm604-5B\{10071\}.

$QGw1.inra-7A\{10071\}$. v: Renan/Recital; favourable allele from Recital \{10071\}. ($R^2=5.2-10.3\%\{10071\}$). ma: Xcfa2049-7A - Xbcd1930-7A\{10071\}.

32. Growth Rate and Early Vigour

QTL analyses in Ae. tauschii: chromosomes 1D, 4D, and 7D carried QTLs for relative growth rate, biomass allocation, specific leaf area, leaf area ratio, and unit leaf rate. Chromosome 2D had QTLs for rate and duration of leaf elongation, cell production rate, and cell length. Chromosome 5D harbored QTLs for total leaf mass and area, number, and growth rate of leaves and tillers (10293).

33. Hairy/Pubescent Auricles

$Pa\{886,042\}$. 4BS\{886,042\}. s: Saratovskaya 29'/Yanetzkiis Probat 4B\{886\}; Saratovskaya 29'/Shabati Sonora 4B\{886\}; Saratovskaya 29'/4/Siete Cerros 4B\{886\}. v: Diamant 1\{886\}; Magali\{886\}; Pirotrix 28\{886\}; Shabati Sonora\{886\}; Siete Cerros\{886\}; Ulyanovka 9 \{886\}.

pa. v: Gabo\{886\}; Saratovskaya 29\{886\}; This phenotype is expressed in Diamant ditelo 4BL\{886\}.

34. Hairy Glume

$Hg\{1494\}$. 1A\{1293\}.1AS\{947\}. i: S-615°11/Jones Fife\{1500\}. s: CS°7/Indian 1A\{1293\}. v: A well-known, widespread and easily identified dominant marker - few examples will be listed. Indian\{1293\}: Jones Fife\{1494\}; Prelude\{1494\}. iv: LD222°11/T. Turgidum var. durum melanops\{1546\}. tv: Golden Ball\{1342,1494\}. dv: T. monococcum lines\{1494\}. ma: Xutv1391-1A (distal) - 3 cM - Bg - 1.6 cM - Hg - 2.4 cM - Gli-A1 (proximal)\{9959\}; Tel...........Hg/GB605525 - 3.8 cM - Xpsp2999(Glu3)-1A\{10193\}.

A 1A gene controlling hairy glumes was mapped in a cross between durum cv. Messapia and T. turgidum ssp. dicoccoides acc. MG4343\{9959\}.

$Hg1\{1405\}$. v: Ulyanovka\{1405\}; Pionerskaya\{715,1405\}. Evidence for multiple alleles in T. monococcum is given in \{744\}. The likelihood of three alleles, $hg$ (hairless), $Hg1$ (weakly hairy) and $Hg$ (very hairy), with $hg1$ being recessive to $Hg$ and causing a short (weak) hairy phenotype, was mentioned in \{1405\}.

35. Hairy Leaf

$Hli\{0316\}$. Weakly hairy. $[Hli\{884\}]$. 4B\{884\}.4BL\{760\}. v: Artemovka\{925\}; Caesium 111\{925\}; Lutescens 53/12\{925\}; Lutescens 62\{925\}; Milturum 321\{884\}; Poltavka\{925\}; Pyrothrix 28\{925\}; Saratov 321\{884\}; Saratovskaya 29\{884,760\}; Sarrubra\{925\}. ma: Xgwm375-4B - 12.1 cM - $Hli$ - 2.1 cM\{10516\}. 


The hairy leaf gene ($H_{Aesp}$) in *Ae. speltoides* introgression line 102/00 was allelic with $Hl2$ {10516}.

Kuspira *et al.* {744} provided evidence for at least three alleles at an $Hl$ locus in *T. monococcum*.

A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous of $Hll$ {10516}.

36. Hairy Leaf Sheath

Levy & Feldman {795} concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides*.

$Hs$ {795}. [Hls {761}]. v: Certain hexaploid derivates of G25 produced in Israel{939}. tv: *T. dicoccoides* G25{761}.

$hs$. v: Most hexaploid wheats{939}. tv: *T. dicoccoides* G7{761}.

37. Hairy Neck/Pubescent Peduncle

$Hp$ {275}. Derived from *Secale cereale*

4BL{T4B.5R}{274,275}. i: S-61511/CS Derivative{1500}.

5BS{T5B-5R}{1298}. v: HN-2 (CS type){1298}.

6D{T6D-5R}{1298}. v: HN-1(CS type){1298}.

4BL{T4B.5R}{274,275}. v: CS Derivative{1304}.

38. Hairy Node/Pubescent Node

Inheritance of hairy (glabrous) node versus non-hairy node was attributed to a single, dominant gene difference {396,837,910,914} and the $Hn/hn$ locus was shown to be linked with $B1$ (awn inhibitor). Observations on 5A trisomics and telosomics of Chinese Spring confirmed this location. Love & Craig {837} studied a cross involving Velvet Node CI 5877, and Gaines & Carstens {396} studied an offtype single plant designated Velvet Node Wash. No. 1981.


$hn$. v: Garnet{722}; Kimno{722}; Pika{722}; Timantii{722}.

Levy & Feldman {795} concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides*.

Multiple alleles were reported in *T. monococcum*{744}.

39. Heat tolerance

QTL: QTLs contributing to grain-filling duration (GFD) under high temperatures were associated with $Xgwm11-1BS$ (11% of variability) and $Xgwm293-5AS$ (23% of variability) in Ventnor (tolerant) // Karl 92 (Non-tolerant) {0327}.

40. Height

$Ht$ is the general symbol.
40.1. Reduced Height : GA-insensitive

**Rht-1** [371,0019].

The *Rht-1* homeologs are orthologous with the *D8* locus in maize and the *GAI* locus in *Arabidopsis*. They encode proteins resembling nuclear transcription factors and are involved in sensing gibberellin levels [0019]. Common wheat and durum NIL pairs are listed in [02102].

**Rht-A1** [0019]. v: Chinese Spring [0019]; All wheats are assumed to be monomorphic.


**Rht-B1a** [116]. v: Tall wheats [116]; e.g. Chinese Spring [0019].

**Rht-B1b** [116]. Partially recessive [024], recessive [357], semi-dominant [408]. [RhtI [015], SdI [015]]. i: Tom Thumb/7* Kharkov/Lancer [1040]; See [408]; v: Minister Dwarf [404]; Selection D6899 (Tom Thumb-Sonora 64/Tacuari) [357]; Tom Thumb [405]; Tom Pouce Blanc [407,1634]; Tom Pouce Barba Rouge [407,1634]; Topo; Tordo. ma: Xmwg634-4B (distal) - 30.6 cM - Rht-B1c - 11.9 cM - Xpsr144-4B (proximal) [117].


**Rht-B1e** [116]. [RhtKrasnodari1 [452], RhtI (B-dw) [1600]]. v: Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezoektaya 1) [1600].


**Rht-B1g** [0019]. v: Highbury mutants M3 103-3 and M3 103-9 [0019]; Allele *Rht-B1g* is a fast neutron-induced mutation of *Rht-B1b* and produces a tall gibberellin responsive phenotype [0019].

**Rht-B1** [371,0019]. tv: *T. turgidum* var. *polonicum* IC12195 [10144].

**Rht-D1** [116]. 4D [411,583,1544]. 4DS [980,1266,116]. i: Common wheat and durum NIL pairs are listed in [02102]. ma: Xpsr1871 (Pki)-4D - 4 cM - Rht-D1 - 6 cM - Xubc821 (PhyA)-4D [410]; Rht-D1 - 2.8 cM - Xglk578-4D [9966]; Xpsr1871 - 1 cM - Rht- D1b - 4 cM - Xpsr821 (PhyA) [0019].

**Rht-D1a** [116]. v: Tall wheats [116]; e.g. Chinese Spring.

**Rht-D1b** [116]. Partially recessive [024], recessive [357], semi-dominant [408]. [Rht2 [015], Sd2 [015]]. 4D [411,414,02102]. i: See [408,414,02102]; v: Biscay [10574]; Combe [567]; Era [407]; Gaines Sib 2 [015]; Jaral [407]; Kite [1174]; Maris Hobbit [411]; Pirat [10574]; Pitic 62 [567]; Rubens [10574]; Songlen [243]. tv: Oleson *Rht-B1b* [357]; Norin 10-Brever, 14 *Rht-B1b* [015]; Selection D6301 *Rht-
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B1b{357}; List in{1386}. ma: The development of allele-specific primers for Rht-D1b was reported in{0378}.

Rht-D1c{116}. Dominant {114}. [Rht10{1266}]. v: Ai-bian{1544,1266}. ma: Xpsr921-4D (4DS) - 0.8 cM - Rht-D1c - 28 cM - Xgwm165-4D (4DL){117}.

Rht-D1d{116}. Semi-dominant {116}. [RhtAi-bian 1a{115}]. v: Ai-bian 1a (spontaneous mutant of Ai-bian 1){115}.

The development of allele-specific primers for Rht-D1b was reported in{0378}. Rht-D1c{116}. Dominant {114}. [Rht10{1266}]. v: Ai-bian{1544,1266}. ma: Xpsr921-4D (4DS) - 0.8 cM - Rht-D1c - 28 cM - Xgwm165-4D (4DL){117}.

Rht-D1d{116}. Semi-dominant {116}. [RhtAi-bian 1a{115}]. v: Ai-bian 1a (spontaneous mutant of Ai-bian 1){115}.

The line XN004, earlier considered to have Rht21{0230}, was shown to carry an allele at the Rht-D1 locus {0231}. Various common wheat and durum N1Ls differing at the Rht-D1 locus are listed in {02102}. Genotype lists in {402,1382,1612,1613}.

Genotypes of Indian semi-dwarf wheats based on the Ellis et al. {0378}.

40.2. Reduced Height : GA-sensitive

Borner et al. {116} found no evidence of orthologous GA-sensitive genes in rye, but reviewed evidence for orthologous GA-insensitive genes. The close linkage of Rht8 and Xgwm261-2D permitted the use of the microsatellite as a marker for the detection of allelic variants at the Rht8 locus{9962}.

Rht4{568}. Recessive. 2BL{10249}. v: Burt ert 937, CI 15076{566,717}. ma: Associated with Xwmc317-2B{10249}.

Rht5{717}. 3BS{10249}. v: Marfed ert 1, M1, CI 13988{717,718,1593}. ma: Approximately 10 cM from Xbarc102-3B{10249}.

Rht6{718}. Recessive. v: Advent 1, Brevor{569}; Burt{569,718}. v2: Norin 10-Brevor, 14 Rht-B1b

Rht7{1602}. 2A{1602}. v: Bersee Mutant A{1602}; Bersee Mutant C{1602}.

Rht8. 2D{772,1601,1598}.2DL. s: Cappelle-Desprez / Mara 2D{1601}. v: Chuan Mai 18{10249}; Novasadska Rana 1{1604}; Sava{1601,414}. v2: Akakomugi Rht9{1191}; Mara Rht9{1191}. ma: Xgwm484-2D (proximal) - 19.9 cM - Rht8 - 0.6 cM - Xgwm261-2D (distal){727}; Close linkage with Xwmc-2D{10249}; A survey of Chinese cultivars showd 13 alleles of Xgwm261-2D{10284}.

The close linkage of Rht8 and Xgwm261-2D permitted the use of the microsatellite as a marker for the detection of allelic variants at the Rht8 locus{9962}.


Rht8c. Associated with a 192 bp fragment of WMS 261 {9962}. v: Akakomugi{1191}; Alfa{9962}; Aquila{9962}; Ardito{9962}; Argelato{9962}; Avrora{9962};
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Banija[9964]; Baranjka[9964]; Beauchamps[9962]; Bezoektaia[9962]; Biserka[9962]; Campodoro[9962]; Centauro[9962]; Chikushi-Komugi (Norin 121)[9962]; Chuanmai 18[10512]; Damiano[9962]; Djerdanka[9964]; Dneprovskaya[9962]; Duga[9964]; Etoile-de-Choisy[9962]; Etruria[9962]; Fakuho-Komugi (Norin 124)[9962]; Farnese[9962]; Favorite[9962]; Fedorovka[0243]; Fiorello[9962]; Fortunato[9962]; Funo[9962]; Gala[9962]; Haya Komugi[9962]; Impeto[9962]; Inerio[9962]; Jarka[9964]; Jugoslavia[9962]; Kavkas[9962]; Kaloyan[0243]; Khersonskaya 50[0243]; Khersonskaya 93[0243]; Khar'kovskaya 50[0243]; Khar'kovskaya 93[0243]; Khersonskaya 86[0243]; Kolubara[9964]; Kosava[9964]; Libellula[9962]; Lonja[9964]; Lovrin 32[9962]; Macvanka-2[9964]; Mara[119,9962]; Marzotto[9962]; Mv 03[0243]; Mv 06[0243]; Mv 17[0243]; N.S. 649[9962]; N.S. 3014[9962]; N.S. 16[1604]; N.S. Rana 1[9962]; N.S. Rana 2[9962]; N.S. 649[9962]; N.S. 3014[9962]; Odesskaya 51[0243]; Odesskaya Krasnokolosaya[0243]; Odesskaya Polukarlikovaya[0243]; Orlandi[9962]; Osjecanka[9964]; OSK 5[9964]; OSK 4[0243]; OSK 3[0243]; Partizanka[9962]; Partizanka Niska[9962]; Poljarka[9964]; Posavka 1[9964]; Posavka 2[9962]; Pomoravka[9962]; Produitore[9962]; Radusa[9962]; Roazon[0243]; Salto[9962]; Sanja[9962]; San Pastore[9962]; Sava[1601,414,9962]; Siete Cerros[9962]; Sirovol Odesskii[0243]; Sikva[0243]; Strumok[0243]; Skopjanka[9962]; Skorospelka 3B[9962]; Slavonija[9964]; Somorka[9964]; Sremica[9964]; Superzlatna[9962]; Svezda[9962]; Tira[0243]; Tisa[9964]; Transilvania[9962]; Ukrainka Odesskaya[0243]; Una[9962]; Villa Glori[9962]; Vype[0243]; Vupleinaya 75[0243]; Zagrebanka[9964]; Zelengora[9964]; ZG 6103/84[9964]; ZG 7865/83[9964]; Zitarka[9964]; Zitnica[9962]; Zlatna Dolina[9964]; Zlatoklasa[9964]; Zolotava[0243].

Although CS carries a 192 bp fragment, sequencing showed it was a different allele than other genotypes with Rht8c [02103].

Although the ‘diagnostic’ association of Rht8c and Xgwm261192 applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives [10512]. The pedigrees of a number of Chinese wheats postulated to have Rht8c on the basis of the marker trace to Italian sources [10515].

Rht8d. Associated with a 201 bp fragment of WMS261 [9962]. v: Pliska[9962]; Courtot[9962].

Rht8e. Associated with a 210 bp fragment of WMS261 [9962]. v: Chino[9962]; Klein Estrello[9962]; Klein 157[9962].

Rht8f. Associated with a 215 bp fragment of WMS261 [9962]. v: Klein 49[9962].

Rht8g. Associated with a 196 bp fragment of WMS261 [[0243]]. v: Mirleben[0243].

Rht8h. Associated with a 206 bp fragment of WMS261 [[0243]]. v: Weihenstephan M1[0243].

Rht9. 7BS[772,1601].5AL[10249]. v: Acciao[718]; Forlani[718]; Mercia 12[10249]. s: Cappelle-Desprez/Mara 5BS-7BS[1601]. v2: Akakomugi Rht8[1601]; Mara Rht8[1601]. ma: Close linkage with Xwmc410-4A[10249].

Rht11[718]. v: Karlrik 1[718].

Rht12[718]. Dominant. 5A[1445,1606]. bin: 5AL-23, based on co-segregation with B1[1606]. v: Karcagi 522M7K[721]. ma: Rht12 is located distally on 5AL cosegregating with B1 and closely linked to b-Amy-A1[1606]; Xgwm291-5A - 5.4 cM - Rht12[726].

Rht12 delayed ear emergence by 6 days[1606].

Rht13[718]. 7BS. v: Magnif 41M1 CI 17689[718]. ma: Associated with Xwms577-7B[10249].
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Rht14{718}. v: Cp B 132 {123} = Castelporziano PI 347331{718}.
Rht15{718}. tv: Durox{718}.
Rht16{718}. v: Edmore M1{718}.
Rht17{718}. v: Chris Mutant CI 17241{1129}.
Rht18{718}. tv: Icaro{718}.
Rht19{718}. v: Vic M1{718}.
Rht20{718}. v: Burt M860{718}.
Rht21{0230}. The existence of this gene was not confirmed {0231}.

40.3. Reduced Height : QTL

In Courtot/CS:

QHt.fcu-4BL{10256}. ma: Associated with Xbarc125-4B (R^2=0.57)\{10256\}.
Reduced height allele in Grandin \{10256\}.

QHt.fcu-6AS{10256}. ma: Associated with Xbarc23-6A - Xcp201-6A (R^2=0.07)\{10256\}.
Reduced height allele in BR34 \{10256\}.

QHt.crc-2D{10287}. 2D\{10287\}. ma: Linked to BE497718-260 (LOD 4.2) in RL4452/AC
Domain\{10287\}.

QHt.crc-4B{10287}. 4B\{10287\}. ma: Linked to Rht-B1 (LOD 7.7) in RL4452/AC
Domain\{10287\}.

QHt.crc-2D\{10287\}. 2D{10287}. ma: Associated with QTLs for lodging and 1000-
grain weight.

QHt.crc-4D{10287}. 4D\{10287\}. ma: Linked to Rht-D1 (LOD 30.9) in RL4452/AC
Domain\{10287\}.

QHt.crc-5B{10287}. 5B\{10287\}. ma: Linked to Xwmc640-5B (LOD=5.8, R^2=15.4\%){10287}.

QHt.crc-7A{10287}. 7A\{10287\}. ma: Linked to Xwmc139-7A (LOD 3.3) in RL4452/AC
Domain\{10287\}.

QHt.fra-1A\{9957\}. ma: Linkage with Xfba393-1A\{9957\}.

QHt.fra-1B\{9957\}. ma: Linkage with Xcdo1188-1B.2\{9957\}.

QHt.fra-4B\{9957\}. ma: Linkage with Xglk478-7A\{9957\}.

QHt.fra-7A\{9957\}. ma: Linkage with XksuD2-7B\{9957\}.

QHt.ipk-4A\{0255\}. 4AL\{0255\}. v: Opata/W-7984 (ITMI) RI mapping population\{0255\}; the
height is contributed by Opata\{0255\}. ma: Associated with Xmwg549-4A, Xabg390-4A and
Xbcd1670-4A\{0255\}.

QHt.ipk-4A coincided with QTLs for ear length (QEl.ipk-4A), grain number (QGnu.ipk-4A)
and grain weight per ear (QQwe.ipk-4A) \{0255\}.

QHt.ipk-6A\{0255\}. 6A\{0255\}. v: Opata/W-7984 (ITMI) RI mapping population\{0255\}; The
height is contributed by W-7984\{0255\}. ma: Associated with Xcdo29-6A and Xfba234-
6A\{0255\}.

QHt.ipk-6A coincided with QTLs for peduncle length (QPdl.ipk-6A) and ear length (QEl.ipk-
Two QTLs for plant height were assigned to chromosome 3A in RSLs from Cheyenne*7/Wichita 3A substitution line{0025}. Seven QTLs on chromosomes 1A, 1D, 2B, 2D and 4B affected plant height among RILs of CS/T. spelta duhamelianum. Effects linked with the CS alleles of Xbcd1160-1A, Xksu127-1D and XksuF11-2D increased height whereas those CS alleles associated with Xpsr131-2B, Xpsr125-2B, Xpsr934-2D and Xcs22.2-4B reduced it {0196}.

QHt.ocs-4A.1{0047}. 4AL{0047}. v: CS/CS(Kanto107 4A) mapping population{0047}. ma: Associated with Xpsr119-4A and Wx-B1{0047}.

QHt.ocs-4A.2{0047}. 4AS{0047}. v: CS/CS(Kanto107 4A) mapping population{0047}. ma: Associated with Xbcd1738-4A and Hd{0047}.

QHt.ocs-5A.1{0068}. 5AL{0068}. v: CS(T. spelta 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. ma: Associated with the intervalXcdo1088-5A - Xbcd9-5A{0068}.

This QTL coincided with a QTL for culm length, QCl.ocs-5A.1 {0068}.

QHt.riso-3A{10067}. ma: Mapped on the centromeric region between SSR markers Xwmc505-3A and Xwmc264-3A (LOD>6){10067}.

41. Herbicide Response

41.1. Difenzoquat insensitivity

Dfq1{1396}. Insensitive. 2B{1396}.2BL{789}. v: CS{1396}.


Busch et al. {153} reported a single dominant gene for tolerance of Era and Marshall compared with the susceptibility of Eureka and Waldron, but its relationship to Dfq1 is unknown.

41.2. 2,4-D tolerance

Randhawa et al. {1190} reported a single dominant gene in each of WL711, CPAN1874 and CPAN1922 controlling tolerance. HD2009 and PBW94 were described as susceptible.

41.3. Chlortoluron Insensitivity

Su1{1402}. Insensitive. 6B{1402}.6BS{799}. v: Cappelle-Desprez{1402}. tv: B-35{735}.

su1. Sensitive. v: Chinese Spring{1402}; Poros{1402}. tv: B-7{735}. ma: Xpsr312-6B - 5.3 cM - Su1 - 6.8 cM - Xpsr477(Pkg2)-6B{736}. ma, tv: Nor2 (6BS) - 2.7 cM - Su1{1401}; Su1 - 5.2 cM - Xpsr371-6B(6BL){735}.

Su1 also controls insensitivity to metoxuron {1402}.

A single dominant gene for tolerance to isoproturon was found in tetraploid wheats derived from a tolerant T. monococcum source {1044}. This gene is presumably different from Su1.

41.4. Imidazolinone resistance

Resistance alleles found in mutagenized populations were incompletely dominant and additive in effect {10099}. Resistance is due to single base pair changes in acetohydroxyacid synthase.
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**Imi1** [10099]. $[A\text{hasL}-D1\{10101\}.F\text{s-4}\{10100\}]$. 6DL{10101}. v: BW755 = Grandin*3/Fidel-FS-4{10099}; CDC Teal IMI 1A{10099}; CDC Teal IMI 9A{10099}; CDC Teal IMI 10A = Fidel-FS-2{10099}; Clearfield WHS Janz = Janz*4/Fidel-FS-2; Clearfield WHS Stiletto = Stiletto*3/Spear/ Fidel-FS-3; Fidel-FS-2 = ATCC40997{10100}. v2: CDC Teal IMI 15A = PTA 3955 Imi3{10099}.

**Imi2** [10099]. $[A\text{hasL}-B1\{10101\}]$. 6BL{10101}. v: CDC Teal IMI 11A = PTA 3953{10099}.

**Imi3** [10099]. $[A\text{hasL}-A1\{10101\}]$. 6AL{10101}. v2: CDC Teal IMI 15A Imi3{10099}.

**dv**: *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}).

Mutant EM2 has a serine to asparagine substitution near the carboxyl end of the enzyme. The same change led to imidazolinone resistance in hexaploid wheat, rice and *Arabidopsis* {10102}.

42. Hybrid Weakness

42.1. Hybrid necrosis

[Progressive lethal necrosis {155}; Firing {971}].

Complementary dominant genes. Descriptive alleles $w$ (weak), $m$ (medium) and $s$ (strong) were allocated by Hermsen {532}. Phenotype is affected by modifying genes (and/or genetic background) and environment {566}. According to Dhaliwal et al. {257} progressive necrosis is suppressed at 28C.

**Ne1** [530]. $[L_e\{155,550\}.F\{971\}.L_e1\{1491\}]$. 5B{1491}. 5BL{1636}. ma: Xbarc216-5B - 8.3 cM - *Ne1* - 2 cM - Xbarc74-5B{10334}.

**Ne1m** [530]. i: S-615’11/Prelude{1500}. v: Carpo{532}; Eskisehir 220-39{532}; Garnet{532}; Klein Aniversario{532}; Koga{532}; Mus XII/80/22{532}; Prelude{532,1491}.

**Ne1s** [530]. v: Big Club{155,532,550}; C306{1475}; Felix{531}; Gaza 141 PI 220429{532}; Luteseens 1163{1264}; Marquillo{115,532,550}; Ponca{532}; Spica{939}; Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60{10334}. tv: Gaza 1E PI 133460; Gaza PI 189262{532}; Iumillo{532}; Kubanka{532}; PI 94587{155,532}; Quanah{532}.

**Ne1s** is common in tetraploid wheats {1080}.

Unknown **Ne1** allele. tv: HW75 {697}; HW178 {697}. Chinese Spring carries the weakest allele {532} and its effect can be observed in CS*7/Atlas 66 2B {939} relative to CS.

**Ne1w** [530].

v: Bobin group {532}: Kenya Farmer {532}; The Bobin selection used in breeding Gabo {532}; and its sister selection, Timstein {532,1556} was in fact Gular. Hence Gular, not Steinwedel, is the presumed source. The Sydney University accession Bobin W39 was the parent of Gabo and Timstein, whereas “true” Bobin carried the accessions number W360. The particular accession tested by Hermsen is not clear. According to Metgzer {1000} Steinwedel is a non-carrier; Federation group {532}: Cadia {532}; Cleveland {971}; Minister group {532}; Rieti group {532}: Mentana {532}; Mara {532}.

**Ne2**. $[L_e2\{155,550,1491\}.F\{971\}]$. 2B{1491}. 2BS{1085}. ma: Xgwm4148-2B - 6.7 cM - *Ne2* - 3.2 cM - Xbarc55-2B{10334}.

**Ne2m** [530]. v: Alsen{10334}; Squarehead group{532}; European wheats{532}; Fronteira group{532}; Sonalika{1475}; South American wheats and derivatives, e.g. Atlas 40{532}; Wheats possessing *Lr13*{939}, e.g. Manitou{939}.

**Ne2m**? [530]. v: Barleta group{532}; South American wheats, e.g. Klein Titan{532}; La Prevision 25{532}; Lin Calel{532}.
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34.

Ne2ms (530). v: Mediterranean group (532): Dawson (155,550); Fultz (550); Fulcaster (550); Fulhard (550); Honor (550); Jones Fife (1491); Shepherd (550,971); Trumbull (155); Vermillion (530); Wabash (155). (Although placed in this group on basis of pedigree, the last three stocks, as well as Fultz selection of CI 19293, appear to have the stronger allele of the Crimean group (532); Mironovskaya (10630); Noe group (532): Vilmorin 27 (532); Unknown Ne2 allele (532); Harvest Queen (532).

Ne2s (530). i: S-615*11/Kharkov (1500). v: Crimean group (532): Blackhull (550); Chiefkan (550); Clarkan (550); Kharkov (1491); Michigan Amber (532); Minhardi (155); Red Chief (550); Stepnaja 135 (1264); Turkey (532). Ne2w (530). v: Vakka (532); Varma (532).

nel ne2. v: Chancellor (531); Elgin (1491); Gladden (155); Leap (155); Purkof (155); Red Bobs (1491); Red Egyptian (1491); Steinwedel (1000); S-615 (1491); Wichita (531). Genotype lists in {531,532,535,640,696,698,1093,1135,1264,1381,1473,1474,1475,1492,1496,1497,1502,1503,1512,1505,1506,1507,1509,1510,1630,1631,1632,1633,1637,1638,1639,0112}.

Rye line 1R136-2 carries Ner1 (1210) that complements wheat gene Ne2 (1289,1210) and rye gene Ne2 (1210) to produce necrosis. Rye lines L155 and L256 carry Ne2 (1210) that complements Nel (630,1210) and Ne1 (1210).


42.2. Hybrid chlorosis type 1

Ch1 (535). [m^6 (1245)]. 2A(538,939). i: Steinwedel’2/Khapli (939); T. macha var. colchicum (535). v: T. macha var. subletschumicum (1245,1493). tv: Khapli (1080,1549); T. dicoccoides var. kotschyanum (535); T. dicoccoides var. straussianum (535).

36 group dicoccon wheats are listed in {697}.


Extremely widespread, very few wheats lack this gene. Allelic variation at the Ch2 locus was suggested (537,1000). Prelude, Reward and Red Bobs were exceptional in producing severe symptoms and death at an early stage. Konosu 25 may carry a weak allele (1000). Different alleles in C306 (strong) and Sonalika (medium) were suggested in (697).

ch1 ch2. v: Alb1(1000,1509); Burt(1000,1509); Chancellor (1000); Garra (1549); Kharkof (535); Steinwedel (1549). su: TAP 67 (= Pawnee 3Ag(3D))(1644).

Lists appear in {535, 697, 1381, 1473, 1474, 1475, 1496, 1497, 1502, 1503, 1512, 1505, 1506, 1507, 1508, 1509, 1510}.

A gene, Chr1, in rye produces chlorosis symptoms in hybrids with wheats such as C306, HD2939 and NI5439 possessing Ch2 (1472). Evidence for multiple alleles of Chr1 was also presented (1472).

Chr1 (1472). dv: Cereal rye lines, EC179188 = WSP527A (1472); EC143825 = WSP506A (1472); EC338685 = Blanco (1472); others (1472).
42.3. Hybrid chlorosis

\textit{Cs1} \{1511\}. [\textit{Chl}]. 5A\{1498\}. \textbf{v}: \textit{T. dicoccum} cv. Hokudai\{1511\}.

Occurs at high frequency in the \textit{T. paleocolchicum} group of emmers.

\textit{Cs2} \{1511\}. [\textit{Chl}]. 4G\{1498\}. \textbf{tv}: Many accessions of \textit{T. timopheevii} and \textit{T. araraticum}\{637,1511\}.

Multiple allelism at the \textit{Cs2} locus is discussed in \{637\}.

42.4. Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4-5 leaf stage. The lethal genotype was designated \textit{apd1 apd1 apd2 apd2} \{10492\}.

\textit{Apd1} \{10492\}. \textbf{v}: WR95 = Kalyansona/Gigas//HD1999/Sonalika/3/\textit{T. earlhcicum}\{10492\}.

\textit{apd2} \{10492\}. \textbf{v}: HD2009\{10492\}; HW2041\{10492\}; Lok-1\{10492\}; others\{10492\}.

\textit{Apd1 Apd2}. \textbf{v}: Atila\{10492\}; Kalyansona\{10492\}; others\{10492\}.

\textit{apd1 apd2}. Lethal genotype.

Uniculm plants occurred as heterozygous segregates among progenies, but homozygous uniculm lines could not be established \{10492\}.

43. Iron Deficiency

\textit{Fe1} \{921\}. 7DL\{927\}. \textbf{v}: Saratovskaya 29\{921\}.

\textit{Fe2} \{921\}. 7BS\{927\}. \textbf{v}: CS\{927\}.

44. Lack of Ligules

The liguleless character is controlled by complementary recessive genes in hexaploid wheat \{077,738,942\} and by a single recessive in tetraploid wheat \{047,050,939,10133\}. One gene at the tetraploid level is allelic with one of those in the hexaploid \{939,10133\}. Evidence for orthology of \textit{lg1} and \textit{lg2} with \textit{lg} of rice \{170\}, \textit{lg1} of maize \{004\}, \textit{li} of barley \{1155\} and \textit{al} of rye was presented in \{725\}. \textbf{al}: Imperial rye chromosome 2R restored the liguled condition to a liguleless CS derivative \{939\}.

\textit{lg1} \{047\}. 2B\{942\}. \textbf{i}: ANK33=Novosibirskaya 67*10/K59990\{10061\}. \textbf{v}: Eligulate W1342 \textit{lg2} \textit{lg3}\{942,10133\}; K31289\{10133\}; K59990\{10061\}; K53660\{10133\}; Liguleless partial backcross derivative of CS\{939\}; Partial backcross derivative of CS\{939\}. \textbf{tv}: K17769\{10133\}; K17784\{10133\}.

\textit{lg2}. 2D\{942\}. \textbf{i}: ANK33=Novosibirskaya 67*10/K59990. \textbf{v}: Eligulate W1342 \textit{lg1} \textit{lg3}\{942,10133\}; Liguleless partial backcross derivative of CS\{939\}.

Because diploid wheats are liguled, polyploid wheats presumably carry a third recessive factor in chromosome 2A.

\textit{lg3} \{10133\}. 2A\{10133\}. \textbf{i}: ANK33=Novosibirskaya 67*10/K59990\{10061\}. \textbf{v}: Present in all hexaploid cultivars.

Genotypes of selected tetraploid wheat \{10133\}
45. Leaf Erectness

QLer.ipk-2A \{0255\}. \text{v}: Opata/W-7984 (ITMI) RI mapping population\{0255\}; The erect leaf phenotype was contributed by Opata\{0255\}. \text{ma}: Associated with Xbcd348-2A\{0255\}.

Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants \{0255\}.

46. Leaf Tip Necrosis

Ltn \{1361\}. \text{v}: Wheats with Lr34/Yr18\{301,1361\}; See Lr34, Yr18.

Ltn1 \{10281\}. [Ltn \{1361\}]. \text{v2}: Parula Ltn2 \{10281\}. \text{ma}: Associated with Xgwm295-7D and Xgwm130-7D\{10281\}. \text{c}: See Lr34.

This gene is identical to Yr18, Pm38 and Ltn and confers stem rust resistance in some genetic backgrounds.

Ltn2 \{10281\}. 1B \{10281\}. \text{v}: Wheats with Yr29/Lr46 \{10281\}; See Yr29, Yr46. \text{v2}: Parula Ltn1 \{10281\}. \text{ma}: Xwmc44-1B - 1.4 cM - Xbac24prot - 9.5 cM - Ltn2 - 2.9 cM - Xbac17R........Xgwm140-1B \{10281\}; Xgwm44-1B - 3.6 cM - Ltn2 - 2.1 cM - Xgwm140-1B \{10281\}.

According to Messmer et al. \{0031\} LTN may be caused by several QTLs and is affected by genetic background and environment.

QLtn.sfr-1B \{0050\}. 1BS \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xgwm18-1B and Xglk483-1B\{0050\}.

QLtn.sfr-3A \{0050\}. 3A \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpstr570-3A and Xpstr543-3A\{0050\}.

QLtn.sfr-4B.1 \{0050\}. 4B \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr921-4B and Xpsr593-4B\{0050\}.

QLtn.sfr-4B.2 \{0050\}. 4B \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr593-4B and Xpsr112-4B\{0050\}.

QLtn.sfr-4D \{0050\}. 4DL \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr302-4D and Xpsr1101-4D\{0050\}.

QLtn.sfr-5A \{0050\}. 5A \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr549-5A and Xglk163-5A\{0050\}.

QLtn.sfr-6A \{0050\}. 6A \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr563-6A and Xpsr966-6A\{0050\}.

QLtn.sfr-7B.1 \{0050\}. 7B \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr350 and Xbzh232(Tha)-7B\{0050\}.

QLtn.sfr-7B.2 \{0050\}. 7B \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xglk750-7B and Xwmg710-7B\{0050\}.

QLtn.sfr-7D \{0050\}. 7DS \{0050\}. \text{v}: Forno/T. spelta var. Oberkulmer mapping population\{0050\}. \text{ma}: Associated with Xpsr160-7D and Xgwm44-7D\{0050\}.

47. Lodging
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QLd.crc-3D\{10287\}. 3D\{10287\}. ma: Linked to Xgwm191-3D (LOD 3.7) in RL4452/AC Domain\{10287\}.

QLd.sfr-1B\{0052\}. 1BS\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr949-1B and Xgwm18-1B\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness and broader leaf width \{0052\}.

QLd.sfr-2A\{0052\}. 2AS\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr919-2A and Xgsk15-2A\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness, broader leaf width, more erect growth habit, later ear emergence and increased culm thickness \{0052\}.

QLd.sfr-2D\{0052\}. 2D\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr918-2D and Xgsk14-2D\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness and reduced culm thickness \{0052\}.

QLd.sfr-3A\{0052\}. 3AS\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr916-3A and Xgsk13-3A\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness and more erect growth habit \{0052\}.

QLd.sfr-4A\{0052\}. 4AS\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xgwm397-4A and Xgsk12-4A\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness and more erect growth habit \{0052\}.

QLd.sfr-5A\{0052\}. 5AL\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr918-5A and Xpsr1201-5A\{0052\}. This QTL coincided with QTL for reduced height, increased culm stiffness, reduced leaf width, more erect growth habit, later ear emergence and increased culm thickness\{0052\}.

QLd.sfr-5B\{0052\}. 5BL\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr370-5B and Xpsr580-5B\{0052\}. This QTL coincided with QTL for increased culm stiffness, broader leaf width and more erect growth habit \{0052\}.

QLd.sfr-6B\{0052\}. 6BL\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr964-6B and Xpsr142-6B\{0052\}. This QTL coincided with QTL for reduced height and later ear emergence \{0052\}.

QLd.sfr-7B\{0052\}. 7BL\{0052\}. v: Forno/T. spelta var. Oberkulmer mapping population\{0052\}. ma: Associated with Xpsr927-7B and Xpsr350-7B\{0052\}. This QTL coincided with QTL for reduced height and later ear emergence \{0052\}.

48. Male Sterility

48.1. Chromosomal

ms1. Recessive alleles for sterility 4B\{268\}.4BS\{064\}.

ms1a\{268\}. v: Briggle’s Chancellor Derivative\{268\}; Pugsley’s Male Sterile\{268\}.

ms1b\{268\}. v: Probus mutant\{268\}.

ms1c\{064\}. v: Cornerstone\{064\}.

ms1d\{0290\}. v: Mutant FS2\{0290\}.

ms1e\{0290\}. v: Mutant FS3\{0290\}.

ms1f\{0290\}. v: Mutant FS24\{0290\}.

ms1g\{10355,10546\}. 4BS\{10354\}. v: Lanzhou Mutant 257A\{10354,10355\}; Male sterile line 257A\{10546\}.

ms2\{806\}. Dominant allele for sterility. [Ta1\{240\}]. 4DS\{806\}. v: Taigu = Line 223\{240,807,806\}; ms2 confers sterility when present in octoploid triticale\{597\}.

ms3\{872\}. Dominant allele for sterility. 5AS\{872\}. i: Chris derivative\{872\}; KS87UP9\{219\}. ma: Xgwm341-5A - 0.8 cM - ms3......cent\{0289\}; Xcdo-677-5A and
Xbcd1130-5A also cosegregated with Xwg341-5A but were located in a different region in the physical map. 

ms4{0293}. Dominant allele for sterility, distinguished from ms2 on the basis of different degrees of recombination with the 4D centromere. 4DS{0293}. v: Konzak's male sterile.

ms5{0290}. 3A{0290}. v: Mutant FS20{0290}.

48.2. Sterility in hybrids with wheat

Shw{0331}. [1HL{0331}]. ad: Additions of 1H and 1HL to wheat and certain translocation lines {0331}. ma: Located in a 16.4 cM interval flanked by Xmwg800-1H and Xmwg943-1H. A possible relationship with Ncc genes is discussed {0331}.

48.3. Photoperiod and/or temperature-sensitive male sterility (PTGMS)

 wtms1{10332}. 2B{10332}. v: BNY-S{10332}. ma: E: AAG/M:CTA163 - 6.9 cM - wtms1 - 4.8 cM - Xgwm374-2B{10332}.

Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10C, but fertile at higher temperatures {10332}.

 wptms1{10333}. 5B{10333}. v: Line 337S wptms2{10333}. ma: Xgwm335-5B - 4.2 cM - wptms1 - 24.4 cM - Xgwm371-5B{10333}.

wptms1 produces sterility only in the presence of wptms2.

 wptms2{10333}. 2B{10333}. v: Line 337S wptms1{10333}. ma: Xgwm374-2B - 6.9 cM - wptms2 - 20.9 cM - Xgwm120-2B{10333}.

wptms2 produces sterility only in the presence of wptms1. wptms1 and wptms2 were analysed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Although mapping data are different a possible relationship between wtms1 and wptms2 needs to be resolved.

49. Manganese Efficiency

 QTL: Variation associated with Xcdo583-4B explained 42% of the variation for Mn efficiency in the durum cross Stojocri 2 (Mn efficient)/Hazar (MN inefficient) {0320}.

50. Maturity time

 QMat.crc-3B{10287}. 3B{10287}. ma: Linked to Xwmc231-3B (LOD 3.0) in RL4452/AC Domain{10287}.

 QMat.crc-4A{10287}. 4A{10287}. ma: Linked to Wx-B1 (LOD 6.1) in RL4452/AC Domain{10287}.

 QMat.crc-7D{10287}. 7D{10287}. ma: Linked to Xgwm130-7D (LOD 17.5) in RL4452/AC Domain{10287}.

51. Megasporogenesis

51.1. Control of megasporogenesis

 Msg{625}. 7AS{625}. tv: Langdon{625}.
52. Meiotic Characters

52.1. Low-temperature pairing

\textit{ltp} \{527\}. \textbf{v:} Chinese Spring\{527\}.
Expressed in the absence of chromosomes 5D at 12°C - 15°C, but not at 20°C. A contrasting allele, \textit{Ltp}, for normal pairing at the lower temperature range was demonstrated in \textit{T. dicoccum}.

52.2. Pairing homoeologous

\textit{Ph1} \{1537\}. \textbf{ma:} PCR-based assays for presence and absence of \textit{Ph1} have been described\{0214,0217,9965,0359\}; The \textit{Ph1} factor(s) was restricted to a region flanked by Xrgc846-5B and Xpsr150-5B\{0219\}; \textit{Ph1} was physically mapped in 5BL to fraction length 0.55, bracketed by deletions 5BL-1 and \textit{ph1b}\{446\}.
A complex \textit{Ph1} candidate structure comprising at least one 5B-specific member of the \textit{cdc2} complex multigenic cluster (involved in chromosome condensation), a unique repeat structure with similarities to repeats on chromosome 3B, and a heterochromatic sub-telomeric insertion from chromosome 3AL was identified \{10240\}.

\textit{ph1a}. - Not applicable - see \textit{ph2b} \{1303\}.

\textit{ph1b} \{1301\}. \textbf{v:} Sears' high pairing mutant\{1301\}. \textbf{ma:} A PCR-based detection system for \textit{ph1b} \textit{ph1b} individuals is described in \{9965\}.

\textit{ph1c} \{593\}. \textbf{tv:} Cappelli \textit{ph1} mutant\{449,593\}; This mutant is deficient for a terminal portion of chromosome 5BL\{449\}. \textbf{ma:} Mutant lines with \textit{ph1b} and \textit{ph1c} carry deletions of the chromosome segment possessing \textit{Ph1} in the respective parent lines\{593,447\}.
Several \textit{ph1} mutants are described in \{0219\}.

\textit{Ph2} \{1302\}. 3DS\{1302\}.

\textit{ph2a} \{1302\}. \textbf{v:} Sears' intermediate pairing mutant\{1301,1302\}.

\textit{ph2b} \{1304,1303\}. \{\textit{ph1a} \{1537\}\}. \textbf{v:} Chinese Spring mutant 10/13\{1537\}.

52.3. Inhibitor of pairing homoeologous

\textit{Ph1\textsuperscript{I}}. \textbf{al:} \textit{Aegilops speltoides}\{1218,439\}.

53. Nitrate Reductase Activity

\textit{Nra} \{424\}. \textbf{v:} UC44-111\{424\}.

\textit{nra} \{424\}. \textbf{v:} Anza\{424\}.

54. Nuclear-Cytoplasmic Compatability Enhancers

\textit{scs} \{869\}. Derived from \textit{T. timopheevii} \{869\}. 1AL\{870,027\}. \textbf{v:} \textit{T. timopheevii}\{869\}. \textbf{ma:} A number of completely linked RAPD makers were identified\{044\}.
Asakura \textit{et al.} \{044\} used the symbol \textit{Ncc} as a synonymn for \textit{scs} pointing out that the effects of the gene are not limited to a single species.

55. Nucleolus Organizer Regions
55.1. 18S - 5.8S - 26S rRNA genes

NORs have been observed as secondary constrictions associated with nucleoli on satellited chromosomes (e.g., 221), and by in situ hybridization to chromosome spreads (039,294,1014) of 18S-5.8S-26S ribosomal-DNA probes (038,433). Allelic variation in gene number has been demonstrated at all wheat Nor sites and at Nor-RI by filter (367) and in situ hybridization (1012). Allelic variants of the Nor loci are detected by hybridization of rDNA probes to restriction endonuclease-treated DNA on Southern blots (037,288,917,1399). Alleles Nor-B2a to Nor-B2f were identified using Taq1 digests of genomic DNAs hybridized to derivatives of the plasmid pTa250 (433) containing spacer-DNA fragments pTa250.4 (367,917) and pTa250.15 (288).

Other variants may have been isolated (1399) using BamHI/EcoRI double digests and pTa71 (433). The variants may or may not be equivalent to those described below.

Nor1a and Nor2a. v: Maris Huntsman (1399).
Nor1b and Nor2b. v: Bezostaya 1 (1399).
Nor1c and Nor2c. v: Cappelle-Desprez, Maris Ranger (1399).

Deletion mapping divided the Nor-B1 in a proximal subregion Nor-B1p (short repeat) and a distal subregion Nor-B1d (long repeat) (0275).

Nor-B1a (918). v: Cheyenne, Chinese Spring, Hope, Kite, Oxley, Teal, Timstein (037,288); Vasco, 8 others (288).

Nor-B1a (918). v: A derivative allele of Nor-B1a with a significantly reduced amount of spacer. Condor 64-1 (918); Sonora 64-1 (918).

Nor-B1b. v: Olympic, Robin, Shortim (917).
Nor-B1c (918). v: Banks (917); Corella (917); Warigal (917); 5 others (917).

Nor-B1c (918). v: Rosella (918).

Nor-B1d (918). v: Maris Huntsman (918).

Nor-Ag1 (374). 1Ag (374). ad: Vilmorin27/Ag. intermedium (374).


Nor-R1. IRS (039). ad: CS/Imperial (039).

Nor-S1. 1SS (294). al: Ae. speltoides (294).

Nor-U1. 1U (906). su: CS/Ae. umbellulata (906).


Nor-B2b (918). v: Blueboy (918); Sonora 64-1 (918).

Nor-B2c (918). v: Banks, Oxley, Shortim, Timstein (037); 12 others (917).

Nor-B2d (918). v: Corella, Robin, Teal, 1 other (917).

Nor-B2d (918). v: H6B (288). v: Hope (037); Olympic (917); Warigal (917).

Nor-B2d (918). v: Harrier (918); Kite (917,918).

Nor-B2e (917). v: Vasco (917).


Nor-B2g (918). v: Falcon; Gluclub; La Prevision (918).

Nor-B2h (918). v: Yakanka (918).

Nor-B2i (918). v: Maris Huntsman; Thatcher (918).

Nor-E2. 6ES (294). ad: CS/E. elongata (294).


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Nor-S2. 6SS[294].  **al:** *Ae. speltoides*{294}.

Nor-A3. 5AS{1014,658}.  **dv:** *T. monococcum, T. urartu* IPSR (PBI) Acc. A.

Nor-D3. 5DS[221,835].  **v:** CS; most wheats{037,288,917}.

Nor-Ag3. 5Ag{374}.  **ad:** CS/Ag. *intermedium*{374}.

Nor-E3. 5ES[294].  **ad:** CS/E. *elongata*{294}.

Nor-H3.  [Rr2{1248}]. 5H[1070,039,1248]. 5HS[794].  **al:** Clipper barley{039}; Sultan barley{794}.

Nor-U3. 5U[906].  **ad, su:** CS/Ae. *umbellulata*{906}.

Nor-D4[1042]. 7DL[1042].  **v:** CS{1042}.

Nor-H4.  [Nor-I4{794}]. 7HS[794,793].  **al:** Sultan barley{794}.

Nor-B6[601]. 1BL[601].  **v:** CS; Cheyenne, Wichita{601}.  **tv:** Langdon{601}.

Nor-A7[601]. 5AL[601].  **v:** CS; Cheyenne, Wichita{601}.  **tv:** Langdon{601}.

Nor-D8[601]. 3DS[601].  **v:** Wichita{601}.

Nor-A9[00120].  [Nor-A1{221,367,835,1012}]. 1AS[282,276].  **v:** *T. spelta*{221,367,835,1012}.

Nor-A10[00120].  [Nor-A3{1014,658}]. 5AS[282,276].  **dv:** *T. monococcum*{282,276}; *T. urartu* IPSR (PBI) Acc. A.

More detailed listings for allelic variation at Nor-B1 and Nor-B2 are given in {917,918}. Two sites designated temporarily as Nor-Ax and Nor-Ay were identified in *T. monococcum* ssp. *boeoticum*, but were absent in ssp. *urartu*.

56. Osmoregulation

Osmoregulation is a specific form of solute accumulation regulating turgor pressure and hydration during periods of stress with positive effects on growth. Wheat lines selected for higher osmoregulation in the greenhouse have greater growth and seed yields under water limited conditions in the field.

**Or**[1030].  **Low osmoregulation.**  **s:** CS (Red Egyptian 7A).  **v:** Cappelle Desprez; Condor 4/3Ag14{1030}; Red Egyptian.  **ma:** Or (proximal in 7AS) - 13 cM - *Xpsr119-7A*{1031}.

**or**[1030].  **High osmoregulation.**  **s:** CS, Condor, Songlen, Takari{1030}.

57. Phenol Colour Reaction of Kernels

Wheat genotypes vary in response when caryopses are treated with weak solutions of phenol, a dark colour response being indicative of a positive response. This response is believed to be related to the action of tyrosinase. There seems to be a genetic relationship with polyphenol oxidase activity which causes a darkening of flour, pasta and noodle products (see also Polyphenol Oxidase (PPO) activity).

**Tc1**[10130]. 2AL[10130,10131].  **su:** Various substitutions of chromosomes 2A into CS[10131].  **suv:** Langdon*/dicoccoides 2A{10130}.  **tv:** Golden Ball{10130}.

**Tc2**[10130]. 2BL[10130].  **suv:** Langdon*/Golden Ball 2B{10130}.  **tv:** Golden Ball{10130}.

**Tc3**[10131].  [Tc{10131}]. 2DL{10130}.  **v:** Chinese Spring (intermediate response){10130}.

**v2:** Timstein *Tc1*{10131}.  **su:** CS/*Timstein 2D{10131}.  **tv:** Cocorit 71{10130}; Langdon{10130}.  **suv:** Langdon*/CS 2D(2A); Langdon*/CS 2B(2D){10130}; *T. dicoccoides* Israel A {10130}. Lines with a negative phenol colour reaction.
58. Pollen Killer

Ki[1306]. Killing allele is dominant. 6BL{1306}. v: Chinese Spring{1306}; Mentana{929}.
ki. v: Probably the majority of wheats including Timstein, Gabo and Yalta{1306}.
Modifiers also appear to be involved as Luig {840, and unpublished} found variation among kiki parents. Some F2 and F3 Sr11sr11 plants from Yalta/Chinese Spring crosses segregated with less than 50% Sr11- phenotypes among the progeny indicating that killing extended to eggs as well as pollen. See also, Gametocidal Activity.

Kato & Maeda {10164} reported both partial pollen and seed sterility in crosses involving certain landraces and Chinese Spring. They attributed sterility to recessive alleles of three complementary genes. The genes were designated Ki2, Ki3 and Ki4 {10164}, but the relationship of Ki3 to the earlier designated Ki was not established. Some genotypes:

**Ki2 Ki3 Ki4:** v: Aka Kawa Aka {10165}; Hope {10165}; Marquis {10165}; Red Russian {10165}

**ki2 Ki3 Ki4:** v: Akadaruma {10165}; Canthatch {10165}; Norin 61{10165}; Pakistani Landrace IL159 {10164}

**Ki2 ki3 Ki4:** v: Gabo {10165}; Thatcher {10165}; Timstein {10165}; Zlatiborka {10165}

**Ki2 Ki3 ki4:** v: Kagoshima {10165}; Komugi Jingoro {10165}; Sakobore {10165}

**ki2 ki3 ki4:** v: Finnish Landrace WAG4339 {10165}; Hungarian Landrace WAG4458 {10165}; Novosadska Jara {10165}

**ki2 Ki3 ki4:** v: Chinese Spring {10165}; Eshima Shinriki {10165}; Ethiopian Landrace IL70 {10164}; Norin 26 {10165}

**Ki2 ki3 ki4:** v: Cadet {10165}; Iraqi Landrace IL171 {10165}; Rex {10165}

59. Polyphenol Oxidase (PPO) Activity

3,4 dihydroxyphenylalanine (L-DOPA) was used as a substrate in a non-destructive test of polyphenol oxidase activity in seeds. Chromosome 2D was shown to carry PPO gene(s) based on Langdon/Chinese Spring (2D) substitution lines and nullisomic-tetrasomic analysis {0342}. An orthologous series of genes affecting PPO activity in both common wheat and durum was proposed in {10149}. See also, Phenol Colour Reaction of Kernels

Chara (mod high)/WW2449(low): DH population: PPO activity Associated with Xgwm294b-2A (R²=0.82), Xwmc170-2A, Xgwm312-2A and Xwmc178-2A (R²>0.7) {10410}.

Chara (medium high PPO)/WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci Xtc1 and XPPO-LDOPA. Xtc1 - 0.6 cM - XPPO-LDOPA/XPPO18/BQ161439 {10484}.

A QTL on 2D, associated with Xfba314-2D was identified in an M6 / Opata 85 population using the L-DOPA assay. The high PPO activity was contributed by M6 {0344}. Markers significantly associated with PPO activity were also detected on chromosomes 2A, 2B, 3B, 3D and 6B in the population NY18 / Clark's Cream {0344}.

A multiplex of markers PPO33 and PPO16 was reliable for selecting genotypes with low PPO activity {10418}.

Tetraploid wheat
60. Red Grain Colour

Red colour is probably due to the polyphenol compounds phlobaphene or proanthocyanidin, synthesized through the flavanoid pathway. Himi & Noda (10107) provided evidence that the D genes were wheat forms of Myb-type transcription factors (Nib10-3A, Myb10-3B, Myb10-3D).

Red colour is dominant to white. At each locus, the white allele is assigned a and the red allele, b. White-grained T. aestivum and amber-grained T. durum wheats carry recessive a alleles at each locus. White-grained CS*7/Kenya Farmer and CS*6/Timstein are considered near-isogenic to CS with R-D1b.


R-A1b. [R2]. i: Novosibirskaya 67°9/Solo{730}. v: Baron{370}; Diamant 2{014}; Hustler{370}; Norin 10- Brevor, 14{017}; Maris Widgeon{370}; Mercia:{370}; Motto{370}; Red Bobs{1003}; Sapphire{370}; Slejpner{370}; Talent{370}; Wembley{370}.

R-B1 [548]. [R3]. 3BL{1003,370}. ma: Xbcd131-3B - 5 cM - R-B1 - 5 cM - Xabc174-3B{410}; Xwmc29-3B - 5 cM - R-B1 - 5 cM - Xbarc-3B{10280}.

R-B1b. [R3]. i: Novosibirskaya 67°9/k-28536{730}. v: Canon{370}; Dollar{370}; Grana{370}; Supreme{370}.

R-D1 [549]. [R1]. 3DL{1291,1293}. ma: Xbcd131-3D cosegregation with R-D1 - 15 cM - Xabc174-3D{410}. v: CS.

R-D1b. [R1]. i: Novosibirskaya 67°9/CS{730}. v: Alexandria{370}; Apollo{370}; Axona{370}; CS{1293}; Dwarf A{370}; Fortress{370}; Jerico{370}; Longbow{370}; Luna{370}; Mardler{370}; Maris Huntsman{370}; Minaret{370}; NFC 75/93/27A; Rapier{370}; Pawnee{549}; Voyage{370}; Vuka{370}.

R-N1 {1018}. 3N{1018}. su: CS/Ae. uniaristata {1018}.

R-R1 {1011}. 3RL{1011}. ad: Holdfast/King II{1011}.

R-V1 {1518}. 3VL{1518}. ad: Creso/D. villosum {1518}.

A 3Ag chromosome from decaploid Ag. elongatum carries an allele for red grain colour which was transferred to Agent and the majority of Sears' 3D-3Ae#1 translocations {939}.

Other studies have identified wheats carrying either one or two, unidentified R-1 alleles: {056,437,549, 631,654,659,1078,1148,1333,1349,1454,370}.

See also Variegated Red Grain Colour.

R-Alb R-B1b R-D1a. [R2,R3]. v: Red Chief{548}; Avalon{370}; Bersee; Cappelle Desprez; Feuvert; Mission; Parade; Rendezvous; Yuri{370}.

R-Alb R-B1a R-D1b. [R2,R1]. v: Broom{370}; Bezostaya 1{370}; Brigand{370}; Brock{370}; Kronjuwel{370}.

R-Ala R-B1b R-D1b. [R3,R1]. v: Kharkov{1003}; Fenman{370}; Norman{370}; Pastiche{370}; Riband{370}; Sperber{370}; Squadron{370}; Urban{370}.

R-Alb R-B1b R-D1b. [R1,R2,R3]. v: Bowie; Frondoso{1148}; Frontiera{437}; Hope{204,206}; Japanese Bearded{1548}; Kanred{1078,1426}; Lin Calel{1078}.

Messopial/T. dicocoides: RILs: Associated with RFLP Xutv1427-2A {10411}.

Jennah Khetifa (high)/Cham 1 (low): Associated with Xgwm312-2AL {10411}.

STS marker PPO18 based on a polyphenol oxidase (PPO) gene (GenBank AY596268) was closely linked to SSR markers Xgwm312 and Xgwm294 on chromosome arm 2AL. PPO18 explained 28-43% of the variation in PPO activity in the cross Zhongyou 9507/CA9632 {10290}.
61. Reaction to Black-Point of Grain
Black-point, a common grain defect, is a dark discoloration of the embryo region of the kernels. Whereas black-point is often attributed to infection by a number of fungi, the presence of such fungi may be a consequence of saprophytic colonization of affected tissues rather than the cause (see \{10148\} for references). The condition may be triggered by high humidity \{0845\}.

QTL: Sunco/Tasman DH population: QTL located in chromosomes 2B (15% of phenotypic variation), 3D, 4A (from Sunco) and 1D, 5A and 7AS (from Tasman \{10148\}. The 2B gene was associated with the presence of Sr36 \{10148\}.

Markers Xgwm319-2B and Xgwm048-4AS were confirmed in a Batavia/Pelsart (resistant) DH population \{10494\}.

Cascades/AUS1408 DH population: QTL from Cascades located in chromosomes 2D (5 cM from Xgwm484-2D, 18% of phenotypic variation), 2A (13%), and 7AS (12%) \{10148\}.

62. Response to Photoperiod
One-gene \{1169\} and two-gene \{638, 1137, 1170\} differences were reported in inheritance studies. In Chinese Spring/Hope substitution lines for chromosomes 1A, 4B and 6B greater sensitivity to short photoperiod was found, whereas substitutions of 3B and 7D were less sensitive \{487\}.

'a' alleles are dominant.

There is an orthologous gene series on the short arms of homoeologous group 2. The "a" alleles confer the insensitive response \{0063\}, the contrasting allele may be referred to as "b".

\textbf{Ppd-A1} \{0063\}. \([Ppd3\{1141\}]\). 2AL\{1268\}. \textbf{v}: C591\{0057\}. \textbf{ma}: Xwmc177-2A - Ppd-A1, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively\{10612\}.

\textbf{Ppd-A1a} \{10612\}. \textbf{tv}: GS100\{10612\}; GS105\{10612\}.

\textbf{Ppd-A1b} \{10612\}. \textbf{tv}: GS101\{10612\}; GS104\{10612\}.

\textbf{Ppd-B1}. \textbf{ma}: Xwhs2002-2B/Xgwm257-2B - PpdB1 - Xgwm148-2B. Actual linkage value varied between crosses\{10129\}; Xpsr666-2B - 1.2 cM - Xpsr109-2B - 4.4 cM - Ppd-B1 - 4.8 cM - Xpsr804-2B ...Cent\{0062\}.

According to \{10611\} the \textit{Ppd-B1} allele from Japanese wheats has a stronger effect than the allele from CS.

\textbf{Ppd-B1a} \{0063\}. \([Ppd2\{1566\}]\). 2BS\{1566, 1268, 1269\}. \textbf{i}: H(C) = Haruhikari*5 / Fukuwasekomugi\{10611\}; H(D) = Haruhikari*5/Fukuwasekomugi \textbf{Ppd-D1a} \{10611\}.

\textbf{s}: Cappelle-Desprez*/CS 2B\{0058\}. \textbf{v}: Chinese Spring\{1268\}; Spica\{557\}; Timstein\{1269\}. \textbf{v2}: Fukuwasekomugi \textbf{Ppd-D1a} \{10611\}; Sharbati Sonora \textbf{Ppd-A1a} \{887\}.

\textbf{Ppd-B1b} \{10611\}. \textbf{v2}: Haruhikari \textbf{Ppd-D1b} \{10611\}.

\textbf{Ppd-B2} \{10628\}. 7BS\{10628\}. \textbf{su}: Favorit (F26-70 7B)\{10628\}. \textbf{v}: F26-70\{0093\}. \textbf{ma}: Xgwm255-7B - 20.7 cM - Ppd-B2 - 4.4 cM - Xgwm537-7B \{10628\}.

This gene confers earlier flowering under long photoperiod conditions \{10628\}.

\textbf{Ppd-D1}. Comparative mapping showed that \textit{Ppd-D1} was co-linear with barley \textit{Ppd-H1} - a member of the pseudo-response regulator (PRR) gene family \{10466\}.

Jagger amplified the 414 bp band \{10466\} associated with daylength sensitivity whereas 2174 amplified the 288 bp band associated with insensitivity \{10722\}.
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**Ppd-D1a** \{0063\}. \([PpdD1a\{1566\}]\). 2DS\{1268\}. i: H(C) = Haruhikari*5 / Fukuwasekomugi\{10611\}; Haruhikari*5 / Saitama 27\{10611\}. s: Capelle Desprez*Ciano 2D\{1598\}; Capelle-Desprez*Mara 2D\{1598\}; CS*Ciano 2D \([Ppd-D1a\{1268\}]\). v: Akakomugi\{1604\}; Bezostaya 1\{1604\}; Festival\{10466\}; Kavkaz\{0917\}; Mara\{1604\}; Orqual\{10466\}; Recital\{10466\}; Saitama 27\{10466\}; Sava\{1604\}; Sideral\{10466\}; Soissons\{10466\}; Sonora 64\{1566\}; Talent\{10466\}; Texel\{10466\}. v: Akakomugi\{1604\}; Bezostaya 1\{1604\}; Festival\{10466\}; Kavkaz\{0917\}; Mara\{1604\}; Orqual\{10466\}; Recital\{10466\}; Saitama 27\{10466\}; Sava\{1604\}; Sideral\{10466\}; Soissons\{10466\}; Sonora 64\{1566\}; Talent\{10466\}; Texel\{10466\}. ma: Stocks with \([Ppd-D1a\{10611\}]-2D\{1268\}\). i: H(D) Haruhikari*/5/Fukuwasekomugi\{10611\}. Ppd-D1a Ppd-D1b. ma: Stocks with \([Ppd-D1a\{10611\}]\)

**Ppd-A1b Ppd-B1b Ppd-D1b**. v: Cheyenne\{1141\}; Diamont 1\{887\}; Lancer\{638\}; Saratovskaya 29\{887\}; Warrier\{638\}. ma: Kna1 was completely linked with Xabc305\{441\} - Xabc305\{441\} - Xgwm497\{502\}.

**63. Response to Salinity**

**63.1. K+/Na+ discrimination**

Variation in K+/Na+ discrimination ratios correlate with salt tolerance, high ratios being indicative of higher tolerance.

**Kna1** \{290\}. 4DL\{290\}.4BS.4BL-4DL\{283\}.4BS.4BL-4DL-4BL\{849\}. v: Hexaploid wheats\{290\}. tv,su: Langdon 4D\{4B\}\{283\}. tv,tr: Various lines\{290\}; Selection 3\{5-4\}\{849\}. ma: Kna1 was completely linked with Xabc305-4B, Xabc305-4D, Xbcd402-4B, Xbcd402-4D, Xpsr375-4D, Xpsr567-4B, Xpsr567-4D, Xwgl99-4B and Xwgl99-4D in recombined \(T. turgidum\) 4B and \(T. aestivum\) 4D chromosomes\{283,849\}. Lophopyrum elongatum chromosome arms 1ES, 7ES, and 7EL enhance K\(^+\)/Na\(^+\) selectivity in wheat under salt stress \{0065\}. Kna1 is a possible orthologue of Nax2 and is the Na\(^+\) transporter TaHKT1;5-D \{10455\}.

**63.2. Salt tolerance**

**QTL:** Opata 85/W7984. 77 QTLs effective at different growth stages were mapped to 16 chromosome \{10384\}.

**63.3. Sodium exclusion**

**Nax1** \{10452\}. 2AL\{10452\}. itv: Tamaroi*6/Line 149 = P06306\{10453\}. tv: Line 149 Nax2 = 126775b\{10452\}. dv: AUS 90382 Nax2 = C68.101 \{10455\} = JIC \(T. aegilopoides\) no. 3. ma: Nax1 was mapped as a QTL in the region Xpsr102-2A - 5.4 cM - Xwmc170-2A - 0.9 cM - Xsud22-2A/Xsud16-2A - 0.8 cM - Xgwm312-2A with \(R^2 = 0.38\) in Tamaroi/Line 149\{10452\}; TmHKT7-A2 was identified as a putative candidate Na\(^+\) transporter\{10454\}. Nax1 promotes withdrawal of Na\(^+\) from xylem in leaf bases and roots \{10453\}. ma: Co-segregation with Xgwm291-5A/Xgwm140-5A/Xgpw2181-
5A(10455); *TmHKTI*:5-A was identified as a candidate for *Nax2*(10455). *Nax2* is a likely orthologue of *Kna1* (10455).

64. Response to Tissue Culture

- **Qtcr.ipk-2B.3**(084).  [ *Tcr-B3*(084)].  **ma**: Linked with *Yr7/Sr9g* (084).
- **QGpp.kvl-2A**(0253).  2AL(0253).  **v**: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano(0253).  **ma**: Associated with *Xpsp3045-2A*(0253).
- **QGpp.kvl-2B.1**(0253).  2BL(0253).  **v**: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano(0253).  **ma**: Associated with *Xgwm388-2B*(0253).
- **QGpp.kvl-2B.2**(0253).  2BL(0253).  **v**: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano(0253).  **ma**: Associated with AFLP markers(0253).

65. Response to Vernalization

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, vernalization requirement is controlled by four major genes designated *Vrn*-1, *Vrn*-2, *Vrn*-3, and *Vrn*-4. The first three genes were identified using map based cloning approaches (10014, 10299, 10421). The *Vrn*-1 gene encodes a MADS-box transcription factor closely related to the Arabidopsis *AP1/FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat (10014).

Deletions in the promoter (*Vrn-A1a, Vrn-A1b*) (10198) or the first intron of this gene (*Vrn-A1c, Vrn-B1a, Vrn-D1a*) (10202) are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide (10617,10695,10709).

The *Vrn*-2 locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain (10299).

Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit (10299).

Among the cultivated tetraploid and hexaploid wheat species the *Vrn*-B2 gene is generally functional whereas the *Vrn*-A2 gene is not (10710). At least one functional copy of *Vrn*-2 combined with homozygous recessive alleles at all three *Vrn*-l loci is required to confer winter growth habit in hexaploid wheat.

The *Vrn*-B3 locus (formerly known as *Vrn*-5 or *Vrn*-B4) is homologous to the Arabidopsis *FT* gene (10421). This dominant allele, found in the variety Hope, is associated with the insertion of a transposable element in the *Vrn*-B3 promoter. Natural variation at the *Vrn*-A3 and *Vrn*-D3 loci has been also described in hexaploid wheat (10533). *Vrn*-3 promotes the transcription of *Vrn*-1 and accelerates flowering (10421).
The Vrn-D4 allele for early flowering was originally identified in the Australian cultivar Gabo {671} and was backcrossed into Triple Dirk to develop the isogenic line TDF {1172}. This locus was mapped on the centromeric region of chromosome 5D between markers Xcfd78 and Xbarc205 {10711}. Natural variation for flowering time at the centromeric region of homoeologous group 5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of Vrn-D4 but molecular markers are now available to separate the incorrect stocks {10711}. Using genetic analyses, Iwaki et al. {10003} found the Vrn-D4 allele for spring growth habit occurred with a higher frequency in India and neighboring regions.

Vrn-I{1398}. Synonymous with TaVRT-I {10019}

Orthologous series in long arms of chromosomes of homoeologous group 5.

Vrn-I is a MADS-box gene similar to Arabidopsis APETALA1 {10014}. Spring types are associated with mutations in the promoter or the first intron {10014, 10198, 10202, 10288}. Reduction of Vrn-I transcripts in transgenic hexaploid spring wheat delays flowering {10300}.

A polymorphism between Jagger and 2174 was associated with vrn-A1a. A point mutation occurred in exon 4 {10695}; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele {10695}.

Vrn-I genotypes in Pacific Northwest USA wheats are listed in {10695}.


Multiple recessive alleles were suggested {745}. Vrn-A1a was mapped on the long arm of chromosome 5A closely linked to the same RFLP markers as Vrn-A1 {279}. Vrn-A1b was mapped to the Xcdo504-5A - Xpsr426-5A region {0312}. In the opinion of the curators this location may not be correct

Multiple alleles also were reported in {9930}, and the dominant allele of Novosibirskaya 67 and the weaker dominant allele of Pirotrix 28 were designated Vrn1a and Vrn1b, respectively.

Vrn-A1b{10198}. v: Marquis PI94548 (GenBank AY616461){10198}. tv: T. turgidum var. durum ST36{10198}.

Vrn-A1c{10198}. This allele is a promoter similar to recessive vrn-A1a from Triple Dirk C {10198} and a large deletion in intron 1 {10202}. v: IL162{10198}; IL369{10198} has a 5.5 kb deletion in Vrn-A1 intron 1{10202}. tv: Aldura PI 486150{10202}; Leeds CI 13796{10202}; Mexicali 75 PI 433760{10202}; Minos CI 15161 {10202}. Most durum genotypes have a 7.2 kb deletion in intron 1{10202}.

Vrn-A1d{10198}. tv: T. turgidum var. dicoccoides Amrim 34{10198}; FA15 (GenBank AY616462){10198}; Iraq 8736{10198}; Tabigha 15{10198}.
**Vrn-A1e**\{10198\}.  **tv**: *T. turgidum var. dicoccum* ST27 = Vernal (GenBank AY616463)\{10198\}.

**Vrn-B1**.  **c**: GenBank AY747604.1\{10695\}.

**Vrn-B1a**\{1398\}.  [\(\text{Vrn4}\{1173\};\text{Vrn2}\{1172\};\text{Ss}\{002\};\text{Vrn2a} = \text{Vrn2}\{921,920\};\text{Vrn2b} = \text{Vrn2}\{921,920\}\)].  **5B**: 885.  **5D***: 635.  **5BL**: 885.  **5B**: 921, 920.  **5BL or 7BL**: 635, 0282.  **i**: Ank-18\{921,920\}; Triple Dirk B\{1172\}.  **s**: Diamant 1\&8/Mironovskaya 5A\{920\}; Diamant 1\&8/Skorospelka 35 5A\{920\}; Rescue/Cadet 5A \(\text{Vrn-A1a}\{885\}\); Saratovskaya 29\&8/Mironovskaya 808 5A\{920\}; Saratovskaya 29\&8/Odesskaya 5A\{920\}.  **v**: Bersee\{557\}; Brown Schlanstedt\{001,002,1171,1172\}; Cadet\{1221\}; Festiguay\{1172\}; Magali; Mara\{1611\}; Milturum 321\{885,920\}; Milturum 885\{885,920\}; Noe\{002\}; Pyrothrix 28\{920\}; Spica\{557\}; *T. spelta* var. *dahamelianum* KT19-1\{10057\}; Ulyanovka 9\{920\}.  **v2**: Borsum \(\text{Vrn1-A1a}\{001\}\); Dala \(\text{Vrn1-A1a}\{001\}\); Diamant 1 \(\text{Vrn1}\{001,920\}\); Gabo \(\text{Vrn4}\{1172\}\); Halland \(\text{Vrn-A1a}\{001\}\); Harukikari \(\text{Vrn-A1a}\{883\}\); Rubin \(\text{Vrn-A1a}\{001\}\); Saratovskaya 29 \(\text{Vrn-A1a}\{920\}\); Shortandinka \(\text{Vrn-A1a}\{1221\}\); Triple Dirk \(\text{Vrn-A1a}\{1173\}\).  **ma**: A dCAPS marker derived from \(\text{Xwg644-5B}\) was 1.7 cM from \(\text{Vrn-B1}\{10006\}\); \(\text{Vrn-B1a} - 1.6\text{ cM - }\text{Xwg644-5B} - 2.5\text{ cM - }\text{Xgwm408-5B}\)\{10004\}; Closely linked to \(\text{Xgwm408-5B}\) in Diamant 1\&8/Mironovskaya 808 5A // Bezostaya 1\{10007\}; A close association of \(\text{Vrn-B1}\) with \(\text{Xcdol326-5B}\) was reported in\{10057\}.  **c**: GenBank AY74603.1\{10695\}.

When mapped as a QTL \(\text{Vrn-B1}\) showed closest association with \(\text{Xgwm408-5B}\)\{10007\}. All common wheat genotypes carrying \(\text{Vrn-B1a}\) studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk B, Bersee, Festiguay, Mara, Milturum, Noe, Spica)\{10202\}. Two variants of \(\text{Vrn-B1a}\) were distinguished in\{920,921\}. Carriers of an earlier designated \(\text{Vrn2b}\) (characterized by Diamant 1\&8/Skorospelka 35 5A) showed accelerated flowering after 15 and 30 days of vernalization, whereas carriers of \(\text{Vrn-2a}\), (characterized by Ank-18 and Saratovskaya 29\&8/Mironovskaya 808 5A) did not respond to these periods of vernalization. This distinction was not made in the above list.

**Vrn-B1b**\{10695\}.  **v**: Alpowa\{10695\}.  **c**: GenBank FJ766015. Relative to \(\text{Vrn-B1a}\) (Triple Dirk B), \(\text{Vrn-b1b}\) has a G-C SNP at position 1656 and a 36 bp deletion at 1661-1696\{10695\}.

**Vrn-D1a**\{1398\}.  [\(\text{Vrn3}\{1172\}\)].  **5DL**: 775,883.  **i**: Triple Dirk E\{1172\}.  **s**: Rescue/Cadet 5A \(\text{Vrn-A1a}\{1221\}\); \(\text{Chinese Spring}\{1172\}\); \(\text{Loro}\{1172\}\); \(\text{Norin 61}\{460\}\); \(\text{Shinchunaga}\{460\}\); \(\text{Shirasagi Komugi}\{460\}\); \(\text{Ushio Komugi}\{460\}\).  **v2**: Rescue \(\text{Vrn-B1a}\{1221\}\).

All the common wheat genotypes carrying \(\text{Vrn-D1a}\) studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk E, Chinese Spring, Norin 61, Shinchunaga, Shirasagi Komugi, Ushio Komugi)\{10202\}.

**Stock: Genotype: Vernalization Response**

Triple Dirk, Kolben: \(\text{Vrn-A1a} \text{Vrn-B1b} \text{Vrn-D1b}\): No

Triple Dirk B, Festiguay: \(\text{Vrn-A1b} \text{Vrn-B1a} \text{Vrn-D1b}\): Yes

Gabo: \(\text{Vrn-A1b} \text{Vrn-B1a} \text{Vrn-D1b}\): Yes

Triple Dirk E, Chinese Spring: \(\text{Vrn-A1b} \text{Vrn-B1b} \text{Vrn-D1a}\): Yes

Triple Dirk F: \(\text{Vrn-A1b} \text{Vrn-B1b} \text{Vrn-D1b} \text{Vrn-D5a}\): Yes

Triple Dirk C: \(\text{Vrn-A1b} \text{Vrn-B1b} \text{Vrn-D1b} \text{Vrn-D5b}\): Yes Winter type.

**Vrn1**\{10014\}.  **Spring type**: \(\text{tv}\): G2528\{10014\}.

**vnr1**\{10014\}.  **Winter type**: \(\text{tv}\): DV92\{10014\}; G1777\{10014\}; G3116\{10014\}.  **ma**: \(\text{Vrn1}\) was completely linked to MADS-box genes *AP1* and *AGLG1*. *AP1* was considered a better candidate than *AGLG1* and differences between winter and spring genotypes appeared to be
related to differences in the promoter region of *API* [10014]; The involvement of *API* in vernalization response conditioned by *Vrn-I* was also reported in [10019].

**Vrn-2** [1398].
Orthologous series in chromosomes of homoeologous group 4. *Vrn-A*m2 was located in *T. monococcum* [279] on chromosome 5A*m* on the 4A*m* translocated region. *Vrn-A*m2 was mapped to the distally located *Xwg114*-5A - *Xwec87*-5A region [0312]. *Vrn-H2(sh/shg1)* occurs in barley chromosome 4H [1455] and is probably orthologous to *Vrn-A*m2 based on comparative maps [279,767]. *Vrn-2* is a zinc-finger/CCT domain transcription factor (*ZCCT1*) [10299], and repressor of flowering down-regulated by vernalization and short days [10301]. Reduction of *Vrn-2* transcripts in transgenic hexaploid winter wheat accelerates flowering [10299].


**Vrn-A2b** [279]. Spring habit, recessive in diploid wheat. dv: DV92[279]; PI 355517{10299}; PI 345242{10299}; PI 352475{10299}; PI 277137{10299}.
Contains a non-functional mutation in the CCT domain [10299].

**Vrn-A2e** [10299]. Spring habit, recessive in diploid wheat dv: PI 352484[10299]; PI 323437[10299]; PI 286068[10299]; PI 591871[10299]; PI 542474[10299]; PI 428175[10299]; PI 237659[10299]; PI 482129[10299]; PI 221329[10299]; PI 225164[10299]; PI 377662[10299]; PI 377648[10299]; PI 362610[10299]. Complete deletion of the *ZCCT1* gene [10299].

**Vrn3** [1398]. Orthologous series in chromosomes of homoeologous group 1 predicted from orthology with *Vrn-H3(Sh3)* in barley chromosome 1H [1455,1316]. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization [773].

**Vrn-B3** [10421]. [Vrn-4B[279],Vrn5,eHi{769,771,779}]. 7BS{768,769,771}. s: CS(Hope 7B) Vrn-D1a{768}. v2: Hope Vrn-A1a[1424]. ma: Vrn-B3 is completely linked to *TaFT* and 1 cM distal to *Xabc158*-7B on the region of 7BS proximal to the translocation with homoeologous group 5[10421].
The dominant *Vrn-B3* allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165) [10421]. Transformation of winter wheat Jagger with the dominant *Vrn-B3* significantly accelerated flowering [10421]. Different Hope seed sources were heterogeneous for this insertion [10421]. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B) [10421].

**Vrn-H3** [10421]. [Sh3]. ma: Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage [1455,1316].

**vrn-B3. v:** Chinese Spring *Vrn-D1* (GenBank DQ890162)[10421]. In both wheat and barley *Vrn-3* is completely linked with a flowering promoter gene homologous to *Arabidopsis FLOWERING LOCUS (FT)* [10421]. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat [10533].

**Vrn4** [279]. [Vrn5{771,769},Vrn-D5{10004}]. 5D{10002}.5DL{10004}. i: Triple Dirk F[10711]. s: CS (Hope 7B) VrnD1a{768}. v2: Gabo Vrn-B1a[1172]; ILA7/Vrn-A1a{10005}. bin: Centromeric region. ma: *Xgdm3-5D* - 11.5 & 4.5 cM - *Vrn4*{10004}; Located in a 1.8 cM interval flanked by markers *Xcjf78*-5D and *Xbarc205*-5D{10711}. Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh [1424] doubted the existence of *Vrn4*. Goncharov [10108] confirmed
the existence of \textit{Vrn4} but failed to confirm its location on chromosome 5D. References to additional studies are given in \{1424\).

\textit{Vrn4} was mapped on the centromeric region of 5D between markers. Incorrect TDF seed stocks generated confusion about \textit{Vrn-D4} existence \{10711\}. Eight land races with only \textit{Vrn4} were detected in \{10003\}; others combined \textit{Vrn4} with other \textit{Vrn} genes. Stelmakh \{1424\} doubted the existence of \textit{Vrn4}. Goncharov \{10108\} confirmed the existence of \textit{Vrn4} but failed to confirm its location on chromosome 5D.

\textit{Vrn-D5a} \{10004\}. \{\textit{Vrn-D5} \{10004\}, \textit{Vrn4} \{1172\}\}. 5D \{10002\}.5DL \{10004\}. \textit{i:} Triple Dirk F\{1172\}. \textit{v2:} Gabo Vrn-B1a\{1172\}; IL47 Vrn-A1a\{10005\}. \textit{ma:} \textit{Xgdm3-5D} - 11.5 & 4.5 cM - \textit{Vrn-D5a} \{10004\}.

Eight landraces with only \textit{Vrn-D5a} were detected in \{10003\}; others combined \textit{Vrn-D5a} with other \textit{Vrn} genes. Stelmakh \{1424\} doubted the existence of \textit{Vrn-D5a}. Goncharov \{10108\} confirmed the existence of \textit{Vrn-D5a} but failed to confirm its location on chromosome 5D. References to additional studies are given in \{1424\}.

QTL: Analysis in Courtot/CS \{0132\}. A QTL on chromosome 5BL was linked to \textit{Xgwm604-5B} (this QTL explained 11\% of the variance in flowering time) \{10075\}.

Three genes up-regulated by vernalization were cloned from \textit{T. monococcum} \{10531\}. These were \textit{VIN3} like genes similar to Arabidopsis \textit{VIN3}.

\textbf{Allelic variations at the \textit{Vrn-1} and \textit{Vrn-B3} loci in Chinese wheat cultivars are summarized in \{10617\}.}

Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization \{773\}.

\textbf{Stem-elongation in winter wheat:} In regions where wheat is used as a dual purpose crop for grazing and grain production a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).

In a Jagger/2174 RIL population, QTL for stem elongation included \textit{Qste.ocs-5A} (associated with the \textit{Vrn-A1} locus, \textit{Qste.ocs-1BL}, \textit{Qste.ocs-2D} (associated with the \textit{Ppd-D1} locus) and \textit{Qste.ocs-6A} \{1010\}. In 2007 the respective \(R^2\) values were 0.289, 0.155, 0.067 and 0.058. Jagger alleles on chromosome 5A, 1B and 6A promoted stem elongation whereas the allele on chromosome 2D had a delaying effect \{10722\}.

\section*{66. Restorers for Cytoplasmic Male Sterility}

\subsection*{66.1. Restorers for \textit{T. timopheevii} cytoplasm}

\textbf{\textit{Rf1}\{823\}.} 1A\{1224,1619,873\}.1AS\{868\}. \textit{v:} L22\{868\}; \textit{(T. timopheevii/Aegilops squarrosa)//3} Dirk\{1619\}. \textit{v2:} \textit{T. timopheevii/3} Marquis \textit{Rf2}\{823\}; \textit{R113} \textit{Rf4}\{873\}.

The second gene referred to as \textit{Rf4}\{1619\} in the last stock was located in chromosome 7D, but its relationship to \textit{Rf2} in \{823\} is unknown.

\textbf{\textit{Rf2}\{823\}.} 7D\{871\}. \textit{v:} \textit{T. timopheevii/3} Marquis \textit{Rf1}\{823\}.

\textbf{\textit{Rf3}\{1453\}.} 1B\{1453\}.1BS. \textit{v:} R18\{10222\}; R9034\{10222\}; \textit{T. spelta} var. \textit{duhamelianum}\{1453\}. \textit{ma:} \textit{Xcdo388-1B} - 1.2 cM - \textit{Xabc156-1B}\{9934\}; RFLP markers
Xcdo442-1B and Xbcd249-1B were found to be associated with Rf3 on 1BS{860}; Mapped as a QTL in the region Xbarc207-1BS - Xgwm131-1BL - Xbarc61-1BL in crosses R18/ND36 and R9034/ND36{10222}.

\( \text{Rf4} \{1619\}. \quad [\text{Rf2}\{1619\}] \cdot 6\text{B}\{1619,873\}.1\text{BS}\{868\}. \quad \text{v: } L3\{868\}; (\text{T. timopheevii}/\text{Aegilops squarrosa}) / 3 \text{ Canthatch } \text{Rf5}\{1619\}; \text{Rf1}\{873\}.\)  

\( \text{Rf6}\{865,859\}.6\text{AS} [\text{T6AL}.6\text{AS}-6U]\{865\}.6\text{BS} [\text{T6BL}.6\text{BS}-6U]\{865\}. \quad \text{tr: } \text{Line 2114}\{865\}; \text{Lines 040}-5; 061-1\{865\}; 061-4\{865\}. \quad \text{Genes } \text{Rfc3} \text{ in chromosome 6RL and } \text{Rfc4} \text{ in chromosome 4RL were reported in } \{225\}. \quad \text{Novel } Rf \text{ genes were identified on 5AL linked to } Xcdo786-5A \text{ and } XksuH1-5A\{860\}. \)

Minor restorer effects were associated with Xbarc330-5A in R18 and Xgdm130-7D in R9034 {10222}. The relationships of these QTL with previously located restorers in chromosomes 5A {860} and 7D (Rf2) are unknown.

66.2. Restorers for Aegilops longissima cytoplasm  
Vi{867}. 1B{870}.1BS{027}. \text{v: T. turgidum}{867}.  
Probably derived from a cv. Selkirk (\text{T. aestivum}) line with \text{Ae. cylindrica} cytoplasm {867}.

66.3. Restorers for photoperiod-sensitive Aegilops crassa cytoplasm  
Morai & Tsunewaki {1047} described photoperiod sensitive CMS caused by \text{Ae. crassa} cytoplasm in wheat cv. Norin 26. Almost complete sterility occurred when plants were grown in photoperiods of 15h or longer.

\( \text{Rfd1}\{1047\}.7\text{BL}\{1047\}. \quad \text{v: Chinese Spring}\{1047\}. \quad \text{A different system of restoration occurs in cv. Norin 61 where at least four chromosomes, 4A, 1D, 3D and 5D, appear to be involved } \{1046\}. \quad \text{Several Japanese wheats carry a similar or equally effective gene combination } \{0335\}. \)

67. Ribosomal RNA  
The 5S-Rrn-1 loci were physically mapped in 1AS, 1BS, and 1DS and the 5S-Rrn-2 loci were physically mapped in 5AS, 5BS and 5DS of Chinese Spring using deletion lines {1043}. Table 1 in {276} lists the chromosome or chromosome arm locations of rRNA loci in 12 Triticeae species.

67.1. 5S rRNA genes  
Within the Triticeae there are basically two sets of 5S rRNA loci. One set, identified by repetitive units 320-468 bp in length, is located on group 1 chromosomes. The other set, identified by repetitive units 469-500 bp in length, is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

\( \text{5S-Rrna-A1}. \quad [\text{5SDna-A1}\{295\}].1\text{AS}\{295,658\}. \quad \text{v: CS}\{1043\}. \quad \text{5S-Rrna-B1}. \quad [\text{5SDna-B1}\{295\}].1\text{BS}\{039,295\}. \quad \text{dv: T. monococcum.} \quad \text{ma: A PCR marker specific 5S-Rrna-B1} \quad \text{was developed}\{9974\}. \quad \text{5S-Rrna-D1}. \quad [\text{5SDna-D1}\{295\}].1\text{D}\{295,758\}.1\text{DS}\{295\}. \quad \text{v: CS}\{295,758\}. \quad \text{dv: Ae. tauschii}\{758\}. \quad \text{ma: A PCR marker specific for 5S-Rrna-D1} \quad \text{was developed in } \{9974\}. \quad \text{5S-Rrna-E1}. \quad [\text{5SDna-E1}\{960\}].1\text{E}\{1290\}. \quad \text{dv: L. elongatum}. \)
68. Seedling Leaf Chlorosis

sc{149}. 3BS{149}. s: CS°/Hope3B{149}. v: Hartog{149}; Suneca{149}; wheats with Sr2{149}.

Leaf chlorosis is affected by temperature and light and is enhanced by infection with pathogens. sc is completely linked with Pbc (pseudo-black chaff) and Sr2 (reaction to Puccinia graminis).

69. Segregation Distortion

See also, Gametocidal Genes.

Qsd.ksu-1D[9931]. 1DL[9931]. dv: Ae. tauschi var. meyeri acc. TA1691; Ae. tauschi var. typica acc. TA1704[9925]. ma: Association with Xcmwg706-1D[9931].

Qsd.ksu-3D[9931]. 3DS[9931]. dv: Ae. tauschi var. meyeri acc. TA1691; Ae. tauschi var. typica acc. TA1704[9925]. ma: Association with Xwgl773-3D[9931].


Qsd.ksu-5D.1[9931]. 5D[9931]. dv: Ae. tauschi var. meyeri acc. TA1691; Ae. tauschi var. typica acc. TA1704[9925]. ma: Association with Xcdc677-5D[9931].


Qsd.ksu-5D.3[9931]. 5DL[9931]. dv: Ae. tauschi var. meyeri acc. TA1691; Ae. tauschi var. typica acc. TA1704[9925]. ma: Association with Xgkl439-7D (syonym 'Xtag439-7D')[9931].

70. Soft Glumes

Sog{10555}. dv: T. monococcum ssp. boeoticum ID49{10555}.
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sog{10555}. 2AS{10555}. dv: T. monococcum ssp. monococcum var. sinskajae (syn. aegilopoides) UD69{10555}. ma: Co-segregation with AFLP loci Xe4232041 and Xe373311(10555). sog was considered to be an homologue of Tg1 and Tg2. See Tenaceous glumes.

71. Sterol Esterification in Kernels - Synthesis of b-Sitosterol Esters
Two sterol-ester phenotypes, p-L (palmitate + linoleate) and L (linoleate) are inherited as alleles at a single locus.

Pln{428}. [ P-L{428}]. 7DS{1476}. v: Aradi{428}; Aragon 03{428}.
pln{428}. [ L{428}].  L{428}. v: Mara{428}; Pane 247{428}.

72. Stem solidness
Solid stem, caused by increased pith in normally hollow stem regions, is associated with resistance to wheat stem sawfly, Cephus cinctus. Solid stem confers resistance to wheat stem sawfly. See also Reaction to Cephus spp.

Qsst.msub-3BL. 3BL{10206}. v: Rampart PI 59388{10206}. ma: Linked to microsatellite markers Xgwm247-3B, Xgwm340-3B, and Xgwm547-3B. These markers explained 76% of the total variation for stem solidness in Rampart/Jerry{10206}.

Qsst.msub-3DL. [Qss.msub-3DL{10395}]. 3DL{10395}. Associated with Xgwm645-3DL (R²=0.31), Xwmc656-3DL (R²=0.1), and Xcfd9-3DL (R²=0.13) {10395}. This gene acted as an enhancer of Qsst.msub-3BL {10395}.

Qsf.spa-3B{10351}. tv: Kyle*2/Biodur (solid stem)//Kofa (hollow) DH population: Qsf.spa-3B was located to a 21.3cM interval flanked by Xgwm247-3B and Xgwm114-3B {10351}. Mapped as a single gene, Xgwm247-3B - 6.9cM - Qsf.spa-3B - 14.4cM - Xgwm114-3B {10351}. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents {10351}.

73. Temperature-Sensitive Winter Variegation
This phenotype involves reduced vigour and chlorotic patches on leaves of certain genotypes in Ae. umbellulata cytoplasm when grown at low temperatures {1596}.

Vgw. Variegation is dominant {1596}. [Vg{1021}]. 5BL{1021}. v: Bersee{1596}; Cappelle-Desprez{1596}; Hobbit Sib{1596}; Mara{1596}.
vgw{1021}. v: Besostaya I{1596}; CS{1596}; Poros{1596}; Sava{1596}; T. spelta{1596}.

74. Tenacious Glumes
Tg1{1240}. Derived from Ae. tauschii. Dominant. [Tg{1240}]. 2DS{1240}. v: Synthetic ABD wheats{652}. ma: Placed in a 12 cM interval between Xwmc112-2D and Xbarc168-2D{10497}.

Tg2{0046}. Derived from T. dicoccoides 2BS{0046}. ma: Tg2 is associated with Xrsq805(Embp)-2B and Xpsr899-2B{0046}.

Tg1 and Tg2 were considered to be homologues of sog for soft glumes in T. monococcum. See Soft glumes.
A QTL analysis of the relationship of glume tenacity (Gt) with threshability (Ft) and the size of the glume base scar (Gba) after glume detachment in two crosses, viz. the ITMI population
and CS*/CS (Ae. tauschii 2D), was undertaken \{10497\}. In the first cross \textit{QF}_{orst}-2D.1 and \textit{QG}_{orst}-2D.1 were closely associated with \textit{Xgwm261}-2D, and \textit{XF}_{orst}-2D.2 and \textit{XG}_{orst}-2D were associated with \textit{Xgwm455}-2D, in the second population only the first pair along with \textit{Xba}_{orst}-2D were detected; these appeared to correspond with \textit{Tg1} \{10497\}.

75. Tiller Inhibition

\textit{tin1} \{1212\}. Restricted tiller number is recessive \{1212\} [\textit{Tin} \{1212\}]. 
\textit{v}: Israel Uniculm 494 \{1212\}; Banks + \textit{tin} \{10193\}; Oligoculm 390 \{10193\}; Uniculm 492 \{10193\}. 
\textit{ma}: \textit{Xpsp2999(Glu3)}-1A - 3.9 cM - \textit{tin1/Xgwm136}-1A - 2.4 cM - \textit{Xwhs179}-1A \{10193\}; the 350 bp allele of \textit{Xgwm136}-1A was diagnostic of \textit{tin1} \{10193\}.

\textit{tin2} \{1212\}. Tiller-reducing affect of this allele was dominant \{9909\}. [\textit{Tin} \{9909\}].

\textit{tin3} \{10329\}. 3A^mL \{10329\}. \textit{dv}: \textit{T. monococcum} TA4443 = TA4342-96 mutant \{10329\}. 
\textit{ma}: \textit{Xbcd131/Xbcd1431}-3A - 9.6 cM - \textit{tin3/Xpsr1205}-3A - 4.7 cM - \textit{Xcfa2076}-3A \{10329\}.

A QTL of large effect on spike number per plant in a DH population of Fukuho-Komugi/Oligoculm mapping to the \textit{Hg} - \textit{Xpsp2999(Glu3)}-1A region \{10218\} probably corresponds to \textit{Tin1}.

76. Uniculm Stunt

Stunting is favoured by a combination of long days and low night temperatures \{581\}. Caused by duplicate recessive genes, \textit{us1} and \textit{us2}, located in chromosomes 4A and 5B, respectively \{200\}. 
Genotypes: Normal \textit{v}: \textit{Us1 us2}: Alfa \{581\}; Jaral \{581\}. Normal \textit{v}: \textit{us1 Us2}: Mabruk \{581\}. Stunted \textit{v}: \textit{us1 us2}: Line 492 \{581\}.

77. Variegated Red Grain Colour

\textit{vg} \{498\}. \textit{v}: Line 10859 \{498\}. 
\textit{vgvg} genotypes in Line 10859 are variegated. The \textit{Vg/vg} locus was independent of the single red gene locus in Line 10859. In a cross to Selkirk (\textit{R-A1b, R-B1b, R-D1b}) \textit{vgvg} was expressed only in plants with one \textit{R} gene \{498\}. Variegated red pericarp was also studied in crosses of cv. Supreme. In this case, two red colour genes were present \{0136\}.

78. Yield and Yield Components

78.1. Grain weight

78.1.1. 50-grain weight

\textit{QFgw.ocs-4A.1} \{0047\}. 4A \{0047\}. \textit{v}: CS/CS(Kanto107 4A) mapping population \{0047\}. 
\textit{ma}: Associated with \textit{Xbcd265-4A} and \textit{Xbcd1738-4A} \{0047\}.

78.1.2. 1000-grain weight

QTL: Two QTLs for 1,000-kernel weight were assigned to chromosome 3A in RSLs from Cheyenne\*7/Wichita 3A \{0025\}. QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL in a RIL population from RS111/CS \{0236\}. Eight QTLs for 1,000-kernel weight (54 % of the variation) were mapped in Forno/Oberkulmer spelt \{0280\}. 

\textit{A QTL of large effect on spike number per plant in a DH population of Fukuho-Komugi/Oligoculm mapping to the \textit{Hg} - \textit{Xpsp2999(Glu3)}-1A region} \{10218\} probably corresponds to \textit{Tin1}.
55  M O R P H O L O G I C A L  A N D  P H Y S I O L O G I C A L  T R A I T S

QGw1.cssu-1A{0165}.  1AS{0165}.  v:  RS111/CS mapping population{0165}.  ma:  Associated with Xwmc333-1A{0165}.
QGwt.crc-3D{10287}.  3D{10287}.  ma:  Linked to Xgwms341-3D - Xwmc552-3D (LOD 4.3) in RL4452/AC Domain{10287}.
QGwt.crc-4A{10287}.  4A{10287}.  ma:  Linked to Xgwms494-Xgwms162 (LOD 6.7) in RL4452/AC Domain{10287}.
QGwt.crc-6D{10287}.  6D{10287}.  ma:  Linked to Xgwms325-6D - Xgwms55-6D (LOD 3.9) in RL4452/AC Domain{10287}.
QTgw.ipk-5A{0255}.  5AL{0255}.  v:  Opata/W-7984 (ITMI) RI mapping population{0255};  The higher yielding allele was contributed by W-7984{0255}.  ma:  Associated with Xfba351-5A and Xcdo1312-5A{0255}.
QTkwt.unl-3A.1{10044}.  3AS{10044}.  v:  Cheyenne/Cheyenne(Wichita 3A) RI mapping population{10044};  a higher kernel weight of 0.27% was contributed by Cheyenne and the QTL explained 12.7% of the phenotypic variation{10044}.  ma:  Associated with Xbarc12-3A and Xtam55-3A{10044}.
QTwt.crc-1B{10287}.  1B{10287}.  ma:  Linked to Xgwms374.1-1B (LOD 3.9) in RL4452/AC Domain{10287}.
QTwt.crc-1D{10287}.  1D{10287}.  ma:  Linked to Xgdm126-1D (LOD 5.8) in RL4452/AC Domain{10287}.
QTwt.crc-2D{10287}.  2D{10287}.  ma:  Linked to Xgwms349-2D - Xbarc59-2D (LOD 5.2) in RL4452/AC Domain{10287}.
QTwt.crc-3B{10287}.  3B{10287}.  ma:  Linked to Xwmc625-3B - Xbarc164-3B (LOD 15.4) in RL4452/AC Domain{10287}.
QTwt.crc-3D{10287}.  3D{10287}.  ma:  Linked to Xbarc71-3D (LOD 5.2) in RL4452/AC Domain{10287}.
QTwt.crc-5D{10287}.  5D{10287}.  ma:  Linked to Xgdm63-5D - Xwmc765-5D (LOD 5.3) in RL4452/AC Domain{10287}.

78.1.3.  Test weight
QTwt.crc-1B{10287}.  1B{10287}.  ma:  Linked to Xgwms374.1-1B (LOD 3.9) in RL4452/AC Domain{10287}.
QTwt.crc-1D{10287}.  1D{10287}.  ma:  Linked to Xgdm126-1D (LOD 5.8) in RL4452/AC Domain{10287}.
QTwt.crc-2D{10287}.  2D{10287}.  ma:  Linked to Xgwms349-2D - Xbarc59-2D (LOD 5.2) in RL4452/AC Domain{10287}.
QTwt.crc-3B{10287}.  3B{10287}.  ma:  Linked to Xwmc625-3B - Xbarc164-3B (LOD 15.4) in RL4452/AC Domain{10287}.
QTwt.crc-3D{10287}.  3D{10287}.  ma:  Linked to Xbarc71-3D (LOD 5.2) in RL4452/AC Domain{10287}.

78.2.  Grain weight/ear
QGwe.ocs-4A.1{0047}.  4AS{0047}.  v:  CS/CS(Kanto107 4A) mapping population{0047}.  ma:  Associated with Xbcd1738-4A{0047}.
QGwe.ipk-2D{0255}.  2DS{0255}.  v:  Opata/W-7984 (ITMI) RI mapping population{0255};  Higher grain weight was contributed by Opata{0255}.  ma:  Associated with Xcdo1379-2D and Xbcd1970-2D{0255}.
QGwe.ipk-4A{0255}.  4AL{0255}.  v:  Opata/W-7984 (ITMI) RI mapping population{0255};  Higher grain weight was contributed by Opata{0255}.  ma:  Associated with Xwmc549-4A, Xabg390-4A and Xbcd1670-4A{0255}.
QGwe.ipk-4A coincided with QTLs for height (QHt.ipk-4A), spike length (XEl.ipk-4A) and grain number (QGnu.ipk-4A) {0255}.

78.3. Grain number per spike
QGnu.ipk-4A{0255}.  4AL{0255}.  v:  Opata/W-7984 (ITMI) RI mapping population{0255};  Higher grain number was contributed by Opata{0255}.  ma:  Associated with Xwmc549-4A, Xabg390-4A and Xbcd1670-4A{0255}.
Morphological and Physiological Traits

QGnu.ipk-4A coincides with QTL for height (QHt.ipk-4A), spike length (XE1.ipk-4A) and grain weight per ear (QGwe.ipk-4A) [0255].

QKps.unl-3A.1 [10044]. v: Cheyenne/Cheyenne(Wichita 3A) RI mapping population [10044]; a higher kernel number of 0.3 kernels was contributed by Wichita and the QTL explained 15.5% of the phenotypic variation [10044]. The QTL coincided with QTLs for grain yield, kernel number per square metre and 1000-kernel weight [10044]. ma: Associated with Xbarc12-3A [10044].

QKps.unl-3A.2 [10044]. v: Cheyenne/Cheyenne(Wichita 3A) RI mapping population [10044]; a higher kernel number of 0.3 kernels was contributed by Cheyenne and the QTL explained 9.5% of the phenotypic variation [10044]. ma: Associated with Xbcd141-3A [10044].

QTL: Three QTLs for kernel number per spike were assigned to chromosome 3A in RSLs from Cheyenne 7/Wichita [0025].

78.4. Grain yield

Non-glaucous (virescent) lines from a Shamrock/Shango DH population had higher yields than glaucous sibs [10543]; see Glaucousness, subsection Epistatic inhibitors of glaucousness.

QGyld.unl-3A.1 [10044]. 3AS [10044]. v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population [10044]; a higher grain yield of 32 kg/ha was contributed by Wichita and the QTL explained 6.6% of the phenotypic variation [10044]. The QTL coincided with QTLs for kernel number per square metre, 1000-kernel weight and kernels per spike [10044].

QGyld.unl-3A.2 [10044]. 3A [10044]. v: Cheyenne/Cheyenne (Wichita 3A) RI mapping population [10044]; a higher grain yield of 82 kg/ha was contributed by Wichita and the QTL explained 28.1% of the phenotypic variation [10044]. The QTL coincided with a QTL for kernel number per square metre [10044]. ma: Associated with Xbarc67-3A and Xbcd366-3A [10044].


QYld.inra-7D [10071]. v: Renan/Recital [10071]. ma: Xcdf69-7D (R^2=3.7-15.7%).

QYld.ndsu-5B [10161]. [QGy.ndsu-5B [10161]]. v: LDN (DIC5B)/LCN, contributed by LDN [10161]. ma: Mapped to the Xbcd1030-5B - Xgwm604-5B interval [10161].


Grain yield under drought stress

QTL: Dharwar Dry (drought tolerant)/Sitta: SSR locus Xwmc89-4AL was the marker most closely associated with QTL for grain yield, grain fill rate, spike density, grains/m², biomass and drought susceptibility index covering a genetic distance of 7.7 cM [10488].

78.5. Spikelet number/ear


78.6. Spike number per square metre
78.7. Spike length

\textbf{QEl.ipk-1B} [0255]. 1BL [0255]. \textit{v}: Opata/W-7984 (ITMI) RI mapping population [0255]; Longer ear was contributed by Opata [0255]. \textit{ma}: Associated with Xbcd388-1B and Xw605-1B [0255].

\textbf{QEl.ipk-4A} [0255]. 4AL [0255]. \textit{v}: Opata/W-7984 (ITMI) RI mapping population [0255]; Longer ear was contributed by Opata [0255]. \textit{ma}: Associated with Xmg549-4A, Xabg390-4A and Xbcd1670-4A [0255].

This QTL is likely to be a pleiotropic effect of the gene underlying the height QTL, \textit{QHt.ipk-4A} [0255].

\textbf{QEl.ipk-5A} [0255]. 5AL [0255]. \textit{v}: Opata/W-7984 (ITMI) RI mapping population [0255]; Longer ear was contributed by W-7984 [0255]. \textit{ma}: Associated with Xmg522-5A [0255].

QTL: Five QTLs for spike length were detected in Courtot/Chinese Spring [0114] but only one on chromosome arm 5AL was consistent for at least two years.

78.8. Tiller number/plant

\textbf{QTn.ocs-4A.1} [0047]. 4AS [0047]. \textit{v}: CS/CS(Kanto107 4A) mapping population [0047]. \textit{ma}: Associated with Xpsr163-4A [0047].

78.9. Kernel number per square metre

\textbf{QKpsm.unl-3A.1} [10044]. 3AS [10044]. \textit{v}: Cheyenne/Cheyenne(Wichita 3A) RI mapping population [10044]; higher kernel number (170 kernels) was contributed by Wichita and the QTL explained 14.6% of the phenotypic variation [10044]; The QTL coincided with a QTL for grain yield [10044]. \textit{ma}: Associated with Xbarc12-3A [10044].


78.10. Grain volume weight

\textbf{QGvwt.unl-3A.1} [10044]. 3A [10044]. \textit{v}: Cheyenne/Cheyenne (Wichita 3A) RI mapping population [10044]; higher grain volume weight (+23 kg/hL) was contributed by Wichita and the QTL explained 43.1% of the phenotypic variation [10044]; the QTL coincided with a QTL for spikes per square metre [10044]. \textit{ma}: Associated with Xbcd1380-3A [10044].

79. Yellow Berry Tolerance

QTL: A QTL for yellow berry tolerance, contributed by RS111, was associated with Xgwm190-5D and Xgwm174-5D in a RIL population from RS111/CS [0237]. A tolerance QTL contributed by CS, the susceptible parent, was detected on 6B [0237].
80. Proteins

80.1. Grain protein content

Thirteen QTLs for grain protein content were identified in a RI population from the cross WL711 (low protein content) and PH132 (high grain content) \{10055\}. The QTLs that were identified using more than one method or in more than one environment are listed below. Also listed is a QTL that was identified in the mean over the four environments and was therefore deemed important \{10055\}.

\textbf{Gpc-B1a.} \[QGpc.ndsu-6Ba\{623\}].

This allele, fixed in cultivated durum, is a non-functional frame-shift mutation \{10438\}. A similar non-functional allele, or a complete deletion of \textit{Gpc-B1}, is fixed in hexaploid wheat \{10438\}.

\textbf{Gpc-B1b} \{10296\}. \[QGpc.ndsu-6Bb\{623,10071\}, Gpc-6B1\{10299\}\]. 6BS. \textbf{ma:} Mapped to a 0.3 cM interval flanked by \textit{Xucw79-6B} and \textit{Xucw71-6B} \{10229\}; \textit{Xodo365-6B} - 1.5 cM - \textit{Gpc-B1} - 1.2 cM - \textit{Xucw67-6B} \{10296\}; A high-throughput codominant marker, \textit{Xuhw89-6B}, was then mapped less than 0.1 cM from \textit{Gpc-B1} \{10297\}.

\textit{Gpc-B1b}, the functional allele \{10438\} in \textit{T. dicoccoides}, affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity \{10298\}.

\textbf{Gpc-B1} is a NAC transcription factor designated \textit{Nam-B1} \{10438\}. A paralogous copy of this gene is present in homologous group 2 (\textit{Nam2}).

\textbf{Pro1} \{777\}. 5DL\{777\}. \textbf{s:} CS\(^{+}\)6/Hope 5D\{777\}.

May be identical to \textit{Vrn-D1}.

\textbf{Pro2} \{777\}. 5DS\{777\}. \textbf{s:} CS\(^{+}\)6/Hope 5D\{777\}.

\textbf{QGpc.ccsu-2B.1} \{10055\}. 2BL\{10055\}. \textbf{v:} WL711/PH132 RI mapping population \{10055\}; higher protein content was contributed by PH132 and the QTL explained 13.4\% of the phenotypic variation \{10055\}. \textbf{ma:} Associated with \textit{Xgwm1249-2B} \{10055\}.

\textbf{QGpc.ccsu-2D.1} \{0015,10055\}. 2DL\{0015, 10055\}. \textbf{v:} WL711/PH132 RI mapping population \{0015,10055\}; higher protein content was contributed by PH132 and the QTL explained 19 \% \{0015\} and 14 \% \{10055\} of the phenotypic variation. \textbf{ma:} Associated with \textit{Xgwm1264-2D} \{10055\}.

\textbf{QGpc.ccsu-3D.1} \{10055\}. 3DS\{10055\}. \textbf{v:} WL711/PH132 RI mapping population \{10055\}; higher protein content was contributed by PH132 and the QTL explained 16.3 \% of the phenotypic variation \{10055\}. \textbf{ma:} Associated with \textit{Xgwm456-3D} \{10055\}.

\textbf{QGpc.ccsu-3D.2} \{10055\}. 3DS\{10055\}. \textbf{v:} WL711/PH132 RI mapping population \{10055\}; higher protein content was contributed by PH132 and the QTL explained 14 \% of the phenotypic variation \{10055\}. \textbf{ma:} Associated with \textit{Xgwm892-3D} \{10055\}.

\textbf{QGpc.ccsu-7A.1} \{10055\}. 7AS\{10055\}. \textbf{v:} WL711/PH132 RI mapping population \{10055\}; higher protein content was contributed by PH132 and the QTL explained 32.4 \% of the phenotypic variation \{10055\}. \textbf{ma:} Associated with \textit{Xgwm1171-7A} \{10055\}.

\textbf{QGpc.ipk.7B} \{10628\}. \textbf{v:} F26-70\{10628\}; Closely associated with \textit{Ppd-B2} \{10628\}. \textbf{su:} Favorit(F26-70 7B)\{10628\}.

See response to Photoperiod.

\textbf{QGpc.ndsu-5B.1} \{10161\}. 5B\{10161\}. \textbf{v:} LDN (DIC5B)/LDN, contributed by DIC5B\{10161\}. \textbf{ma:} Nearest marker, \textit{Xgwm604-5B} \{10161\}.

\textbf{QGpc.ndsu-5B.2} \{10161\}. 5B\{10161\}. \textbf{v:} LDN (DIC5B)/LDN, contributed by DIC5B\{10161\}. \textbf{ma:} Nearest marker, \textit{Xabc310-5B} \{10161\}.

\textbf{QGpc.ndsu-5B.3} \{10161\}. 5B\{10161\}. \textbf{v:} LDN (DIC5B)/LDN, contributed by DIC5B\{10161\}. \textbf{ma:} Nearest marker, \textit{Xwg909-5B} \{10161\}.
80.2.1. Acid phosphatase

**Acph-A1** [504]. [Acph2[516],Acph3[516],Acph-B1[936]]. 4AS[504,516]. v: CS.

**Acph-B1** [504]. [Acph4[516],Acph8[516],Acph-A1[936]]. 4BL[504,516]. v: CS.

**Acph-D1**. [Acph5[516],Acph6[516]]. 4DL[504,516]. v: CS.

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QTLs for grain protein content were detected on chromosome arms 6AS (associated AFLP marker, XE38M60200) and 1BL (associated RFLP marker, Xcd01188-1B) in Courtot/Chinese Spring {0141}.

Nine QTLs (51% of the variation) were mapped in cross 'Forno'/ 'Oberkulmer' spelt {0280}. A QTL for grain and flour protein content, contributed by CS, was associated with Xtri-1D/centromere in a RSL population from the cross Cheyenne (high quality wheat)/CS {0251}.

For QTLs conferring grain protein content detected in the cross Renan/Recital {10071}, only QTLs stable over at least 4 of 6 locations are presented. Renen contributed the four alleles for high grain protein content.

Ning 7840/Clark: RILs: QTLs from Ning 7840 were detected on chromosomes 3AS (Xwmc749-3AS - Xgwm369-3AS; R²=0.09-0.11) and 4B (Xgwm368-4B - Xwmc617-4B, R²=0.08-0.11) {10702}.

Durum: In 3BIL-85 (high protein introgressed from T. dicoccoides/Latino QTL were detected in chromosomes 2AS (associated with Xcfa2164-2A, R²=17%), 6AS (Xp39M37250-6A, R²=17%) and 7BL (Xgwm577-7B, R²=9%) {10338}.

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80.2. Enzymes

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Aph-D2 \{10309,10407\}. \(\text{Aph-D2}_{100}\) and \(\text{Aph-D2}_{95}\) alleles distinguished accessions of \textit{Ae. tauschii} ssp. \textit{tauschii} and \textit{strangulata}, respectively\{10309\}. \(\text{Aph}\): \textit{Ae. tauschii}\{10407\}. \(\text{ma}\): Cent ... \(\text{Aph-D2} - 4\text{ cM} - \text{Xgwm157} - 2\text{D}(10309)\).

\(\text{Aph-H1}\)\{1153\}. \(\text{ad}\): CS/Betzes.

\(\text{Aph-M'}1\)\{237\}. \(\text{Aph-M'}1\{985\} - 4\text{M'}\{237\}. \(\text{tr}\): H-93-33\{984\}.

\(\text{Aph-R1}\). 7R\{1457\}.7RS\{506\}. \(\text{ad}\): CS/Imperial.

Acid phosphatase gene loci were reported for 7RL in \textit{S. cereale} \{1251\}, chromosomes L1 (= 7Ag') and L4 (= 4Ag') of \textit{Thin. intermedium} \{361\}, and chromosome E of \textit{Ae. umbellulata} \{69\}. Two loci on 7R were separated by 25 +or- 5.2cM \{1354\}. Wehling \{1559\} identified four acid phosphatase loci in \textit{S. cereale}, three of which were located in 7R.

\(\text{Aph-S'}1\)\{1140\}. \(\text{Aph-S'}1\{1140\} - 4\text{S'}\{1140\}. \(\text{ad}\): CS/T. searsii.

80.2.2. Alcohol dehydrogenase (Aliphatic)

\textit{Adh-A1} \{502\}. \(\text{Adh-A1}_{502}\); \textit{Adh-B1} \{504\}. \(\text{Adh-B1}_{504}\) - 4A\{502\}.4AL\{504,516\}. \(\text{v}\): CS.

\textit{Adh-B1} \{501,502\}. \(\text{Adh-B1}_{501}\); \textit{Adh-B1} \{504\}. \(\text{Adh-B1}_{504}\) - 4B\{502\}.4BS\{504,516\}. \(\text{v}\): CS.

\textit{Adh-B1a} \{1442\}. \(\text{Adh-B1a}_{501}\); \textit{Adh-B1a} \{1442\} - 4A\{502\}.4AL\{504,516\}. \(\text{v}\): CS. Malavika\{1442\}.

\textit{Adh-B1b} \{1442\}. \(\text{Adh-B1b}_{501}\); \textit{Adh-B1b} \{1442\} - 4B\{502\}.4BS\{504,516\}. \(\text{v}\): CS. Rageni derivative\{1443\}.

\textit{Adh-B1b} was the only variant \textit{Adh-1} allele detected in study of a large number of \textit{T. aestivum} and \textit{T. turdium} accessions \{503\}.

\textit{Adh-C1} \{1278\}. \(\text{G}\{1278\} - 4\text{C}\{1278\}. \(\text{ad}\): \textit{T. aestivum} cv. Alcedo / \textit{Ae. caudata} line G.

\textit{Adh-D1} \{504\}. \(\text{Adh-D1}_{504}\) - 4D\{502\}.4DS\{504,516\}. \(\text{v}\): CS. \(\text{ma}\): \textit{Adh-D1} \{\textit{Adh1}, \textit{Adh2}\} - 4D\{502\}.4DS\{504,516\}. \(\text{Aph}\): \textit{T. aestivum} \{361\}. \(\text{v}\): CS. \(\text{Adh-D1}\) \{1443\} - 4D\{502\}.4DS\{504,516\}. \(\text{v}\): CS. PI 226951\{501\}; \textit{Caribo/Th. intermedium}; Malavika\{1442\}.

\textit{Adh-D1} \{504\} - 4D\{502\}.4DS\{504,516\}. \(\text{v}\): CS. \(\text{ma}\): \textit{Adh-D1} \{\textit{Adh1}, \textit{Adh2}\} - 4D\{502\}.4DS\{504,516\}. \(\text{Adh-D1}\) \{1443\} - 4D\{502\}.4DS\{504,516\}. \(\text{v}\): CS. PI 226951\{501\}; \textit{Caribo/Th. intermedium}; Malavika\{1442\}.

\textit{Adh-E1} \{518\}. \(\text{Adh-E1}_{518}\) - 4ES\{518\}. \(\text{ad}\): CS/\textit{E. elongata}.

\textit{Adh-H1} \{520\}. \(\text{Adh-H1}_{520}\) - 4H\{520\}. \(\text{ad}\): CS/Betzes.

\textit{Adh-M'}1 \{984\}. \(\text{Adh-M'}1\{984\} - 4\text{M'}\{984\}. \(\text{v}\): H-93-33.

\textit{Adh-R1} \{1457\}. \(\text{Adh-R1}\{1457\} - 4\text{R}\{582,1457\}.4RS\{506\}. \(\text{ad}\): CS/Imperial\{1457,506\}; FEC28/Petkus\{404\}; Holdfast/King II\{582\}.

\textit{Adh-V1} \{1026,242\}. \(\text{Adh-V1}_{1026}\). \(\text{v}\): CS/D. villosum.

Three \textit{Adh} genes were identified in \textit{Hordeum vulgare} and \textit{H. spontaneum} \{144,490,493,520\}. Two of these were tightly linked at the \textit{Adh-H1} locus \{144\}. The third gene was tentatively located in 5H \{490\}.

A low-level of aliphatic alcohol dehydrogenase activity is commonly observed on zymograms in the absence of added substrate \{513\}; this may account for the observation of wheat lactate dehydrogenase that was reported in \{1465\}.

The gene series formerly designated \textit{Adh-2} and \textit{Adh-3} appear under Aromatic Alcohol Dehydrogenase

80.2.3. Aminopeptidase

\textit{Amp-A1} \{504\}. \(\text{Amp-A1}_{504}\); \textit{Amp-A1a} \{1533\}.

\textit{Amp-A1b} \{504\}; \textit{Vitka}\{1533\}. \(\text{v}\): CS.

\textit{Amp-B1} \{504\}. \(\text{Amp-B1}_{504}\); \textit{Amp-B1a} \{1533\}.

\textit{Amp-B1a} \{1533\}. \(\text{v}\): CS/\textit{D. villosum}.
**Proteins**

**Amp-B1b** v: Iskra{1533}.

**Amp-B1c**{703,1244}. Null allele v: *T. spelta* IPSR 1220017{703}; Sivalocho M.A{1244}.

**Amp-C1**{1278}. 6D{1278}. ad: Alcedo/Ae. caudata line D.

**Amp-D1{504}**. 6DS{504,516}. v: CS.

**Amp-D1α**{703}. v: CS.

**Amp-D1β**{703}. v: Sears’ Synthetic IPSR1190903.

**Amp-Ag1**{1575}. 6Ag{1575}. ad, su: Rescue/Th. elongatum.

**Amp-Ag1**{703}. 6Ag{703}. ad: Vilmorin 27/Th. intermedium.

**Amp-E1**{518}. 6E{518}. ad: CS/E. elongata.

**Amp-H1**{520}. 6H{520}. ad: CS/Betzles.

**Amp-R1**{1457}. 6R{1457,1280}. ad: CS/Imperial{1457}; Holdfast/King II{1280}.

**Amp-A2**{703}. 4AL{703}. v: CS.

**Amp-A2α**{703}. v: CS.

**Amp-A2β**{703}. v: T. spelta IPSR 122017.

**Amp-B2**{703}. 4BS{703}. v: CS.

**Amp-B2α**{703}. v: CS.

**Amp-B2β**{703}. v: Timstein.

**Amp-B2c**{703}. v: Hope.

**Amp-D2**{703}. 4DS{703}. v: CS.

**Amp-D2α**{703}. v: CS.

**Amp-D2β**{703}. v: Sears’ Synthetic IPSR 1190903.

**Amp-D2c**{703}. v: Bersee.

**Amp-Ag2**{703}. 4Ag{703}. ad: Vilmorin27/Th. intermedium.

**Amp-E2**{703}. 4E{703}. ad: CS/E. elongata.

**Amp-H2**{703}. 4H{703}. ad: CS/Betzles.

**Amp-H2β**{703}. 4Hβ{703}. ad: CS/H. chilense.

**Amp-J2**{703}. 4J{703}. ad: CS/Th. junceum.

**Amp-M2**{235}. 4Mβ{235}. su: H-93-33{235}.

**Amp-R2**{703}. 4R{703}. 4RS{702,093}. ad: CS/Imperial.

**Amp-S2**{703}. 4SL{703}. ad: CS/Ae. sharonensis{180}. tr: 4DS.4DL-4S1L{660}.

**Amp-V2**{703}. 4V{703}. ad: CS/D. villosum.

**Amp-A3**{703}. 7AS{703}. v: CS.

**Amp-A3α**{703}. v: CS.

**Amp-A3β**{703}. v: Timstein.

**Amp-H3**{703}. 7H{703}. ad: CS/Betzles.

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### 80.2. Alpha-amylase

**a-Amy-A1**{007}. [Amy6A{1082}]. 6AL{412,1082}. v: CS.

**a-Amy-A1α**{007}. [Amy 6A1{1084}]. v: CS.

**a-Amy-A1β**{007}. v: Bezostaya 1; Kavkaz.

**a-Amy-A1γ**{007}. [Amy 6A1m{1084}]. v: Aka.

**a-Amy-B1**{007}. [Amy6B{1082}]. 6BL{412,1082}. v: CS.

**a-Amy-B1α**{007}. [Amy 4{1084}, Amy 6B1{1084}, Amy 6B2w{1084}]. v: CS{007}; Rare.

**a-Amy-B1β**{007}. [Amy 4m{1084}, Amy 6B1m{1084}, Amy 6B2{1084}]. v: Mara{007}.

**a-Amy-B1ε**{007}. [Amy 4{1084}, Amy 6B1ε{1084}, Amy 6B2w{1084}]. v: Sava{007}; Rare.

**a-Amy-B1d**{007}. [Amy 4m{1084}, Amy 6B1d{1084}, Amy 6B2w{1084}]. v: Sicco{007}; Rare.

**a-Amy-B1e**{007}. [Amy 4m{1084}, Amy 6B1e{1084}, Amy 6B2w{1084}]. v: Cappelle-Desprez{007}.
Two types of nomenclature were assigned to the genes encoding the a-AMY-1 isozymes. In one, allelic states were defined for individual isozymes [1084] whereas in the other, several isozymes were considered to be the products of compound loci [007,412]. This listing shows the 'alleles' described in [007] which are assumed in [007] to be synonymous with the a-AMY-1 through a-AMY-B1h nomenclature. Amy 4 and Amy 4' are unmarked alternatives [1084] which appear to be identical to zymogram bands [bands 9 and 9b [007]] forming part of the a-AMY-B1 phenotype. Amy 6B1 [with forms Amy 6B1', and Amy 6B1''] considered to be mutually exclusive [1084] and Amy 6B2 [with forms Amy 62 and Amy 6B2' [1084]] describe further aspects of a-AMY-B1 [007]. See a-Amy1 below for further consideration of Amy 6B2 [1084].

**a-Amy-D1** [007]. [Amy6D1{1082}]. 6DL{412,1082}. v: CS.

**a-Amy-D1a** [007]. [Amy6D1{1084},Amy 6D2{1084}]. v: CS.

**a-Amy-D1b** [007]. [Amy6D1{1084},Amy 6D2{1084}]. v: Prelude{1082}; Capelle-Desprez{007}.

**a-Amy-D1c.** [Amy6D1''{1084},Amy 6D2{1084}]. v: T. spelta var. duhamelianum.

**a-Amy-Ag1** [374]. 6Ag'1[374]. ad: Vilmorin 27/Th. intermedium.


**a-Amy-H1.** [a-Amy1{146}]. 6H[146,1051]. ad: CS/Betzes.

**a-Amy-R1** [013]. 6RL[013]. su,ad: CS/Imperial; CS/King II; Holdfast/King II.

**a-Amy-R1** [013]. 6R[L1013]. ad: CS/S. montanum.


It was estimated [902] that there are two a-AMY-1 genes in 6A and five or six in both 6B and 6D, and three or four a-AMY-2 genes at each of the 7A, 7B, and 7D loci.

**a-Amy-A2** [007]. [Amy7A{1082}]. 7AL{412,1082}. v: CS.

**a-Amy-B2** [007]. [Amy7B{1082}]. 7BL{412,1082}. v: CS.

**a-Amy-B2a** [412]. [Amy 7B1{1084},Amy 7B2{1084}]. v: CS.


The alternative states of Amy 7B2, namely, Amy 7B2 and Amy 7B2'' {1084}, are identical to the variation in band 2 [412]. The complete description of the a-AMY-B2 variation also includes variation in band 11 [412].

**a-Amy-D2.** [Amy7D{1082}]. 7DL{412,1082}. v: CS.

**a-Amy-D2a** [412]. [Amy 7D1{1084}]. 7DL{412,1082}. v: CS.

**a-Amy-D2b** [417]. [Amy 7D1''{1084}]. v: Largo{007}; Sears' Synthetic{007}; VPM1{417}.

**a-Amy-Ag2** [374]. 7Ag'1[374]. ad: Vilmorin 27/Th. intermedium.

**a-Amy-E2** [013]. 7EL[013]. ad: CS/E. elongata.

**a-Amy-H2.** [a-Amy2{146}]. 7HL[146,1051,793]. ad: CS/Betzes.

**a-Amy-H2** [1015]. 7H[1015,793]. su,ad: CS/H. chilense.

**a-Amy-R2** [013]. 7RL[013]. su,ad: CS/Imperial; CS/King II; Holdfast/King II.

**a-Amy-S2** [013]. 7S[013]. ad: Holdfast/Ae. bicorin.

**a-Amy-U2** [013]. 7U[013]. ad: CS/Ae. umbellulata.

Three other a-AMY loci, namely, Amy 6B2, Amy 6D2, and Amy 7B2, were reported [1084]. No variation was observed for the products of Amy 6D2 and Amy 7B2, although nullisomic analysis located the genes in 6DL and 7B, respectively. In accordance with the Guidelines, these genes are assumed to be part of the a-AMY-D1 and a-AMY-B2 loci, respectively. Amy 6B2 was observed to produce alternative phenotypes [1084]. In a test of the segregation of these phenotypes relative to two alternative products of Amy 6B1, the two loci were found to
be linked with a recombination frequency of 20.6% [1084]. However, an attempt to confirm the presence of more than one $a$-Amy locus in 6BL was unsuccessful [007].

$a$-Amy1{1084,1083}. [Amy 6B2{1084}, Amy-B2{1083}]. 6BL{1084,1083}. v: CS.

$a$-Amy1a{1083}. [Amy-B1a]. v: CS.

$a$-Amy1b{1083}. [Amy-B1b]. v: CS.

$a$-Amy1c{1083}. [Amy-B4]. tv: T. durum ssp. georgicum.

The presence of $a$-Amy1 reported in {1084} was confirmed by segregational tests in a CS/Jones Fife population and in a population derived from a tetraploid cross {1083}. The recombinations with $a$-Amy1 were 9.3% and 22.3%, respectively.

A further set of a-amylase genes, Xa-Amy5 [$a$-Amy3], was identified in 5A, 5B and 5D by cross-hybridization with a-AMY-1 and a-AMY-2 probes {080}. Only one gene copy appears to be present at each locus. In rye, evidence was obtained for three $a$-Amy-l genes, two or three $a$-Amy-2 genes and three $a$-Amy-3 genes [007].

Synthesis of a-amylase isoymes controlled by $a$-Amy-1 genes on chromosomes 6A and 6D is reduced in DT6BS compared to euploid CS. This result suggests the presence of a gene(s) on the long arm of chromosome 6B, which is (are) required for GA-induced alpha-amylase synthesis in the aleurone {0072}.

80.2.5. Beta-amylase

$b$-Amy-A1{008,227}. [b-Amy-A2{008}, b-Amy-B1{1331}]. 5AL{008,227}. v: CS{008}. s: CS/Federa{227}.

$b$-Amy-A1a{008}. [b-Amy-A2a{008}, b-Amy-B1a{936}]. v: CS.

$b$-Amy-A1b{008}. [b-Amy-A2b{008}, b-Amy-B1b{936}]. v: Koga II.

$b$-Amy-A1c{008}. [b-Amy-A2c{008}, b-Amy-B1c{936}]. v: T. macha IPSR 1240005.


$b$-Amy-A1e{008}. [b-Amy-A2e{008}, b-Amy-B1e{936}]. v: Bezostaya I.

$b$-Amy-B1{628}. [b-Amy-A1{008}]. 4BL{008,628}. v: CS.

$b$-Amy-B1a{1330}. [b-Amy-A1a{008}, b-Amy-B1a{1330}]. v: CS.

$b$-Amy-B1b{1330}. [b-Amy-A1b{008}, b-Amy-B1b{1330}]. v: Sears' Synthetic IPSR 1190903.

$b$-Amy-B1c{1330}. [b-Amy-A1c{008}, b-Amy-B1c{1330}]. v: Ciano 67.


$b$-Amy-C1{1278}. B{1278}. ad: Aestivum cv. Alcedo / Ae. caudata line B.

$b$-Amy-D1{008}. 4DL{008,628}. v: CS.

$b$-Amy-D1a{008}. v: CS.

$b$-Amy-D1b{008}. v: Bersee.

$b$-Amy-D1e{008}. v: Sears' Synthetic. Rare.

Previously listed alleles $b$-Amy-D1d and -D1e were found to be $b$-Amy-B1 alleles [400]. Two $b$-Amy-D1 alleles were predominant in 60 accessions of T. tauschii [1578].

$b$-Amy-Ag1{168,013}. 4Ag1{168}. ad: Vilmmori27/Th. intermedium.

$b$-Amy-E1{661}. 5E1{661}. tr: 5AS.5E1L.

$b$-Amy-H1{1153}. ad: CS/Beetz.

$b$-Amy-H1a{013}. 4H1b{013}. ad: CS/H. chilense.

$b$-Amy-R1. [b-Amy-R2{013}, b-Amy-R1{043}]. 5R{103,1280}.5RL{043}. ad: FEC 28/Petkus{043,82}; Holdfast/King II{043,1280}. tr: CS/Imperial 5BL-5RL{043}.

$b$-Amy-Sh1{013}. 4S1{013}.D{013}. ad: CS/Ae. sharonensis D{013}. su: CS/Ae. sharonensis. ad: CS/Ae. longissima.

$b$-Amy-U1{013}. [b-Amy-U2{013}]. 5U{013}. su: CS/Ae. umbellulata.

A second set of loci with homology to $b$-Amy-1 genes was identified in 2AS, 2BS and 2DS and designated the Xb-Amy-2 [b-Amy-2 {1331}] set. Evidence for these genes derives from cross-hybridization with a b-AMY-H1 cDNA probe [1331]. Further members of the same set
were identified in 2H \{732\}, and 2R and 2U \{1331\}. Sixty \textit{Ae. tauschii} lines revealed two \textit{b-Amy-D'I} alleles \{1578\}.

**80.2.6. Endopeptidase**

\textit{Ep-A1} \{516\}. 7AL\{516\}. \textit{v}: CS.

\textit{Ep-A1a} \{516,708\}. \textit{v}: CS.

An EP isozyme encoded by \textit{Ep-A1a} of CS is visible on zymograms following starch gel electrophoresis \{516\}. The product of this allele is not observable, however, on zymograms following isoelectric focusing \{708\}.

\textit{Ep-A1b} \{708\}. \textit{v}: Cappelle-Desprez\{708\}; Hobbit\{704\}; Rendezvous\{1603\}.

\textit{Ep-A1c} \{708\}. \textit{v}: Sears' Synthetic.

An EP isozyme encoded by \textit{Ep-A1a} of CS is visible on zymograms following starch gel electrophoresis \{516\}. The product of this allele is not observable, however, on zymograms following isoelectric focusing \{708\}.

\textit{Ep-B1} \{516\}. 7BL\{516\}. \textit{v}: CS.

\textit{Ep-B1a} \{708\}. \textit{v}: CS.

\textit{Ep-B1b} \{708\}. \textit{v}: Cappelle-Desprez.

\textit{Ep-B1c} \{708\}. \textit{v}: Ciano 67.

\textit{Ep-B1d} \{708\}. \textit{v}: Bersee.

\textit{Ep-B1e} \{708\}. \textit{v}: Sears' Synthetic.

\textit{Ep-D1} \{516\}. 7DL\{516\}. \textit{v}: CS.

\textit{Ep-D1a} \{708\}. \textit{v}: CS.

\textit{Ep-D1b} \{708\}. \textit{v}: Cappelle-Desprez.

\textit{Ep-D1c} \{708\}. \textit{v}: CS.

\textit{Ep-D1d} \{1587\}. \textit{Null allele}. \textit{v}: Wheats with \textit{Lr19}\{1587\}.

\textit{Ep-D1e} \{894\}. \textit{Isozyme 5}. \textit{v}: PI 294994\{894\}.

\textit{Ep-E1} \{518\}. 7EL\{518\}. \textit{al}: CS/E. elongata.

\textit{Ep-H1} \{520\}. 7HL\{520\}. \textit{al}: CS/Betzkes.

\textit{Ep-H1ch} \{708\}. 7H\textit{ch}\{708\}. \textit{su}: CS/H. chilense.

\textit{Ep-H1t} \{1037\}. 7H\textit{st}\{1037\}. \textit{ad}: CS/E. trachycaulus.

\textit{Ep-M1} \{985\}. \textit{[Ep-M'1}\{985\}\]. 7M\textit{v}\{7D\}. \textit{su}: 7M\textit{v}\{7D\}.

\textit{Ep-R1} \{092,266,708\}. 6RL\{092\}. \textit{ad}: CS/Imperial.

\textit{Ep-S1} \{708\}. 7S\textit{b}\{708\}. \textit{su}: Holdfast/Ae. bicornis.

\textit{Ep-S1} \{517\}. 4S\textit{b}\{517\}. \textit{ad}: CS/Ae. longissima.

\textit{Ep-S1} \{1140\}. 7S\textit{b}\{1140\}. \textit{ad}: CS/T. searsii.

\textit{Ep-U1} \{708\}. 7U\{708\}. \textit{su}: CS/Ae. umbellulata.

\textit{Ep-V1} \{708\}. 7V\{708\}. \textit{ad}: CS/D. villosum.

\textit{Ep-B2} \{599\}. 6BS\{599\}.

An \textit{Ep} locus was located in 4RS in King II \{1280\}, using Holdfast/King II addition lines and in 4R in Imperial \{266\} using Chinese Spring/Imperial addition lines.

**80.2.7. Esterase**

Genetic control of esterases [carboxylic ester hydrolases (E.C.3.1.1.1)] was the subject of a comparative study \{814\}.

**80.2.7.1. EST-1**
EST-1 is a dimeric enzyme that electrofocuses around pH 4.0 and is expressed in all tissues except endosperm [814].

**Est-A1**. \([\text{Est}_A\{061\}]\). 3AS\{060\}. \(v\): CS.

**Est-B1**. \([\text{Est}_B\{061\}]\). 3B\{060\}.3BS\{100\}. \(v\): CS.

**Est-D1**. \([\text{Est}_D\{061\}]\). 3D\{060\}.3DS\{100\}. \(v\): CS.

**Est-E1**. 3ES\{518\}. \(v\): CS./E. elongata.

**Est-H1**. 3H\{814\}. \(v\): CS./Betzes.

**Est-R1**. \([\text{Est}_R\{061\}]\). 3R\{061\}.1254. \(v\): CS./Imperial; Holdfast/King II\{100\}; Kharkov/Dakold\{100\}.

**Est-S1**. 3S\{814\}. \(v\): CS./Ae. longissima.

Each of 208 hexaploid accessions carried the same Est-1 alleles except accessions of \(T.\) compactum var. rubriceps, each of which carried an Est-B1 or Est-D1 electrophoretic mobility variant [585].

80.2.7.2. EST-2

EST-2 is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.

**Est-A2**. \([\text{Est}_2\{585\}]\). 3A\{585\}. \(v\): CS.

**Est-B2**. \([\text{Est}_2\{585\}]\). 3BL\{585\}. \(v\): CS.

**Est-D2**. \([\text{Est}_2\{585\}]\). 3DL\{585\}. \(v\): CS.

Among 208 hexaploid accessions, an apparent Est-B2 null allele occurred frequently in accessions of \(T.\) macha and \(T.\) sphaero occum and occasionally in accessions of \(T.\) compactum. The allele was not observed in \(T.\) aestivum and \(T.\) spelta accessions [585].

80.2.7.3. EST-3

EST-3 is a monomeric enzyme that is expressed in young seedlings (this enzyme was not observed in [814]).

**Est-B3**. \([\text{Est}_3\{585\}]\). 7BS\{585\}. \(v\): CS.

**Est-D3**. \([\text{Est}_3\{585\}]\). 7DS\{585\}. \(v\): CS.

**Est-H3**. 520. \(v\): CS./Betzes.

One accession carrying an apparent Est-B3 null allele and one carrying an apparent Est-D3 null allele were found among 208 hexaploid accessions [585].

A 7AS locus encodes three esterase isozymes in immature grains [009].

80.2.7.4. EST-4

EST-4 is a monomeric, leaf-specific enzyme that electrofocuses around pH 4.5.

**Est-A4**. \([\text{Est}_4\{585\}]\). 6AL\{585,919\}. \(v\): CS.

**Est-B4**. \([\text{Est}_4\{585\}]\). 6BL\{585,919\}. \(v\): CS.

**Est-D4**. \([\text{Est}_4\{585\}]\). 6DL\{585,919\}. \(v\): CS.

Probable Est-A4 and Est-D4 null alleles were detected in several accessions of \(T.\) compactum var. rubriceps [585]; otherwise, no Est-4 variant occurred among 208 hexaploid accessions [585].

An esterase gene was located in chromosome L7 (= 6Ag i) of \(Th.\) intermedium [361].

80.2.7.5. EST-5

EST-5 consists of 20 or more monomeric, grain-specific isozymes that electrofocus between pH 5.6 and 7.0.

**Est-A5** [009]. 3AL\{009\}. \(v\): CS.
Proteins

Est-A5a[009]. v: CS.
Est-A5b[009]. v: Kalyansona[009]; T. compactum AUS12084[756].
Est-B5[009]. 3BL[009]. v: CS.
Est-B5a[009]. v: CS.
Est-B5b[009]. v: Big Club.
Est-B5c[009]. v: Timstein.
Est-B5d[009]. v: Sears' Synthetic.
Est-D5[009]. 3DL[009]. v: CS.
Est-D5a[009]. v: CS.
Est-D5b[009]. v: T. macha.
Est-D5c[009]. v: Big Club.
Est-D5d[009]. v: Timstein.
Est-D5e[009]. v: T. macha WJR 38548.

Encoding of the endosperm esterases of hexaploid wheat by 12-15 genes in five compound loci located in 3AL, 3BL, 3DL, 3AS and 3DS was postulated in [1204]. Three and six alleles at Est-D5 (in Ae. tauschii) were reported in [756] and [1578], respectively.

In S. cereale, in addition to Est-R1, genes encoding leaf esterases were located in three chromosomes [1561]. These included a gene designated Est8 in 6R in cvs. Imperial and King II, a gene designated Est2 and two genes, designated Est6 and Est7, which are part of a separate compound locus [1560], in 5RL in Imperial, and a gene designated Est10 in 4R of King II and 4RL of Imperial. In Hordeum vulgare, genes encoding leaf esterases were located in 3H {1071; see also, 520, 580} and 7H {520}.

Est-Ag5[374]. 3Ag[374]. ad: Vilmorin 27/Th. intermedium.
Est-H5[010]. 3H[010]. ad: CS/Betzes.
Est-H5ch[010]. 3Hch[010]. ad: CS/H. chilense.
Est-R5[010]. [EstA[737]]. 6R[043,1280]. ad: CS/Imperial[010,043]; Kharkov/ Dakold 6RL[010,1280]; CS/King II[010]; Holdfast/King II[043,1280].

A second S. cereale gene encoding grain esterases, designated EstB, was located in 4RL in King II and Petkus and in 7RS in Imperial [737].

Est-S5[010]. 3S[010]. su,ad: CS/Ae. bicornis.
Est-S5[010]. 3S[010]. ad: CS/Ae. longissima.

Sixty Ae. tauschii lines revealed six Est-D5 alleles {1578}.

80.2.7.6. EST-6

EST-6 is a dimeric enzyme that electrofocuses around pH 7.6 and is specific to endosperm.

Est-A6[1130]. 2AS[1130]. v: CS.
Est-A6a[1130]. v: CS.
Est-A6b[1130]. v: Ceska Previvka.
Est-B6[1130]. 2BS[1130]. v: CS.
Est-B6a[1130]. v: CS.
Est-B6b[1130]. v: Hope.
Est-D6[1130]. 2DS[1130]. v: CS.
Est-D6a[1130]. v: CS.
Est-D6b[1130]. v: Sears' Synthetic IPSR 1190903.
Est-M6[1130]. 2MS[1130]. su: CS/Ae. comosa.
A group of leaf esterase isozymes controlled by the long arms of the homoeologous group 3 chromosomes were reported \cite{919}. The relationship of these esterases to EST-2 and to the leaf esterase designed EST-6 reported in \cite{629} has not been determined.

\subsection*{80.2.7.7. EST-7}

EST-7 is a monomeric enzyme that electrophoretically focuses in the same region as EST-6 but is specific to green tissues.

- **Est-A7**: 2AL. \( v: \text{CS} \).
- **Est-B7**: 2BL. \( v: \text{CS} \).
- **Est-D7**: 2DL. \( v: \text{CS} \).
- **Est-D7a**: \( v: \text{CS} \).
- **Est-D7b**: Synthetic \{IPSR 1190903\}.

\subsection*{80.2.7.8. EST-8}

EST-8 consists of about 10 isozymes that electrophoretically focus between pH 4.5 and 6.5 and are expressed only in vegetative tissues. EST-8 is likely to be the enzyme previously described in \cite{919} and \cite{629}.

- **Est-A8**: 3AL. \( v: \text{CS} \).
- **Est-B8**: 3BL. \( v: \text{CS} \).
- **Est-D8**: 3DL. \( v: \text{CS} \).
- **Est-R8**: 6RL. \( \text{ad: CS/Imperial, CS/King II} \).

\subsection*{80.2.7.9. EST-9}

EST-9 is a monomeric enzyme that electrophoretically focuses around pH 5.0 and is expressed only in embryos.

- **Est-A9**: 3AS. \( v: \text{CS} \).
- **Est-B9**: 3BS. \( v: \text{CS} \).
- **Est-D9**: 3DS. \( v: \text{CS} \).

EST-2, EST-5 and EST-8 are controlled by genes on 3L and where a recombination test was possible between \textit{Est-D5} and \textit{Est-D8}, no segregation was observed. The different gene symbols were retained because of the different tissue specificities and polymerisation profiles of the enzymes. The same arguments surround the EST-1 and EST-6 genes located in the 3S arms \cite{814}.

The \textit{Est-6} gene of rye was mapped \cite{249}. The \textit{Est-6} genes of wheat were mapped comparatively in the proximal regions of chromosomes 2S \cite{256}. The \textit{Est-2, Est-5 and Est-8} were mapped to the extreme distal regions in the 3L arms \cite{247}.

\subsection*{80.2.8. Glucosephosphate isomerase}

- **Gpi-A1**: 1AS. \( v: \text{CS} \).
- **Gpi-B1**: 1BS. \( v: \text{CS} \).
- **Gpi-D1**: 1DS. \( v: \text{CS} \).
Glutamic oxaloacetic transaminase

Gpi-D1a\{195\}. \(v\): CS.

Gpi-D1b\{195\}. \(v\): CS variant and certain CS aneuploids. Rare.

Varietal differences in GPI zymograms were noted in \{1127\}.

GPI zymogram phenotypes observed in *Triticum* and *Aegilops* species are reported in \{456,457\}.

No allelic variation at Gpi-D1 was found in 60 accessions of *Ae. tauschii* \{1578\}.

Gpi-Ag\{7\}1\{361\},\{374\}. [Gpi-X1\{361\}]. 1Ag\{361\}. \(ad\): Vilmorin 27/Th. intermedium.

Gpi-E1\{518\}. 1ES\{518\}. \(ad\): CS/E. elongata.

Gpi-H\{1153\}. 1HS\{1153\}. \(ad\): CS/Betzes.

Gpi-H\{h\}1\{195\}. 1H\{h\}\{195\}. \(ad\): CS/H. chilense.

Gpi-R1\{195\}. 1R\{195\}.1RS\{779\}. \(ad\): CS/King II\{195\}. \(al\): 2a, 2b, and R14\{779\}.

Gpi-R\{n\}1\{195\}. 1R\{195\}. \(ad\): CS/S. montanum.

Gpi-S\{l\}1\{1228\}. 1S\{517\}.1S\{S\}1\{1228\}. \(ma\): In *Ae. longissima* 2 x *Ae. longissima* 10, Gpi-S\{l\}1, two glutenin loci, and three gliadin loci were mapped relative to one another as follows: Glu-S\{l\}1 - 15.9 cM - Gpi-S\{l\}1 - 38 cM - Gli-S\{l\}4 - 7.1 cM - Glu-S\{l\}3 - 0.9 cM - Gli-S\{l\}1 - 5.6 cM - Gli-S\{l\}5\{1228\}. Glu-S\{l\}1 is located in 1S\{l\}1 and the other loci are in 1S\{S\}1.

Gpi-S\{s\}1\{1140\}. 1S\{S\}{1140}. \(ad\): CS/Ae. searsii.

Gpi-U1\{195\}. 1U\{195\}. \(ad\): CS/Ae. umbellulata.

Gpi-V1\{1026\}. 1V\{1026,241\}. \(ad\): CS/D. villosum.

80.2.9. Glutamic oxaloacetic transaminase

Got-A1\{505\}. 6AS\{505\}. \(v\): CS.

Got-B1\{505\}. 6BS\{505\}. \(v\): CS.

Got-D1\{505\}. 6DS\{505\}. \(v\): CS.

Got-A2\{505\}. 6AL\{505\}. \(v\): CS.

Got-B2\{505\}. 6BL\{505\}. \(v\): CS.

Got-D2\{505\}. 6DL\{505\}. \(v\): CS. \(ma\): Cent - Got-D2 - 2 cM - Xpsr154-6D\{757\}.

Got-Ag\{2\}1\{1575\}. 6Ag\{2\}\{1575\}. \(ad\),\(su\): Rescue/Th. elongatum.

Got-E2\{518\}. 6EBeta\{518\}. \(ad\): CS/E. elongata.

Got-H2\{520\}. 6H\{520\}. \(ad\): CS/Betzes.

Got-R2\{1457\}. [Got\{3\}{1559}]. 6R\{1457\}.6RL\{1280\}. \(ad\): CS/Imperial 6R\{1457\}; Holdfast/King II 6RL\{1280\}.

Got-V2\{1026,242\}. 6V\{1026\}. \(ad\): Creso/D. villosum.

Got-H\{2\}2\{1037\}. 6H\{2\}\{1037\}. \(ad\): CS/E. trachycaulus.

Got-A3\{505\}. 3AL\{505\}. \(v\): CS.

Got-B3\{505\}. 3BL\{505\}. \(v\): CS.

Got-C3\{1278\}. F\{1278\}. \(ad\): *T. aestivum* cv. Alcedo / *Ae. caudata* line C.

Got-D3\{505\}. 3DL\{505\}. \(v\): CS.

Got-Ag\{3\}2\{521\}. 3Ag\{3\}L\{521\}. \(ad\): CS/TAP 67. \(su\): CS/TAP 67. \(tr\): Certain CS 3D/Ag lines.

Got-E3\{518\}. 3EL\{518\}. \(ad\): CS/E. elongata.

Got-H3\{\}. [Got-b\{3\}\{90\}]. 3H\{90\}. \(ad\): CS/Betzes.

Got-H\{h\}3\{351\}. 3H\{h\}\{351\}. \(ad\): MA/H. chilense.

Got-R3\{1457\}. [Got\{3\}{1559}]. 3R\{1457\}. \(ad\): CS/Imperial\{1457\}; Holdfast/ King II\{1253\}; Kharkov/Dakold\{1253\}.

Got-S\{3\}3\{1140\}. 3S\{3\}\{1140\}. \(ad\): CS/Ae. searsii.

Got-V3\{1518,242\}. 3VL\{1518\}. \(ad\): Creso/D. villosum.

Got-R4\{\}. [Got\{1\}7R\{1203\},Got\{2\}{1559}]. 7RL\{1203\}. \(al\): *S. cereale*.

Wehling \{1559\} identified a GOT locus designated *Gotl* in 4RL of *S. cereale*. 
80.2.10. Hexokinase

Hexokinase

\(Hk-B1\{006\}. 1B{006}. \ v: \ CS.\\nHk-D1\{006\}. 1D{006}. \ v: \ CS.\\nHk-A2\{810\}. 3A\{810\}. \ v: \ CS.\\nHk-A2a\{810\}. \ v: \ CS.\\nHk-A2b\{810\}. \ s: \ CS/Sears' Synthetic 3A. \ v: \ Sears' Synthetic IPSR 1190903.\\nHk-B2\{006\}. 3B\{006,810\}. \ v: \ CS.\\nHk-D2\{810\}. 3D\{810\}. \ v: \ CS.\\nHk-D2a\{810\}. \ v: \ CS.\\nHk-D2b\{810\}. \ v: \ Sears' Synthetic IPSR 1190903.\\nHk-E2\{006\}. 3E\{006\}. \ ad: \ CS/E. elongata.

Allelic variation was observed in three of 55 hexaploid accessions \{006\}.

80.2.11. Lipoxygenase

The wheat \(Lpx-1\) gene in wheat corresponds to barley \(LoxA\) (GenBank L35931). The \(Lpx-B1\) locus is duplicated, with the \(Lpx-B1.1\) and \(Lpx-B1.2\) loci corresponding to GenBank sequences DQ474240 and DQ474241, respectively. The \(Lpx-B1b\) allele corresponds to a deletion associated with a 4.5-fold reduction in lipoxygenase activity. The \(Lpx-2\) gene in wheat corresponds to the barley \(LoxC\) gene (GenBank L37358) whereas the \(Lpx-3\) gene in wheat corresponds to the barley \(LoxB\) gene (GenBank L37359).

\(Lpx-A1\{516\}. [Lpx-B1\{516\}]. 4A\{516\}. \ v: \ CS\{516\}. \ ma: \ Xksu919(Lpx-1)-4A\{0091\}.\\nLpx-B1\{516\}. [Lpx-A1\{516\}]. 4B\{516\}. \ v: \ CS\{516\}. \ ma: \ Xcn119(Lpx-1)-4B\{0091\}.\\nLpx-B1\{516\}. [Lpx-A1\{516\}]. 4BS\{516\}. \ v: \ CS\{516\}. \ ma: \ Xksu919(Lpx-1)-4B\{0091\}.\\nLpx-B1a\{516\}. [Lpx-A1a\{936\}]. \ v: \ Bosanka\{1533\}.\\nLpx-B1b\{516\}. [Lpx-A1b\{936\}]. \ v: \ Bosanka\{1533\}.\\nLpx-B1.1\{10303\}. 4B\{10303\}. \ ma: \ Xksm62-4B - 8 cM - LpxB1.1 - 13 cM - Xwmc617b-4B\{10303\}.\\nLpx-B1.1a\{10303\}. tv: \ UC1113\{10303\}.\\nLpx-B1.1b\{10303\}. tv: \ Kofa, deletion\{10303\}.\\nLpx-B1.2\{10303\}. 4B\{10303\}. \ v: \ CS.\\nLpx-D1\{516\}. 4DS\{516\}. \ v: \ CS.\\nLpx-E1\{518\}. 4ES\{518\}. \ ad: \ CS/E. elongata.\\nLpx-H1\{716\}. 4H\{716\}. \ ad: \ CS/Betzes.\\nLpx-A2\{516\}. 5AL\{516,10303\}. \ v: \ CS. \ ma: \ Xksu919(Lpx-2)-5A\{0091\}.\\nLpx-B2\{516\}. 5BL\{516,10303\}. \ v: \ CS. \ ma: \ Xksu919(Lpx-2)-5B\{0091\}; Xcn119(Lpx-2)-5B\{0269\}.\\nLpx-D2\{516\}. 5DL\{516\}. \ v: \ CS.\\nLpx-E2\{518\}. 5EL\{518\}. \ ad: \ CS/E. elongata.\\nLpx-H2\{716\}. 5H\{716\}. \ ad: \ CS/Betzes.\\nLpx-S\{1140\}. 5S\{1140\}. \ ad: \ CS/Ae. searsii.\\nLpx-V2\{242\}. 5V. \ ad: \ CS/D. villosum.\\nLpx-A3\{10303\}. 4AL\{10303\}. tv: \ UC1113 (GenBank DQ474244) and Kofa (GenBank DQ474242)\{10303\}. \ ma: \ Xwmc617a-4A - 10 cM - Lpx-A3 - 15 cM - Xgwm192b-4A\{10303\}.\\nLpx-B3\{10303\}. 4B\{10303\}. tv: \ UC1113 and Kofa (GenBank DQ474243)\{10303\}.

80.2.12. Malate dehydrogenase

\(Mdh-A1\). [Mdh2A\{087\}]. 1A\{087\}. \ v: \ CS.
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**Mdh-B1.** [Mdh2B{087}]. 1BL{101,087}. v: CS.

**Mdh-D1.** [Mdh2D{087}]. 1DL{087}. v: CS.

**Mdh-H1**{1153}. 1HL{1153}. ad: CS/Betzes.

**Mdh-Hch1**{195}. 1Hch{195}. ad: MA/H. chilense.

**Mdh-R1.** [Mdh2-1{1252}]. 1RL{1252}. ad: CS/Imperial 1R; Kharkov/Dakold 1R; Holdfast/King II 1RL.

**Mdh-S1**{1140}. 1S{1140}. ad: CS/T. searsii.

**Mdh-H2.** [Mdh2-b2{090}]. 3H{090}.

**Mdh-R2.** [Mdh2-2{1252}]. 3R{1252}. ad: CS/Imperial.

A third set of dimeric MDH isozymes identified in mature grain are separable from MDH-1 and MDH-2 by their higher pI's in IEF {811}.

**Mdh-A3{811}**. 5AS. v: CS.

**Mdh-A3a{811}.** v: CS.

**Mdh-A3b{811}.** v: Bersee.

**Mdh-B3{811}**. 5BS. v: CS.

**Mdh-B3a{811}.** v: CS.

**Mdh-B3b{811}.** v: Hope.

**Mdh-D3{811}**. 5DS. v: CS.

**Mdh-D3a{811}.** v: CS.

**Mdh-D3b{811}.** v: Sears' Synthetic.

**Mdh-E3{811}**. 5ES. ad: CS/E. elongata.

**Mdh-H3{811}**. 5H. ad: CS/Betzes.

**Mdh-U3{811}**. 5U. ad: CS/Ae. umbellulata.

**Mdh-R4{360}**. 1RL{360}. v: Various crosses.

80.2.13. Peroxidase

Peroxidase (EC1.11.1.7) isozymes have high tissue specificity. Staining and electrophoretic systems are reviewed in {118}. PER-1, -2, -3, -4 and -5 are all reported in {816}.

80.2.13.1. PER-1

PER-1 is expressed in leaf {012} and coleoptile {816} tissues.

**Per-B1{012}**. 1BS{012,919}. v: CS.

**Per-D1{012}**. 1DS{012,919}. v: CS.

**Per-D1a{012}**. v: CS.

**Per-D1b{012}**. v: Sears' Synthetic.

**Per-Hsth1{012}**. 1Hsth{012}. ad: CS/H. chilense.

**Per-R1{012}**. [Prx{1561}] 1RS{012,1561}. ad: CS/King II{012}; Holdfast/King II{1561}.

tr: Veery 'S'{012}.

**Per-V1{241}**. 1V{241}. ad: Creso/D. villosum.

80.2.13.2. PER-2

PER-2 is expressed in young leaf {118}, coleoptile and root {816} tissues.

**Per-A2.** 2AS. v: CS.

**Per-A2a{816}.** v: CS.

**Per-A2b{816}.** v: Timstein.

**Per-B2{118}.** 2BS{118}. v: CS.

**Per-B2a{816}.** v: CS.

**Per-B2b{816}.** v: Sears' Synthetic IPSR1190903.

**Per-D2{118}.** 2DS{118}. v: CS.
80.2.13.3. PER-3

PER-3 is expressed in embryo {119,816} and scutellar {119} tissues.

Per-A3[119]. 3AL[119]. v: CS.
Per-A3a[816]. v: CS.
Per-A3b[816]. v: Timstein.
Per-A3c[816]. v: Hobbit 'S'.
Per-B3[086],[119]. [Per4{961}]. 3BL[086,119]. v: CS.
Per-B3a[816]. v: CS.
Per-B3b[816]. v: Hope.
Per-B3c[816]. v: T. macha IPSR1240005.
Per-B3d[816]. v: Timstein.
Per-B3e[816]. v: Sears' Synthetic IPSR1190903.

80.2.13.4. PER-4

PER-4 is expressed in endosperm tissue {086,119}.

Per-A4a[816]. v: CS.
Per-A4b[816]. v: Hope.
Per-A4c[816]. v: Sicco.
Per-B4a[816]. v: CS.
Per-B4b[816]. v: Hope.
Per-B4c[816]. v: Thatcher.
Per-D4[695],[119]. [Per1{961}]. 7D[695].7DS[694,086,119]. v: CS.
Per-D4a[816]. v: CS.
Per-D4b[816]. v: Thatcher.
Per-Ag'4. 7Ag'S[694]. tr: Certain CS 7D/Ag' lines.
Per-Ag4. [Per-Ag3{374}]. 7Ag'[168]. ad: Vilmorin 27/Th. intermedium.
Cultivar variation for Per-4 was reported in {094}.

80.2.13.5. PER-5

PER-5 is expressed in roots {816}.

Per-D5[816]. 2DS[816]. v: CS.
Per-S5[816]. 2S'[816]. ad: CS/Ae. longissima.
80.2.14. Phosphodiesterase

<table>
<thead>
<tr>
<th>Gene</th>
<th>Loci</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pde-B1</td>
<td>3B[1590],3BS[1589]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Pde-D1</td>
<td>3DS[1590]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Pde-S1</td>
<td>3S[172]</td>
<td>ad: CS/Ae. longissima.</td>
</tr>
<tr>
<td>Pde-V1</td>
<td>3VS[1518]</td>
<td>ad: CS/D. villosum.</td>
</tr>
</tbody>
</table>

80.2.15. Phosphogluconate dehydrogenase

<table>
<thead>
<tr>
<th>Gene</th>
<th>Loci</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PgdR1</td>
<td>4RL[1191]</td>
<td>ad: CS/Imperial; Holdfast/King II.</td>
</tr>
<tr>
<td>PgdR2</td>
<td>6RL[1191]</td>
<td>ad: CS/Imperial; Holdfast/King II.</td>
</tr>
</tbody>
</table>

Loci were also identified in 6B [1435], 1EL [1435], 1HL [147,1072], 1H ch [352] and 1RL [779].

80.2.16. Phosphoglucomutase

<table>
<thead>
<tr>
<th>Gene</th>
<th>Loci</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pgm-A1</td>
<td>4AL[088]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Pgm-D1</td>
<td>4DS[088]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Pgm-Ag1</td>
<td>4Ag[361]</td>
<td>ad: Vilmorin 27/Th. intermedium.</td>
</tr>
<tr>
<td>Pgm-H1</td>
<td>4H[085]</td>
<td>ad: CS/Betzes.</td>
</tr>
<tr>
<td>Pgm-R1</td>
<td>4RS[1561,1253]</td>
<td>ad: CS/Imperial 4RS[1253,1561]; Kharkov/Dakold 4R[1253]; Holdfast/King II 4RS[1253,1561].</td>
</tr>
</tbody>
</table>

80.2.17. Shikimate dehydrogenase

<table>
<thead>
<tr>
<th>Gene</th>
<th>Loci</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Skdh-A1</td>
<td>5AS[706,1065]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Skdh-B1</td>
<td>5BS[706,1065]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Skdh-D1</td>
<td>5DS[706,1065]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Skdh-H1</td>
<td>5H[085]</td>
<td>ad: CS/Betzes.</td>
</tr>
<tr>
<td>Skdh-Hf1</td>
<td>5Hf[1037]</td>
<td>ad: CS/E. trachycaulus.</td>
</tr>
<tr>
<td>Skdh-Mf1</td>
<td>5Mf[985]</td>
<td>su: 5Mf'(5A), 5Mf'(5D).</td>
</tr>
<tr>
<td>Skdh-R1</td>
<td>5RS[706],5R[085]</td>
<td>ad: CS/King II[085]; CS/Imperial[706]; Kharkov/Dakold[085].</td>
</tr>
<tr>
<td>Skdh-S1</td>
<td>5S[085]</td>
<td>ad: CS/Ae. longissima.</td>
</tr>
<tr>
<td>Skdh-Sf1</td>
<td>5Sf[1140]</td>
<td>ad: CS/Ae. searsii.</td>
</tr>
<tr>
<td>Skdh-V1</td>
<td>5V[085]</td>
<td>ad: CS/D. villosum.</td>
</tr>
<tr>
<td>Skdh-U1</td>
<td>5U[706]</td>
<td>ad,su: CS/Ae. umbellulata.</td>
</tr>
</tbody>
</table>

80.2.18. Superoxide dismutase

<table>
<thead>
<tr>
<th>Gene</th>
<th>Loci</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sod-A1</td>
<td>2AL[1066]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Sod-B1</td>
<td>2BL[1066]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Sod-D1</td>
<td>2DL[1066]</td>
<td>v: CS.</td>
</tr>
<tr>
<td>Sod-E1</td>
<td>2V[808],8E[808]</td>
<td>ad: CS/E. elongata.</td>
</tr>
<tr>
<td>Sod-H1</td>
<td>2H[716]</td>
<td>ad: CS/Betzes.</td>
</tr>
<tr>
<td>Sod-R1</td>
<td>2R[1066]</td>
<td>ad: CS/Imperial.</td>
</tr>
<tr>
<td>Sod-Sf1</td>
<td>2Sf[1140]</td>
<td>ad: CS/Ae. searsii.</td>
</tr>
</tbody>
</table>
Sod-VI\{1026\}. 7V\{1026\}. ad: CS/D. villosum.

80.2.19. Triosephosphate isomerase

\textit{Tpi-A1}\{1139\}. 3AS\{1139\}. v: CS.
\textit{Tpi-B1}\{1139\}. 3BS\{1139\}. v: CS.
\textit{Tpi-D1}\{1139\}. 3DS\{1139\}. v: CS.
\textit{Tpi-E1}\{1139\}. 3E\{1139\}. ad: CS/E. elongata.
\textit{Tpi-H1}\{1139\}. 3H\{1139\}. ad: CS/Betzes.
\textit{Tpi-R1}\{1139\}. 3R\{1139\}. ad: CS/Imperial; Kharkov/Dakold.
\textit{Tpi-S1}\{1139\}. 3S\{1139\}. ad: CS/Ae. elongata.
\textit{Tpi-A2}\{1139\}. 5AL\{1139\}. v: CS.
\textit{Tpi-B2}\{1139\}. 5BL\{1139\}. v: CS.
\textit{Tpi-D2}\{1139\}. 5DL\{1139\}. v: CS.
\textit{Tpi-H2}\{1139\}. 5H\{1139\}. ad: CS/Betzes.
\textit{Tpi-R2}\{1139\}. 5R\{1139\}. ad: CS/Imperial; Kharkov/Dakold.
\textit{Tpi-S2}\{1139\}. 5S\{1139\}. ad: CS/Ae. elongata.
\textit{Tpi-U2}\{1139\}. 5U\{1139\}. ad: CS/Ae. umbellulata.
\textit{Tpi-Ag2}\{374\}. 5Ag\{'374\}. ad: Vilmorin 27/Th. intermedium.

80.2.20. Aromatic alcohol dehydrogenase

\textit{Aadh-A1}. [\textit{Adh-A2}\{584\}]. 5AL\{584\}. v: CS. ma: \textit{XksuG44-5A}(proximal) - 6.9 cM - \textit{Aadh-A1} - 24.7 cM - \textit{Xcdo412-5A}(distal){9959}.
\textit{Aadh-A1a}. v: CS; 133 other accessions\{584\}.
\textit{Aadh-A1b}. v: \textit{T. spelta}; K-24696; other accessions\{584\}.
\textit{Aadh-B1}. [\textit{Adh-B2}\{584\}]. 5BL\{584\}. v: CS.
\textit{Aadh-B1a}. v: CS\{1533\}.
\textit{Aadh-B1b}. v: Drina \{1533\}.
\textit{Aadh-C1}\{1278\}. C\{1278\}. ad: Alcedo/Ae. caudata line C.
\textit{Aadh-D1}. [\textit{Adh-D2}\{584\}]. 5DL\{584\}. v: CS.
\textit{Aadh-E1}. [\textit{Adh-E2}\{518\}]. 5EL\{518\}. ad: CS/E. elongata.
\textit{Aadh-R1}. 5RL\{1280\}. ad: Holdfast/King II.
\textit{Aadh-A2}. [\textit{Adh-A3}\{508\}]. 6A\{1279\}.6AL\{513,587\}. v: CS\{513\}; Carola\{1279\}.
\textit{Aadh-B2}. [\textit{Adh-B3}\{508\}]. 6B\{1279\}.6BL\{513\}. v: CS\{513\}; Carola\{1279\}.
\textit{Aadh-D2}. [\textit{Adh-D3}\{508\}]. 6D\{1279\}.6DL\{513\}. v: CS\{513\}; Carola\{1279\}.
\textit{Aadh-Ag2}\{1575\}. 6Ag\{'1575\}. ad, su: Rescue/Th. elongatum.
\textit{Aadh-E2}. [\textit{Adh-E3}\{518\}]. 6EBeta\{518\}. ad: CS/E. elongata.
\textit{Aadh-R2}. 6RL\{1280\}. ad: Holdfast/King II.
\textit{Aadh-V2}\{241\}. 6V\{241\}. ad: CS/D. villosum.

The \textit{Aadh-1} and \textit{Aadh-2} loci were designated with the synonyms \textit{Adh-2} and \textit{Adh-3}, respectively, in a number of publications in addition to \{508,518,584\}. These include: \{510,509,511,519,517,587,1066,1139\}.

80.2.21. Aconitase

\textit{Aco-A1}\{189\}. 6AL\{189\}. v: CS.
\textit{Aco-A1a}. v: CS\{1533\}.
\textit{Aco-A1b}. v: Dubravka\{1533\}.
\textit{Aco-B1}\{189\}. 6BL\{189\}. v: CS.
\textit{Aco-B1a}. v: CS\{1533\}.
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Aco-B1b. v: Dubravka{1533}.
Aco-B1c. v: Slavonka{1533}.
Aco-D1{189}. 6DL{189}. v: CS.

Further alleles at Aco-A1 and Aco-B1 are listed in {1127}; these have not been tested against those found in {1533}.
Aco-Ag1{1575}. 6Ag{1575}. ad, su: Rescue/Th. elongatum.
Aco-EI{189}. 6Ebeta{189}. ad: CS/E. elongata.
Aco-H1{147},{189}. [Aco-J{147}]. 6H{147}.6HL{189}. ad: CS/Betzes.
Aco-R1{189}. 6RL{189}. ad: Sturdy/PI 252003.
Aco-S1{147}. 6S{189}. ad: CS/A. longissima.
Aco-S2{1140}. 4S{1140}. ad: CS/Ae. searsii.
Aco-U1{189}. CSU-31{189}. ad: CS/Ae. umbellulata.
Aco-A2{189}. 5AL{189}. v: CS.
Aco-B2{189}. 4BL{1513}. v: CS.
Aco-B2a{1513}. v: CS.
Aco-B2b{1513}. v: PI 278437.
Aco-B2c{1513}. v: PI 182575.
Aco-B2d{1513}. v: PI 157589.
Aco-D2{189}. 4DL{1513}. v: CS.
Aco-E2{189}. 4EL{189}. ad: CS/E. elongata.
Aco-M2{1341}. [Aco-M2{985}]. 5M{5}. ad: 5M{5}(5A),5M{5}(5D).
Aco-R2{189}. 5RL{189}. ad: CS/King II 5R; Holdfast/King II 5RL.
Aco-S2{1140}. 4S{1140}. ad: CS/Ae. searsii.

80.2.22. NADH dehydrogenase

80.2.22.1. Ndh-1

Ndh-A1a{1533}. [Ndh-B1a{936}]. v: CS.
Ndh-D1{513}. 4DS{513}. v: CS.
Ndh-H1{147},{513}. [Nadhd-I{147}]. 4H{147}.4HS{813}. ad: CS/Betzes.
Ndh-Hf8{813}. 4Hf{813}. ad: CS/H. chilense.
Ndh-VI{241}. 4V{241}. ad: CS/D. villosum.
Ndh-R1{813}. 4R{362}.4RS{813}. ad: CS/Imperial, CS/King II{813,362}; CS/Dakold{362}.
Ndh-S1{813}. 4S{813}. ad: CS/Ae. longissima.
Ndh-U1{362}. A{362}. ad: CS/Ae. umbellulata.

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the Ndh1 (NADH dehydrogenase) and Dia3 (diaphorase) represent the same locus {0356}.

80.2.22.2. Ndh-2

Ndh-A2{813}. 7A{813}. v: Hope.
Ndh-D2{813}. 7DS{813}. v: CS.
Ndh-R2{813}. 7RS{813}. ad: CS/Imperial, CS/King II, Holdfast/King II (7R).
Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the \textit{Ndh-2} (NADH dehydrogenase) and \textit{Dia2} (diaphorase) represent the same locus \{0356\}.

80.2.22.3. \textit{Ndh-3}

\textit{Ndh-A3} \{813\}. 3AL \{813\}. \textit{v}: CS.
\textit{Ndh-B3} \{813\}. 3BL \{813\}. \textit{v}: CS.
\textit{Ndh-B3a} \{813\}. \textit{v}: CS.
\textit{Ndh-B3b} \{813\}. \textit{v}: Carmen.
\textit{Ndh-D3} \{813\}. 3DL \{813\}. \textit{v}: CS.

A \textit{Ndh} locus, designated \textit{Nadh2}, was mapped 27 cM from \textit{Est-D10} in an \textit{Ae. taushii} F\textsubscript{2} population derived from VIR-1954/VIR-1345 \{10046\}. This locus may be homologous to \textit{Ndh-D3}

\textit{Ndh-H3} \{813\}. 3HL \{813\}. \textit{ad}: CS/Betzes.
\textit{Ndh-R3} \{813\}. 6RL \{813\}. \textit{ad}: Holdfast/King II, CS/Imperial (6R). CS/King II (6R).
\textit{Ndh-S3} \{813\}. 3SL \{813\}. \textit{ad}: CS/\textit{Ae. longissima}; CS/\textit{Ae. sharonesis} (3S).

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that \textit{Ndh-3} (NADH dehydrogenase), \textit{Dia1} (diaphorase) and \textit{Mnr1} (menadione reductase) represent the same locus \{0356\}.

80.2.22.4. \textit{Ndh-4}

\textit{Ndh-A4} \{813\}. 3AS \{813\}. \textit{v}: CS.
\textit{Ndh-B4} \{813\}. 3BS \{813\}. \textit{v}: CS.
\textit{Ndh-E4} \{813\}. 3ES \{813\}. \textit{ad}: CS/\textit{E. elongata}.
\textit{Ndh-H4} \{813\}. 3HS \{813\}. \textit{ad}: CS/Betzes.
\textit{Ndh-R4} \{813\}. 3RS \{813\}. \textit{ad}: CS/King II, CS/Imperial (3R).

80.2.23. \textit{Dipeptidase}

\textit{Dip-A1} \{454\},\{700\}. [\textit{Pept-A1} \{454\}]. 6AL \{454,700\}. \textit{v}: CS.
\textit{Dip-A1a} \{700\}. \textit{v}: CS.
\textit{Dip-A1b} \{700\}. \textit{v}: Cheyenne.
\textit{Dip-B1} \{454\},\{700\}. [\textit{Pept-B1} \{1533\}]. 6BL \{454,700\}. \textit{v}: CS.
\textit{Dip-B1a} \{700\}. \textit{v}: CS.
\textit{Dip-B1b} \{700\}. \textit{v}: Cappelle-Desprez.
\textit{Dip-D1} \{700\}. 6DL \{700\}. \textit{v}: CS.
\textit{Dip-H1} \{147\},\{700\}. [\textit{Pept-I} \{147\}, Dip 1 \{145\}]. 6H \{147,145,700\}. \textit{ad}: CS/Betzes.
\textit{Dip-J1} \{700\}. 6J \{700\}. \textit{ad}: CS/\textit{Th. junceum}.
\textit{Dip-V1} \{700\}. 6V \{700\}. \textit{ad}: CS/\textit{D. villosum}.

80.2.24. \textit{Malic enzyme}

A dimeric enzyme extractable from mature grains.
\textit{Mal-A1} \{809\}. 3AL. \textit{v}: CS.
\textit{Mal-B1} \{809\}. 3BL. \textit{v}: CS.
\textit{Mal-B1a} \{809\}. \textit{v}: CS.
\textit{Mal-B1b} \{809\}. \textit{v}: \textit{T. spelta} IPSR line 1.
\textit{Mal-B1c} \{809\}. \textit{v}: Sears' Synthetic.
80.2.25. Adenylate kinase

<table>
<thead>
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<th>Description</th>
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<tbody>
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<td>[Adk-a(091)]</td>
<td>7AL{091}</td>
<td>CS</td>
</tr>
<tr>
<td>Adk-B1</td>
<td>[Adk-b(091)]</td>
<td>7BL{091}</td>
<td>CS</td>
</tr>
<tr>
<td>Adk-D1</td>
<td>[Adk-d(091)]</td>
<td>7DL{091}</td>
<td>CS</td>
</tr>
<tr>
<td>Adk-E1</td>
<td></td>
<td>7E{091}</td>
<td>CS/E. elongata</td>
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<tr>
<td>Adk-H1</td>
<td></td>
<td>7H{091}</td>
<td>CS/Betzes</td>
</tr>
<tr>
<td>Adk-M1</td>
<td>[Adk-M(985)]</td>
<td>7M{985}</td>
<td>CS/Ae. umbellulata</td>
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<tr>
<td>Adk-R1</td>
<td></td>
<td>7RL{091}</td>
<td>CS/Imperial; Holdfast/King II</td>
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<tr>
<td>Adk-U1</td>
<td></td>
<td>E{091}</td>
<td>CS/Th. intermedium</td>
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<td>CS/DV92</td>
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80.2.26. Glutamate-pyruvate transaminase

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<td>CS/E. elongata 1E</td>
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<tr>
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<td>1H{1435}</td>
<td>H. vulgare cv. Betzes</td>
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</table>

80.2.27. Catalase

A catalase locus, designated Cat2, was mapped 6 cM proximal to Aco-D2 in an Ae. tauschii F2 population derived from VIR-1954/VIR-1345 cross {10046}. This locus may be orthologous to Cat-B1 {10046}.

<table>
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<td>Cat-B1</td>
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80.2.28. Beta-glucosidase

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<td></td>
<td>2A{282}</td>
<td>DV92</td>
</tr>
<tr>
<td>b-Glsb</td>
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80.2.29. Starch branching enzyme I

<table>
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<td>1DL{9937}</td>
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<td>SbeI2</td>
<td></td>
<td>7BL{9937}</td>
<td>CS</td>
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</table>

80.2.30. Starch branching enzyme II

SbeII.

Suppression of SBEIIb expression alone had no effect on amylose contents, however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose {10534}.
80.2.31. Benzoxinones

The putative role of benzoxinones sets \( \text{Bx-1 to Bx-5} \) is to catalyze the pathway Indole-3-glycerol phosphate to DIBOA. Primers designated from maize sequences were used to generate RT-PCR products utilised to screen a cDNA library from CS seedlings. Full-length cDNAs were heterologously expressed in yeast and the Bx gene products had enzymatic action. The Bx genes located by Southern analysis of CS deletion stocks occurred as clustered groups in homoeologous groups 4 \((\text{Bx-1, Bx-2})\) and 5 \((\text{Bx-3, Bx-4, Bx-5})\) \(\{10103\}\).

80.2.32. Acetohydroxyacid synthase (EC 4.1.3.18)

An orthologous series was mapped as the active target sites of imidazolinone herbicides. See section: Herbicide Response: Imidazolinone resistance.

\(\text{AhasL-A1}\{10101\} \) \(\text{Imi3}\{10099\}\). \(\text{6AL}\{10101\}\). \(\text{v2: CDC Teal IMI 15A Imi3}\{10099\}\). \(\text{dv: T. monococcum mutant EM2 (mutant of susceptible line TM23}\{10102\}\).

\(\text{AhasL-B1}\{10101\} \) \(\text{Imi2}\{10099\}\). \(\text{6BL}\{10101\}\). \(\text{v: CDC Teal IMI 11A=PTA3953}\{10099\}\).

\(\text{AhasL-D1}\{10101\} \) \(\text{Imi1}\{10099\}\). \(\text{6DL}\{10101\}\). \(\text{v: BW755=Grandin*3/Fidel-Fs-4}\{10099\}\).

80.2.33. Phytoene synthase

Phytoene synthase, which condenses two molecules of geranyl geranyl diphosphate to produce phytoene, is the first of the specific enzyme necessary for carotene biosynthesis in plants.

80.2.33.1. Phytoene synthase 1 (EC 2.5.1.32)

Homology with the same gene in rice (\(\text{Psy1}\) \(\{10230\}\). Phytene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Flour colour and Grain quality parameters: Flour, semolina and pasta colour). The gene \(\text{Psy-A1}\) was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents \(\{10501\}\). Most hexaploid wheat cultivars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aranoa with high yellow pigment. The \(\text{Psy-B1b}\) allele from tetraploid wheat Kofa is the result of a B-A intergenomic conversion event that probably occurred in Cappelli \(\text{ph1c}\) mutant 1 \(\{10530\}\). An EMS mutation in the \(\text{Psy-E1}\) gene is associated with whiter endosperm in lines carrying the \(\text{Th. elongatum 7EL}\) translocation.

\(\text{Psy1-A1}\{10230\}. 7\text{AL}\{10230\}. \text{tv: Kofa}\{10230\}. \text{ma: Xwmc809-7A - 5.8 cM - Yp7A}\{10501\}\).

\(\text{Psy1-Ab}\). \(\text{v: Chinese common wheats with low yellow pigment content}\{10501\}; \text{PH82-2}\{10501\}; \text{Shaan 9314}\{10501\}; \text{Xinong 336}\{10501\}. \text{c: GenBank EF600064}\{10501\}. 37-bp insertion intron 2 (231 bp fragment for marker \(\text{Yp7A}\) \(\{10501\}\). 676-bp insertion in intron 4 \(\{10501\}\).\)

\(\text{Psy1-Alc}\{10230\}. \text{v: M564}\{10650\}. \text{c: GenBank EU650391}\{10650\}; \text{No 37-bp insertion in intron 2 and no 676-bp insertion in intron 4}\{10530\}; \text{High yellow pigment cultivars: Arrona (PI 464647)}\{10530\}; \text{Dundee (PI 89424, PI 106125)}\{10530\}; \text{Raven (PI 303633, PI 330959)}\{10530\}.\)

\(\text{Psy1-Alf}\{10651\}. \text{tv: Langdon}\{10651\}; \text{T. dicoccum DM28}\{10652\}. \text{c: GenBank EU263018}\{10651\}; \text{FJ393515}\{10652\}.\)

\(\text{Psy1-Alg}\{10652\}. \text{dv: T. urartu PI 428326}\{10652\}. \text{c: FJ393516}\{10652\}.\)

\(\text{Psy1-Alh}\{10652\}. \text{dv: T. urartu UR1}\{10652\}. \text{c: FJ393517}\{10652\}.\)
Psy1-AIh[10652]. dv: T. boeticum BO1[10652]; T. monococcum MO5[10652]. c: FJ393518[10652]; FJ393519[10652].
Psy1-AI[10652]. dv: T. monococcum MO1[10652]. c: FJ393520[10652].
Psy1-AI[10652]. tv: Kofa[10230,10550]; Strongfield[10653]; T. dicoccoides DS6[10652]. c: EU096090[10230,10530]; FJ393524[10652].
Psy1-Aln[10652]. v: Spelt SP9[10652]. c: FJ393526[10652].
Psy1-Alo[10653]. tv: Commander[10653]. c: FJ234424[10653].
Psy1-All[10654]. v: Tasman[10654]. c: EU649792[10654].
Psy1-Alq[10654]. v: Cranbrook[10654]. c: EU649793[10654].
Psy1-Als[10654]. v: Schomburgk[10654]. c: EU649795[10654].
Psy1-Bl[10650]. GenBank EU096093[10530]. [[10530]]. v: Chinese Spring[10530,10650,10564]; Spelt SP9[10652]. tv: T. dicoccoides DS4[10652]. c: FJ393529[10652]; FJ393528[10652]; EU650392[10650]; EU096094[10530]; EU649789[10654].
Psy1-BIb[10650]. v: Neixiang 188[10650]. c: EU650393[10650].
Psy1-BI[10650]. v: CA 9648[10650]. c: EU650394[10650].
Psy1-Bld[10650]. v: Ning 98084[10650]. c: EU650395[10650].
Psy1-Blf[10651]. tv: Langdon[10651]. c: EU263020[10651].
Psy1-Blg[10651]. tv: DR1[10651]; T. dicoccoides DS6[10652]. c: EU650396[10651]; FJ393530[10652].
Psy1-Bil[10652]. tv: T. dicoccoides DS3[10652]. c: FJ393531[10652].
Psy1-BI[10652]. tv: T. dicoccoides DS8[10652]. c: FJ393532[10652].
Psy1-Bln[10530]. Previously designated Psy1-Blb[10656]. tv: Kofa. c: EU096092[10530]; DQ642439[10230].
Psy1-D[10652]. 7DL[10652].
Psy1-Dla[10652]. v: Chinese Spring[10652]. c: EU650397[10652]; EU649790[10654].
Psy1-Dlb[10652]. dv: Ae. tauschii Ae34[10652]. c: FJ393542[10652].
Psy1-Dlc[10652]. dv: Ae. tauschii Ae46[10652]. c: FJ393543[10652].
Psy1-Dle[10652]. v: Spelt SP9[10652]. c: FJ393545[10652].
Psy1-Dlg[10652]. v: Zhonliang 88375[10652]. c: FJ807498[10652].
Psy1-Dlh[10652]. dv: Ae. tauschii Ae37[10652]. c: FJ807499[10652].
Psy1-Dli[10652]. dv: Ae. tauschii Ae38[10652]. c: FJ807500[10652].
Psyl-D1j {10652}. dv: Ae. tauschii Ae42 {10652}. c: FJ807501 {10652}.
Psyl-D1k {10655}. v: Nongda 3291 {10655}. c: FJ807495 {10655}.
Psyl-D1l {10655}. v: Ning 97-18 {10655}. c: FJ807497 {10655}.
Psyl-D1m {10655}. v: Nongda 3291 {10655}. c: FJ807495 {10655}.

Psyl-E1. [Psy-E1].

Psyl-E1a {10655}. GenBank EU096095 {10655}. [Psy-E1a {10655}]. v: Agatha (7EL translocation) {10655}.

Psyl-E1b {10655}. = EU096095 with P to L mutation at amino acid 422 {10655}. [Psy-E1b {10655}]. v: EMS mutant Agatha-28-4 {10655}; Wheatear {10655}.

Psyl-S1 {10652}. al: Ae. speltoides Ae48 {10652}.

Psyl-S1a {10652}. al: Ae. speltoides Ae48 {10652}. c: FJ393536 {10652}.
Psyl-S1b {10652}. al: Ae. speltoides Ae49 {10652}. c: FJ393537 {10652}.
Psyl-S1c {10652}. al: Ae. speltoides Y162 {10652}. c: FJ393538 {10652}.

80.2.33.2. Phytoene synthase 2 (EC 2.5.1.32)
Homology with the same gene in rice (Psy2) {10230}.

Psyl-A1 {10230}. 5A {10230}. tv: Kofa {10230}.

Psyl-B1 {10230}. 5B {10230}. tv: Kofa {10230}. ma: Xgwm191-5B - 17 cM - Psy-B2 {10230}.

80.2.34. Polyphenol oxidase
High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.
Primers different from those in {10386} were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) were similar. A null allele of Ppo-D1 was identified for this locus using primer pair WP3-2 {10504}.

Ppo-A1 {10386}. PPO-2A {10385}. 2AL {10385}. ma: Detected with STS markers PPO18 {10385}; and PPO33 {10386}; Xgwm321-2A - 1.4 cM - Ppo-A1 - 5.8 cM - Xgwm294-2A {10385}.

Ppo-A1a {10386}. PPO-2Aa {10385}. v: Nongda 139 {10386}; Zhongyou 9507 {10386,10385}; others {10386,10504}. c: EF070147 {10386}.
Wheats with this allele tend to have lower PPO activity {10385,10386}.

Ppo-A1b {10386}. PPO-2Ab {10385}. v: Chinese Spring {10386}; CA 9632 {10385,10386}; Nongda 183 {10504}; others {10386,10504}. tv: T. dicoccoides DS4 {10386}. c: EF070148 {10386}.
Wheats with this allele tend to have lower PPO activity {10385,10386}.

Ppo-A1c {10386}. dv: T. urartu UR1 {10657}. c: EU371651 {10657}.

Ppo-A1d {10657}. dv: T. boeoticum BO1 {10657}. c: EU371652 {10657}.

Ppo-A1e {10657}. dv: DR8 {10657}. dv: T. monococcum MO1 {10657}. c: EU371653 {10657}.

Ppo-A1f {10657}. tv: T. dicoccoides DS3 {10657}. c: EU371654 {10657}.

Ppo-A1g {10657}. tv: Langdon {10657}. c: EU371655 {10657}.

Ppo-B1 {10658}. v: Chinese Spring {10658}.

Ppo-B1a {10658}. v: Chinese Spring {10658}. c: GQ303713 {10658}.

Ppo-D1 {10386}. ma: Detected with primers PPO16 and PPO29. Xwmc41-2D - 2.0 cM - Ppo-D1 {10386}.
80.2.35. **Protein disulfide isomerase (EC 5.3.4.1)**

*Pdi-A1*{10422}.  4AL{10422}.  v: {10422}.

*Pdi-B1*{10422}.  4DS{10422}.  v: {10422}.

*Pdi-D1*{10422}.  4BS{10422}.  v: {10422}.

The genes for PDI and their promoters were sequenced in {10423}. A related sequence on 1BS was shown to be a partial, non-expressed copy in {10424}, but not detected in {10409}. PCR-RFLP markers for [TaPDI-4A] and [TaPDI-4B] were designated [Xvut(PDI)-4A] and [Xvut(PDI)-4B] in {10409}. These were also closely associated with Germin (oxalate oxidase {10441}) genes {10409}.

80.2.36. **Isoamylase 1**

*Iso-1*{10295}.  [ISA-1{10295}].  dv: *Ae. tauschii*{10295}.

80.2.37. **Polygalacturonase-inhibiting proteins**

PGIPs are leucine-rich repeat (LRR) proteins involved in plant defence.

*Pgip1*{10390}.  7BS{10390}.  v: CS ditelo 7BL{10390}.  v2: Chinese Spring *Pgip2*{10390}.

*Pgip-A1*{10608}.  v: Langdon{10390}.

*Pgip-1*{10608}.  7DS{10390}.  v: CS ditelo 7DL{10390}.  v2: Chinese Spring *Pgip1*{10390}.

*Pgip-B1*{10608}.  [Tapgip1{10610}].  7BS{10610,10608}.  ma: Xs13M50-7B - 5 cM - *Pgip-B1* - 11.7 cM - Xmgb105s-7B{10608}.

*Pgip-B1a*{10608}.  Tapgip1a {10608}.  tv: Messapia{10608}.

*Pgip-B1b*{10608}.  Tapgip1b, AM884195 {10608}.  tv: *T. turgidum* ssp. *dicoccoides* MG4343{10608}.

This non-expressed allele produces a large amplicon in southern blots using the *Pgip* sequenced as probe, due to an insertion of a Vacuna mutator element {10608}.

*Pgip-D1*{10608}.  [Tapgip2{10610}].  7DS{10610}.  tv: Langdon 7D(7A){10610}; Langdon 7D(7B){10610}.

80.3. **Endosperm storage proteins**

80.3.1. **Glutenins**
These are heterogeneous mixtures of proteins comprising subunits linked by disulfide bonds. 'A' are high-molecular-weight (HMW) and 'B', 'C' and 'D' are low-molecular-weight (LMW) subunits.

Using proteomic analysis of 2D gels of seed storage proteins in 39 ditelocentric lines of cv. CS, 105 protein spots were resolved. Locations of structural genes controlling 26 spots were identified in 10 chromosomal arms (4 on 1BL, 5 on 1BS, 4 on 1DL, 4 on 1DS, 2 on 6AS, 3 on 6BS, 1 on 6DL, 1 on 6DS, 1 on 3BS and 1 on 3BL). Multiple regulators of the same protein located on various chromosome arms were observed. Two novel subunits, named 1Bz and 1Dz, were found to have very similar structures to HMW glutenin subunit 12 (encoded by Glu-D1-2a - see the relevant list below) and were located to chromosome arms 1BL and 1DL, respectively.

80.3.1.1. Glu-1
The Glu-1 loci, all of which are compound, encode HMW glutenin subunits. Each Glu-1 locus in hexaploid wheat contains two genes, the products of which were described as 'x-type' and 'y-type' based on differences in molecular weight and isoelectric point.

Other evidence has shown that these gene products differ in electrophoretic fingerprint pattern and cysteine content, and the genes themselves differ in nucleotide sequence. Although early evidence suggested up to 6 genes in total at each locus, it appears likely that only a single copy of each gene is present at the 1AL, 1BL, and 1DL loci. No 'y-type' protein from the Glu-A1 locus has been demonstrated in hexaploid wheat, although they are found in diploid wheats, and sequencing experiments have shown the presence of two stop codons in the transcribed portion of the gene. Definitive evidence that subunit 21* has a mobility close to that of subunit 21, is a 'x-type' protein rather than a 'y-type' protein has not been obtained. The gene coding for 'x-type' proteins within Glu-A1 is also often silent.

The symbols for the genes within the Glu-1 loci coding for 'x-type' and 'y-type' proteins will be Glu-I-1 and Glu-I-2, respectively, rather than Glu-1x and Glu-1y. The genes are closely linked but recombination has been observed between Glu-B1-1 and Glu-B1-2 with a frequency of 3 in 3,450. It is now evident that all 11 Glu-1 genes may be present in a single wheat chromosome, rather than the 3 chromosomes that made up the group in the early studies.

The subunit nomenclature used is that devised in 1987; however, an alternative system based upon molecular weight was proposed in 1988. A system of naming the Glu-A1-1, Glu-A1-2, Glu-B1-1 and Glu-B1-2 alleles in T. turgidum var. dicoccoides is given in 1996.

In 00115, a comparison between spelt wheats (T. spelta) and bread wheat was carried out for the glutenins using a nomenclature system described in 00118. The Glu-I loci may be recognised by the DNA probe pTag1290 and probe pwhe1(Dy10) and probe pwhe1(Dy10). Individual Glu-I-1 loci on 1A, 1B and 1D and the Glu-I-2 loci may be recognised by specific primers.

In 00105, the evolution of the high molecular weight glutenin loci of the A, B, D and G genomes of wheat was explored; 30 partial allele sequences were compared, designated by Greek letters (alpha, beta, gamma, etc.) (5 of which were cited as Schlumbaum, pers. comm.; the remaining 25 were deposited as GenBank, accession nos. X98583-X98592, X98711-
X98715 and Y12401-Y12410). These partial alleles derive from all six Glu-1-1 and Glu-1-2 loci in current-day samples taken from seven species of wheat, as well as from DNA extracted from charred grain of two samples from archaeological excavations, dated 3000 and 5000 years old, respectively.

Following the first listing which considers the Glu-1 set for hexaploid wheat as a single locus, there is a provisional listing based on x- and y- type glutenins. These are not referenced.

The importance of the HMW glutenin subunits for bread-making quality was first noted from observations in wheat cultivars of related pedigree on the effects of the presence of subunit 1 encoded by Glu-A1a [0197], effects that have repeatedly been confirmed since (for example {0198,0199,01100}).

A nomenclature system for prolamin banding patterns of triticale was proposed in {03139}. Extensive allelic variation in triticale at A1 nomenclature system for prolamin banding patterns of triticale was proposed in {03139}. Glu-1 alleles: reported in {03121}. Extensive allelic variation in triticale at A1 nomenclature system for prolamin banding patterns of triticale was proposed in {03139}. The importance of the HMW glutenin subunits for bread making quality was first noted from observations in wheat cultivars of related pedigree on the effects of the presence of subunit 1 encoded by Glu-A1a [0197], effects that have repeatedly been confirmed since (for example {0198,0199,01100}).

Primers were designated that enabled Ax2* to be distinguished from Ax1 or Ax-null [10641].

Glu-A1{780,1125}. [Glu-A1{420},Glu-A2{420},Glu 1{1415}]. 1A{780}.1AL{781,1125}.

s: CS/Bezostaya 1. v: CS{780,781}; various{420}.

Primers were designated that enabled Ax2* to be distinguished from Ax1 or Ax-null [10641].

Glu-A1a{1116}. 1{1116}. v: Hope.

Glu-A1b{1116}. 2{1116}. v: Bezostaya 1.

Glu-A1c{1116}. Null allele{1116}. v: CS.

Glu-A1d{1535}. v: V74, Spain[1115].

Glu-A1e{1535}. v: 132c, Poland[1115].

Glu-A1f{1535}. v: 112-29, Sudan[1115].

Glu-A1g{1535}. v: Landrace 1600.


Glu-A1i{1527}. [GLU-A1-II{1527}]. tv: CI 12213, India, T. dicoccum; Lambro{1523}.


Glu-A1k{478}. 26{478}. v: BT-2288{478}.

Glu-A1l{847}. tv: Chinook, Canada.

Glu-A1m{1069}. tv: Nugget Biotype 1, Canada, T. durum.


Glu-A1p{1146}. 3'1146. v: David 1.


Glu-A1r{1232}. 39+40{1232}. i: T. thaoudar, IPSR 1020006/6^Sicco.

Glu-A1s{1231}. 41+42{1231}. i: T. thaoudar, G3152/6^Sicco.


The allele designated Glu-A1u and Glu-A1-lu in the appropriate list below encodes a high molecular weight glutenin subunit (denominated 2^B) that is identical to subunit 2* apart from one amino acid difference involving the exchange of serine for cysteine (which itself is due to a C to G point mutation at the 1181 bp point of the coding region of 2*). The authors of {02106} suggest that the additional cysteine residue facilitates the formation of further disulphide bonds (cf. the 1Dx5 subunit) which might lead to an improvement in gluten quality characters.

Glu-A1x{10327}. 2'{10327}. v: TR14165/91{10327}.
Glu-A1y{10535}. [2''{10535}]. v: 211.12014{10535}.

There is a possibility that Glu-A1 alleles i, j (1527) and k (478) correspond to alleles d, e, f or g (1535) that were published shortly earlier. Glu-A1m [(1526)] was changed to n, because the m allele in (1069) has precedence. Allele n [(1526)] was changed to o. An earlier reference to an allele designated Glu-A1d [1411] was withdrawn (1114). There appears to be a minor band associated with subunit 2 encoded by Glu-A1b (1516); this may be the same as a band named A5 in (420).

Six combinations involving 5 HMW subunits [1A (u-z)] are listed in (420), from a study of 109 genotypes including representatives of botanical varieties. A number of alleles in T. turgidum var. dicoccoides populations, 12 at Glu-A1-1 and 3 at Glu-A1-2, were described in (798). In a further study using different germplasm of this species (205), 14 alleles at Glu-A1 were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at Glu-A1-1 (with up to 10 not previously observed), and 5 alleles at Glu-A1-2 (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.

In a study including emmers (T. dicoccum) (00115), new subunits named 1* and 2* were found in accesses MG4378/1 and MG5380/1, respectively, and provisionally assigned to Glu-A1. Until confirmed, they are not included in the Glu-A1 list.

Glu-B1(107),[1125]. [Glt-B1[420],Glt-B2[420],Glt-B3[420],Glu IB[1415]].

1BL{107.780,1125}. v: CS.

Glu-B1a{1116}. 7{1116}. v: Finlor.

Glu-B1b{1116}. 7+{1116}. v: CS.

Glu-B1c{1116}. 7+9{1116}. v: Bezostaya 1.

Glu-B1d{1116}. 6+{1116}. v: Hope.

Glu-B1e{1116}. 20{1116}.20x+20y{03133}. v: Federation.

Glu-B1f{1116}. 13+16{1116}. v: Lancota (rare).

Glu-B1g{1116}. 13+19{1116}. v: NS 335 (rare).

Glu-B1h{1116}. 14+15{1116}. v: Sappo (rare).

Glu-B1i{1116}. 17+18{1116}. v: Gabo.

Glu-B1j{1116}. 21{1116}.21x+21y{03116}. v: Dunav (rare); Foison{03116}.

Glu-B1k{1116}. 22{1116}. v: Serbian (rare).

Glu-B1l{778}. 23+24{778}. v: Spica D.

Glu-B1m{1527}. [GLU-B1-I[1527]]. tv: PI 94640, Iran, T. dicoccum.

Glu-B1n{1527}. [GLU-B1-II[1527]]. tv: PI 355505, Germany, T. dicoccum.


Glu-B1p{1527}. [GLU-B1-IV[1527]]. 23+18{125}. tv: Dritto{1523}; Ethiopia, PI 94655, T. dicoccum{1527}.


Glu-B1r{1527}. [GLU-B1-VII[1527]]. 19{125}. tv: PI 94669, Bulgaria, T. dicoccum{1527}; Lambro{1523}.

Glu-B1s{478}. 7+11{478}. v: BT-2288.

Glu-B1t{847}. v: Supreza, Canada.

Glu-B1u{1069}. 7''+{1146}. v: Owens{1069}; Fiorello{1146}.

Glu-B1v{1069}. v: Mondor.

Glu-B1w{1069}. 6' +8' {1146}. v: Dawbull{1069}; Sieve{1146}.

Glu-B1x{1526}. [GLU-B1-VIII[1526],Glu-B1t{959}]. tv: Canoco de Grao Escuro, Portugal, T. turgidum.

Glu-B1y{1526}. [Glu-B1-VIII[1526],Glu-B1u{959}]. tv: Tremez Mollez, Portugal, T. durum.


Glu-B1ak (899). 7+8 [899]. v: Norstar.


Other genotypes are listed in [10196].

Many of the cultivars carrying the over-expressed subunit 7 encoded by Glu-B1al show %UPP values that transcend the normal range observed for cultivars that lack this subunit (10089), which presumably is associated in some way with its unusually high amount in the grain. The underlying cause of the increased amount may be due to an increased transcriptional rate compared to other alleles, for which a known difference in promoter sequence compared to other alleles expressing normal levels of this subunit (10090) may be responsible.


Glu-B1ar (1229). 34+35 [1229]. v: Jeja Almendros.


Glu-B1bc (03138). 6+17 [03138]. v: ICDW 20975 [03138].


Glu-B1be (10186). tv: T. dicoccoides Israel-A [10186].

Glu-B1bf (10186). tv: T. dicoccoides PI 481521 [10186].

Glu-B1bg (10186). tv: T. dicoccoides PI 478742 [10186].

Glu-B1bh (10327). 13+22 [10327]. v: Grado [10327]; KU-1026 [10327]; KU-1086 [10327]; KU-1094 [10327]; KU-1139 [10327].

The alleles formerly designated \( \text{Glu} \quad \text{Glu} \quad \text{Glu} \quad \text{Glu} \quad \text{Glu} \quad \text{Glu} \quad \text{Glu} \quad \text{Glu} \) - \( \text{By9} \)

that this is in fact true. 6+17, ap

Although alleles assigned to MG5333/1 and MG5507) and 13 accessions MG5400/5 and MG30835/1), 8 of these alleles were distinct from each other, or from others previously observed. Glu-19 alleles included 11 alleles at species {205}, 19 alleles at populations were described in {798}. In a further study using different germplasm of Eight alleles at subunits encoded by a

Glu-By8, for distinguishing subunit

Possible low gene expression at doubled intensity of restriction fragments carrying the gene in Southern blotting {998} as evidenced by increased intensity of the subunit in SDS PAGE and by approximately

Variation in the staining intensity of subunit 7 in different lines was observed {1069}; a

Glu-7 has precedence; also, {1523} states that

A duplication of the gene encoding subunit 7 probably occurred in cultivar 'Red River 68', as evidenced by increased intensity of the subunit in SDS-PAGE and by approximately doubled intensity of restriction fragments carrying the gene in Southern blotting (9989). Possible low gene expression at Glu-B1 was noted for Glu-B1w, where subunits 6*+8* stain very faintly {1146}.

One of the Glu-B1af subunits was numbered 26 in {1146}; 26 was previously used to number the subunit encoded by Glu-Alk {478}. Subunit 28 of Glu-B1ag (28+29) {1146} is referred to as subunit 19* in {1068}. Subunit 23 of Glu-B1p {23+18} and Glu-B1ad (23+22) {125} may not be the same subunit as that numbered 23 of Glu-B1l {23+24} {778}. Glu-B1z carried by Roccia was numbered (7+15) and named Glu-B1-XII in {125}; however, the earlier name, Glu-B1-IX {1523}, has precedence; also, {1523} states that the Glu-B1-IX subunit of faster mobility is slightly slower than subunit 15. Subunit 11 of Glu-B1s {7+11} was so numbered in {478} because its mobility is the same as one of the subunits encoded by a Glu-D1 allele (2+11) described in {755}.

Eight alleles at Glu-B1-1 and 10 alleles at Glu-B1-2 in T. turgidum var. dicoccoides populations were described in {798}. In a further study using different germplasm of this species {205}, 19 alleles at Glu-B1 were observed, including 15 not previously observed; the 19 alleles included 11 alleles at Glu-B1-1 and 14 alleles (including the null allele) at Glu-B1-2, although, as the authors pointed out, it was not conclusively clear how many of these alleles were distinct from each other, or from others previously observed.

In a study including emmer wheats (T. dicoccon) {00115}, new subunits named 7* (in accessions MG5400/5 and MG30835/1), 8* (in accessions MG5400/5, MG30835/1, MG5333/1 and MG5507) and 13* (in accession MG5282/2) were found and provisionally assigned to Glu-B1. Until confirmed, they are not included in the Glu-B1 list. Although alleles Glu-B1i encoding subunits 17+18, and Glu-B1bc encoding subunit 6+17, apparently share a common subunit (Ax17 and By17, respectively) it is not clear that this is in fact true.

Primers were designed to distinguish subunit By8 from By8*, for distinguishing subunit By9-containing alleles from non-By9 alleles, and for diagnosing the presence of Glu-B1f.

Glu-B1bp {10643}. 7* +8 {10643}. v: XM1368-2{10643}; XM1404-2{10643}.
Glu-B1hq{10643}. 7+8** {10643}.

Glu-D1[1100,1125]. [Glt-D1{420},Glt-D2{420},Glu 1D{1415}].

1DL{107,150,780,1100,1125}. v: CS.

Primers were designated that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12 {10641}.

Glu-D1a{1116}. 2+12{1116}. v: CS.

Glu-D1b{1116}. 3+12{1116}. v: Hobbit.

Glu-D1c{1116}. 4+12{1116}. v: Champlein.

Glu-D1d{1116}. 5+10{1116}. v: Hope.

Glu-D1e{1116}. 2+10{1116}. v: Flinor (rare).

Glu-D1f{1116}. 2.2+12{1116}. v: Danchi (rare).

Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality {10573}.

Glu-D1g{478}. 5+9{478}. v: BT-2288.

Glu-D1h{1145}. 5+12{1145}. v: Fiorello, Italy.

Note that the cultivar Fiorello is given as a standard for Glu-D1h encoding subunits 5+12 and for Glu-D1w encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1i{107}. null{107}. v: Nap Hal, Nepal.

Glu-D1j{1146}. 2+12'1146}. v: Tudest.

Glu-D1k{421}. 2{421}. s: CS/Timstein 1D.

Glu-D1l{759}. 12{759}. v: AUS 10037, Afghanistan.

Glu-D1m{759}. 10{759}. v: AUS 13673, Afghanistan.

Glu-D1n{759}. 2.1+10{759}. v: AUS 14653, Afghanistan.

Glu-D1o{755}. 2.1+13{755}. v: AUS 14519, T. macha.

Glu-D1p{1233}. 36{1233}. i: Iranian landrace accession 3048/5* Sicco.

Glu-D1q{124}. 2+11{124}. v: Flinor.

Glu-D1r{1229}. 2.3+12{1229}. v: PI 348465.

Glu-D1s{1032}. 38{1032}. v: Leningradka.

Glu-D1t{668}. 43+44{668}. i: Ae. tauschii accession TA2450/2*.

Glu-D1u{836}. 2+10'{836}. v: Coker 68-15.

Glu-D1v{755}. 2.1+10.1{755}. dv: Ae. tauschii.

Glu-D1w{03124}. 5*+10{03124}. v: Fiorello{03124}.

Note that the cultivar Fiorello is given as a standard for Glu-D1h encoding subunits 5+12 and for Glu-D1w encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1x{755}. 2+T{755}.2+12.2'03124}. dv: Ae. tauschii.

Glu-D1y{755}. 3+T{755}.3+12.2'03124}. dv: Ae. tauschii.

Glu-D1z{755}. 3+10{755}. dv: Ae. tauschii.

Glu-D1aa{755}. 3+10.3'755. dv: Ae. tauschii.

Glu-D1ab{755}. 4.1+10{755}. dv: Ae. tauschii.

Glu-D1ac{755}. 4+10{755}. dv: Ae. tauschii.

Glu-D1ad{755}. 5.1+10.2{755}. dv: Ae. tauschii.

Glu-D1ae{1578}. 2.1+T{1578}.2.1*+12.2'{03124}. dv: Ae. tauschii.

Glu-D1ag{1578}. 1.5+T{1578}.1.5*+12.2'{03124}. dv: Ae. tauschii.

Glu-D1ah{1578}. 1.5+10{1578}. dv: Ae. tauschii.

Glu-D1ai{1578}. 2.1+10.5{1578}. dv: Ae. tauschii.

Glu-D1aj{1578}. 1.5+12{1578}. dv: Ae. tauschii.

Glu-D1ak{1578}. 3+10.5{1578}. dv: Ae. tauschii.

Glu-D1al{02107}. 2.2'02107}. v: MG315.

Glu-D1am{03122}. [Glu-D1-I{03122}]. 2+12'{03122}. v: PI 348495 spelt {03122}.
Glu-D1\text{an} \{03122\}. \ [Glu-D1-II\{03122\}]$. 2+12$^t\{03122\}. \ v: \ PI \ 348672 \ spelt \ \{03122\}.

Glu-D1\text{ao} \{03122\}. \ [Glu-D1-III\{03122\}]$. 2.4+12\{03122\}. \ v: \ PI \ 348473 \ spelt \ \{03122\}.

Glu-D1\text{ap} \{03122\}. \ [Glu-D1-IV\{03122\}]$. 2.5+12\{03122\}. \ v: \ PI \ 348572 \ spelt \ \{03122\}.

Glu-D1\text{aq} \{03124\}. 1.5^t+10.1^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{ar} \{03124\}. 2^t+10.1^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{as} \{03124\}. 1.5^t+10.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{at} \{03124\}. 3^t+10.1^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{au} \{03124\}. 2.1^t+10.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{av} \{03124\}. 2^t+12.3^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{aw} \{03124\}. 1^t+10^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{ax} \{03124\}. 1^t+12^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{ay} \{03124\}. 1^t+10.1^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{az} \{03124\}. 4^t+12.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{ba} \{03124\}. 1^t+12.3^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bb} \{03124\}. 1.5^t+11^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bc} \{03124\}. 1.5^t+10.3^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bd} \{03124\}. 1^t+11^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{be} \{03124\}. 2.1^t+12.4^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bf} \{03124\}. 2^t+12.1^t\{03124\}. \ dv: \ Ae. \ tauschi\{03124\}.

Glu-D1\text{bg} \{03124\}. 3^t+10.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bh} \{03124\}. 4^t+10.1^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bi} \{03124\}. 4^t+10.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bj} \{03124\}. 5^t+11^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bk} \{03124\}. 5^t+10.1^t\{03124\}. \ dv: \ Ae. \ Tauschii.

Glu-D1\text{bl} \{03124\}. 5^t+12.2^t\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bm} \{03124\}. 5^n+null\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bn} \{03124\}. 5^t+12\{03124\}. \ dv: \ Ae. \ tauschii.

Glu-D1\text{bo} \{01099\}. 5^t+12\{01099\}. \ v: \ W958\{10091\}.

This putative new allele encodes two subunits that have very similar electrophoretic mobilities compared to subunits 5+12 encoded by Glu-D1h, but analysis using the specific PCR primers for Dx5 described in \{01009\} and \{01009\} shows that the x-type subunit of Glu-D1bo, provisionally denominated 5' \{10091\}, does not appear to be the same protein as subunit 5 \{10091\}. Definitive evidence awaits sequencing information (See note to allele Glu-D1ls).

Glu-D1k \{421\} appears to have arisen as the result of a deficiency of subunit 12 from Glu-D1a (2+12); subunits 2 and 12 are referred to as D1 and D5 in \{421\}. One of the Glu-D1o subunits has been numbered 13 in \{755\}; 13 was previously used to number a subunit encoded by Glu-B1f (13+16) and Glu-B1g (13+19) \{1116\}. Subunit 9 of Glu-D1g (5+9) was so numbered in \{478\} because its mobility is the same as one of the subunits encoded by Glu-B1c (7+9).

Glu-D1h \{10327\}. 2.1^t+12\{10327\}. \ v: \ KU-1034\{10327\}.

Glu-D1\text{tg} \{10304\}. [Glu-D1h\{10304\}]. 2.6+12\{10304\}. \ v: \ Baidongmai\{10304\}; Hongdongmai\{10304\}; Hongkedongmai\{10304\}; Jinbaojin\{10304\}.

The complete sequence of this subunit was determined \{10319\}.

Glu-D1\text{br} \{10426\}. 5^n+10.1t\{10426\}. \ tv: \ Ae. \ tauschii \ TD81\{10426\}.

Subunit 10.1t possesses a mobility slightly lower than subunit 10 in SDS-PAGE and its deduced amino acid sequence is similar to subunit 12 (8 amino acid differences) \{10426\}; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that Glu-1 gene duplication event probably occurred about 16.83 million years.
Five combinations involving 6 HMW subunits [1D (p-t)] are listed in [420]. Eleven additional Glu-D1 alleles in T. tauschii were described [755].

Seven transfers of Glu-D1a and 10 of Glu-D1d (5+10) from chromosome 1D to chromosome 1A in triticale were described [846].

The subunit 2.2* encoded by Glu-D1al and Glu-D1-lm in the appropriate list below has an unusually high Mr. Comparison of its N-terminal sequence and amino acid composition with those of subunit 2 (encoded by Glu-D1-1a) indicated that its greater Mr, could be due to the presence of a larger central repetitive domain, although further evidence suggested that this does not affect the conformational properties of the subunit [02107]. The alleles originally designated Glu-D1w (encoding 'subunits' 2 (or 2') denoting its origin in the Ae. tauschii genome) +T1+T2), Glu-D1af (encoding 3 (or 3')+T1+T2) and Glu-D1ag (encoding 1.5 (or 1.5')+T1+T2) share the component T1 that was originally classified as a HMW glutenin. However, it has since been shown [02108] that this protein is soluble in aqueous ethanol, casting doubt upon this classification. More recently, it was shown [02109], from one and two dimensional gel electrophoresis based upon SDS-PAGE and A-PAGE, and from N-terminal sequencing, that this protein is an omega-gliadin of unusually low electrophoretic mobility in SDS-PAGE, encoded by a locus located on the short arm of chromosome 1D, though distant (13.18 cM) from the principle gliadin-encoding locus on 1D, Gli-D1, and 40.20 cM from the high molecular weight encoding locus, Glu-D1. The authors named the locus Gli-DT1 (see Gliadins). Reference to T1 was consequently removed from the Glu-D1 list. As a consequence of this finding, allele Glu-D1w was reused for a distinct allele, and Glu-D1af was omitted and will be reused for a future allele, since the combinations of subunits that these alleles originally represented are no longer unique.

In [03124], null alleles were observed for both Glu-D1-1 and Glu-D1-2, which, naturally, are not necessarily the same as those previously reported for this locus, meaning that composite alleles involving them in this study and corresponding to combinations apparently already listed in the Catalogue, may, in fact, represent novel alleles. It is also found that certain subunits of apparently identical relative mobility in SDS-PAGE showed different surface hydrophobicities in RP-HPLC; and the reverse situation was also observed (the same hydrophobicity, but different electrophoretic mobilities).

It was shown [03126] that the relatively small size of a y-type HMW glutenin subunit, named 12.4' (encoded by Glu-D1-1t [03124] - see below) and carried by accession CPI110750 of Ae. tauschii, is due to the deletion of blocks of repetitive motifs, amounting to approximately 200 amino acids, probably caused by unequal crossing-over.

Alleles and subunits at Glu-Al-1 and Glu-Al-2; Glu-Al-1 encodes X-type glutenins and Glu-Al-2 encodes y-type glutenins.

Glu-D1bs(10642). 1.6+12.3' {10642}. dv: Ae. tauschii TD16{10642}.

Glu-D1bt(10568). 2.1'+12.3' {10568}. v: Syn 396{10568}.

Glu-Al-1.

Glu-Al-1a. Null. v: CS.

Glu-Al-1b. 1. v: Hope.

Glu-Al-1c. 2'. v: Bezostaya 1.

A PCR marker specific for the Glu-Al-1c (Ax2') allele was developed in [0147].

Glu-Al-1d. v: V74, Spain.

Glu-Al-1e. v: 132c, Poland.

Glu-Al-1f. v: 112-29, Sudan.

Glu-Al-1g. v: Landrace 1600.
Glu-A1-1i. tv: CI 12213, India, T. dicoccum.
Glu-A1-1j. tv: PI 352359, Germany, T. dicoccum; Lambro.
Glu-A1-1l. tv: Chinook, Canada.
Glu-A1-1m. tv: Nugget Biotype 1, Canada.
Glu-A1-1r. i: T. thaoudar IPSR 1020006/6 Sicco.
Glu-A1-1s. i: T. thaoudar G3152/6 Sicco.

Glu-A1 is a provisional designation; definitive evidence that subunit 21*, which has a mobility similar to that of subunit 21, is a 'x-type' and not a 'y-type' protein has not been obtained.

Glu-A1-1v{10327}. 2.1*{10327}. v: Grado{10327}; KU-1026{10327}; KU-1086{10327}; KU-1094{10327}; KU-1139{10327}.
Glu-A1-1w{10327}. 2'1{10327}. v: TR114165/91{10327}.
Glu-A1-1x{10535}. 2''{10535}. v: 211.12014{10535}.

Glu-A1-2c. 42. i: T. thaoudar G3152/6 Sicco.

Glu-B1.
Glu-B1-1a. 7. v: CS.

A PCR marker (2373 bp) for the Glu-B1-1a (Bx7) allele was developed in {0145}.
Glu-B1-1b. 7. v: Flinor, Bezostaya 1, Owens, Norstar.
Glu-B1-1c. 7. v: Adonis.
Glu-B1-1d. 6. v: Hope.
Glu-B1-1e. 20. v: Federation.
Glu-B1-1f. 13. v: Lancota.
Glu-B1-1g. 14. v: Sappo.
Glu-B1-1h. 17. v: Gabo.
Glu-B1-1i. 21.21x{03116}. v: Dunav; Foisson{03116}.
Glu-B1-1j. 23. v: Spica D.
Glu-B1-1k. tv: PI 94640, Iran, T. dicoccum.
Glu-B1-1l. tv: PI 355505, Germany, T. dicoccum.
Glu-B1-1m. tv: PI 352354, Ethiopia, T. dicoccum.
Glu-B1-1n. tv: PI 94633, Morocco, T. dicoccum.
Glu-B1-1o. v: Supreza, Canada.
Glu-B1-1p. v: Mondor.
Glu-B1-1q. tv: Canoco de Grao Escuro, Portugal.
Glu-B1-1r. tv: Tremez Mollez, Portugal.
Glu-B1-1s. tv: Quaduro, Italy.
Glu-B1-1t. tv: Athena, Italy.
Glu-B1-1v. 28. v: Forlani.
Glu-B1-1w. Null. v: Olympic mutant.
Glu-B1-1x. 30. v: Marinar.
Glu-B1-1y. 32. v: BG-1943.
Glu-B1-1z. 34. v: Jeja Almendros.
Glu-B1-1aa. 37. v: Shedraya Polesja.
Glu-B1-1ab. 6*. v: Dawbill.
Glu-B1-1ac{03116}. 6.8{03116}. v: Carnac hexaploid triticale{03116}.
Glu-B1-1ad{03122}. 13*{03122}. v: PI 348767 spelt {03122}.
Glu-B1-1ae{010327}. 14*{010327}. v: TRI1553/92{010327}.
Glu-B1-1af{010327}. 6.1{010327}. v: Hercule{010327}; KU-3418{010327}; KU-3446{010327}; Rouguin{010327}; Schwabenkorn{010327}; SP3{010327}; Steiners Roter Tiroler{010327}; TRI4613/75{010327}.
Glu-B1-1ag{010643}. 7**{010643}. v: XM1368-2{010643}.

Glu-B1-2.
Glu-B1-2a. 8. v: CS.
Glu-B1-2b. 9. v: Bezostaya 1.
Glu-B1-2c. 16. v: Lancota.
Glu-B1-2d. 19. v: NS 335.
Glu-B1-2e. 15. v: Sappo.
Glu-B1-2f. 18. v: Gabo.
Glu-B1-2g. 22. v: Serbian.
Glu-B1-2h. 24. v: Spica D.
Glu-B1-2i. tv: PI 355505, Germany, T. dicoccum.
Glu-B1-2k. tv: PI 94633, Morocco, T. dicoccum.
Glu-B1-2l. 11. v: BT-2288.
Glu-B1-2m. v: Supreza, Canada.
Glu-B1-2n. v: Mondor.
Glu-B1-2o. 8*. v: Dawbull.
Glu-B1-2q. tv: Tremez Mollez, Portugal, T. durum.
Glu-B1-2r. tv: Quaduro, Italy, T. durum.
Glu-B1-2s. 18*. v: David.
Glu-B1-2t. 27. v: Cologna 1.
Glu-B1-2u. 29. v: Forlani.
Glu-B1-2w. 31. v: Marinar.
Glu-B1-2x. 33. v: BG-1943.
Glu-B1-2y. 35. v: Jeja Almendros.
Glu-B1-2z{03116}. 20y{03116}. v: Carnac hexaploid triticale{03116}.
Glu-B1-2aa{03122}. 18’{03122}. v: PI 348631 spelt {03122}.
Glu-B1-2ab{03116}. 21y{03116}. v: Foison{03116}.
Glu-B1-2ae{010327}. 22*{010327}. v: Grado{010327}; KU-1026{010327}; KU-1086{010327}; KU-1094{010327}; KU-1139{010327}.
Glu-B1-2ad{010327}. 22.1{010327}. v: Hercule{010327}; KU-1135{010327}; Rouguin{010327}; Schwabenkorn{010327}; SP3{010327}; Steiners Roter Tiroler{010327}.
Glu-B1-2ae{010327}. 15*{010327}. v: TRI1553/92{010327}.
Glu-B1-2af{010327}. 19*{010327}. v: KU-3410{010327}; Rechenbergs Frueher Dinkel{010327}; Renval{010327}; SP1{010327}; TRI9885/74{010327}; Zeiners Weiser Schlegel{010327}.
Glu-B1-2ag{010643}. 8**{010643}. v: XM1404-2{010643}.

Glu-D1.
Glu-D1-1a. 2. v: CS.


**PROTEINS**

\[\text{Glu-D1-1b.} \quad 3. \ v: \text{ Hobbit.} \]
\[\text{Glu-D1-1c.} \quad 4. \ v:\text{ Champlein.} \]
\[\text{Glu-D1-1d.} \quad 5. \ v: \text{ Hope.} \]
   
   PCR markers specific for the \textit{Glu-D1-1d} (Dx5) allele were developed in \{0145\} and \{0147\}.
\[\text{Glu-D1-1e.} \quad 2.2. \ v: \text{ Danchi.} \]
\[\text{Glu-D1-1f.} \quad \text{Null.} \ v:\text{ Nap Hal, Nepal.} \]
\[\text{Glu-D1-1g.} \quad 2.1. \ v:\text{ AUS 14653, Afghanistan.} \]
\[\text{Glu-D1-1h.} \quad 2.3. \ v:\text{ PI 348465.} \]
\[\text{Glu-D1-1i.} \quad 38. \ v:\text{ Leningradka.} \]
\[\text{Glu-D1-1j.} \quad 43\{668\}. \ i:\text{ Ae. tauschii accession TA2450/2\textsuperscript{*}.} \]
\[\text{Glu-D1-1k.} \quad 4.1\{755\}. \ dv:\text{ Ae. tauschii.} \]
\[\text{Glu-D1-1l.} \quad 1.5\{1578\}. D'x1.5\{10306\}. \ dv:\text{ Ae. tauschii accession SQ-214\{10306\}.} \]
   
   A restriction enzyme based method named the 'restricted deletion method' was used to characterize the ORF of this subunit \{10306\} (as in the case of subunit D'y10 encoded by \textit{Glu-D1-2u} \{10306\}. Allele-specific PCR markers were developed based upon SNPs located at the non-repetitive N-terminal \{10320\}.
\[\text{Glu-D1-1m.} \quad 02107. \ 2.2\{02107\}. \ v:\text{ MG315.} \]
\[\text{Glu-D1-1n.} \quad 03122. \ 2.4\{03122\}. \ v:\text{ PI 348473 spelt\{03122\}.} \]
\[\text{Glu-D1-1o.} \quad 03122. \ 2.5\{03122\}. \ v:\text{ PI 3484572 spelt\{03122\}.} \]
\[\text{Glu-D1-1p.} \quad 03124. \ 1\{03124\}. \ dv:\text{ Ae. tauschii\{03124\}.} \]
\[\text{Glu-D1-1q.} \quad 03124. \ 5\{03124\}. \ dv:\text{ Ae. tauschii\{03124\}.} \]
\[\text{Glu-D1-1r.} \quad 755. \ 5.1\{755\}. \ dv:\text{ Ae. tauschii.} \]
   
   This allele was designated \textit{Glu-D1-1j} in the 1998 Catalogue edition.
\[\text{Glu-D1-1s.} \quad 10091\{10091\}. \ 5\{10091\}. \ v:\text{ W958\{10091\}.} \]
   
   This putative allele encodes a subunit, provisionally denominated 5' \{10091\}, that has a very similar electrophoretic mobility compared to subunit 5 encoded by \textit{Glu-D1-1d}, but analysis using the specific PCR primers for Dx5 described in \{10092\} and \{10093\} shows that it does not appear to be the same protein as subunit 5 \{10091\}. Definitive evidence awaits sequencing information (See note to allele \textit{Glu-D1bo}).
\[\text{Glu-D1-1t.} \quad 10304\{10304\}. \ 2.6\{10304\}. \ v:\text{ Baidongmai\{10305\}; Jinbaojin\{10305\};} \]
   
   Hongdongmai\{10305\}; Hongkedongmai\{10305\}.
\[\text{Glu-D1-1u.} \quad 10327\{10327\}. \ 2.1\{10327\}. \ v:\text{ KU-1034\{10327\}.} \]
\[\text{Glu-D1-1v.} \quad 10642\{10642\}. \ [1.6\{10642\}]. \ dv:\text{ Ae. tauschii TD16\{10642\}.} \]

**Glu-D1-2.**

\[\text{Glu-D1-2a.} \quad 12. \ v:\text{ CS.} \]
   
   A PCR marker (612 bp) for the \textit{Glu-D1-2a} (Dy12) allele was developed in \{0145\}.
\[\text{Glu-D1-2b.} \quad 10. \ v:\text{ Hope.} \]
   
   PCR markers (576 bp and 2176bp) for the \textit{Glu-D1-2b} (Dy10) allele were developed in \{0145\} and \{0147\}, respectively.
\[\text{Glu-D1-2c.} \quad 9. \ v:\text{ BT-2288.} \]
\[\text{Glu-D1-2d.} \quad \text{Null.} \ v:\text{ Nap Hal, Nepal.} \]
\[\text{Glu-D1-2e.} \quad 12^{*}. \ v:\text{ Tudest.} \]
\[\text{Glu-D1-2f.} \quad 13. \ v:\text{ AUS 14519, T. macha.} \]
\[\text{Glu-D1-2g.} \quad 36. \ i:\text{ Iranian landrace 3048/5\textsuperscript{*} Sicco.} \]
\[\text{Glu-D1-2h.} \quad 11. \ v:\text{ Flinor.} \]
\[\text{Glu-D1-2i.} \quad 668\{668\}. \ i:\text{ Ae. tauschii TA2450/2\textsuperscript{*}.} \]
\[\text{Glu-D1-2j.} \quad 836\{836\}. \ v:\text{ Coker 68-15.} \]
\[\text{Glu-D1-2k.} \quad 755\{755\}. \ T1\{755\}. \ dv:\text{ Ae. tauschii.} \]
\[\text{Glu-D1-2l.} \quad 755\{755\}. \ T2\{755\}. \ dv:\text{ Ae. tauschii.} \]
\[\text{Glu-D1-2m.} \quad 755\{755\}. \ 10.1\{755\}. \ dv:\text{ Ae. tauschii.} \]
Glu-D1-2n\{755\}. 10.2\{755\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2\textit{o}\{755\}. 10.3\{755\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2\textit{p}\{1578\}. 10.5\{1578\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2q\{03122\}. 12’\{03122\}. \textit{v}: PI-348495 spelt wheat accession\{03122\}.

Glu-D1-2r\{03124\}. 12.1’\{03124\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2s\{03124\}. 12.3’\{03124\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2t\{03124\}. 12.4’\{03124\}. \textit{dv}: \textit{Ae. tauschii}.

Glu-D1-2u\{10306\}. D’y10\{10306\}. \textit{v}: \textit{Ae. tauschii} accession SQ-214\{10306\}.

A restriction enzyme based method named the 'restricted deletion method' was used to characterize the ORF of this subunit \{10306\} (as in the case of subunit 1.5 (or D’y1.5 \{10306\}) encoded by \textit{Glu-D1-1I} \{10306\}). This subunit was first recognized as being different from subunit 1- encoded by \textit{Glu-D1-2b} in hexaploid wheat in \{10307\}.

\textit{Glu-Ag1}\{374\}. 1Ag\{374\}. \textit{ad}: Vilmorin 27/\textit{Th. intermedium}.

\textit{Glu-E1}\{781\}. 1ES\{781\}. \textit{ad}: \textit{CS/E. elongata}.

HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced \{10439\} and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain, but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intra-molecular disulphide bond formation.

Four \{10660, 10661\} and 11 \{10662\} alleles were observed in \textit{Agropyron elongatum} (\textit{E}e genome, \textit{2n} = 10\textit{X} = 70) and named \textit{Aex1} to \textit{Aex5} (producing \textit{x-type} subunits) and \textit{Aey1} to \textit{Aey10} (producing \textit{y-type} subunits). \textit{Aex4}, \textit{Aey7} and \textit{Aey9} were very similar to three alleles in the diploid progenitor \textit{Lophopyrum elongatum} \{10439, 10663\}. The C-terminal regions of three of the \textit{y-type} subunits (products of \textit{Aey8}, \textit{Aey9} and \textit{Aey10}) were more similar to \textit{x-type} subunits than to other \textit{y-type} subunits \{10662\}. The subunit from \textit{Aex4} contained an additional cysteine residue, which may be associated with good processing quality in wheat introgression lines \{10662\}. Allele \textit{Aey-4} was a chimeric gene formed by recombination of two other genes \{10662\}.

\textit{Glu-E1a}\{781\}. \textit{ad}: \textit{CS/L. elongatum} W0622\{781\}.

\textit{Glu-E1b}\{10644\}. \textit{ad}: Langdon/L. elongatum DGE-1\{10644\}. \textit{al}: \textit{L. elongatum} PI 53179\{10644\}.

\textit{Glu-H1}\{781\}. \textit{[Hor 3\{1337\}]. 1H\{781\}.1HL\{1337\}. \textit{ad}: \textit{CS/Betzes}\{781\}. \textit{al}: Various barley cultivars\{1337\}.

\textit{Glu-HI}\{1037\}. 1H\{1123\}. \textit{ad}: \textit{CS/H. chilense}.

38 accessions (natural populations) of \textit{Hordeum chilense} carrying the following 10 subunits were used as the maternal parents of 121 lines of primary tritordeum, and evaluations for associations with bread-making quality initiated \{03114\}. Subunits 1\textit{Hch}, 2\textit{Hch} and 3\textit{Hch} were previously referred to as \textit{Hch}a, \textit{Hch}b and \textit{Hch}c \{03112\}.

\textit{Glu-Hch1a}\{03114\}. 1H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H1\{03114\}.

\textit{Glu-Hch1b}\{03114\}. 2H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H11\{03114\}.

\textit{Glu-Hch1c}\{03114\}. 3H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H7\{03114\}.

\textit{Glu-Hch1d}\{03114\}. 4H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H16\{03114\}.

\textit{Glu-Hch1e}\{03114\}. 5H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H47\{03114\}.

\textit{Glu-Hch1f}\{03114\}. 6H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H220\{03114\}.

\textit{Glu-Hch1g}\{03114\}. 7H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H293\{03114\}.

\textit{Glu-Hch1h}\{03114\}. 8H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H297\{03114\}.

\textit{Glu-Hch1i}\{03114\}. 9H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H252\{03114\}.

\textit{Glu-Hch1j}\{03114\}. 10H\textit{ch}\{03114\}. \textit{al}: \textit{H. chilense} Accession H210\{03114\}.

\textit{Glu-HI}\{1037\}. 1HL\{1037\}. \textit{ad}: \textit{CS/E. trachycaulum}.
Five new x-type subunits (plus the null allele) and four y-type subunits were reported in {10094}. They vary principally through duplications and deletions of the tri-, hexa- and nona-peptide motifs found in the central repetitive region of the subunits. Orthologous genes were found to be more closely related than paralogous genes, supporting the hypothesis that gene duplication occurred before Triticaceae speciation {10095, 10094}. From study of chromosome substitutions in bread wheat {03117}, it was found that a chromosome 1R carrying HMW secalin subunit 6.5 (Glu-R1e), originally derived from the ‘Petkus’ rye population, was associated with bread making quality (i) intermediate between chromosome 1A carrying the null allele Glu-A1c and chromosome 1A carrying HMW glutenin subunit 2’ encoded by Glu-A1b; (ii) equivalent to a chromosome carrying HMW glutenin subunit 7 encoded by Glu-B1a; and (iii) inferior to chromosomes 1D with distinct alleles.

Glu-R1-1.
Glu-R1-1a {03116}. 1’{03116}. v: Indiana hexaploid triticale{03116}.
Glu-R1-1b {03116}. 2’{03116}. v: Graal hexaploid triticale{03116}.
Glu-R1-1c {03116}. 6’{03116}. v: Alamo hexaploid triticale{03116}.
Glu-R1-1d {03115}. 0.8’{03115}. v: Carmara hexaploid triticale{03115}.
Glu-R1-1e {03115}. 5.8’{03115}. v: Arrayan hexaploid triticale{03115}.

Glu-R1-2. 1R, 1RL.
Glu-R1-2a {03116}. 4’{03116}. v: Indiana hexaploid triticale{03116}.
Glu-R1-2b {03116}. 6.5’{03116}. v: Graal hexaploid triticale{03116}.
Glu-R1-2c {03116}. 13’{03116}. v: Alamo hexaploid triticale{03116}.
Glu-R1-2d {03116}. 9’{03116}. v: Olympus hexaploid triticale{03116}.

Glu-R2{1339}. 1R{1339}, 1RL{1339,1340}. ad: CS/S. montanum {1339,1340}.

Glu-S1{1228}. 1S1L{1228}. ma: In Ae. longissima 2/Ae. longissima 10, Glu-S1, Glu-S3, one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one and other {1228} as follows: Glu-S1 - 15.9 cM - Gpi-S1 - 38 cM - Glu-S4/5 - 7.1 cM - Glu-S3 - 0.9 cM - Gli-S1 - 5.6 cM - Gli-S5. Glu-S1 is located in 1S1L and the other loci are in 1S5S.

Glu-U1{150}. 1U{150,781}. ad: CS/Ae. umbellulata {150,781}.

Glu-V1{111,242,1026}. 1V{1026,1111}. ad: CS/D. villosum; Creso/D. villosum.
Glu-V1a {1651}. 71{1651}. al: D. villosum.
Glu-V1b {1651}. 72{1651}. al: D. villosum.
Glu-V1c {1651}. 73{1651}. al: D. villosum.
Glu-V1d {1651}. 74{1651}. al: D. villosum.

Glu-R1{781,1356}. [Sec 3{1336}]. 1R{781,1336}, 1RL{1356,1340}. ad: CS/Imperial; Holdfast/ King II{1340}. tr: CS Imperial 1DS, 1RL{1356}.
Glu-R1a {03116}. 1’{03116}. v: Indiana hexaploid triticale{03116}.
Glu-R1b {03116}. 2’{03116}. v: Graal hexaploid triticale{03116}.
Glu-R1c {03116}. 6’{03116}. v: Almo hexaploid triticale{03116}.
Glu-R1d {03116}. 2’{03116}. v: Olympus hexaploid triticale{03116}.
Glu-R1e {03116}. 6.5’{03116}. v: Clercal hexaploid triticale{03116}.
Glu-R1f {03115}. 0.8’{03115}. v: Carmara hexaploid triticale{03115}.
Glu-R1g {03115}. 5.8’{03115}. v: Arrayan hexaploid triticale{03115}.

There is a difficulty in the assignment of subunit 6’ in the Glu-R1-1 and Glu-R1-2 lists, since it appears as an x-type subunit in allele Glu-R1c and as a y-type subunit in allele Glu-R1f. It is currently provisionally assigned to the Glu-R1-1 list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

The Glu-R1-1 and Glu-R1-2 lists are not free of ambiguity. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.
Alleles and subunits at Glu-V1 and GLU-V1-2: The following is analogous to the Glu-I-1 and Glu-I-2 lists given earlier to identify x-type and y-type subunits in wheat. It was assumed that where an allele at Glu-V1 produces only a single subunit, it is an x-type subunit and so encoded by Glu-V1-1 rather than by Glu-V1-2; the electrophoretic mobilities of the subunits are all greater, though some only marginally so, than subunit 7 encoded by Glu-B1-1a (an x-type subunit), and extend beyond the mobility of subunit 12 encoded by Glu-D1-2a (a y-type subunit) \(1651\); therefore, it is quite possible that any one of the subunits designated as encoded by Glu-V1-1 is, in fact, encoded by Glu-V1-2. The designation given here is intended to be the most practically useful until the identities of the genes encoding the alleles are directly established.

### Glu-V1-1.

<table>
<thead>
<tr>
<th>Allele</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glu-V1-1a (1651)</td>
<td>(71{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1b (1651)</td>
<td>(72{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1c (1651)</td>
<td>(73{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1d (1651)</td>
<td>(74{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1e (1651)</td>
<td>(75{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1f (1651)</td>
<td>(76{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1g (1651)</td>
<td>(77{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1h (1651)</td>
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<td>Glu-V1-1i (1651)</td>
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<td>Glu-V1-1j (1651)</td>
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<td>Glu-V1-1k (1651)</td>
<td>(null{1651}. \text{al}: D. villosum.</td>
</tr>
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<td>Glu-V1-1l (1651)</td>
<td>(81{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1m (1651)</td>
<td>(83{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-1n (1651)</td>
<td>(85{1651}. \text{al}: D. villosum.</td>
</tr>
</tbody>
</table>

### Glu-V1-2.

<table>
<thead>
<tr>
<th>Allele</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glu-V1-2a (1651)</td>
<td>(null{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-2b (1651)</td>
<td>(82{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-2c (1651)</td>
<td>(84{1651}. \text{al}: D. villosum.</td>
</tr>
<tr>
<td>Glu-V1-2d (1651)</td>
<td>(86{1651}. \text{al}: D. villosum.</td>
</tr>
</tbody>
</table>

A Chinese cultivar of \(T. aestivum\), Xiaoyanmai 7, carries a subunit with electrophoretic mobility in 10% SDS-PAGE well beyond that of subunits so far observed in \(T. aestivum\). It may derive from \(Agropyron elongatum\), which was used in the breeding programme that led to the variety \(1538\). It has not been given a subunit number or allelic designation, because its genetic control has not been elucidated.

### Glu-Ta1 \(10449\).

<table>
<thead>
<tr>
<th>Allele</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glu-Ta1a (10449)</td>
<td>(Ta. crinitum) PI 204577{10449}.</td>
</tr>
<tr>
<td>Glu-Ta1b (10449)</td>
<td>(Ta. crinitum) PI 204577{10449}.</td>
</tr>
<tr>
<td>Glu-Ta1c (10449)</td>
<td>(Ta. crinitum) PI 561094{10449}; (Ta. asperum) PI 561091{10449}; PI 561092{10449}.</td>
</tr>
<tr>
<td>Glu-Ta1d (10449)</td>
<td>(Ta. caput-medusae) PI 598389{10449}.</td>
</tr>
</tbody>
</table>
Glu-Ta{10449}. al: Ta. caput-medusae PI 577708{10449}.
Glu-Ta{10449}. al: Ta. caput-medusae PI 577710{10449}.

Each allele identified to date encodes two subunits, an x-type and a y-type. The x-type subunits are slower or equal in mobility to subunit Dx2 of wheat, whereas the y-type subunits are faster than subunits Dx12 {10449}. Phylogenetic analysis based upon the sequence of two genes designated Tax and Tay isolated from Ta. crinitum PI 204577 suggest that the Tax subunit was most closely related to Ax1, Cx (Ae. caudata), Ux (Ae. umbellulata) and Dx5, and the Tay subunit to Ay, Cy and Ry (Secale cereale) {10449}.

80.3.1.2. Glu-2
Glu-B2{819,277}. [XGlu-B2{277}]. 1BS. s: CS*/Cheyenne 1B{277}. stv: Langdon*/T. turgidum var. dicoccoides 1B{277}.
Glu-B2a{00114}. 12{00114}. tv: Mexicali.
Glu-B2b{00114}. Null{00114}. tv: Langdon.

Gli-B3 was designated Glu-B2 {589} until the name of the locus was changed in {1119}.
Glu-B2c{10215}. 12*{10215}. tv: Alcala la Real{10215}.

80.3.1.3. Glu-3

The Glu-3 loci are defined as the cluster of LMW glutenin genes previously considered a component of the compound Gli-1 loci.

More than 30 LMW glutenin complete genes, partial genes or pseudogenes have been sequenced from Triticum species (reviewed in {0245}).

In T. aestivum, only Glu-B3 was shown to recombine with the gliadin genes (1.7 +/- 0.8) {1355,1358}. However, in T. durum, recombination was observed for both Glu-A3 and Glu-B3 with their respective Gli-1 loci: the map distance between Glu-A3 and Gli-A1 has been estimated as 1.3 +/- 0.4 cM {1242}, and that between Glu-B3 and Gli-B1 as 2.0 +/- 0.8 in {1144} and as 2.0 +/- 0.4 in {1242}. It appears that Glu-B3 is proximal to Gli-B1, and there is some evidence, albeit only tentative as the authors acknowledge, that Glu-A3 is proximal to Gli-A1 {1242}.

Whereas hitherto it has been widely thought that all the LMW subunits of glutenin were encoded by genes located on the chromosomes of homoeologous group 1, it has been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of the C subunits must be controlled by loci elsewhere in the genome {482}.

A novel type of polymeric protein (Mr approx. 71,000) was reported in the Australian advanced breeding line DD118 {03125}. It participates in the polymeric structure of glutenin (possibly as a chain terminator), and with an Mr of approximately 71,000, could be considered as a D-subunit of LMW glutenin. However, N-terminal sequencing suggests it to be a Gli-B1 type omega-gliadin that has acquired a cysteine residue through mutation.

In an electrophoretic survey of 51 primary tritordeums {03113}, 20 distinct whole banding patterns (a-t), each consisting of between one and three bands, were observed for D-zone prolamin exhibiting glutenin-like solubility characteristics.

In 85 Japanese common wheat cultivars and 61 elite F{sub 6} breeding lines, 3 alleles were observed at each of Glu-A3 and Glu-B3, and 2 alleles at Glu-D3 were named according to their parental origins in three doubled haploid mapping populations {03135}.

C-type LMW glutenin subunits in CS were assigned to chromosome groups 1 and 6, and
shown to have sequences very similar to those of alpha- and gamma-gliadins (03134). The authors suggest that they may be encoded by novel genes at loci tightly linked or present within the Gli-1 and Gli-2 loci, unlike other LMW glutenin subunits encoded by the Glu-3 loci.

The HMW and LMW glutenin subunits carried by chromosome 1A\textsuperscript{n} of \textit{T. monococcum} accession G1777 were characterised electrophoretically and evaluated for quality characteristics using recombinant chromosome substitution lines with chromosome 1A of CS (03142). The HMW subunits from G1777 are promising for bread-making quality, whereas its LMW subunits are promising for biscuit-making quality.

The bread wheat cv. Salmone has been shown to carry two DNA fragments designated as SF720 and SF750 located on the chromosome 1B satellite and associated with the presence of two LMW glutenin subunits (03143). However, the authors suggest that they occur at a locus other than \textit{Glu-B3} due to their relatively high frequency of recombination with \textit{Gli-B3}.

A naming system in which roman numerals are assigned to whole banding patterns for the LMW glutenin subunit is given in (03131) as an alternative to the LMW-1/2 system described in (03136). A further system naming whole banding patterns from LMW-1 to LMW-23 in emmer wheat is described in (03137).

In (00111), in a study of common and durum wheats from Portugal, the authors used the nomenclature system described in (00113) for the LMW subunits in common wheat, and that described in (00114) for the LMW subunits in durum wheat. The latter system was updated according to (02110), but has been changed herein to new alleles with the earlier durum designation (00114) given as synonyms. In (03116), it was suggested that \textit{Glu-B3} (common wheat standard genetic stock) is equivalent to \textit{Glu-B3r} (durum wheat standard genetic stock), and that (referring to article (03127)) LMW subunits observed in some Portuguese triticales could be of the durum type.

A novel storage protein gene with chimerical structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated \textit{Ch1} to \textit{Ch8}, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci \textit{Gli-1} and \textit{Glu-3}. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated (10307).

\textbf{Glu-A3} (1358). 1AS (1358). \textbf{v}: CS.

The first 7 alleles were distinguished using 5 allele-specific primer sets (10185). Further mainly Australian genotypes with alleles \textit{a} to \textit{f} are listed in (10185).

\textit{Glu-A3a} (481). \textbf{v}: CS.
\textit{Glu-A3b} (481). \textbf{v}: Gabo.
\textit{Glu-A3c} (481). \textbf{v}: Cheyenne.
\textit{Glu-A3d} (481). \textbf{v}: Cappelle Desprez, Orca; Suneca (10185).
\textit{Glu-A3e} (481). \textbf{v}: Halberd (10185); Hope, Insignia.
\textit{Glu-A3f} (481). \textbf{v}: Rescue.
In 112 common wheat cultivars from Argentina, 11 microsatellite alleles plus a null allele were found at the Glu-A3 locus \{03123\}.

Three different approaches were employed to identify putative SNPs used to design gene-specific primers for LMW-GS genes, and six functional STS markers, three for Glu-B3 and three for Glu-D3 \{10664\}. These markers distinguished cultivars with different haplotypes at the Glu-B3 and Glu-D3 loci, but there was no clear correlation between the alleles of cultivars defined by protein electrophoretic mobility and the separation patterns of the DNA
markers, since all three Glu-3 loci were multiple gene loci and each protein electrophoretic
mobility allele was controlled by 3-6 coding genes {10665}.

Glu-D3a{481}. v: CS.
Glu-D3b{481}. v: Gabo.
Glu-D3c{481}. v: Insignia, Cappelle Desprez.
Glu-D3d{481}. v: Norin-61A.
Glu-D3e{481}. v: Orca, Thatcher.
Glu-D3f{10548}. v: Cheyenne{10548}.
Glu-D3g{10558}. v: Hira-1{10558}.
Glu-D3h{10558}. v: India 115{10558}.
Glu-D3i{10558}. v: Orca, Thatcher.
Glu-D3j{10558}. v: Hira-2{10558}.
Glu-D3k{10558}. v: Lincoln{10558}.

Glu-E3{480}. 1ES{480}. su: CS/E. elongata.
Glu-S3{480,1228}. 1S{480}.1S{1228}. su: CS/Ae. longissima{480,1228}. ma: In Ae. longissima 2/Ae.longissima 10 glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one another in {1228} as follows: Glu-S1 - 15.9 cM - Gpi-S1 - 38 cM; Gli-S4 - 7.1 cM - Glu-S3 - 0.9 cM - Gli-S1 - 5.6 cM - Gli-S5. Glu-S1 is located in 1S1 and the other loci are in 1S1S.

Glu-U3{480}. 1U{480}. su: CS/Ae. umbellulata.
A series of papers {00106, 00107, 00108 and 00109} describe considerable variation in primitive wheats not present in bread wheat (A genome species T. boeoticum, T. urartu, T. thaoudar, T. aegilopoides, T. monococcum, and D-genome species T. tauschii) for the low molecular weight subunits, sufficient to use them as a source for potentially changing flour properties in bread wheat.

In {00110}, variants for LMW glutenin subunits were reported from study of twenty-four accessions of einkorn wheat (T. monococcum ssp. monococcum). Nine of these showed two electrophoretic bands for LMW subunits, arbitrarily designated 'a' and 'b', that appeared to be associated with good bread-making quality. The isolation of a new low-molecular-weight glutenin subunit gene, located on chromosome 1D, was reported in {0350}.

80.3.1.4. Glu-4

The following loci, Glu-D4 and Glu-D5, encoding low molecular weight subunits of glutenin (30-32 kDa) were described in {02111}; the proteins encoded by them were first observed earlier {02114, 02115}, and the former was later tentatively assigned the symbol Glu-4 {02116}, before its chromosomal location was established and the locus definitively named as Glu-D4 in {02111}. While this locus is located on chromosome 1D (in accordance with the position on the group 1 chromosomes of the remaining glutenin encoding loci found to date), the locus Glu-D5 is located on chromosome 7D. In SDS-PAGE, the proteins from both loci are detected only in the presence of 4-vinlypyridine added to the sample extract. Their amino acid compositions do not match those of the major prolamin groups; nonetheless, they classify as glutenins based upon solubility, immunological behaviour and N-terminal amino acid sequence (the latter suggesting an evolutionary link with the major (B and C) low molecular weight glutenin subunits).

Glu-D4{02111}. 1D{02111}. su: CS/Langdon 1D(1A); CS/Langdon 1D(1B){02111}.
Glu-D4a{02111}. v: J 24.
Glu-D4b{02111}. v: PBW 154.
Glu-D4c{02111}. Null allele. v: NI 4.
80.3.1.5. Glu-5

Glu-D5a\{02111\}. 7D\{02111\}.  su: CS/Langdon 7D(7A); CS/Langdon 7D(7B)\{02111\}. 
Glu-D5b\{02111\}.  v: PBW 154. 
Glu-D5c\{02111\}.  Null allele.  v: K 68.

A collection of 173 Ae. tauschii accessions were analysed for low molecular weight glutenin subunits by SDS-PAGE \{02112\}. Thirty three different patterns for B-subunits and 43 for C-subunits were identified, some of which were of identical electrophoretic mobility to those observed in common wheat. Also observed were subunits with the same mobilities as the D-subunits and as the subunits encoded by the Glu-D4 and Glu-D5 loci. This variation represents a source of novel germplasm of potential value for breeding programmes aimed at improving the D-genome of common wheat in the context of bread-making quality.

PCR amplification of genomic DNA was used to isolate three LMW glutenin genes in cultivar Chinese Spring, named LMWG-MB1, LMWG-MB2 and LMWG-MB3 \{01101\}. The deduced amino-acid sequences showed a high similarity between these ORFs and with those of other LMW glutenin genes. The authors state that the study provided direct evidence that insertions and/or deletions provide a mechanistic explanation for the allelic variation, and hence the resultant evolution, of prolamin genes, and comment on relationships with gamma-secalins and beta-hordein families. Single-base substitutions at identical sites generate premature stop codons in both LMWG-MB2 and LMWG-MB3, indicating that these clones are pseudogenes.

80.3.2. Gliadins

These are heterogeneous mixtures of alcohol-soluble polypeptides without quaternary structure. The Gli-1 loci are compound and are now considered to comprise the omega-gliadin and gamma gliadin \{982,1415\} multigene families \{494\}, which in some circumstances may be divided into Gli-1-1 and Gli-1-2, respectively. The LMW glutenin multigene families, which are closely linked to the Gli-1 loci \{588\}, are listed separately as the Glu-3 set \{1358\}; information on map distance and gene order in relation to Glu-3 and the centromere is given in the preamble for the Glu-3 loci. There is evidence that a few of the omega-gliadin genes are separated from the main omega-gliadin gene cluster \{993\}. Variation at the Gli-1 loci was described earlier \{634,996,1126\} and applied in mapping experiments \{1243,1125,196,422,1120\}. A rational system of naming the alleles was produced by Dr. E.V. Metakovsky\{988\}. This nomenclature is reproduced below. A considerable number of alleles were added to the original list given in \{988\}, and referenced here accordingly. A few alleles have been deleted, because, following much detailed comparison, there is now doubt that they can be reliably distinguished from existing alleles \{9981\}. The allelic letter in these cases has not been reused. To facilitate practical use of the list, the aim was to give at least three standard cultivars from a range of countries for each allele \{9981\}. This was achieved for the vast majority of entries and is a change from the original list compiled from \{988\}, where up to two standards were given. While the three or more standards described almost always include the original standards, some have been replaced for various reasons, such as international awareness of the cultivar, availability of seed, or the ease with which an allele can be identified in a particular genetic background \{9981\}. In the original list, where two cultivars were given as prototypes for an allele, the first named was from the USSR and the second from elsewhere; this is no longer the case, although care was taken to include a Russian cultivar where possible, to maintain a wide base of germplasm in which the alleles are available, as well as to acknowledge the research groups in the country where much of the pioneering work was carried out.
For discussion of null alleles at the Gli-1 and Gli-2 loci, see (9984). Recombination was observed within the gliadin multigene family at XGli-A1 (277). These closely linked genes may correspond to Gli-A1 and Gli-A5, but they were temporarily designated XGli-A1.1 and XGli-A1.2 until orthology with Gli-A1 and/or Gli-A5 is established.

Note: The catalogue entries reproduced here only refer to alleles in T. aestivum; there is, however, enormous variation in the gliadins in the close relatives of wheat; see, for example, (989) for studies in T. monococcum (more than 80 gliadin electrophoretic patterns observed in 109 accessions), (990) for studies in T. boeoticum (more than 50 electrophoretic patterns in 60 accessions), and (1076) studies in T. durum (19 electrophoretic patterns, referring only to variation in the omega-gliadins, in 243 accessions). In (00110), variants for omega-gliadins were reported from study of twenty-four accessions of einkorn wheat (T. monococcum ssp. monococcum). In (00111), in a study of common wheat and durum from Portugal, the authors used the nomenclature system described in (00112) for the omega-gliadins. In (00116), a comparison between spelt and common wheat was carried out for the gliadins using a nomenclature system described in (00118). The Gli-1 loci may be recognised by probes pcP387 (372) and pTag1436 (065), and by specific microsatellites primers (252). Furthermore, it was shown that probe pTag1436 differentiates gliadins alleles rather well; using this probe, families of gliadin alleles and some of their relationships were described (9988).

Twenty eight gamma-gliadin gene sequences from GenBank were grouped into nine subgroups in (10063). Primers were developed against some of the subgroups and the chromosomal locations of the gamma-gliadin genes were determined (10063).

Based upon morphological observation and RFLP analysis, it was proposed that the cultivar 'Chinese Spring' is a strain of the landrace 'Chengdu-guangtou' from the Chengdu Plain, Sichuan Province; this proposal is supported by the observation that CS and the landrace share the same alleles at all nine Gli-1, Gli-2 and Glu-1 loci (see 01102). PCR primers GAG5 and GAG6 were applied to 35 cultivars of closely related spelt and hexaploid wheat, and to eight cultivars of durum, to yield products originating from two gamma-gliadin genes mapped to chromosomes 1B (termed GAG56B) and 1D (termed GAG56D) (01103). Two alleles for GAG56D (differing in a 9 bp deletion/duplication and single nucleotide polymorphism) were found, one a new allele and the other previously published (01104). Meanwhile two alleles found for GAG56B among the durum wheats correlated with the presence of gluten quality markers, gamma-gliadins 42 or 45.

1B and 1D sulphur-poor omega-gliadins in cultivar Butte 86 were characterised by RP-HPLC, SDS-PAGE, two-dimensional PAGE, amino acid composition determination and sequencing, matrix assisted laser desorption ionisation-time of flight mass spectrometry and circular dichroism spectroscopy to reveal the detailed nature of the peptides belonging to the two groups, and showing that the complexity of mixtures of the peptides of the 1B group was greater than that of the 1D group (01105). Although circular dichroism spectra were similar for the two groups of peptides, and suggested a mainly flexible random structure, there was evidence for a significant amount of left-handed polyproline II helical conformation in the case of the 1D components. The authors placed some of the results in the context of the possible ancestor of the B-genome and relationships with the barley C-hordeins and rye omega-secalins. Eleven new gliadin alleles were found in a collection of 52 Spanish landraces of common wheat (03141). These will be added to the Gli-1 and Gli-2 allelic lists in a later Supplement.
A new family of low-molecular-weight gliadin genes located on groups 4 and 7 were reported in [10117]. They appear to influence rheological properties and seem to be closely related to the 17kDa epsilon hordein, important in beer foam stability.

A novel storage protein gene with chimerical structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated Ch1 to Ch8, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci Gli-1 and Glu-3. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated [10307].

Transcriptome analysis showed the presence of proteins called avenin-like a and b. The former contained a duplicated sequence of about 120 residues and corresponded to the LMW-gliadins. The latter was not previously characterized, but may form part of the glutenin fraction and hence influence quality. These avenin-like proteins showed higher expression levels in three Aegilops species (Ae. caudata, Ae. cylindrica and Ae. tauschii) than in common wheat [10321].
**PROTEINS**

**Gli-B1null** [9984,9987]. v: Saratovskaya 29 (mutant)[9987]; E. Mottin[9981].


**Gli-B1a** [988]. v: CS[988].

**Gli-B1b** [988]. v: Bezostaya 1[988]; Carat[991]; Marquis[988]; Liocorno[9986]; Soisson[991].

**Gli-B1c** [988]. v: CS* /Cheyenne[634].

**Gli-B1d** [988]. v: CS[988].

**Gli-B1e** [988]. v: CS[988].

**Gli-B1f** [988]. v: CS[988].

**Gli-B1g** [988]. v: CS[988].

**Gli-B1h** [988]. v: CS[988].

**Gli-B1i** [988]. v: CS[988].

**Gli-B1j** [988]. v: CS[988].

**Gli-B1k** [988]. v: CS[988].

**Gli-B1l** [988]. v: CS[988].

**Gli-B1m** [988]. v: CS[988].

**Gli-B1n** [988]. v: CS[988].

**Gli-B1o** [988]. v: CS[988].

**Gli-B1p** [988]. v: CS[988].

**Gli-B1q** [988]. v: CS[988].

**Gli-B1r** [988]. v: CS[988].

**Gli-B1s** [988]. v: CS[988].

**Gli-B1t** [988]. v: CS[988].

**Gli-B1u** [988]. v: CS[988].

**Gli-B1v** [988]. v: CS[988].

**Gli-B1w** [988]. v: CS[988].

**Gli-B1x** [988]. v: CS[988].

**Gli-B1y** [988]. v: CS[988].

**Gli-B1z** [988]. v: CS[988].

**Gli-B1null** [9984,9987,991]. v: Touzelle[991]; Florence Aurora[9985].

In 112 bread wheat cultivars from Argentina, 12 microsatellite alleles plus a null allele were found at the Gli-B1 locus tightly linked to Glu-B3 [03123].

**Gli-D1** [121,1125]. [Gld ID[1415],Gld-D1[420],Gld-D2[420],Gld-D3[420]]. 1DS[121,150,634,1334,1607]. s: CS/Cheyenne[634]. v: CS[121,150,1334,1607].

**Gli-D1a** [988]. v: CS[988].

**Gli-D1b** [988]. v: CS[988].

**Gli-D1c** [988]. v: CS[988].

**Gli-D1d** [988]. v: CS[988].

**Gli-D1e** [988]. v: CS[988].

**Gli-D1f** [988]. v: CS[988].

**Gli-D1g** [988]. v: CS[988].

**Gli-D1h** [988]. v: CS[988].

**Gli-D1i** [988]. v: CS[988].

**Gli-D1j** [988]. v: CS[988].

**Gli-D1k** [988]. v: CS[988].

**Gli-D1l** [988]. v: CS[988].

**Gli-D1m** [988]. v: CS[988].

**Gli-D1n** [988]. v: CS[988].

**Gli-D1o** [988]. v: CS[988].

**Gli-D1p** [988]. v: CS[988].

**Gli-D1q** [988]. v: CS[988].

**Gli-D1r** [988]. v: CS[988].

**Gli-D1s** [988]. v: CS[988].

**Gli-D1t** [988]. v: CS[988].

**Gli-D1u** [988]. v: CS[988].

**Gli-D1v** [988]. v: CS[988].

**Gli-D1w** [988]. v: CS[988].

**Gli-D1x** [988]. v: CS[988].

**Gli-D1y** [988]. v: CS[988].

**Gli-D1z** [988]. v: CS[988].

**Gli-D1null** [9984,9987,991]. v: Touzelle[991]; Florence Aurora[9985].
Gli-D1j{988}.  v: Aubain{991}; Chinook{995}; Inia{985}; Petrel{991}; Promin{988}.
Gli-D1k{988}.  v: Cargimarec{991}; Kremena{988}; Mara{986}; Pippo{986}.
Gli-D1l{988}.  v: Artaban{991}; Corin{991}; Longbow{988}.
Gli-D1m{991}.  v: Heurtebise{991}.
Gli-D1n{981}.  v: Blanquillo de Toledo (MCB-0950){9981}.
Gli-D1null{984,987,991}.  v: Darius{991}; Touzelle{991}; Saratovskaya 29 (mutant){987}.
Gli-Ag1'.  1Ag{168}.  ad: Vilmorin 27/Th. intermedium.
Gli-D1I{02109}.  1D1S{02109}.  v: L/18913 (synthetic).  dv: Ae. tauschii AUS18913.

A locus designated Gli-D1I controlling an omega-gliadin of Ae. tauschii was mapped on the short arm of chromosome 1D between loci Gli-D1 (strictly Gli-D1') and Glu-D1 (strictly Glu-D1'), 13.18 cM proximal to the former and 40.20 cM from the latter {02109}. The only omega-gliadin to date identified as being encoded by this locus, namely T1, is of unusually low electrophoretic mobility in SDS-PAGE gels and was formally thought to be a high molecular weight glutenin encoded by the Glu-D1 locus of Ae. tauschii (see note following the Glu-D1 list in section 'Glutenins'). The authors speculate that, due to their similar relative map positions, the loci Gli-A4, Gli-D4, Gli-R3, Gli-S4 and this locus, Gli-D1I, form a series of 'Gli-4' orthologous loci. However, this should be interpreted in the light of the above discussion on Gli-A3 and Gli-A4.

A 1,200 bp Dra I RFLP was identified as a gene-specific probe for the T1 omega-gliadin {10645}.

Gli-E1{781}.  1ES{781}.  ad: CS/E. elongata.
Gli-H1{1037}.  1H1p{1037}.  ad: CS/E. trachycaulum.
Gli-R1{1334}.  [SecR1{1356},Sec1{1336}].  1RS{781,1334,1336,1340}.  ad: CS/Imperial{781,1334,1336,1340}; Holdfast/King II{1334,1340}.  tr: CS 1DS. Imperial 1RL{1356}.
Sec-12 and Sec13 are given as allelic alternatives in 1BL.1RS translocation lines by {03132}.

Gli-R1m{1340}.  1R1m{1340}.  ad: CS/S. montanum.
Gli-S1{573}.  1S1{573}.  ad: CS/Ae. longissima.
Gli-U1{1335}.  1U{1335,150}.  ad: CS/Ae. umbellulata.
Gli-V1{1026,111}.  1V{1026,111}.  ad: CS/D. villosum{1026}; Cresol/D. villosum{111}.

In barley, the B and C hordeins are controlled by the Hor2 and Hor1 loci, respectively, which are linked {1341} on chromosome 1HS {1063,1153}. The map distances and homology of the proteins indicate that Hor1, the locus closest to the centromere, is equivalent to the omega-gliadins (Gli-1-1) in Gli-1 {1338}.

Three alleles at each of the Gli-1-1 (omega gliadin) loci were noted {1358}. The complexity of the Gli-1 compound loci is further emphasized by a report of individual genes being separable by recombination, where Gld1-1A (a block of gamma and omega genes) is separable by 0.3% from Gld4-1A (omega gliadins) which is in turn, separable by 1.5% from Gld3-1A (omega gliadins) {1103}.

Elsewhere, variation was described {634,996,1126} and applied in mapping experiments {107,196,422,1120,1125,1243}. Sixteen combinations of Gli-B1 and 4 combinations of Gli-D1 subunits are listed in {420}. Multiple alleles described in {996}, number 15 at Gli-A1, 18 at Gli-B1, and 8 at Gli-D1.

The Gli-1 alleles present in 57 Yugoslav wheat varieties were reported in {994}.

80.3.2.2. Gli-2
Gli-A2{1334,1125}.  [Gld 6A{1415}].  6A{1334}.6AS{1122}.  v: CS.
Gli-A2a{988}.  v: Cabezorro{9985}; CS{988}; Insignia{988}; Rieti DIV{9986}.  
Gli-A2b(988). v: Aradi(995); Bezostaya 1(988); Rivoli(991); Tiberio(986).
Gli-A2c(988). v: Eagle(00119); Escualo(985); Loreto(986); Prinqual(991); Siete Cerros 66(988).
Gli-A2d(988). v: Dneprovskaya 521(988); Kenyon (biotype)(995); Mocho Sobarriba(985).
Gli-A2e(988). v: Adalid(988); Gala(991); Maris Freeman(988); Sistar(986).
Gli-A2f(988). v: Cappelle-Desprez(991); Ducat(988); Mahissa 1(988); Mara(986).
Gli-A2g(988). v: Apollo(991); Basalt(981); Hereward(988); Montjuich(985); N. Strampelli(986).
Gli-A2h(988). v: Krasnodonka(988); Lesostepka 75(988).
Gli-A2i(988). v: Cajeme 71(995); Capitole(991); Clement(991); Pliska(988); S. Lorenzo(986); Yecora 70(9985).
Gli-A2j(988). v: Candeal Alcala(988); Montcada(988); Saratovskaya 39(988).
Gli-A2k(988). v: Genial(991); Open(991); Riband(988).
Gli-A2l(988). v: Akmolinka 1(988); Estica(991); Pyrotrix 28(988); Renan(991); Zena(986).
Gli-A2m(988). v: Chamorro(985); Champlein(991); Longbow(988).
Gli-A2n(988). v: Marquis(988); Rex(991); Suneca(00119).
Gli-A2p(988). v: Calatrava(985); Castan(991); Glenwari(9881); Lontra(9986); Touzelle(991).
Gli-A2r(988). v: Blanquillo de Barcarrota (MCB-0932){9981}.
Gli-A2s(988). v: Hembrilla Soria (MCB-1298){9981}.
Gli-A2t(988). v: Gente del Rey (MCB-0892){9981}.
Gli-A2u(988). v: Bezenchukskaya 98 (biotype){988}.
Gli-A2v(988). v: Kzyl-Bas(988).
Gli-A2w(988). v: Bezenchukskaya 98 (biotype){988}.
Gli-A2x(988). v: Solo(988).
Gli-A2y(9981). v: Gentil Rosso 202(9981); PI 191245(9981).
Gli-A2z(9986). v: Gallo(986); Giuliana(986).
Gli-A2ac(9981). v: Blanquillo de Barcarrota (MCB-0893){9981}.
Gli-A2ad(9981). v: Hembrilla Soria (MCB-1298){9981}.
Gli-A2ae(9981). v: Candeal de S.Lorenzo Parrilla (MCB-0932){9981}.
Gli-A2af(9981). v: Barbilla de Leon (MCB-1292){9981}.
Gli-A2ah(9981). v: Candeal de Nava del Rey (MCB-0892){9981}.
Gli-A2ai(9981). v: Blanquillo (MCB-0908){9981}.
Gli-A2null(9984,9987). v: Saratovskaya 29 (mutant){9987}.
Gli-B2a(988). v: CS{988}.
Gli-B2b(988). v: Bezoastaya 1(988); Cobra{991}; Gladio{9986}; Sideral{991}.
Gli-B2c(988). v: Courtot{991}; Escualo{985}; Gabo{988}; Loreto{986}; Manital{9986}; Prinqual{991}; Siete Cerros 66{988}; Sinton{995}; Yecora 70{9985}.
Gli-B2d(988). v: Akmolinka 1(988); Cesar{9981}; Friedland{991}; Tselinnaya 20{9988}.
Gli-B2f(988). v: Basalt{9981}; Maris Freeman{988}; Master{991}. 

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Gli-B2g [988]. v: Capitole [991]; Capelle-Desprez [991]; Galahad [988]; Forlani [9986].
Gli-B2h [988]. v: Castan [991]; Mentana [9886]; Pane 247 [9985]; Partizanka [994]; Sadovo 1 [988]; Sistar [9986].
Gli-B2i [988]. v: Insignia [988]; Robin [9981].
Gli-B2j [988]. v: Farnese [986]; Funo R250 [9986]; Novosadska Rana 1 [994].
Gli-B2k [988]. v: Scala [988].
Gli-B2l [988]. v: Clement [991]; Longbow [988]; Tracy [991].
Gli-B2m [988]. v: Mironovskaya 808 [988]; Open [991]; Renan [991].
Gli-B2n [988]. v: Japhet [9981]; Rouge de Bordeau [9981]; Solo [988].
Gli-B2o [988]. v: Hardi [9981]; Mara [9986]; Odesskaya 16 [988]; Pippo [9986]; Rivoli [991]; Slavjanka [9981].
Gli-B2p [988]. v: Pliska [983]; Champtal [991]; Oderzo [9986]; Recital [991]; Gazul [9986].
Gli-B2q [988]. v: Palata [9986]; Pembina [995]; Rieti DIV [9986].
Gli-B2r [991]. v: Arminda [991]; Estica [991]; Genial [991].
Gli-B2s [988]. v: Aquila [9981]; Saratovskaya 36 [988].
Gli-B2t [988]. v: Tselinogradka [988].
Gli-B2x [994]. v: Super Zlatna (biotype) [994]; Prostor [9981]; 251/83 [9981].
Gli-B2y [9986]. v: Declic [991]; Garant [991]; Libellula [9986]; Mahissa 1 [9985]; Poljarka [9886].
Gli-B2z [9985]. v: Maestro [9885].
Gli-B2ab [991]. v: Bordier [9981]; Orepi [991].
Gli-B2ac [991]. v: Scipion [991]; Artaban [991]; Riol [991]; Lontra [9981].
Gli-B2ad [991]. v: Champion [991]; Chopin [991].
Gli-B2ae [991]. v: Priam [991]; Et.d'Choisy [991]; Campeador [9885]; Krajinka (biotype) [994].
Gli-B2ag [9981]. v: Jeja del Pais [9985]; Barbilla de Leon (MCB-1292) [9981].
Gli-B2ah [9981]. v: Rojo de Humanes (MCB-1262) [9981]; Grano de Miracolo [9981].
Gli-B2ai [9981]. v: Javelin 48 [9981].
Gli-B2ak [9981]. v: Eagle [9981]; Glenwari [9981].
Gli-B2am [9981]. v: Veda [9981]; Magnif 27 [9981].
Gli-B2an [9981]. v: Winglen [9981]; Isis [9981].
Gli-B2ax [9981]. v: Winglen [9981]; Isis [9981].
Gli-B2b [988]. v: CS [988]; Maris Freeman [988]; Sistar [9986]; Tracy [991].
Gli-B2c [988]. v: Escualo [9985]; Eridano [9886]; Rieti DIV [9986]; Siete Cerros 66 [988].

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*Gli-D2e* [988]. v: Dollar [985]; Lada [981]; Mironovskaya 808 [988]; Open [991].

*Gli-D2f* [988]. v: Creneau [991]; Kirgizskaya Yubileinaya [988]; Rempart [991].

*Gli-D2g* [988]. v: Capelle-Desprez [991]; Futur [991]; Galahad [988]; Ghurka [988]; Mec [986].

*Gli-D2h* [988]. v: Capitole [991]; Chinook [995]; Eagle [00119]; Garant [991]; Sadovo 1 [988]; Thatcher [995].

*Gli-D2i* [988]. v: Insignia 49 [00119]; Lario [996].

*Gli-D2j* [988]. v: Arcane [991]; Gallo [996]; Gazul [995]; Inia 66 [9985]; Mentana [986].

*Gli-D2k* [988]. v: Crvenapa [944]; Kzyl-Bas [988]; Skala [988].

Omitted. No reliable differences compared to existing alleles [9981].

*Gli-D2l* [988]. Omitted. No reliable differences compared to existing alleles [9981].

*Gli-D2m* [988]. v: Marquis [988]; Rex [991]; Rinconada [9985]; Suneca [00119]; Veronese [986]; Yecora 70 [9985].

*Gli-D2n* [988]. v: Castan [991]; Champlein [991]; Mahissa 1 [9985]; Mercia [988]; Pippo [9986].

*Gli-D2o* [988]. v: Omskaya 12 [988].

Note: cultivars Salmone and Resistente, which carry *Gli-D2aa* [9981], were erroneously given as standards for allele *Gli-D2o* in [9986].

*Gli-D2p* [988]. v: New Pusa [988].

*Gli-D2q* [988]. v: Cook [9981]; E. Mottin [9981]; Fournil [991]; Volshebnitsa (biotype) [988]; Winglen [9981]; Soissons [991].

*Gli-D2r* [988]. v: Kremena [988]; Mara [986]; Montcada [9895].

*Gli-D2s* [988]. v: Akmolinka 1 [988]; Bezenchukskaya 98 [988]; Selkirk (biotype) [995].

*Gli-D2t* [988]. v: Golia [988]; Gabo [9881]; Manital [9896]; Bokal [9891].

*Gli-D2u* [991]. v: Epiroux [991]; Arbon [991].

*Gli-D2w* [988]. v: Navarro 150 [9985]; Javelin [9981]; Hoppis [9981]; Canaleja [9895].

*Gli-D2x* [991]. v: Montjuich [9895]; Blanquillo [9895].

*Gli-D2y* [9985]. v: Candeal Alcala [9985].

*Gli-D2z* [9895]. v: Aragon 03 [9985].

*Gli-D2aa* [9981]. v: Salmone [9981]; Resistente [9981].

*Gli-D2ab* [9981]. v: Rojo de Boadilla de Campos (MBC-1031) [9981].

*Gli-D2ac* [9981]. v: Albatros [9981].

*Gli-D2ad* [9981]. v: Hembrilla Soria (MBC-1298) [9981].

*Gli-D2-null* [9984,9987]. v: Saratovskaya 29 (mutant) [9987].

*Gli-Ag* [2][374]. 6Ag [374]. ad: Vilmorin 27/Th. intermedium.

*Gli-R2* [781]. [Sec 2[1336]]. 2R [781,1336],2RS [1340]. ad: CS/Imperial [781,1336,1340]; Holdfast/King II [1340].

*Gli-R2a* [03116]. d1 [03116]. v: Carnac hexaploid triticale [03116].

*Gli-R2b* [03116]. d2 [03116]. v: Mostral hexaploid triticale [03116].

*Gli-R2c* [03116]. t1 [03116]. v: Alamo hexaploid triticale [03116].

*Gli-R2d* [03116]. null [03116]. v: Triticor hexaploid triticale [03116].

*Gli-R2e* [03115]. t2 [03115]. v: Tornado hexaploid triticale [03115].


The location of *Gli-R2* in *S. cereale* is thought to have evolved from *S. montanum* [1339] via a translocation between 2R and 6R [1530].

*Gli-S* [573]. 6S [573]. ad,su: CS/Ae. longissima.

*Gli-U2* [1335]. 6U [1335]. ad: CS/Ae. umbellulata.

Prior to the publication of [988], allelic variation was demonstrated at all of the wheat Gli-2 loci, including 13 alleles at Gli-A2, 11 at Gli-B2, and 10 at Gli-D2, in a study of 39 cultivars [996].

The Gli-2 alleles present in 57 Yugoslav wheat varieties were determined [994].

80.3.2.3. Gli-3

A Gli-3 set of loci coding for omega-type gliadins are located 22 to 31 cM proximal to Gli-1 on the short arms of group 1 chromosomes [422,1403,589].


Each of the following Gli-A3 alleles, apart from Gli-A3d, which is a null, controls one minor omega-gliadin with molecular mass about 41k that occurs in the middle of the omega-region of APAGE fractionation. Gliadins controlled by these alleles differ in their electrophoretic mobility in APAGE in that the fastest of three known Gli-A3-gliadins is controlled by Gli-A3a and the slowest by Gli-A3c [9983].


Gli-B3[422,1119]. [Gld-B6[422],Gluten-B2[589]]. 1BS[422,589]. s: CS*Thatcher1B[422].

v: Sicco[589].

Gli-B3a[422,589,1119]. v: CS.

Gli-B3b[589]. v: Sicco.

Gli-B3c[422,1119]. s: CS*Thatcher1B.

Gli-R3[164]. 1RS[164]. al: Four inbred lines (R2, J14, 8t, E2666).

Gli-S3[1228]. 1S1S[1228]. ad, su: CS/Ae. longissima. ma: In Ae. longissima 2/Ae. longissima 10, three gliadin loci, one glucose phosphate isomerase, and two glutenin loci were mapped relative to one another [1228] as follows: Gli-S1 15.9 cM - Gpi-S1 - 38 cM - Gli-S4 - 7.1 cM - Gli-S5 - 0.9 cM - Gli-S1 - 5.6 cM - Gli-S5. Gli-S1 is located in 1S1L and the other loci are in 1S1S.


80.3.2.4. Gli-4

It is not clear how Gli-S4 and Gli-S5 relate to the Gli-4 and Gli-5 sets described below. A locus designated Gli-A4 controlling omega-gliadins in cv. Perzivan biotype 2 was mapped at 10 cM proximal to Gli-A1 on the short arm of chromosome 1A [1205].

However, Metakovsky et al. [9983] have since shown that this locus and Gli-A3 are, in fact, the same locus. Furthermore, Dubcovsky et al. [277] did not find evidence for the simultaneous presence of both Gli-A3 and Gli-A4 in five 1A or 1A*m mapping populations and concluded that Gli-A4 should be considered to be Gli-A3 until conclusive evidence for the former is obtained. For these reasons, the locus Gli-A4 is deleted from the catalogue.

80.3.2.5. Gli-5

A locus designated Gli-5 controlling omega-gliadins was mapped to the short arms of chromosomes 1A and 1B, distal to Gli-1 [1147]. The map distance between Gli-B5 and Gli-B1 was estimated as 1.4 cM (recombination value of 1.4 +/- 0.4%), although there was significant variation in recombination values over crosses, ranging from 0% to 5.9% over the six crosses analysed. This variation was attributed to genotypic influence on the frequency of recombination.
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Gli-A5\{1147\}. 1AS\{1147\}. v: Salmone.
Gli-A5a\{9983\}. Null\{9983\}. v: CS.
Gli-A5b\{9983\}. v: Marquis.
Allele Gli-A5b controls two slow-moving, easily recognizable omega-gliadins. It is present in all common wheat cultivars having alleles Gli-A1m and Gli-A1r (and, probably, in those having Gli-A1e, Gli-A1l and Gli-A1q), because earlier (for example, in \{988\}) two minor omega-gliadins encoded by Gli-A5b were considered to be controlled by these Gli-A1 alleles \{9983\}.

Gli-B5\{1147\}. 1BS\{1147\}. v: Salmone.
Gli-B5a\{9983\}. v: CS.
Gli-B5b\{9983\}. v: Salmone.
In \{988\}, omega-gliadins controlled by Gli-B5 (allele Gli-B5b) were attributed to alleles at the Gli-B1 locus (alleles Gli-B1c, i, k, m, n and o).

80.3.2.6. Gli-6
Gli-A6\{9983,993\}. 1AS\{9983\}.
Gli-A6 was first explicitly described in \{9983\}, but it was first observed without designation in \{993\}. There is strong evidence that it is distinct from Gli-A3 and Gli-A5, mapping distally to Gli-A1, with which it recombines at a frequency of 2-5%. Currently three alleles are known, of which Gli-A6c is particularly well-described in \{9983\}: the molecular mass of the omega-gliadin controlled by this allele is slightly lower than those of the omega-gliadins controlled by Gli-A3 alleles. In \{988\}, the omega-gliadin controlled by Gli-A6c was attributed to Gli-A1f. Gli-A6c is rather frequent in common wheat and may relate to dough quality (preliminary data \{9983\}). Gli-A6a is null \{9983\}.

Gli-A6a\{9983\}. Null\{9983\}. v: CS, Bezostaya 1.
Gli-A6b\{9983\}. v: Bezenchukskaya 98.
Gli-A6c\{9983\}. v: Courtot, Anda, Mironovskaya 808.

80.3.2.7. Gli-7
Gli-A7\{10547\}. 1DS\{10547\}. dv: AUS18913\{10547\}.
The gamma-gliadin encoded by this locus co-segregated with the T1 omega-gliadin encoded by the Gli-D'T1 locus (currently included in the Catalogue as locus (Gli-D'T1)). Gli-A7 was located 0.69 cM from Gli-D'T1 \{10547\}.

Four new classes of low molecular weight proteins related to gliadins, though not sufficiently similar to be classified as such, were reported in \{02113\}. One of the classes has no close association to previously described wheat endosperm proteins.

80.3.3. Other endosperm storage proteins
Tri-A1\{1357, 1358\}. 1AS\{1357\}. v: CS.
Tri-A1a. [cs\{1358\}]. v: CS.
Tri-A1b. [h\{1358\}]. v: Hope.
Tri-D1\{1357,707,1358\}. 1DS\{1357\}. v: CS.
Tri-D1a. [cs\{1358\}]. v: CS.
Tri-D1b. [i\{1358\}]. v: India 115.

80.3.3.1. Triticin proteins
The triticin proteins (1360) or [Triplet proteins (1357)] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species (1360). Triticin gene segments including its hypervariable region were PCR-amplified, with preferential amplification of Tri-D1 for the only pair of primers giving consistent results (10322).

80.4. Enzyme Inhibitors

80.4.1. Trypsin inhibition

\textit{Ti-H1}. \{lhc \{528\}\}. 3H\{528\}. \textbf{ad}: CS/Betzes.
\textit{Ti-R1}. 3R\{529\}. \textbf{ad}: CS/Imperial.

\textit{Ti-A2\{699\}}. 5AL\{699\}. \textit{v}: CS.
\textit{Ti-B2\{699\}}. 5BL\{699\}. \textit{v}: CS.
\textit{Ti-D2\{699\}}. 5DL\{699\}. \textit{v}: CS.
\textit{Ti-D2a\{699\}}. \textit{v}: CS.
\textit{Ti-D2b\{699\}}. \textit{v}: Champlein.
\textit{Ti-D2c\{699\}}. \textit{v}: Synthetic.
\textit{Ti-Ag\{699\}}. 5Ag\{699\}. \textbf{ad}: Vilmorin 27/\textit{Th. intermedium}.
\textit{Ti-M\{699\}}. 5M\{699\}. \textbf{ad}: CS/Ae. mutica.
\textit{Ti-R2\{699\}}. 5RL\{699\}. \textbf{ad}: CS/Imperial. \textbf{su}: CS/King II.
\textit{Ti-S\{699\}}. 5S\{699\}. \textbf{ad}: CS/Ae. sharonensis.
\textit{Ti-U2\{699\}}. 1U\{699\}. \textbf{ad}: CS/Ae. umbellulata.

80.4.2. Subtilisin inhibition

\textit{Si-R1\{529\}}. 2R\{529\}. 2RS\{701\}. \textbf{ad}: CS/Imperial, Holdfast/King II.
\textit{Si-H1\{528\}}. \{isa l\{528\}\}. 2H\{528\}. \textbf{ad}: CS/Betzes.

\textit{Si-B2\{701\}}. 1BS\{701\}. \textbf{su}: Bersee {Koga II}.
\textit{Si-D2\{701\}}. 1DS\{701\}. \textit{v}: Koga II.
\textit{Si-H2\{528\},\{701\}}. \{ica l\{528\},ica 2\{528\}\}. 1H\{528\}. \textbf{ad}: CS/Betzes.
\textit{Si-R2\{529\},\{701\}}. 1R\{529\}. 1RS\{701\}. \textbf{ad}: CS/Imperial\{529\}. \textbf{tr}: Gabo 1BL.1RS\{701\}.
\textit{Si-S\{701\}}. 1S\{701\}. \textbf{ad}: CS/Ae. longissima.
\textit{Si-U2\{701\}}. 1U\{701\}. \textbf{ad}: CS/Ae. umbellulata.

Considerable genetic variation for \textit{Si-2} was noted in \{701\}. A chromosome location for \textit{Si-H2} on 1HL was inferred in \{528\} but questioned in \{701\}.

Three subunits of the wheat tetrameric inhibitor of insect a-amylase, CM1, CM3 and CM16, with homology to the dimeric and monomeric a-amylase inhibitors and the trypsin inhibitors, were located by Southern analysis of cDNAs pCT1, pCT2, and pCT3 to 4A, 4B, 4D; 7A, 7B, 7D; and 4A, 4B, 4D, respectively \{427\}.

Genes encoding proteins which inhibit the action of mammalian and insect, but not cereal, a-amylases, were located in chromosomes 3BS, 3DS and 6DS of Chinese Spring \{1260\}. Also, genes encoding inhibitors of insect a-amylases were located in \textit{H. chilense} chromosomes 4H\textsuperscript{ch} and 7H\textsuperscript{ch} \{1262\}.

80.4.3. Inhibitors of alpha-amylase and subtilisin
Orthologous genes were identified in *Ae. speltoides* and *T. timopheevii* {908}. All durum wheats investigated had the genotype *Isa-A1b*, *Isa-B1b*.

### 80.4.4. Inhibitors (dimeric) of heterologous alpha-amyloses

Chromosome 3BS has duplicated loci controlling two dimeric inhibitors of exogenous alpha-amyloses, one known as 0.53 or Inh I {1260}, and the other as WDA I-3 {1260}. Chromosome 3DS has a homeologous locus controlling a dimeric inhibitor of exogenous alpha-amyloses, known as 0.19 or Inh III {1260,0124}, that is closely related to 0.53/Inh I. Intervarietal polymorphism for the WDA-3 protein was identified by isoelectric focusing of water-soluble endosperm proteins {0124}. This was interchromosomally mapped on 3BS using both a DH population of Cranbrook/Halberd, and a set of RILs of Opata 85/W-7984 (ITMI population) {0125}.

Three genome allele specific primer sets were designed for the 3BS and 3DS alpha-amylose inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu*, *Triticum monococcum*, *Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24kDa dimeric alpha-amylose inhibitors in cultivated wheat are encoded by a multigene family {10323}, previously proposed in {10324}, as the result of phylogenetic analysis of sequences characterized by cSNPs.

### 80.5. Other proteins

#### 80.5.1. Lipopurothionins

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<td><strong>Pur-A1</strong> {351}</td>
<td>1AL{351}</td>
<td>v:</td>
<td>CS{351}</td>
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</table>
| A PCR marker specific for **Pur-A1** was developed in {9976}.

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| A PCR marker specific for **Pur-B1** was developed in {9976}.

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<td>1DL{351}</td>
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<td>CS{351}</td>
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</table>
| A locus in chromosome 5DS affects the level of lipopurothionin {351}. PCR marker specific for **Pur-D1** was developed in {9976}.

**Pur-R1.** 1RL{1261} = 1RS.1BL.. **ad:** CS/Imperial. **su:** Several 1R(1B) lines. **tr:** Aurora, Kavkaz.

A PCR marker specific for **Pur-R1** was developed in {9976}.

#### 80.5.2. Lectins
80.5.3. Iodine binding factor

A monomeric water soluble protein from mature grain which preferentially binds iodine {818}.

\textit{Ibf-A1}{818}. 5AL{818}. \textit{v}: CS.

\textit{Ibf-A1a}{818}. \textit{v}: CS.

\textit{Ibf-B1}{818}. 5BL{818}. \textit{v}: CS.

\textit{Ibf-B1a}{818}. \textit{v}: CS.
\textit{Ibf-B1b}{818}. \textit{v}: Cappelle-Desprez.
\textit{Ibf-B1d}{818}. \textit{v}: Sears' Synthetic.

\textit{Ibf-D1}{818}. 5DL{818}. \textit{v}: CS.

\textit{Ibf-D1a}{818}. \textit{v}: CS.
\textit{Ibf-D1b}{818}. \textit{v}: Cappelle-Desprez.
\textit{Ibf-D1c}{818}. \textit{v}: Purple Pericarp.
\textit{Ibf-D1d}{818}. \textit{v}: Sears' Synthetic.

\textit{Ibf-Ag}{818}. 5Ag{818}. \textit{ad}: Vilmorin/\textit{Th}. \textit{intermedium}.

\textit{Ibf-E1}{818}. 5EL{818}. \textit{ad}: CS/\textit{E}. \textit{elongata}.

\textit{Ibf-H1}{818}. 4H{818}. \textit{ad}: CS/Betzes.

\textit{Ibf-R1}{818}. 5RL{818}. \textit{ad}: CS/Imperial, CS/KingII.

\textit{Ibf-S1}{818}. 5S{818}. \textit{ad}: CS/\textit{Ae}. \textit{sharonensis}.

\textit{Ibf-U1}{818}. 5U{818}. \textit{ad}: CS/\textit{Ae}. \textit{umbellulata}.

80.5.4. Water soluble proteins

WSP-1 are monomeric grain endosperm proteins identified by their high pI's {817}.

\textit{Wsp-A1}{817}. 7AL{817}. \textit{v}: CS.

\textit{Wsp-A1a}{817}. \textit{v}: CS.
\textit{Wsp-A1b}{817}. \textit{v}: Huntsman.
\textit{Wsp-A1c}{817}. \textit{v}: Hope.

\textit{Wsp-B1}{817}. 7BL{817}. \textit{v}: CS.

\textit{Wsp-B1a}{817}. \textit{v}: CS.
\textit{Wsp-B1b}{817}. \textit{v}: Hope.
\textit{Wsp-B1c}{817}. \textit{v}: Condor.

\textit{Wsp-D1}{817}. 7DL{817}. \textit{v}: CS.

\textit{Wsp-D1a}{817}. \textit{v}: CS.
\textit{Wsp-D1b}{817}. \textit{v}: Sears' Synthetic IPSR 1190903.
\textit{Wsp-D1c}{893}. \textit{v}: T4 = Agatha{893,890}; Indis{890,892}.

\textit{Wsp-E1}{817}. 7E{817}. \textit{ad}: CS/\textit{E}. \textit{elongata}.

\textit{Wsp-H1}{817}. 7H{817}. \textit{ad}: CS/Betzes.
80.5.5. Salt soluble globulins

GLO-1 are endosperm proteins (23-26 kDa) soluble in salt but not in water {455}.


Glo-B1 {455}.  1BS {455}.  v: CS.

Glo-D1 {455}.  1DS {455}.  v: CS.  ma: Distally located: Glo-D1(distal) - 2.9 cM - Gli-D1{1077}.

Glo-E1 {455}.  1ES {455}.  ad: CS/E. elongata.

Glo-R1 {455}.  1RS {455}.  ad: CS/Imperial.  su: 1B/(1R), eg., Salzmunde 14/44.

80.5.6. Waxy proteins

Waxy protein (granule-bound starch synthase = ADP glucose starch glycosyl transferase, EC 2.4.1.21 = GBSSI) is tightly bound within endosperm starch granules and is involved in the synthesis of amylose {1616}. Waxy variants, characterised by starch granules containing increased amyllopectin and reduced amylose, are preferred for Japanese white salted or "udon" noodles {1650}. Similar waxy phenotypes are controlled by orthologous genes in barley, maize and rice but are not known to occur in rye {725}. All combinations of the null alleles were produced in Chinese Spring {0018}. Partial genomic clones of various diploid, tetraploid, and hexaploid wheats were sequenced {0278,0279}. A multiplex PCR assay for identifying waxy genotypes is described in {10032}.

Wx-A1 {180,1053}.  [Xwx-7A {179,180}, Wx-B1 {1053,1054}].  7AS {180,1053}.  v: CS.  ma: Variation in the microsatellite gene Xsun1-7A provides a co-dominant marker for this locus{0116}.

The complete genomic sequences for the Wx-A1a allele from CS {0073} and the cDNA sequence for the Wx-A1b allele from Kanto 107 {0075} were determined.


Wx-A1b {1054}.  [Wx-B1b {1054}].  Null allele.  v: California {10032}; Kanto 79; Kanto 107; Shino {10032}; Shirodaruma {1617}; Sturdy {1617,10032}.  v2: Mochi-Otome Wx-B1b Wx-D1b {10032}; Nebarigoshi Wx-b1b {10032}.  tv: Asrodur{0111}; MG826{03101}; A variant allele was present in one Iranian and one Italian accession{03101}.

Wx-A1c {1617}.  v: Pakistan Zairaishi selection {10629}; QT105 {1617}; WB6 {1617}.

Wx-A1d {1616}.  tv: T. dicoccoides KU 8937B {1616}.

Wx-A1e {1616}.  tv: KU 3659 {10629}; T. durum KU 3655 and KU 3659 {1616}.

Wx-A1f {10187}.  Null allele  v: Turkey-124 {10187}; Turkey-140 {10187}; Turkey-171 {10187}; Turkey-280 {10187}; Turkey-299 {10187}.

Lines with this allele produce a PCR product with a 173 bp insertion in an exon {10187}.

Wx-A1g.  Wx-A1 {10587}.  v: PI 348476 {10587}; Spelt accessions PI 348576 {10587}; 2778 Epeautre Noir Velu {10587}.

Wx-B1 {180,1053}.  [Xwx-4B {179,180}, Xwx-4A {961}, Wx-A1 {1053,1054}].  4AL {180,1054}.  v: CS.  tv: A variant allele was present in three accessions{03101}.


The complete genomic sequence for Wx-B1a from CS was determined {0073}.
**Proteins**

**Wx-B1b** (1054). [Wx-Alb(1054)]. Null allele. v: Kanto 79; Kanto 82; Kanto 107; Norin 98; Gabo[1617]; Reward[10032]; Satanta[1617]; Yukon[10032]. v2: Mochi-Otome Wx-Alb Wx-D1b[10032]; Nebarigoshi Wx-Alb[10032]. v: For list of Australian wheats, see{1650}. tv: Blaquetta (BG-13701){0111}.

An ELISA-based method was developed for distinguishing wheat lines carrying this null allele {10325}.

**Wx-B1c** (1617). v: AF24{10629}; Chousen 40{0094}; Cikotaba{1617,10629}; Junguk 12{1617,10629}.

**Wx-B1d** (1616). tv: T. durum KU 4213D{1616}; KU 4213D{10629}; KU 4224C{1616}.

**Wx-B1e** (0027). v: Blue Boy II{0027}; Canthatch{0027}; Eureka{0027}; Gotz{0027}; Norin 44{0027}; Turkey Red{0027}.

**Wx-B1f** (0111). tv: BG-12413{0111}; BG-12415{0111}.

**Wx-S1g** (10587). al: Ae. speltoides 33{10587}.

**Wx-SL1h** (10587). al: Ae. longissima 12{10587}.

**Wx-D1** (180,1053). [XWx-7D(179,180)]. 7DS{180,1053}. v: CS.

**Wx-D1a** (1054). v: CS.

**Wx-D1b** (1617). Null allele. v: Bai Huo (Baihuomai){1617}; DHWx12 {0117}. v2: Mochi-Otome Wx-Alb Wx-B1b(10032). ma: STS marker Xsun1-7D produces a distinct band of about 260bp (compared with the standard 840bp), indicative of a smaller PCR product, but the gene is non-functional{0116,0117}; Xsun4(Wx) is a perfect marker{0118}.

**Wx-D1c** (1617). v: Scoutland[1617].

**Wx-D1d** (0118). v: K107Wx1{0118}; K107Wx2{0118}; One Iranian and one Italian accession{03101}.

**Wx-D1e** (0117). Null allele{0117}. v: NP150{0117}.

STS marker Xsun1-7D fails to produce a PCR product {0117}

**Wx-D1f**. [Wx-d1e{0234}]. v: Tanikei A6599-4{0234}; Relative to Kanto 107, Tanikei A6599-4 carries an alanine to threonine substitution at position 258 in the mature protein{0234}.

Various hard and soft wheats with the alleles Wx-Alb, Wx-B1b and Wx-D1b are listed in {0304}. 15% of Chinese wheats possessed Wx-B1 null alleles {10357}.

**80.5.7. Starch granule proteins**

The proteins, designated SGP-1, are starch synthases, encoded by SsII-Al, SsII-B1 and SsII-D1 {0042}.

**Sgp-Al** (1615). 7AS{1615}. v: CS.

**Sgp-Ala** (1615). v: CS.
The proteins, designated SGP-A1 to SGP-D3 are identical to wheat starch synthase I, encoded by SsI-A1, SsI-A2 and SsI-D1. A triple null stock (SGP-1 null wheat) is reported in [0137]. Deletion mapping indicated that the gene order on the 7S arms is; centromere - Sgp-1 - Sgp-3 - Wx[1615].

### 80.5.8. Puroindolines and grain softness protein

Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see ‘Grain Hardness’). The name ‘puroindoline’ and the complete amino acid sequence of puroindoline a were given in [0382] from cv Camp Remy. Hard grain texture in hexaploid wheat results from unique changes in the puroindoline amino acid sequence or, currently, four null forms (0295) of the completely linked genes (max. map distance 4.3 cM) [452]. Tetraploid (AABB, AAGG) wheats lack puroindolines and are consequently very hard [03103]. A searchable database of wheat varieties and their puroindoline genotype is available at http://www.wsu.edu/~wwql/php/puroindoline.php. Grain softness protein-1 is a closely related gene which is closely located to the puroindoline genes [03111,1185]. ‘GenBank’ and ‘dbEST’ refer to sequence databases available at NCBI (also available through EMBL and DDB).

Recent reviews [10522, 10523] provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave [10524] reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al. [10525, 10526] developed a CS line (PI 651012) carrying a 5A<sup>m</sup>S.SAS translocation from T. monococcum; the translocated chromatin carries A-genome Pina, Pinb and Gsp-1 alleles that confer softer kernel texture.

**Pina-A1**{03103,03108,03104}. **dv:** T. urartu unspecified accession {03103}; TA763(GenBank AJ302094){03108,03104}; TA808(GenBank AJ302095){03108,03104}.
This locus has a large deletion encompassing genes *Pina-D1*, *Pinb-D1* and *Gsp-D1*. This allelic combination confers a harder kernel texture than *Pina-D1a/Pinb-D1b* (10077).

**Pina-D1a** \(^{(452)}\). \(v\): CS (GenBank DQ363911){03108}; Capitole (GenBank X69914){03110}; Courtot{0249}; Fortuna{0249}; Galaxie{0249}; Heron{1035}; Renan (GenBank CR626934){10440}; Soissons{0249}. \(v2\): Aurelio *Pina-D1a*{0249}; Bezostaja *Pinb-D1b*{0249}; Bilancia *Pina-D1a*{0249}; Bolero *Pina-D1a*{0249}; Brasilia *Pinb-D1b*{0249}; Centauro *Pina-D1a*{0249}; Cerere *Pinb-D1b*{0249}; CS *Pina-D1a*{452,0249}; Colfiorito *Pinb-D1b*{0249}; Cologna 21 *Pinb-D1b*{0249}; David *Pinb-D1b*{0249}; Democrat *Pinb-D1b*{0249}; Etruria *Pinb-D1b*{0249}; Francia *Pinb-D1b*{0249}; Gemini *Pinb-D1b*{0249}; Genio *Pinb-D1b*{0249}; Gladio *Pinb-D1b*{0249}; Lampo *Pinb-D1a*{0249}; Leone *Pinb-D1a*{0249}; Leonardo *Pinb-D1a*{0249}; Libero *Pinb-D1a*{0249}; Marberg *Pinb-D1b*{0249}; Mentana *Pinb-D1a*{0249}; Mieti *Pinb-D1b*{0249}; Mose *Pinb-D1a*{0249}; Neviana *Pinb-D1a*{0249}; Newana *Pinb-D1b*{0249}; Oscar *Pinb-D1a*{0249}; Pandas *Pinb-D1b*{0249}; Pascal *Pinb-D1b*{0249}; Penawawa *Pinb-D1a*{03104}; Sagittario *Pinb-D1b*{0249}; Salgemma *Pinb-D1b*{0249}; Saliente *Pinb-D1b*{0249}; Salmone *Pinb-D1b*{0249}; Serena *Pinb-D1a*{0249}; Serio *Pinb-D1b*{0249}; Veda *Pinb-D1b*{0249}; Zena *Pinb-D1b*{0249}. \(dv\): *Ae. tauschii* unspecified accession (GenBank AJ249935){03103}; TA2475 (GenBank AY252037) *Pinb-D1i*, *Gsp-D1b*{03105}; TA1599 (GenBank AY252011) *Pinb-D1j*, *Gsp-D1g*{03105}; TA1691 (GenBank AY252013) *Pinb-D1j*, *Gsp-D1h*{03105}; *Ae. tauschii* unidentified accession (GenBank AJ249935){03103}; *Ae. tauschii* CPI 110799 (GenBank CR626926){10440}. *Pina-D1a* is present in all soft hexaploid wheats and possibly all hard hexaploid wheats that carry a hardness mutation in puroindoline b \{452,1035,0082,0204,0295\}.

**Pina-D1b** \(^{(1035)}\). Null allele. \(i\): Falcon/7 Heron, Heron/7 Falcon{03109}; Gamunya sel.{0298,0203}; Heron/7 Falcon sel.{0298,0203}; PI 644080 (Alpowa/ID377s//7*Alpowa*){10429}; Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar and Explorer{10527}. \(v\): Butte 86{1035}; Eridano{0249}; Falcon{1035}; Glenlea (GenBank AB262660). This BAC clone also contains *Pinb-D1a*{10431}; Kalyansona{0249}; Super X{0249}; Yecora Rojo{0204}. \(v2\): Amidon *Pina-D1a*{0249}; Ciano *Pinb-D1a*{0249}; Dorico *Pinb-D1a*{0249}; Golia *Pinb-D1a*{0249}; Guadalupe *Pinb-D1a*{0249}; Barra *Pinb-D1a*{0249}; Inia 66 *Pinb-D1a*{0249}; Indice *Pinb-D1a*{0249}; Jecora *Pinb-D1a*{0249}; Manital *Pinb-D1a*{0249}; Mendos *Pinb-D1a*{0249}; Prinqual *Pinb-D1a*{0249}; Sibilia *Pinb-D1a*{0249}. Present only in some hard hexaploid wheats. *Pina-D1b* is associated with harder texture than *Pinb-D1b* \{0177,0206\}. This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls \{10428,10391\}.

**Pina-D1c** \(^{(03105)}\). \(dv\): *Ae. tauschii* TA2369 (GenBank AY252031) *Pinb-D1h*, *Gsp-D1c*; TA2527 (GenBank AY252015) *Pinb-D1h*, *Gsp-D1e*{03108}; *Ae. tauschii* TA10 (GenBank AY649746){03108}.

**Pina-D1d** \(^{(03105)}\). \(dv\): *Ae. tauschii* PI452131 (GenBank AJ302098) *Pinb-D1i*{03104}; PI554318 (GenBank AJ302099) *Pinb-D1k*{03104}; TA1694 (GenBank AY252012) *Pinb-D1h*, *Gsp-D1f*{03105}; TA2374 (GenBank AY251996) *Pinb-D1i*, *Gsp-D1d*{03105}; TA2512 (GenBank AY252042) *Pinb-D1i*, *Gsp-D1e*{03105}; TA2455 (GenBank AY252022) *Pinb-D1i*, *Gsp-D1f*{03105}; TA2536 (GenBank AY252043){03105}; *Ae. tauschii* TA 1704 (GenBank AY649744){03108}.
**Proteins**

**Pina-D1e** (03105).  **dv:** *Ae. tauschii* TA2458 (GenBank AY252034) *Pinb-D1i*, *Gsp-D1d* (03105); TA2495 (GenBank AY252041) *Pinb-D1i*, *Gsp-D1e* (03105).

**Pina-D1f** (03105).  **dv:** *Ae. tauschii* TA2436 (GenBank AY251998) *Pinb-D1i*, *Gsp-D1d* (03105).

**Pina-D1g** (03105).  **dv:** *Ae. tauschii* TA2436 (GenBank AY251998) *Pinb-D1i*, *Gsp-D1d* (03105).

**Pina-D1h** (10118).  **v:** *X. aegiloptriticum* CIGM86.946-1B-0PR-0B (GenBank AY573898) *Pinb-D1o* (10118).

**Pina-D1i** (10118).  **v:** *X. aegiloptriticum* CIGM87.2784-1B-0PR-0B (GenBank AY573899) *Pinb-D1o* (10118).

**Pina-D1j** (10118).  **v:** *X. aegiloptriticum* CIGM88.1363-1B-0PR-0B (GenBank AY573900) *Pinb-D1o* (10118).

**Pina-D1k** (10118).  **v:** *X. aegiloptriticum* CIGM86.946-1B-0PR-0B (GenBank AY573898) *Pinb-D1o* (10118).

**Pina-D1l** (10118).  **v:** *X. aegiloptriticum* CIGM86.946-1B-0PR-0B (GenBank AY573898) *Pinb-D1o* (10118).

**Pina-D1m** (10208).  **v:** *Baimangchun* (GenBank EF620907) (10208).

**Pina-D1n** (10208).  **v:** *Hongheshang* (GenBank EF620907) (10208).

**Pina-D1o** (10311).  **dv:** *Ae. tauschii* RM0182 (GenBank AY608595) (10311).

**Pina-D1p** (10316).  **v:** *T. aestivum* Jing 771 (GenBank AY599893) (10316).

**Pina-D1q** (10316).  **v:** *U29* (GenBank AB181238) (10316); Muu-27 (homonym 'a2', *Pina-D1p*) (10316).

**Pina-A** (0083).  **dv:** *T. monococcum* DV92 (cultivated), G3116 (spp. *aegilopoides*) (GenBank AJ242715) (0083); unspecific accession (GenBank AJ249933) (03103); PI277138 (GenBank AJ302093) (03104); PI418582 (GenBank AJ302092) (03104); *T. monococcum* spp. *monococcum* TA2025, TA2026 (GenBank AY622786), TA2037 (GenBank AJ242715) (03108); *T. monococcum* spp. *aegilopoides* TA183, TA291, TA546, TA581 (GenBank AY622786) (03108).

In *T. monococcum* Pina-A*’*1 is completely linked to *Gsp-A**’*1 (0083).

**Pina-S1** (03108).  **dv:** *Ae. speltoides* PI 393494 (GenBank AJ302096) (03104); PI 369616 (GenBank AJ302097) (03104); *Ae. speltoides* spp. *speltoides* TA2368 (GenBank AY622787), TA1789 (GenBank AY622788) (03108); *Ae. speltoides* spp. *ligustica* TA1777 (GenBank AY622789) (03108).

**Pina-S2** (03108).  **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942 (03108).
**Proteins**

*Pina-S'I* (03108). **dv:** *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622790){03108}; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622791){03108}.

*Pina-S'I* (03108). **dv:** *Ae. searsii* TA1837, TA1355 (GenBank AY622792){03108}.

*Pina-S'II* (03108). **dv:** *Ae. sharonensis* TA1999 (GenBank AY622796){03108}.

*Pina-AI* (03108,03104). **dv:** *T. urartu* TA763 (GenBank AJ302103){03104}; TA808 (GenBank AJ302104){03104}.

*Pinb-DI* 5DS{452}. **v:** CS{452}; Capitole (GenBank X69912){03110}.


*Pinb-DIa* is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pina-DIb*, -D1c, -D1d, -D1e, or -D1f mutations {452,1035,0082,0204,0295}.

*Pinb-DIb* {452}. **5DS{452}**. **i:** Paha'2/Earlo Blackhull/5*Paha*{0298,0203}; Early Blackhull der./5*Nugaines sel.*{0298,0203}; hard sib sel. from Weston{03107}; PI 644081 (Alpowa/ND2603//7*Alpowa*{10429}; s: CS'7/Cheyenne 5D{452}. **v:** Thatcher{0204}; Wanser{452}; hard component of Turkey{0204}; Cheyenne (GenBank DQ363914){10315}; Renan (GenBank CR626934){10440}. **v2:** Bastion *Pina-DIa*{0317}; Bezostaya *Pina-DIa*{0249}; Brasilia *Pina-DIa*{0249}; Cerere *Pina-DIa*{0249}; Colfiorito *Pina-DIa*{0249}; Cologna 21 *Pina-DIa*{0249}; David *Pina-DIa*{0249}; Democrat *Pina-DIa*{0249}; Etruria *Pina-DIa*{0249}; Francia *Pina-DIa*{0249}; Gemini *Pina-DIa*{0249}; Genio *Pina-DIa*{0249}; Gladio *Pina-DIa*{0249}; Marberg *Pina-DIa*{0249}; Mieti *Pina-DIa*{0249}; Newana *Pina-DIa*{0249}; Pandas *Pina-DIa*{0249}; Pascal *Pina-DIa*{0249}; Sagittario *Pina-DIa*{0249}; Salgemma *Pina-DIa*{0249}; Saliente *Pina-DIa*{0249}; Salmone *Pina-DIa*{0249}; Serio *Pina-DIa*{0249}; Veda *Pina-DIa*{0249}; Zena *Pina-DIa*{0249}.

*Pinb-DIb* is a "loss-of-function" mutation resulting from the replacement of a glycine by a serine at position 46 {452}.

*Pinb-DIc* {0082}. **i:** PI 644082 (Alpowa/Red Bobs//7*Alpowa*{10429}. **v:** Avle{0082}; Bjorke{0082}; Portal{0082}; Reno{0082}; Tjalve{0082}.

*Pinb-DIc* is a "loss-of-function" mutation resulting from the replacement of a leucine by a proline at position 60 {0082}.

*Pinb-DId* {0082}. **i:** PI 644083 (Alpowa/Mjolner//7*Alpowa*{10429}. **v:** Bercy{0082}; Mjolner{0082}; Soissons (homonym 'b1'){10433}.

*Pinb-DId* is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a arginine at position 44 {0082}.

*Pinb-DIe* {0204}. **i:** PI 644084 (Alpowa/Canadian Red//7*Alpowa*{10429}. **v:** Gehun{0204}; Canadian Red{0204}; Chiefkan{0204}; Yunxianxiaomai{10427}.

*Pinb-DIe* is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 39 {0204}.
Pinb-D1f[0204].  i: PI 644085 (Alpowa/Sevier/7*Alpowa){10429}.  v: Abyssinia AV12.4{10430}; The hard component of Utac[0204].  
Pinb-D1f is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 44 [0204].

Pinb-D1g[0204].  i: PI 644086 (Alpowa/Andrews/7*Alpowa){10429}.  v: Andrews[0204].  
Pinb-D1g is a "loss-of-function" mutation resulting from the replacement of a cysteine by a stop codon at position 56 [0204].

Pinb-D1h[03105].  dv: Ae. tauschii TA2369 (GenBank AY251983) Pina-D1c, Gsp-D1c(03105); TA2527 (GenBank AY251965) Pina-D1c, Gsp-D1e(03105); TA1649 (GenBank AY251963) Pina-D1d, Gsp-D1f(03105); TA10 (GenBank AY649748)(03108); CPI110799 (GenBank AY159804){10037}.

Pinb-D1i[03105].  dv: Ae. tauschii TA2475 (GenBank AY251989) Pina-D1a, Gsp-D1b(03105); TA2536 (GenBank AY251993) Pina-D1c, Gsp-D1d(03105); TA2374 (GenBank AY251948) Pina-D1d, Gsp-D1d(03105); TA2512 (GenBank AY251992) Pina-D1d, Gsp-D1e(03105); TA2455 (GenBank AY251972) Pina-D1d, Gsp-D1f(03105); TA2458 (GenBank AY251986) Pina-D1e, Gsp-D1e(03105); TA2495 (GenBank AY251991) Pina-D1e, Gsp-D1e; TA2436 (GenBank AY251947) Pina-D1f, Gsp-D1d(03105); Ae. tauschii TA1704 and TA2381 (GenBank AY649747){03108,10315}; Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2){10314}; Ae. tauschii CPI 110799 (GenBank CR626926){10440}.  
Q03-002, TA1704, and TA2381 were incorrectly assigned Pinb-D1w in the 2006 supplement.

Pinb-D1j[03105].  dv: Ae. tauschii TA1599 (GenBank AY251962) Pina-D1a, Gsp-D1g(03105); TA1691 (GenBank AY251964) Pina-D1a, Gsp-D1h(03105); Ae. tauschii TA1691 (GenBank AY251946){03108}.

Pinb-D1k.  dv: Ae. tauschii PI554318 (GenBank AJ302108) Pina-D1d{03104}.

Pinb-D1l[10119].  v: GaoCheng8901{10119}.  
{10208} reported Pinb-D1b in Gaocheng 8901.

Pinb-D1m[10118].  v: X. aegilotropicum CIGM87.2783-1B-0PR-0B (GenBank AY573901) Pina-D1c{10118}.

Pinb-D1n[10118].  v: X. aegilotropicum CIGM92.1708 (GenBank AY573902) Pina-D1d{10118}.

Pinb-D1o[10118].  v: X. aegilotropicum CIGM93.247 (GenBank AY573903) Pina-D1e{10118}.

Pinb-D1p[10121].  [Pinb-D1z(10316)].  v: Dahuangpi (GenBank AY581889){10316}; Nongda 3213{10121}; Nongda 3395{10121}; QinDao landrace{10305}; Qitoubai{10305}; Shijiazhuang 34{10305}; Zigan{10305}.  
The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213. homonym: Pinb-D1i(t) {10305}. This homonym sequence (allele) was incorrectly assigned Pinb-D1z, 'b3', Pinb-D1u.

Pinb-D1q[10077].  s: CS*/Red Egyptian 5D substitution line, Pina-D1k, Gsp-D1i{10077}.  v: Jingdong 11 (GenBank EF620909){10313}.  
This allele was used originally (2004 supplement) in combination with Pina-D1k and Gsp-D1i to denote the large deletion that encompasses Pina-D1, Pinb-D1, and Gsp-D1 {10077} (cf. Pins-D1k). The haplotype nomenclature of this deletion is under review. Pinb-D1q is currently used to denote the C-to-G SNP at position 218 {10313}.

Pinb-D1r[10209].  [Pinb-D1h[10209]].  v: Hyb65 (NCBI AJ619022){10209}.  
G insertion: open reading frame shift and premature stop codon; hard kernel texture {10209}.
**Pinb-D1s** [10209].  v: NI5439 (NCBI AJ619021)[10209].

G insertion as in Pinb-D1r and an A-to-G substitution; hard kernel texture [10209].

**Pinb-D1t** [10208].  v: Guantouxiannmai (GenBank EF620910)[10208]; Hongmai[10208].

G-to-C substitution: Glycine-47 to arginine; hard kernel texture [10208].

**Pinb-D1u** [10427].  v: Tiekemai (GenBank EF620911)[10427]; 31 hard Yunnan endemic wheats (*T. aestivum* ssp. *yunnanense* King)[10427].

Possesses a G deletion at position 127 leading to a shift in ORF [10427].

**Pinb-D1v** [10305,10316].  

[Pinb-D1i(t)[10305], Pinb-D1r[10316]] v: Qingdao Landrace 1[10305]; Qitoubai[10305]; Shijiazhuang 34[10305]; Tachun 3 (GenBank AY598029)[10305]; GenBank AY649747[10305].

The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in [10305] are Pinb-D1p as listed above for that allele. The following variety/sequence was assigned Pinb-D1v in the 2006 supplement; but the original assignment of [10316] is now unchanged.

**Pinb-D1w** [10314].  

[Pinb-D1q[10316]. v: Jing 771 (GenBank AY640304, AB180737)[10316]; Ae. tauschii 002 (GenBank DQ257553)[10314]; Ae. tauschii ssp. tauschii TA1704 (GenBank AY649747)[10315]; Ae. tauschii ssp. anathera TA2381 (GenBank AY649747[10315].

This variety/sequence was incorrectly assigned Pinb-D1x in the 2006 supplement; the original assignment of [10316] is now unchanged.

**Pinb-D1x** [10528].  

Kashibaipi (GenBank AM909618)[10528].

**Pinb-D1y**.

The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in [10305] is Pinb-D1v as listed above. The original assignment of [10316] is now unchanged. Currently there is no assignment for this allele.

**Pinb-D1z**.

This allele/sequence is identical to, and listed under Pinb-D1p. Currently there is no assignment for this allele.

**Pinb-D1aa** [10391].  v: Changmangtoulongbai (GenBank EF620912)[10391]; Hongtutou 1[10391]; Hongtutou 2[10391].

**Pinb-D1ab** [10432].  v: KU3062[10432]; KU3069[10432]; Tuokexunyihao[10528].

**Pinb-D1ac** [10570].  v: Kashibaipi[10570]; Red Star[10570].

G to A substitution at position 257 and C to T substitution at position 382 [10570].

**Pinb-A"m1** [0083].  5A"m15[0083].  dv: *T. monococcum* DV92 (cultivated) cds (GenBank AJ242716) complete BAC sequence (GenBank AY491681), G3116 (spp. *aegilopoides*)[0083]; is identical to allele Pina-D1h[03105]; PI277138 (GenBank AJ302102)[03104]; PI418582 (GenBank AJ302101)[03104]; *T. monococcum* TA2025 (GenBank AY662279)[10315]; *T. monococcum* TA2026 (GenBank AY6622798)[10315]; *T. monococcum* TA183 (GenBank AY6622799)[10315].

In *T. monococcum* Pinb-A"m1 is 0.1 cM proximal to Pina-A"m1 and both loci are less than 36 kb apart [0083].

**Pinb-S1** [03108].  dv: Ae. speltoides PI393494 (GenBank AJ302105)[03104]; PI 369616 (GenBank AJ302106)[03104]; Ae. speltoides spp. speltoides TA2368 (GenBank AY6622797), TA1789 (GenBank AY6622802)[03108]; Ae. speltoides spp. *ligustica* TA1777 (GenBank AY6622803)[03108].

**Pinb-5"1** [03108].  dv: Ae. bicornis spp. *typica* TA1954 (GenBank AY6622807), TA1942 (GenBank AY6622808)[03105].
Grain softness protein

Pinb-SI (03108).  **dv:** Ae. longissima spp. longissima TA1912 (GenBank AY622800) (03108); Ae. longissima spp. nova TA1921 (GenBank AY622804) (03108).

Pinb-SI (03108).  **dv:** Ae. searsii TA1837 (GenBank AY622805), TA2355 (GenBank AY622806) (03105).

Pinb-S4I (03108).  **dv:** Ae. sharonensis TA1999 (GenBank AY622809) (03105).

Pinb-D1b, Pinb-D1c, Pinb-D1d, Pinb-D1e, Pinb-D1f, or Pinb-D1g are present in hard hexaploid wheats not carrying the Pinb-D1b (null) mutation (452,1035,0082,0204).

Wheats with Pinb-D1b were slightly softer and a little superior to those with Pinb-D1b in milling and bread-making characteristics although there was considerable overlap (0206).

Transgenic rice with the Pinb-D1a and Pinb-D1a alleles possessed softer grain (0207).

Genotypes for a selection of North American wheats are given in (0204).

In *T. monococcum* the gene order was reported to be : tel - Gsp-1 - Pina - Pinb (0083, 10122) whereas in *Ae. squarrosa* it was : tel - Gsp-1 - Pinb (10037).

Ikeda et al. (10305) reported a double-null with apparently no Pinb-D1 or Pinb-D1 genes present in : Bindokku, Cheyenne ‘A’, Chosen 68, Saiiku 18, Saiiku 44, and tentatively assigned it Pinb-D1b/Pinb-D1h(t). How this deletion compares with the double null mutation reported by Tranquili et al. (10077) which was assigned Pinb-D1h/Pinb-D1h(t) is unknown.

### 80.5.9. Grain softness protein

**Gsp-I** (1185).

**Gsp-AI** (614).  [**GSP** (614)].  5A (614,0383).  **v:** CS (614,0383); Rosella (GenBank AF177218) (0383).

In (1185) partial-sequence clone TSF61 from cv. Soft Falcon (GenBank X80380) was identical to this allele.

**Gsp-BI** (614).  [**GSP** (614)].  5B (614).  **v:** CS (614); Glenlea (0385).

In (1185) sequence of clone TSF33 from cv. Soft Falcon (GenBank X80379) was identical to this allele, as are ESTs for cv. CS (dbEST BJ235798) and cv. CNN (dbEST BE423845).

**Gsp-DI** (614).  [**GSP** (614)].  5DS (614).  **v:** CS (614); Glenlea (0385).  **dv:** *Ae. tauschii* CPI1110799 (GenBank AF177219) (0383).  **ma:** Co-segregation of Gsp-D1 and Ha (614).

In (1185) sequence of clone TSF69 from cv Soft Falcon (GenBank S72696) is identical, as are ESTs for cv CS (dbEST BJ237450) and cv CNN (dbEST BE422565).

This locus has a large deletion encompassing genes Pinb-D1, Pinb-D1 and Gsp-D1 (10077).

**Gsp-DIb** (03105).  **dv:** *Ae. tauschii* TA1583 (GenBank AY252079) Pinb-D1a, Pinb-D1a (03105); TA2475 (GenBank AY252087) Pinb-D1a, Pinb-D1a (03105).

**Gsp-DIc** (03105).  **dv:** *Ae. tauschii* TA2369 (GenBank AY252081) Pinb-D1c, Pinb-D1h (03105); CPI110799 (GenBank AF177219) (0383).

**Gsp-DIId.  dv:** *Ae. tauschii* TA2536 (GenBank 252093) Pinb-D1c, Pinb-D1i (03105); TA2374 (GenBank AY252046) Pinb-D1d, Pinb-D1i (03105); TA2458 (GenBank AY252084) Pinb-D1e, Pinb-D1i (03105); TA2436 (GenBank AY252048) Pinb-D1f, Pinb-D1i (03105).

**Gsp-DIe.  dv:** *Ae. tauschii* TA2527 (GenBank AY252066) Pinb-D1e, Pinb-D1i (03105); TA2512 (GenBank AY252092) Pinb-D1d, Pinb-D1i (03105); TA2495 (GenBank AY252091) Pinb-D1e, Pinb-D1i (03105).

**Gsp-DIf.  dv:** *Ae. tauschii* TA1649 (GenBank AY252063) Pinb-D1f, Pinb-D1h (03105); TA2455 (GenBank AY252073) Pinb-D1d, Pinb-D1i (03105).
80.5.10. Starch synthase

**Gsp-D1g**. **dv**: *Ae. tauschii* TA1599 (GenBank AY252062) *Pina-D1a*, *Pinb-D1j*{03105}.

**Gsp-D1h**. **dv**: *Ae. tauschii* TA1691 (GenBank AY252064) *Pina-D1a*, *Pinb-D1j*{03105}.

**Gsp-D1i**{03105}. **v**: Yecora Rojo (GenBank AY255771) *Pina-D1b*, *Pinb-D1a*{03105}.

**Gsp-D1j**{10077}. **s**: CS*/Red Egyptian 5D, *Pina-D1*, *Pinb-D1* and *Gsp-D1*{10077}.

80.5.11. Histone H1 Proteins

**HstH1-A1**{0215}. 5A{0215}. **v**: CS{0215}.

**HstH1-B1**{0215}. 5B{0215}. **v**: CS{0215}.

**HstH1-D1**{0215}. 5D{0215}. **v**: CS{0215}.

**HstH1-D1a**{0215}. **v**: CS{0215}; 18 others{0215}.

**HstH1-D1b**{0215}. **v**: Grekum 114{0215}; Kirgizsky Karlik{0215}.

**HstH1-A2**{0215}. 5A{0215}. **v**: CS{0215}.

**HstH1-A2a**{0215}. **v**: CS{0215}.

**HstH1-A2b**{0215}. Null allele{0215}. **v**: Mara{0215}; 10 others{0215}.

**HstH1-B2**{0215}. 5B{0215}. **v**: CS{0215}.

**HstH1-B2a**{0215}. **v**: CS{0215}; 19 others{0215}.

**HstH1-B2b**{0215}. **v**: Excelsior{0215}.

**HstH1-D2**{0215}. 5D{0215}. **v**: CS{0215}.

The relationship of this gene series with a **Hst-A1**, **Hst-B1**, **Hst-D1** series in group 5 chromosomes {0216} based on DNA hybridization studies was not established.
Pathogenic Disease/Pest Reaction

For disease/pest reaction gene guidelines see Introduction, no. 8.

Note: In listings of multiple alleles, the chromosomes locations and ma: citations with generally be given with the particular allele that was located of mapped.

### 81. Reaction to Barley Yellow Dwarf Virus

**Disease:** Cereal yellow dwarf

**Bdv1** {1363,1379}. 7D{1379}.7DS{1363}. i: Jupeteco 73R (compared to Jupeteco 73S){1363}. v: Anza{1379}; Condor BW3991{1379}; Tyrant BW3872{1379}; Hahn BW4097{1379}; Parrot BW10817{1379}; Siren BW18643{1379}; Many CIMMYT genotypes. **Bdv1** is completely linked with **Ltn**, **Lr34** and **Yr18**. See **Ltn**, **Lr34**, **Yr18**.

**Bdv2** {058}. 7DL = T7DS.7DL-7Ai#1L{552,0182}.7D = T7DS-7Ai#1S.7Ai#1L group. tr: TC14{059,0201}; H960642{0182}. v: Glover (with TC6){10491}; Mackellar = LH64C (from tissue culture){10177}; TC14′2/Hartog{0225}; TC14′2/Spear{0201}; TC14′2/Tatiara{0225}; Yw243, Yw443, Yw642 and Yw1029 (derived by *phl* induced recombination) see{10177}. ma: Distal 10% of 7DL, translocation point between RFLP markers Xpsr680 and Xpsr965{0182}; Complete association with Xpsr129-7D, Xpsr548-7D, XksuD2-7D, XcslH81-7D, and Xgwm37-7D selected as a diagnostic marker{0225}; Two RGAP and 1 RAPD markers developed for the Yw series also effective for at least TC14{10177}.

**Bdv3** {10159}. Derived from *Th. intermedium* cv. Ohahe {10158} 7DS.7DL-7EL{10157}. v: P961341 PI 634825{10157}; P98134{10159}. ad: P107{10159}. su: P29 (7D{7E}){10156}. ma: A SSR-BDV marker is described in {10159}.

*Bdv3* in wheat shows distored inheritance that varies with genetic background

### 82. Reaction to Bipolaris sorokiniana

**Diseases:** Spot blotch and common root rot.

**Spot blotch**

**QTL**

**Yangmai 6** (R)/Sonalika (S): RIL population: AUDPC was controlled by four QTLs derived from Yangmai 6, viz. **Qs.bhu-2AL** (**Xbarc353**-2A - **Xgwm445**-2A, $R^2$=0.148), **Qs.bhu-2BS** (**Xgwm148**-3B - **Xgwm375**-2B, $R^2$=0.205), **Qs.bhu-5BL** (**Xgwm67**-5BL - **Xgwm371**-5BL, $R^2$=0.386) and **Qs.bhu-6DL** (**Xbarc173**-6D - **Xgwm372**-6DL, $R^2$=0.225) {10719}.

### 83. Reaction to Blumeria graminis DC.
83.1. Designated genes for resistance

Note: Chancellor, used as a susceptible genetic background, for some near-isogenic lines probably carries Pm10 and Pm15 [1479]. 33 NILs, including 22 resistance genes and 3 genetic backgrounds are listed in {10389}.

**Pm1.**

**Pm1a** [562]. [Pm1{130}, Mlt{1175}, Mla{348}]. 7A{1293}, 7AL{1305}. i: Axminster/8’Chancellor{132}; CI 14114 = As II/8’Chancellor{132}; CI 13836/8 Chancellor{132}; Kenya C6041/5 Federation{1168}; Norka/8’Chancellor{132}. s: CS 5/Axminster 7A{1293}. v: Anfield{098}, As II{130}, Axminster{130,1175}; Birdproof{165}; Bonus{1554}; CI 13836{130}; Converse{1175}; Fedka{939}; Festival{1554}; Fram I{130}; Huron CI 3315{1175,1554}; Kenora{1554}; Kenya W744 = C6041{130,1175}; Norka{130,1175}; Pika{130}; Sweden W1230{1554}; Thew{1175}; TU 4{130}; Zhengzhou 871124{570}. v2: Anfield Pm9{1287}; BGRC 44514 Pm3a{1628}; Mephisto Pm2 Pm9{540}; Normandie Pm2 Pm9{165}; Pompe Pm9{1287}; Ring Pm9{1287}; Sappo Pm2 Pm4b (Carries Lr20){310}; Solo Pm2 Pm4b{052}. ma: Co-seg. with Xcdo347-7A using NILs{864}; Co-segregation or close linkage with three RAPDs; one RAPD converted to a STS{570}. Note: In Solo, Pm1 is translocated to chromosome 7D{052}; Complete cosegregation of several markers including Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbz232(Tha)-7A, Xrgc607-7A and Xsts638-7A with Pm1 and Lr20 was reported in {0323}.

**Pm1b** [562]. v: MocZlatka{562}.

**Pm1c** [562]. [Pm18{853,562}]. v: Blaukorn{0011}; M1N{1628,562}; In{540}; M1N was described as an undesignated subline of Weihenstephan M1. ma: AFLP marker 18M2 was diagnostic for Pm1c{0011}.

**Pm1d** [562]. v: T. spelta var duhamelianum TR12258{562}. ma: AFLP marker 18M1 - various Pm1 alleles 0.9 cM{0011}.

T. spelta duhamelianum also possesses Pm10 and Pm11 which confer resistance to certain hybrids of B. g. tritici and B. g. agropyri.

**Pm1e** [0322]. [Pm22{1134}]. v: Elia{1134}; Est Mottin{1134}; Ovest{1134}; Tudest{1134}; Virest{1134}.

**Pm2** [130]. [Mlt{1175}, Mlx{1088}]. 5D{1007}, 5DS{945}. i: CI 14118 = Ulka/8’ Chancellor{132}; CI 14119 = CI 12632/8 Chancellor{132}; Federation 4/Ulka{1168}. v: Avalon{096}; Bounty{096}; Fenman{096}; Galahad{1531}; H8810/47{130}; Longbow{1531}; Maris Beacon{1592}; Maris Nimrod{1592}; Maris Sportman{096}; Maris Templar{1592}; Norman{096}; Orestis{1079}; PI 92378{1168}; PI 181374{1168}; Sea Island{130}; Sentry{096}; S2303{945}; Synthetic(lumillo/Ae. taudsi){1168}; TP 114/2 Stark deriv{626}; Ulka{130,1175}; XX186 = T. durum Santa Maria/Ae. squarrosa BGRC 1458 Pm19{853}. v2: Apollo Pm4b Pm8{541}; Brigand Pm6{096}; Brimstone Pm6{1531}; CI 12632 Pm6{130}; CI 12633 Pm6{133}; Compal Pm4b{854}; Crossbow Pm5 Pm6{098}; Gawain Pm6{1531}; Halle Stamm 13471 Mld{097}; Heiduc Pm6{541}; Hustler Pm6{096}; Hornet Pm8{1531}; Kinsman Pm6{096}; Mardler Pm6{096}; Maris Dove Mld{1592}; Maris Fundin Pm6{096}; Maris Huntsman Pm6{1592}; Mephisto Pm1 Pm9{540}; Normandie Pm1 Pm9{165}; Parade Pm5 Pm6{1531}; Rendezvous Pm4b Pm6{1531}; Solo Pm1 Pm4b{052}; Timmo Pm4b{096}; TP 114 Pm6{626}; Virtue Pm6{096}; Walter Pm4b Pm6{1428}. dv: Ae. squarrosa BGRC 1458{853}; Forty accessions of Ae. taudsi{852}. ma: Pm2 - 3.5 cM - Xbcd1871-5D using F2s{864}; Xcfd81-5D - 2.0 cM - Pm2{10366}.

Disease: Powdery Mildew.

Resistance genes and their molecular associations are reviewed in {10141}. 
**Pm3**. 1A. **ma**: Xgdms33-1A - 2.3 cM - Pm3/Xpsp2999-1A{0313}.

Genotype list: {0313, 10405, 10406} The Pm3a, Pm3b, Pm3d and Pm3f alleles form a true allelic series based on sequence analysis {10292}.

Following the cloning and sequencing of Pm3b {10064}, 6 other alleles were sequenced {10405}. The Chinese Spring (susceptible) allele, Pm3CS, considered to be ancestral and present in many hexaploid and tetraploid wheats, was also transcribed {10405, 10406}. Other wheats possessed a truncated sequence (e.g. Kavkaz), or were null {10405,10406}. Unique markers were developed for all 8 transcribed alleles, and for individual alleles {10405}.

Alleles Pm3b, Pm3d, and Pm3f were detected in Scandinavian varieties using allele-specific markers {10681}.

**Pm3a**{130,132}. [Mla{1168}]. 1A{1007}.1AS{943,947}. i: Asosan/8 Chancelor {132} = CI 14120; Asosan/3 Federation{1168}. v: Asosan{130,1168}; BGRC 44514  

**Pm4a**{1629}; Coker 797{786}; Florida 301{786}; Florida 302{786}; Hadden{097}; Halle Stamm{097}; Norin 3{1134}; Norin 29{1134}; PI 46890{1439}; Saluda{786}; Tyler{1419}. ma: Xbcd1434-1A - 1.3 cM - Pm3 using NILs{864}; Xwhs179-1A - 3.3 cM - Pm3{522}.

Sequence AY939880 {10292}.

**Pm3b**{130,132}. [Mlc{165},Pm3j{10405}]. 1A{1007}. i: Chul^8/Chancelor{132}; T. sphaerococcum^8/Chancelor = CI 15887{539}. v: Chul{165}. ma: Xbcd1434-1A - 1.3 cM - Pm3b using NILs{864}.

The isolation of Pm3b is reported in {10064}. The Pm3b gene (GenBank AY325736) is a coiled-coil NBS-LRR type of disease resistance gene {10064}.

**Pm3c**{130,132}. [Mls{1175},Pm3i{10405}]. 1A{134,1007}. i: Sonora/8 Chancelor {132} = CI 14122; Sonara/4 Federation{1168}; Triticale/8 Chancelor{539}. s: CS^7/Indian {134}. v: Borens{854}; Cawnpore{1628}; CI 3008{130}; CI 4546{130}; Hindukush{1628}; Indian{1175}; Sonora{130,1168}; Sturgeon{1175}.

Sequence DQ251587, DQ517917 {10405}.

**Pm3d**{1628}. [Ml-k{540},Mlk{434},Pm3h{10405}]. 1A{1628}. v: Axona{0313}; Cornette{0313}; Herold{540}; Indian 4{0313}; Kadett{0313}; Kanzler{0011}; Kleiber{0313}; Kolibri{540,542,1628}; Ralle{540}; Socrates {heterogeneous}{540}; Star {heterogeneous}{540}; Syros{540}. v2: Kadett Pm4b{540}; Turbo Pm4b{540}.

Sequence AY939881 {10292}. DQ251488, DQ517518 {10405}.

**Pm3e**{1628}. v: Sydney University Accession W150 =AUS 6449(939,1628).

**Pm3f**{1628}. i: Michigan Amber/8 Chancelor{1628}; This allele was distinguished from Pm3c with only one of 13 pathogen cultures.

Sequence DQ071554 {10292}.

**Pm3g**{0070}. [Mlar{854}]. 1A{0070}.1AS{0363}. v: Avo{1629}; Aristide{1629}; Champetre{0313}; Courtot{1629}; Lutin{0313}; Oradian{0313}; Rubens{0313}; Soissons{0313}; Valois{0313}. ma: Pm3g - 5.2 cM - Gli-A5 - 1.9 cM - Gli-A1{0070}; Pm3g was completely linked to microsatellite Xpsp2999{0363}.

Sequence DQ251489, DQ517919 {10405}.

**Pm4**{131}.

**Pm4a**{1464}. [Pm4{131}]. 2AL{1464}. i: CI 14123 = Khapli/8 Chancelor{131}; CI 14124 = Yuma/8 Chancelor{131}. v: Steinwedel2/Khapli{939}; Yangmai 10{10176}; Yangmai 11{10176}. tv: Khapli{131}; Valgerado{097}; Yuma{131}.

ma: Co-seg with Xbcd1231-2A & Xcd678-2A using F2s{864}; Xbcd1231-2A - 1.5 cM - Pm4 - 1.56 cM - Xbcd292-2A{864}; Pm4a - 3.5 cM - AFLP markers 4aM1 and 4aM2{0011}; Xbcd1231-2A was converted to a STS marker{0069,10176}; and to a Pm4a-specific dominant PCR marker{10176}; Xgwm356-2A - 4.8 cM - Pm4a{10176}.
**Pathogenic Disease/Pest Reaction**

*Pm4b* [1464]. *Mle* [1591]. 2A [052], 2AL [1464]. *i*: Federation \(^7\) T. *arthelicum* W804 [1464]. *v*: Achill [540]; Ajax [540]; Arkas [540]; Armada [096]; Atlantis [0011]; Boheme [0011]; Botri (heterogeneous) [854]; ELS [1591]; Facta [854]; Factor (heterogeneous) [854]; Fakon [854]; Fazit [854]; Hermes [540]; Horizont [540]; Maris Halberd; Max [540]; Olym [540]; Orbis [540]; RE714 [1220]; Renan [0016]; Ronos [1079]; S-25 [052]; S-28 [052]; TP 229 [626, 1591]; Weißenstephan M1 [1591]; VPM1 [097]. *v2*: Apollo *Pm2* *Pm8* [541, 802]; Boxer *Pm5* [541]; Compal *Pm2* [854]; Kadett *Pm3d* [540]; Kronjuwel *Pm8* [541]; Mission *Pm5* 78, 541, 1531; *Rang Pm1* [052]; Rendezvous *Pm2* *Pm6* [1531]; Solo *Pm1* *Pm2* [052, 540]; Sorbas *Pm6* [541]; Timmo *Pm2* *Pm6* [096]; Turbo *Pm3d* [540]; Walter *Pm2* *Pm6* [1428]. *ma*: *Pm4b* - 4.8 cM - Xgbx3119b-2A [0272]; Xgwm382-2A - +/- 10 cM - *Pm4b* - +/- 2 cM - XgbxG303-2A [0354]; STS241 - 4.9 cM - *Pm4b* - 7.1 cM - SRAP Me8/Em7220 - 4.7 cM - Xgwm382-2A [10553].

*Pm4c* [10583]. *Pm23* [1618] 2AL [10583]. earlier reported on 5AL [1618]. *v2*: 81-7241 *Pm8* suppressed [10583, 1618]. *ma*: Xbarc122-2A - 1.4 cM - *Pm4c* - 3.5 cM - Xgwm356-2A [10583].

*Pm5*.

*Pm5a* [0257]. *Pm5a* was transferred to hexaploid wheat from *T. dicoccum* via Hope and H-44. Recessive. *Pm5* [787], *mlH* [771]. 7B [964], 7BL [771]. *i*: Hope/8* Chancellor = CI 14125 [570]. *s*: CS6/8* Hope 7B [771,964]. *v*: Alidos [854]; Aotea [964]; Caldwell [786]; Ga 1123 [0257]; Galaxie [0257]; Glenwari [964]; Hardired [786]; Hope [964]; H-44 [964]; Kontrast [854]; Kormoran [1079]; Kutulkuska [0257]; Lambros [0257]; Lawrence [964]; Navid [0257]; Pagode [0257]; Redcoat [097]; Redman [964]; Regina [0257]; Renown [964]; Selpek [540]; Sicco [096, 0257]; Spica [964]; Tarasque [0257]; Warigo [964]; Zolotistaya [0257]. *v2*: Arthur *Pm6* [786]; Coker 983 *Pm6* [786]; Double Crop *Pm6* [786]; Granada *Pm8* [541]; Saar *Pm38* *Pm39* [10481]; Sensor *Pm8* [541].

*Pm5b* [0257]. *Mli* [540, 558]. *v*: Aquila [096, 541]; Carimulti [541]; Cariphus [541]; Cucurova [0257]; Dolomit [541]; Falke [541]; Flanders [096]; Fruhprobst [0257]; Ilona [0257]; Ibis [096]; Kirkpinar-79 [0257]; Kontrast [0257]; Kormoran [541]; Krakat [541]; Markant [541]; Mercia [1531]; Milan [541]; Nadadores [0257]; Reiher [541]; Rektor [541]; Rothwell Perdix [096]; Siete Cerros [0257]; Severin [541]; Sicco [096]; Sperber [541]; Tukan [541]; Una [0257]; Urban [541]; Wattines [541]; Wettiness [0257]. *v2*: Bert *Pm6* [541]; Boxer *Pm4b* [541]; Crossbow *Pm2* *Pm6* [098]; Kristall *Pm8* [541]; Mission *Pm4b* [541, 1531]; Parade *Pm2* *Pm6* [1531].

*Pm5c* [0257]. 7B [0257]. *v*: *T. sphaerococcom* cv. Kollandi [0257].

*Pm5d* [0257]. 7B [0257], 7BL, FL 0.86 [10542]. *i*: IGV 1-455 = CI 10904/7* Prins [0257]; CI 10904/7* Starke [0257]. *v*: Dream [10542]. *ma*: Xgwm611-7B - 2.1 cM - *Pm5d* - 2.0 cM - Xgwm577-7B - 1.0 cM - Xwmc581-7B [10542].

*Pm5e* [0258]. Recessive and hemizygous effective [0258]. *mlfc* [0259]. *v*: Fuzhuang 30 [0258]. *ma*: Xgwm1267-7B - 6.6 cM - *Pm5e* - 12.6 cM - Xucb405s282B [0258].

*Pm6* [627]. *Ml* [626]. 2B [1088]. *i*: CI 13250/7* Prins [0069]; CI 12559/8* Prins [0069]; Eight Prins derivatives [10576]; PI 170914/7* Prins 6 NILs based on Prins [0139]. [0069]. *v*: 1969 IVGS Line C [626]; Abe [097, 1256]; Coker747 [786, 1079]; Mengavi [097]; Oasis [786]; Timgalen [098]; TP 114/2 Starke deriv. B [626]. *v2*: Arthur *Pm5a* [097, 786]; Brigant *Pm2* [096]; Brimstone *Pm2* [1531]; CI 12632 *Pm2* [626, 1088]; CI 12633 *Pm2* [626, 1088]; Crossbow *Pm2* *Pm5* [098]; Double Crop *Pm5a* [786]; Garwain *Pm2* [1531]; Greif *Pm5a* [0017]; Heiduck *Pm2* [541]; Hustler *Pm2* [096]; Kinsman *Pm2* [096]; Mardler *Pm2* [096]; Maris Fundin *Pm2* [096]; Maris Huntsman *Pm2* [1592]; Parade *Pm2* *Pm5* [1531]; Rendezvous *Pm2* *Pm4b* [1531]; Sorbas *Pm4b* [541]; Timmo *Pm2* *Pm4b* [096]; TP 114 *Pm2* [626]; Virtue *Pm2* [096]; Walter *Pm2* *Pm4b* [1428]. *ma*: Close
linkage with \(Xbcd135-2B\) (1.5+1.4 cM), \(Xbcd307-2B\) (4.7+2.5 cM) and \(Xbcd266-2B\) (4.5+2.4 cM); Mapped to the interval \(Xbcd35-2B\)-\(Xpsr934-2B\) (0139); However, the fact that Timgalen and a 'C112632/Cc' line lacked the critical \(T.\ timopheevii\) markers (0139) is cause for concern; RFLP marker \(Xbcd135-2B\) was converted to STS markers NAU/STS\_BCD135-1 and NAU/STS\_BCD135-2 which showed linkage of 0.8 cM with \(Pm6\) (10576).

**Pm7.** Derived from \(S.\ cereale\) cv. Rosen. 4BL\{270,271,389\} = T4BS.4BL-5RL\{543\}, but more recently revised to T4BS.4BL-2R\#IL\{380,389\}. \(\text{i:}\) Translec\#8 'Chancellor. \(\text{v:}\) Translec\{269\}; Translec\{273\}.

**Pm8.** Derived from Petkus rye - see \(Yr9,\ Lr26,\ Sr31\). 1R\{1B\}.1BL.1RS. \(\text{i:}\) MA1 and MA2, four-breakpoint double translocation lines 1RS-1BS-1RS-1BS. 1BL in Pavon (0084). \(\text{v:}\) Corinthian\{1531\}; Dauntless\{1531\}; Ambassador\{1531\}; Disponent\{541\}; GR876\{753\}; Halle Stamm\{097\}; Hammer\{098\}; Others\{1208\}; ST1-25\{201\}; Slejtnar\{1531\}; Steston\{1531\}; Stuart\{096\}. \(\text{v:2}\) Apollo \(Pm2\) \(Pm4b\)\{541\}; Granada \(Pm5\)\{541\}; Hornet \(Pm2\)\{1531\}; Kristall \(Pm5\)\{541\}; Kronjuwel \(Pm4b\)\{541\}; Sensor \(Pm5\)\{541\}. \(\text{tv:}\) Cando*2/Veery = KS91WGRC14\{381\}. 1BS/1RS recombinants 2.9 cM proximal to \(Gli-B1/GluB3\) (0084). Crosses between three lines with \(Pm8\) and Helami-105, a 1BL.1RS line with \(Pm17\), indicated that \(Pm8\) and \(Pm17\) were allelic\{524\}. Earlier, these genes were reported to be genetically independent\{1463\}. A STS marker distinguished \(Pm17\) from \(Pm8\) (0286).

**Pm9\{347\}.** 7A\{347\}.7AL. \(\text{v:}\) N14\{562\}. \(\text{v:2}\) Anfield \(Pmla\)\{1287\}; Mephistro \(Pmla\) \(Pm2\)\{540\}; Normandie \(Pmla\) \(Pm2\)\{347\}; Pompe \(Pmla\)\{1287\}; Ring \(Pmla\)\{1287\}.

**Pm10\{1482\}.** 1D\{1482\}. \(\text{v:}\) Norin 4\{1482\}; Norin 26\{1482\}; Norin 29\{1482\}; Penjamo 62\{1482\}; Shinchunaga\{1482\}. \(\text{v:2}\) \(T.\ spelta\) duhamelianum \(Pm11\)\{1481\}. \(Pm10\) was detected using a culture derived from a hybrid of \(B.\ g.\ triticici\) and \(B.\ g.\ agropyri\). \(Pm11\)\{1481\}. 6BS\{1481\}. \(\text{v:}\) Chinese Spring\{1481\}; Salmon\{1481\}; \(T.\ compactum\) No. 44\{1481\}. \(\text{v:2}\) \(T.\ spelta\) duhamelianum \(Pm10\)\{1481\}. \(Pm11\) was detected using a culture derived from a hybrid of \(B.\ g.\ triticici\) and \(B.\ g.\ agropyri\).

**Pm12\{1017\}.** Derived from \(Ae.\ speltoides\) The earlier location of 6A \{1017\} was not correct. 6B = 6BS-6SS.6SL\{598,572\}.6S\#1\{598\}. \(\text{v:}\) Wembley\#6/\(Ae.\ speltoides\) #31\{1017,598\}. \(\text{al:}\) \(Ae.\ speltoides\) CL214008 = K\{1017\}. \(\text{ma:}\) \(Pm12\) was mapped to a translocated segment proximal to \(Xpsr551\)-\(6B\)\{598\}; Secondary recombination analysis indicated that \(Pm12\) was located in the long arm of 6S between \(Xwmc\)\{105\} and \(Xc2\)\{10576\}.

**Pm13.** Derived from \(Ae.\ longissima\) \(\text{ma:}\) STS marker \(Xutv13\)\{0036\}; several other markers located in introgressed segments\{0036\}. 3B\{173\} = T3BL.3BS-3S\#1\{389\}. \(\text{v:}\) R1A\{174\}; R1B\{055\}; R4A\{055\}; R6A\{055\}. \(\text{ma:}\) \(Pm13\) was mapped to a translocated 3S\#1 segment distal to \(Xcdo-460-3B\)\{0036\}. 3D\{173\} = T3DL.3DS-3S\#1\{389\}. \(\text{v:}\) R2A\{055\}; R2B\{055\}. \(\text{tv:}\) R1D\{174\}. 3S\#1\{S. \(\text{al:}\) \(Ae.\ longissima\).

**Pm14.** 6B\{1478\}. \(\text{v:2}\) Akabozu \(Pm10\)\(Pm15\)\{1478\}; Kokeshikomugi \(Pm15\)\{1478\}; Norin 10 \(Pm15\)\{1478\}. \(Pm14\) and \(Pm15\) were detected using hybrids between \(B.\ g.\ triticici\) and \(B.\ g.\ agropyri\) cultures.

**Pm15.** 7DS\{1478\}. \(\text{v:2}\) Akabozu \(Pm14\)\{1478\}; Chinese Spring \(Pm11\)\{1478\}; Kokeshikomugi \(Pm14\)\{1478\}; Norin 4 \(Pm10\)\{1478\}; Norin 10 \(Pm14\)\{1478\}; Norin 26 \(Pm10\)\{1478\}; Shinchunaga \(Pm10\)\{1478\}; \(T.\ macha\) subletschumicum \(Pm10\)\{1478\}; \(T.\ compactum\) No. 44 \(Pm11\)\{1478\}. \(Pm14\) and \(Pm15\) were detected using hybrids between \(B.\ g.\ triticici\) and \(B.\ g.\ agropyri\) cultures.

**Pm16**\{1201\}. 4A\{1201\}5B\{10217\}. \(\text{v:}\) Line 70281 = Norman\#3 Beijing 837\{10217\}; Norman lines with resistance from \(T.\ dicoccoides\) CL1060025\{1201\}. \(\text{tv:}\) \(T.\ dicoccoides\) CL1060025\{1201\}. \(\text{ma:}\) \(Pm16\) - 5.3 cM - \(Xgwm\)\{159-5B\}\{10217\}. To account for the different chromosome locations a 4A-4B translocation was suggested
Based on the 5B location and similar disease responses Pm16 and Pm30 may be the same [10217].

**Pm17**[979,838,544]. 
1A5 = T1AL.1R#2S(1624,185,389). v: Amigo[561]; Century[216]; Nekota[0021]; Neobrara[0021]; TAM107[216]; TAM200[216]; TAM201[216]; TAM202[0021]. 
1BS = T1BL.1R#2S[561]. v2: Helami 105 Pm5[561]. ma: A STS marker distinguished Pm17 from Pm8[0286]; Pm7 - 7.8 cM - Xwmg68-1R - 10.9 cM - Sec-I in 1RS[10167]. 
Pm8 and Pm17 were reported to be allelic [524], see note under Pm8.

**Pm18.** Deleted, see Pm1c.


**Pm21**[1177]. 6AS = T6AL.6VS[1177]. v: 9 independent translocations[1177]. ma: RAPD OPH17[1900] (synonym 'OPH17-1900') was associated with Pm21 and RAPD OPH17[1000] (synonym OPH17-1000) with its absence[1176]; RAPD OPH17[1400] and SCAR markers SCAR[1400] and SCAR[1265] associated with Pm21 are described in[0014]; Marker NAU/Xibao15, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying Pm21[10519]. 
Three lines, Pm97033, Pm97034 and Pm07035, with a 6DL.6VS translocation were infection, acts as a co-

**Pm22**[1134]. Deleted. See Pm1e.

**Pm24**[571]. 6D[571].1DS[0150]. v: Chiyacao[571]. ma: Xgwm789-1D/Xgwm603-1D - 2.4 cM - Pm24 - 3.6 cM - Xbarc229-1D[10109].

**Pm25**[1343]. [PmTmb[1343,1344]]. 1A[1343]. v: NC94-3778[1344]. v2: NC96BGTA5 = Saluda 3/PI 427662 Pm3a[1343]. dv: T. monococcum PI 427662[1343]. ma: Linked with 3 RAPDs, the nearest, OPAG04950, at 12.8 +/- 4.0 cM[1343]; Associated with 3 RAPDs[1344].


**Pm28**[0022]. 1B[0022]. v: Meri[0022].

**Pm29**[0129]. v: Pova[0129]. ma: Location confirmed by co-segregation with molecular markers[0129].

**Pm30**[0163]. [MIC20] 5BS[0163]. v: 87-1/C20/2*8866 Seletion[0163]. ma: Pm30 - 5.6 cM - Xgwm159-5B[0163]. Pm30 could be the same as Pm16[10217].


**Pm32**[10025]. Derived from Ae. speltoides [10025]. 1B=1BL.1SS[10025]. v: L501 = Rodina*6/Ae. speltoides[10025].

Complex genotypes:


be different from NC96BGT4 (a single resistance gene was identified on chromosome 7AL in hexaploid germplasms 599036 = Saluda*3/PI 427772 {10479}).

A further gene derived from Pm1 was about 15 cM proximal to a cluster of markers that earlier c segregated with Pm1 {10372}; A cross indicated linkage between Pm37 and Pm1 {10372}; Xgwm332-7A - 0.5 cM - Pm37 - 0.5 cM - Xwmc790-7A - 15.5 cM - Pm1 {10372}.

10.7 cM with Lr34/Yr18 - 11.9 cM - Xwmc790 {10372}; A cross indicated linkage between Lr34/Yr18/Pm39 - 2.7 cM {10374}; see also, Reaction to Puccinia triticina and Reaction to Puccinia striiformis.

This gene is identical to Yr18, Lr34 and Ltn and confers stem rust resistance in some genetic backgrounds.

Pm39 {10481}.  Adult plant resistance 1BL {10480, 10481}.  i: Avocet-R+Lr46/Yr29 = Avocet-R*3/Lab mono 1B*4/Pavon 76 {10480}.  v: Genotypes with Lr46/Yr29; see Reaction to Puccinia triticina.  v2: Saar Pm5a Pm39 {10481}.  ma: Xgwm1220-7D - 0.9 cM - Lr34/Yr18/Pm38 - 2.7 cM {10374}; see also, Reaction to Puccinia triticina and Reaction to Puccinia striiformis.

This gene is identical to Yr18, Lr34 and Ltn and confers stem rust resistance in some genetic backgrounds.

Pm40 {10539}.  Derived from Th. intermedium {10539}.  7BS {10539}.  v: GRY19 {10539}; Partial amphiploid TAI7047 {10539}; YU {10539}; YU24 {10539}.  ma: Xwmc426-7B - 5.9 cM - Xwmc334-7B - 0.2 cM - Pm40 - 0.7 cM - Xgwm297-7B - 1.2 cM - Xwmc364-7B {10539}.

Pm41 {10551}.  Derived from T. dicoccoides.  3BL {10551}.  v: XXX = 87-1B*4/Langdon/IW2 {10551}.  tv: Langdon/IW2 Seln. XXX {10551}; T. dicoccoides IW2 {10551}.  ma: BE499472 - 0.8 cM - Pm41 - 1.9 cM - Xwmc687-3B {10551}. Pm41 and associated marker alleles showed strongly distored inheritance with reduced frequencies relative to Langdon alleles {10551}.

Pm42 {10559}.  Derived from T. dicoccoides, Recessive.  2BS {10559}.  bin: 0.75-0.84.  v: P63 = Yanda 1817/G303-1M/3*aJing 411 {10559}.  tv: T. dicoccoides G303-1M {10559}.  ma: BF146221 - 0.9 cM - Pm42 - Xgwm148-2B {10559}.

Pm43 {10560}.  Derived from Th. intermedium.  2DL {10560}.  v: Line CH5025 = 76216-96/TAI7045/2*Jing 411 {10560}; Partial amphiploid TAI7045 {10560}.  al: Th. intermedium Z1141 {10560}.  ma: Xwmc412-2D - 2.3 cM - Pm43 - 4.2 cM - Xbarc11-2D {10560}.

A further gene derived from T. monococcum PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3/PI 427772 {10479}.

A single resistance gene was identified on chromosome 7AL in hexaploid germplasms NC96BGT4 (a T. monococcum derivative). This gene was proximal to Pm37, although possibly allelic {10274}.


Complex genotypes:
Suppressors of Pm

Some wheats which, on the basis of cytological and rust tests carry IRS from Petkus rye, do not express resistance due to presence of a suppressor [385]. Zeller & Hsam [1625] located a suppressor of Pm8 and Pm17 in chromosome 7D of Caribo. Mildew resistance was suppressed in Florida, Heinrich, Ikarus, Olympia and Sabina, which are derivatives of Caribo with 1BL.1RS. According to Ren et al. [1209], SuPm8 does not suppress Pm17. Hanusova et al. [492] listed 16 wheats that carry a suppressor of Pm8; 111 wheats did not carry the suppressor. In contrast, a high frequency of suppression occurred in CIMMYT wheats {108, 1208}. Further genotypes are identified in [491]. Although Line 81-7241 carries Pm8 as well as Pm23, evidence was presented to indicate that Pm8 was suppressed in Line 81-7241 {1618} and, by inference, indicated that Chinese Spring possessed SuPm8.


Temporarily designated genes for resistance to Blumeria graminis

Pm2026 [10604]. pm2026 [10604], Recessive [10604]. 5AL17-0.78-1.00 [10604]. dv: T. monococcum TA2026 [10604]. ma: Xcfd39-5A - 1.8 cM - Xcfd1493-5A/Xmg2170-5A - 0.9 cM - Pm2026 - 2.5 cM - Xgwm126-5A [10604].

PmCN17 [10686]. 1BS=1BL.1RS [10686]. v: Chuannong 17 [10686]. al: S. cereale R14 [10686].

PmHNK [10706]. 3BL [10706]. v: Zhourmai 22 [10706]. ma: Xgwm108-3BL - 10.3 cM - PmHNK - 3.8 cM - Xwmc291-3BL [10706].

PmLK906 [10476]. Resistance is recessive [10476, 10477]. 2AL [10476, 10477]. v: Lankao 90(6)21-12 [10476]; Zhengzhou 9754 [10476]. ma: TacsAetPR5-2A/Pm4 - 3.9 cM - Xgwm265-2A - 3.72 cM - Pm39 - 6.15 cM - Xgdm93-2A [10476, 10477]; TacsAetPR5-2A was converted to a STS marker [10477].

PmPS5A [10205]. 2AL [10205]. tv: AM4 [10205]. tv2: T. turgidum subsp. carthlicum P5 Pm33 [10205]. ma: Xgwm356-2A - 10.2 cM - PmPS5A; PmPS5A is located at or near the Pm4 locus [10205].


PmYm66 [10619]. 2AL [10619]. v: Yumai 66 [10619]. ma: XKsum193-2A - 2.4 cM & 3.6 cM - PmYm66 [10619].

MI-Ad [854]. v: Adlungs Alemannen [854].

MI-Br [854]. v: Bretonischer Bartweizen [854].

Mld [1096]. 4B [1097]. v2: Halle 13471 Pm2 [1096]; H8810/47 Pm2 [1096]; Maris Dove Pm2 [1096]. tv: T. durum line [1096].

MI-Ga [854]. v: Garnet [854]; many old German cultivars [854].

MIW72 [10545]. 7AL [10545]. bin: FL 0.86 [10545]. tv: T. dicoccoides IW72 [10545]. ma: Xmag1759-7A - 8.2 cM - MIW72 - 3.3 cM - Xmag2185-7A - 1.6 cM - Xgwm344-7A [10545].

83.4. QTLs for resistance to *Blumeria graminis*

QTL: Several QTLs were detected in two RE714/Hardi populations when tested at two growth stages and with different cultures over three years. The most persistent and effective QTL was located in the vicinity of *Xgwm174-5D* (0272). Three QTLs, *QPm.vt-1B*, *QPm.vt-2A* and *QPm.vt-2B*, with additive gene action, accounted for 50% of the variation in a population developed from Becker/Massey (0284). These QTLs were confirmed by the addition of extra markers to the Becker/Massey map and in a separate analysis of USG 3209 (A Massey derivative)/Jaypee (susceptible) (10505). USG 3209 possessed *Pm8* (1BL.1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL (10505).

QTLs on chromosomes 1A, 2A, 2B, 3A, 5D, 6A and 7B were detected in a RE714/Festin population in multiple locations and over multiple years. The QTL on chromosome 5D was detected in all environments and all years and was associated with markers *Xgwm639-5D* and *Xgwm174-5D*. Resistance was contributed by RE714. A QTL coinciding with *MIRE* on 6A was also detected in all environments. The QTL on chromosome 5D and 6A accounted for 45% to 61% of the phenotypic variation (0354).

Avocet R(S)/Saar (R) F6 RILs: QTL located on chromosomes 1BL (close to *Xwmc44-1B*) (*Pm39*), 7DS (*Xgwm1220-7D*) (*Pm38*) and 4BL (*XwPt-6209*) (resistance allele from Avocet R (10481)).

*QPm.sfr-1A* (0051). 1A (0051). v: Forno/T. spelta var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer (0051). ma: Associated with *Xpsr1201-1A* and *Xpsr941-1A* (0051).
Resistance was contributed by Opata\(^{0255}\).

Associated with var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer\(^{0051}\).

Resistance was contributed by Forno\(^{0051}\).

Resistance was contributed by Oberkulmer\(^{0051}\).

Resistance was contributed by Oberkulmer\(^{0051}\).

Resistance was contributed by Forno\(^{0051}\).

Resistance was contributed by Forno\(^{0051}\).

Resistance was contributed by Oberkulmer\(^{0051}\).

Resistance was contributed by Forno\(^{0051}\).
### 84. Reaction to *Cephus* spp.

**Pest:** Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*.

Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).

Tetraploid wheat

**Qsf.spa-3B**{10351}.

See Stem solidness.

### 85. Reaction to *Cochliobolus sativus* Ito & Kurib.

**Disease:** Cochliobolus root rot.

**Crr**{764}. Recessive. 5BL{764,765}. v: Apex{764}; Cadet{765}.

### 86. Reaction to *Diuraphis noxia* (Mordvilko)

**Insect pest:** Russian aphid, Russian wheat aphid.

**Dn1**{286}. 7D{1288}, 7DS{0211}. i: Betta-Dn1:PI 634768{0004,0211,10277}; Caledon{0004}; Gariep{0004}; Karee-Dn1{0211}; Limpopo-Dn1{0004}; Tugela-
Dn1: PI591932 {0004, 0211, 10277}. v: PI 137739 {286}. ma: Xgwm111-7D-7D_{210} - 3.20 +/- 0.20 cM - Dn1 {0211}.

Dn2 {286}. 7DL {863} .7DS {0211}. i: Betta-Dn2: PI 634769 {0211, 10277}; Karee-Dn2: PI 663774 {0211, 10277}; Tugela-Dn2: PI 634772 {0211, 10277}. v: PI 262660 {286, 863}. ma: XksuA1-7D - 9.8 cM - Dn2 {863}; Myburg et al. {9968} identified two SCAR markers that mapped 3.3 cM proximal to Dn2 {9968}; Xgwm111-7D_{200} - 3.05 +/- 0.18 cM - Dn2 {0211}; XksuA1-7D - 9.9 cM - Dn2 - 2.8 cM - Xgwm437-7D {0353}. According to Saidi & Quick {1250}, Dn1 and Dn2 are probably allelic. Reference stocks with each gene showed allelism with a gene in PI 262605.

Dn3 {1086}. Recessive. v: Ae. tauschii SQ24/T. turgidum TD65 {1086}. dv: Ae. tauschii SQ24 {1086}.

Dn4 {1250}. 1DL {863}. i: Yumar {10397}. v: Ankor {10397}; CORWAI {260}; CI 2401 {260}; Halt {0209}; PI 151918 {260}; PI 372129 {1250}; Prairie Red {10397}. ma: Xabc156-1D - 11.6 cM - Dn4 {863}; Xgwm106-1D - 7.4 cM - Dn4 - 12.9 cM - Xgwm337-1D {0352}; Xgwm106-1D - 5.9 cM - Dn4 - 9.2 cM - Xgwm337-1D {10128}.

Dn5 {1249}. 7D {259}.7DL {287, 10310, 10396}.7DS {0211}. i: Betta-DN5 {0211}; Palmiet derivative 92RL28 {287}; Palmiet DNS {0004}. v: STARS - 9302W-sib {259}; PI 294994 {259}. ma: A SCAR marker developed from the RAPD fragment OPF14_{1083} mapped 5.5 cM proximal to Dn5 {0172}; Xgwm111-7D_{220} - less than 3.20 cM - Dn5 {0211}. Issues relating to the confused arm location and mapping of Dn5 is discussed in {10310}. Genetic mapping indicated that Dn5 is located in chromosome 7DS, but cytological analysis showed it was located in 7DL {10396}. It was also suggested {10396} that the Palmiet Dn5 line {0004} may not have Dn5 {10396}.

Dn6 {1250}. v: CI 6501 {260}; PI 243781 {1250, 1249}. ma: Dn6 - 3.0 cM - Xgwm111 {0352}.

Dn7 {9918}. Derived from S. secale cv. Turkey 77 {9918} [Dn2414 {10478}]. 1B = 1BL.1RS {9918}.1R {9918}. v: 93M45-14 {9918}; 94M370 {10188}; ST-ARS 02RWA2414-11 {10474}. ma: Xbcd1434-1R - 1.4 cM - Dn7 - 7.4 cM - Xksud14-1R {10188}; Xhor2-1R - 1.7 cM - Dn7 - 1.0 cM - Xscb241-1R {10474}; Marker Xrems1303 {320} was amplified only in genotypes resistant to biotype 3 and presumably possessing Dn7 {10474}.

Dn8 {0211}. 7DS {0211}. i: Karee-Dn8: PI 634775 {10277}. v2: PI 294994 Dn5Dn9 {0211}. ma: Xgwm635-7D_{100} - less than 3.20 cM - Dn8 {0211}.

Dn9 {0211}. 1DL {0211}. i: Betta-DN9: PI 634770 {10277}. v2: PI 294994 Dn5Dn9 {0211}.

Dnx {0211}. 7DS {0211}. v: PI 220127 {0211}. ma: Xgwm111-7D_{210} - 1.52 +/- 0.15 cM - Dnx {0211}.

Dnx was considered to be located at a locus different from Dn1, Dn2 or Dn5 {0211}, which were likely to be identical or allelic.

Dn1881 {10145}. 7BS {10145}. tv: Line 1881 {10145}. ma: Xgwm46-7BS - 10.1 cM - Dn1881 - 12.8 cM - Xgwm333-7BL {10145}.

QTL: QTLs for antixenosis were associated with Xpsr687-7D (7DS) and Xgwm437-7D (7DL) in CS/CS (Synthetic 7D) {10136}. Separate antibiotic effects were demonstrated for the same chromosome {10136}.

A QTL, QDn.unlp.6A, for antixenosis was associated with Xgwm1393-6AL and Xgwm1150-6AL in a CS/CS (Synthetic 6A) DH population {10216}.

87. Reaction to Fusarium spp.

87.1. Disease: Fusarium head scab, scab
Type II resistance. Whereas much of the recent genetic work involved FHB caused by *Fusarium graminearum*, according to {10514}, *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction and DON/NIV contamination.

**Fhb1**{10214,10403}. [QFhs.ndsu-3B]{9925,0175}. 3BS{9925}. ma: HC374/8*98B69-147{10214}; Sumai3*S*Thatcher{10214}. v: HC-147-126{10444}. v2: BW278 Fhb2{10225}; Sumai 3 Fhb2{10314}. 6BS{10225}. ma: Xgwm133-6B - 4 cM - Fhb1 - 1.1 cM - Xgwm644-6B{10225}. The relationship of Fhb2 to Fhs1 or Fhs2 {1096} is unknown.

**Fhb2**{10225}. 6BS{10225}. v: pBE85{10444}. v2: BW278 Fhb1{10225}; Sumai 3 Fhb1{10225}. ma: Xgwm133-6B - 4 cM - Fhb2 - 2 cM - Xgwm644-6B{10225}. The relationship of Fhb2 to Fhs1 or Fhs2 {1096} is unknown.

**Fhb3**{10529}. 7DS = T7AL.Lr1S{10529}. v: TA 5608{10529}. al: *Leymus racemosus*{10529}. ma: Three PCR markers, Be586744-STS, BE404728-STS and BE586111-STS, were developed{10529}. The level of type 2 resistance conferred by Fhb3 was similar to that of Sumai 3 {10529}.

**Fhs1**{1096}. v: Line A{1096}. v2: Ning 7840 Fhs2{1096}.

**Fhs2**{1096}. v: Line B{1096}. v2: Ning 7840 Fhs1{1096}.

A major QTL was associated with several linked AFLP markers tentatively located in chromosome 7BL of Ning 7840{0005}.

QTLs for resistance to *Fusarium graminearum* detected in the cross Renan/Recital {10069}. All resistance alleles, except QFhs.inra-3A, were contributed by Renan. LOD scores and percent of variation explained by the QT (R^2) are average of three years of field tests.

**QFhs.inra-2A**{10069}. ma: Associated with Xgwm382c-2A (LOD=6.3, R^2=14.4%).

**QFhs.inra-2B**{10069}. ma: Associated with Xgwm374-2B (LOD=7.6, R^2=12%).

**QFhs.inra-3A**{10069}. ma: Associated with Xbcd372-3A (LOD=3.7, R^2=6.2%).

**QFhs.inra-3B**{10069}. ma: Associated with Xgwm383b-3B (LOD=5.4, R^2=10.5%).

**QFhs.inra-5A.1**{10069}. ma: Associated with Xpsr170a-5A (LOD=3.8, R^2=5%).

**QFhs.inra-5A.2**{10069}. ma: Associated with Xgwm639b-5A 8LOD=6.6, R^2=14%).

**QFhs.inra-5A.3**{10069}. ma: Associated with B1 (LOD=6.3, R^2=8.5%).

**QFhs.inra-5D**{10069}. ma: Associated with Xcfd29-5D (LOD=4.4, R^2=7%).

**QFhs.inra-6D**{10069}. ma: Associated with Xcfd42-6D (LOD=2.7, R^2=6.6%).

**QFhs.ndsu-2A**{9925,0175}. 2AL{9925}. v: Sumai 3/Stoa RI mapping population; the QTL was contributed by Stoa{9925}. ma: Association with RFLP XksuHI6-2A (LOD>3){9925,0175}.

**QFhs.ndsu-3A.3**{10482}. 3AS{0372}. tv: *T. turgidum* var. *dicoccoides*. Recombinant substitution lines LDN and LDN(Dic-3A). The resistant allele was contributed by T. *dicoccoides*{0372}. ma: Associated with Xgwm2-3A (explained 37% of the phenotypic variation){0372}; QFhs.ndsu-3AS was placed within a 11.5 cM region flanked by TRAP marker loci Xfcp401-3A and Xfcp397-2-3A{10482}; This gene is unlikely to be a homoeologue of Qfhs.ndsu-3BS = Fhb1{10482}.

**QFhs.ndsu-3B**{9925,0175}. 3BS{9925}. v: Sumai 3/Stoa RI mapping population; the QTL was contributed by Sumai 3{9925,0175}. ma: Association with Xbcd907-3B.2 (LOD>3) {9925} and microsatellite markers Xgwm1533-3B and Xgwm493-3B{0175}; QFhs.ndsu-3B from Sumai 3 was associated with microsatellite loci Xgwm533-3B and Xgwm274-3B in...
certain Sumai 3 derivatives \{10062\}. In Ning 894037 the QTL has the same location and similar SSR bands to Sumai 3 \{10085\}. STS marker SRST.3B1 was mapped between \textit{Xgwm533-3B} and \textit{Xgwm389-3B} and associated with \textit{QFhs.ndsu-3B} \{10072\}. \textit{QFhs.ndsu-3B} was associated with markers \textit{Xgwm533-3B}, \textit{Xbard133-3B}, \textit{Xbarc147-3B} and \textit{Xgwm493-3B} \{10073\}.

This QTL explained 42\% of the variation in Sumai 3/Stoa \{0175\}. Two additional QTL for resistance to \textit{Fusarium graminearum} were identified in the cross Sumai3/Stoa \{0175\}. The QTL on 4BS was associated with \textit{Xwg909-4B} and the QTL on 6BS was associated with \textit{Xbarc101-6B} and \textit{Xbcd1383-6B} \{0175\}. The QTL associated with markers \textit{Xgwm493-3B}/\textit{Xgwm389-3B} (explaining 24.8 \% of the variation), and \textit{Xbarc101-6B}/\textit{Xbcd1383-6B} were also identified in a RIL population from the cross ND2603/Butte 86 \{0175\}. In addition, one QTL on chromosome 3AL associated with \textit{Xbcd941-3A} and one on chromosome 6AS associated with \textit{XksuH4-6A} were identified in RILs from the cross ND2603/Butte 86 \{0175\}.

Resistance QTL on chromosome 3BS associated with \textit{Xgwm493-3B} and \textit{Xgwm533-3B} was also identified in a DH population of the cross Remus/CM-82036 (a Sumai 3 derivative) \{0240\}. Additional QTL in this cross were detected on chromosome 5A, associated with \textit{Xgwm293-5A} and \textit{Xgwm304-5A}, and possibly on 1B, associated with \textit{Glu-B1} \{0240\}.

Two major genes with additive effects were reported in crosses between Sumai 3 (resistant) and two susceptible cultivars\{0174\}. One of the genes was assigned to 5AL based on linkage to the dominant awn suppressor B1 (RF 15.1-21.4\%).

QTLs were located in 3BS, 2BL and 2AS in Ning 7840/Clark. The most effective QTL was probably in interval, flanked by deletions 3BS-3 and -8 and was close to \textit{Xgwm533-3B} and \textit{Xbarc147-3B} \{0328\}.

A marker study found that 14 of 66 wheats with putative FHB resistance shared markers indicative of the 3BS QTL in Ning 7840, Sumai 3, Wangshuibai and possibly Wuhan 3, plus Japanese landraces Shinchunaga and Shirasu No 1 \{10115\}. The original source may be the landrace 'Taiwan Wheat' rather than Funo \{10115\}. Four QTLs on chromosomes 3BS (associated with \textit{Xbarc133-3B}), 3BL (\textit{Xgwm247-3B}) and 3AS (\textit{Xgwm5-3A}) from Huapei 57-2, and 5BL (\textit{Xbarc59-5B}) from Patterson, were reported in the cross Huapei 57-2/Patterson \{10026\}. Huapei 57-2, Ning 7840 and Sumai 3 carried common alleles in the \textit{Xgwm533-3B}, \textit{Xgwm493-3B}, \textit{Xbarc147-3B} and \textit{Xbarc133-3B} region \{10026\}.

Wuhan-1/Nyubai \{10623\}: Two QTLs were located on chromosomes 2DL and 3BS (distal) \{10020\}.

G16-92(R)/Hussar(S): Two QTL for resistance to \textit{F. culmorum} were identified on chromosome 1A (resistance from Hussar) (\(R^2 = 0.01\)) and 2B (resistance from G16-92) (\(R^2 = 0.14\)) \{10588\}.

Of 54 lines with reported FHB resistance, 6, including CM-82036, Ning 7840 and Wuhan 3, had the same 5-marker haplotype as Sumai 3, and 4 lines possessed 4 of the markers. Twenty-nine lines, including Frontana, has no marker allele in common with Sumai 3, whereas 13 lines had 1 to 3 alleles in common with it \{10113\}. \textit{QFhs.ndsu-3B} and the 5 marker loci were placed in 3BS deletion bin 0.78-0.87 \{10144\}.
Nanda2419(S)/Wangshuibai(R): 8 QTLs were identified; those with large effects were associated with Xgwm533-3B.3 - Xgwm533-3B.1 (W), Xwmc539-6B (W) and Xs1021m-2B - Xgwm47-2B [10190].

Type I resistance (% infected plants) in this cross was attributed to 10 chromosome regions among which Qfhi.nau-4B (Xwmc349-4B - Xgwm149-4B - r² = 0.75), XFhi.nau-5A (Xwmc96-5A - Xgwm304-5A - r² = 0.27) and Qfhi.nau-5B (Xgwm408-5B - Xbarc140-5B) from Wangshuibai were detected in at least 3 of 4 years [10282]. A significant additive effect of QTL on 6D and 2A was also observed [10282].

Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTLs, four from Wangshuibai. Those with the largest effects included QFdk.nau-2B (from Nanda 2419), QFdk.nau-3B and QFdk.nau-4B [10577] with each accounting for more than 20% of the phenotype variation.

Pelikan (S)/G93010 (=Bussard / Ning 8026) (R). Qfhs.Ifl-7BS/5BL and Qfhs.Ifl-6BS (probably Fhb2) from Ning 8026 reduced disease severity by 30% and 24%, respectively, and by 46% when combined [10594]. Other resistance genes were located on chromosomes 1AS (Qfhs.Ifl-1AS from Pelikan), and 2AL and 7AL (from Ning 8026) [10594].

Spark (MR)/Rialto(S) DH population: Of nine QTLs identified across all environments, seven alleles for resistance came from Spark and two from Rialto. The largest effect on Type 1 resistance (Xfhs.jic-4D.2) was associated with the Rht-D1b allele in Rialto which made lines more susceptible. Other QTLs occurred on chromosomes 1B (1B.1R), 4D (Qfhs.jic-4D.2), 2A,3A (each, 2 QTLs), 5A and 7A. Xfhs.jic-4d.2 had little effect on Type 2 resistance [10603].

Wangshuibai/Seri 82:F3:F5 population: QTL on chromosome 3BS (Xgwm533-3B - Xs18/m12-3B) and 2DL(Xgwm539-2D - Xs15/m24-2D) accounted for 17% and 11%, respectively, of the phenotypic variance [10264].

Wangshuibai/Alondra 'S': A stable QTL was associated with Xgwm533-3B in each of 3 years, QTLs in 5B (Xgwm335-5B), 2D and 7A were detected in 2 years [10268].

Wangshuibai(R)/Wheaton(S): QTLs located in chromosome 3BS (Xbarc147-3B, R² = 37% & Xbarc344-3B, R² = 7%), 7AL (Xwms1083-7A, R² = 10%) and 1BL (Xwms759-1B, R² = 12%) [10200].

Chokwang (R)/Clark (S): Qfhs.ksu-5DL.1 associated with Xbarc239-5D (R² = 0.24) [10276], Qfhs.ksu-4BL.1 associated with Xbarc1096-4B (R² = 0.13) [10276], and Qfhs.ksu-3BS.1 marginally associated with the region of Fhb1 (R² = 0.1) [10276].

Ernie(Res)/MO94-317(Sus): 243 F8 RIL population. Four QTLs from Ernie detected as follows: Qfhs.umc-2B, linked to Xgwm278-2BS, R² = 0.04 [10456]. Qfhs.umc-3B, linked to Xgwm285-3BS, R² = 0.13 [10456]. Qfhs.umc-4B, linked to Xgwm495-4BL, R² = 0.09 [10456]. Qfhs.umc-5A, linked to Xgwm165-5A, R² = 0.17 [10456]. Evidence was provided to suggest the QTL acted additively [10456].

Associations between response to FHB caused by *F. culmorum* and the semi-dwarfing locus *Rht-D1* in crosses Apache/Biscay, Romanus/Pirat and History/Rubens (Biscay, Pirat and
Rubens carry $Rht-D1b$ were reported in \{10574\}. Genotypes with the semi-dwarf alleles tended to be more susceptible.

A review of 52 mapping studies is provided in \{10593\}. Seedling resistance to *Fusarium graminearum* (FSB). A QTL for FSB resistance in the Wuhan/Nyubai population was associated with the $Qwmc75-5B$ locus, $R^2 = 0.138$. The relationship of this resistance to crown rot resistance is unknown \{10624\} (see Reaction to *F. pseudograminearum*).

Tetraploid wheat

Langdon/Langdon (DIC-2A) RICL population: Increased susceptibility of the *T. dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22 cM interval spanned by $Xgwm558-2A$ and $Xgwm445-2A$ \{10613\}.

$QFhs.pur-2D$ \{10085\}.  $v$: Alondra \{10085\}.  $ma$: Located on 2DS between SSR markers $Xgwm296-2D$ and $Xgwm261-2D$ \{10085\}.

$QFhs.pur-7El$ \{10489\}.  $7e_1$ \{10489\}.7DS.7DL-7e_1 \{10489\}.  $su$: K2630 \{10489\}.  $v$: K11695 = 7DS.7DL-7e_1 \{10489\}; KS10-2 = 7e_1.S.7e_2-7DL \{10489\}; KS24-1 and KS24-2 = 7DS.7e_1 \{10489\}.  $ma$: $Qfhs.pur-7e_1$ was flanked by $BE445653$ and $Xcfa2270$-7D \{10489\}; These markers were also present in KS10-2 \{10489\}.


$Qfhs.crc-2BL$ \{10445\}.  $tv$: Strongfield \{10445\}.  $ma$: Spanning 16 cM, this QTL peaking on $Xgwm55-2B$ explained 23% of the phenotypic variation \{10445\}.

$Qfhs.ndsu-3AS$ \{10402\}.  $sutv$: LDN-DIC 3A \{10402\}.  $tv$: *T. dicoccoides* \{10402\}.  $ma$: Located in an interval spanning 29.3 cM this QTL accounted for 37% of the phenotypic variation; peak marker, $Xgwm293$-5A, $Xgwm304$-5A, $Xgwm1057$-5A, $Xbarc117$-5A, $Xbarc186$-5A, $Xbarc100$-5A and $Xbarc40$-5A \{10073\}.

$Qfhs.crc-6BS$ \{10445\}.  $tv$: *T. turgidum* var. *carthlicum* cv. Blackbird \{10445\}.  $ma$: Spanning 23 cM and peaking on $Xwmc397$ this QTL accounted for 23% of the phenotypic variation \{10445\}.

$Qfhs.fcu-7AL$ \{10401\}.  $sutv$: LDN-DIC 7A \{10401\}.  $tv$: *T. turgidum* var. *dicoccoides* PI 78742 \{10401\}.  $ma$: Located in an interval 39.6 cM thie QTL accounted for 19% of the phenotypic variation in a RIL population of Langdon/LDN-DIC 7A; nearest marker $Xbarc121-7A$ \{10401\}.

Strongfield/*T. carthlicum* (Blackbird): Field resistance identified in chromosome 2BL ($Xgwm55-2B$), and 6BL($Xwmc397-6B$) (coincident with *Fhb2* \{10225\}).

Patterson (mod sus)/Fundulea 201R RILS: QTLs accounting for 19% and 13% of phenotypic variation were found on chromosomes 1BL ($Xbarc8-1BS - Xgwm131$-1BL region) and 3AS ($Xgwm674$-3A/$Xbarc67$-3A region) \{10114\}. Two weak QTLs were possibly associated with chromosomes 3D (Patterson allele) and 5AS \{10114\}.

Arina(R)/Forno(S): Three QTLs, $QFhs.fal-6DL$ ($R^2=22\%$), $QFhs.fal-5BL.1$ (in Forno, $R^2=14\%$) and $QFhs.fal.4AL$ ($R^2=10\%$) and 5 minor QTLs in 2AL, 3AL, 3BL, 3DS and 5DL were detected \{10172\}.
Arina/Riband DH lines: QTL affecting ADUPC were identified in 1BL(2), 2B, 4DS, 6BL and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of \( Rht-D1a \) rather than height \( \text{per se} \) \{10464\}.

Kansas (moderately resistant)/Ritmo (susceptible): Map based analysis across environments revealed seven QTL, \( QFhs.whs-1BS \) (1RS), \( QFhs.whs-3B \) (not \( Fhb1 \)), \( QFhs.whs-3DL \), \( QFhs.whs-5BL \), \( QFhs.whs-7AL \) and \( QFhs.whs-7BL \) (cumulatively, \( R^2 = 0.56 \)). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread \{10503\}. There were significant correlations of FHB response with height and heading date \{10503\}.

More detailed mapping led to the relocation of the 5B QTL to chromosome 1BL. The renamed \( Qfhs.lfl-1BL \) reduced FHB severity by 42% relative to line lacking it \{10698\}. This gene was also present in Biscay, History and Pirat \{10698\}.

Three RGA sequences putatively assigned to chromosome 1A explained 3.37-12.73% of the phenotypic variation in FHB response among F7 and F10 populations \{10364\}. STS marker FHBSTS1A-160 was developed from one of the RGA.

Dream(R)/Lynx(S) RIL population. Following inoculation with \( F. culmorum \) 4 QTL for AUDPC were identified on chromosomes 6AL (\( R^2=19\% \)), 1B (12\%), 2BL (11\%) and 7BS (21\%). The resistance allele in 1B came from Lynx and was associated with T1BL.1RS \{10260\}.

Dream*4/Lynx lines were developed by selection of QTL on chromosomes 6AL, 7BS and 2BL. Lines carrying \( QFhs.lfl-6AL \) and \( QFhs.lfl-7BS \) were more resistant than lines lacking them; the 2BL QTL effect was not verified \{10470\}.

Frontana(R)/Remus(S): Major QTLs in chromosomes 3AL (\( Xgwm270-3AL - Xdupw227-3A \) region) and 5A (\( Xgwm129-5A - Xbarc-5A \) region) accounted for 16\% and 9\% of the phenotypic variation (mainly type 1 resistance) over 3 years \{10174\}.

Frontana(MR)/Seri82(S), F3 and F3:5 populations: QTLs were located in chromosomes 1BL (\( R^2=7.9\% \)), flanked by AFLP markers, 3AL (\( R^2=7.7\%)\), flanked by \( Xgwm720-3A \) and \( Xgwm121-3A \), 7AS (\( R^2=7.6\% \)), flanked by an AFLP and \( Xgwm233-7A \) \{10349\}.

Veery (S) / CJ9306 (R): Four QTLs, \( XQFhs.ndsu-3BS \) (\( Xgwm533b - Xgwm493 \)), \( QFhs.nau-2DL \) (\( Xgwm157 - Xwmc-041 \)), \( QFhs.nau-1AS \) (\( Xwmc024 - Xbarc148 \)) and \( QFhs.nau-7BS \) (\( Xgwm400 - Xgwm573 \)) accounted for 31, 16, 10 and 7\%, respectively, of the average phenotypic variation over three years \{10490\}.

Type I resistance and DON accumulation: Hobbit Sib/T. macha 4A DH population: Both traits were assigned to a small region distal to \( Xgwm601-4A \) and cosegregating with \( Xgwm165-4A \) \{10254\}.

DH181(R)(Sumai 3/HY 386 Seln.): QTL identified in 2DS, 3AS, 3BS, 3B Cent. region, 4DL, 5AS, 6BS \{10213\}.

Field resistance: Wuhan-1/Maringa, QTLs were located on chromosomes 2DS, 3BS (Proximal) and 4B \{10020\}.
Resistance to DON accumulation: Wuhan-1/Maringa, QTLs were located on chromosomes 2DL and 5DS \{10020\}.

Veery/CJ 9306 (R): Four QTLs contributed to resistance; QFhs.ndsu-3BS nearest marker Xgwm533b ($R^2 = 0.23$), QFhs.nau-2DL, Xgwm539 ($R^2 = 0.2$), QFhs.nau-1AS, Xbarc148 ($R^2 = 0.05$) and QFhs.nau-5AS, Xgwm425 ($R^2 = 0.05$) \{10496\}.

Haplotype diversity among a large number of FHB resistant and susceptible (mainly Canadian) germplasms indicated similarities in Asian, Brazilian and other materials \{10173\}. Brazilian cv. Maringa was more similar to Asian than to other Brazilian lines \{10173\}.

For review see\{0283\}.

Mesterhazy et al.\{0006\} reported a strong genetic correlation in resistance to different species of \textit{Fusarium}.

Bobwhite plants transformed with AtNPR1, an \textit{Arabidopsis thaliana} gene that regulates activities of SAR, displayed a heritable type II response equal to that of Sumai 3 \{10237\}.

In cross Patterson (open)/Goldfield (closed) RILs, narrow flower opening which was correlated with FHB resistance. The major QTL effect associated with narrow flower opening and low FHB incidence occurred in map interval Xbarc200 - Xgwm210 (29% of variation in FHB incidence); these genes were probably located in chromosome 2BS \{10243\}.

Wangshuibai/Annong8455:RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosome 3B ($R^2=0.17$) and 2A ($R^2=0.12$) and for DON levels in 5A ($R^2=0.13$), 2A ($R^2=0.85$) and 3B ($R^2=0.06$) \{10447\}. The regions involved were Xgwm533-3B - Xbarc133-3B, Xgwm425-2A, and Xgwm186-5A - Xgwm156-5A \{10447\}.

In a reciprocal backcross analysis of Chris monosomics/Frontana, Frontana chromosomes 3A, 6A and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B and 7A increased the same traits \{10398\}.

Soissons (relatively resistant)/Orvantis (susceptible): Soissons carried QFhs.jic-4D ($R^2=0.106-0.161$) associated with Rht-D1a (tall allele) \{10718\}. FHB susceptibility tended to be associated with the Rht-D1b allele \{10718\}. Supporting studies with NILs indicated that the presence of Rht-B1b led to reduced type 2 resistance relative to presence of Rht-B1b or the tallness alleles at both loci \{10718\}.

87.2. Disease: Crown rot caused by \textit{Fusarium pseudograminearum}, \textit{F. culmorum} and other \textit{Fusarium} species.

QTL: Kukri(R)/Janz(S) DH population. Simple interval mapping in the region Pst1 ACG.Mse1 CAC - Xgwm251-4B accounted for 48% of the variation in crown rot response \{10034\}.

Lang (S)/CSCR6(R):RIL population: tested under controlled conditions with \textit{F. pseudograminearum} and \textit{F. graminearum}: Qcrs.cpi-3BL from CSCR6, $R^2=0.49$ and Qcrs.cpi-4B from Lang $R^2=0.23$ \{10703\}. 
2-49 (partially Resistant) / Janz(susceptible) DH population: Analysis of partial seedling resistance indicated major QTL in chromosomes 1D ($R^2=0.21$) and 1A ($R^2=0.09$) and minor QTL in 2A, 2B (from Janz), 4B and 7B [10132].

W21NMT70/Mendos: DH population: three consistent QTLs for seedling resistance were identified with CIM; these were located in chromosome 5D and 2D (resistance alleles from W21NMT70) and 2B (resistance allele from Mendos) [10358].

88. Reaction to *Heterodera avenae* Woll.

Cereal root eelworm; cereal cyst nematode.

**Cre1.** [Cre[1388]]. 2B[1388].2BL[1579,1580]. i: AP = Prins’s8/AUS10894[1579]. v: AUS 10894[1056]; Beulah[10013]; Chara[10163]; Goldmark[10013]; Goroke[10013]; Kellalac[10013]; Loros CI 3779[10013]; Mira[10163]; Mitre[10163]; Ouyen[10013]; RE8670[10013]; Silverstar[10013]; VI252[10013]; VI727[10013]. ma: Xglk605-2B - 7.3 cM - Cre1 - 8.4 cM - Xcdo588-2B/Xabc451-2B [1579]; A PCR-based assay was developed from Xglk605-2B[1580]; Co-segregation with Xcsl107-2B. Four of 6 land varieties possessed Xcsl107-2B. A variant haplotype of Xcsl107-2B was present in AUS4930[10013]; Xcdo36-2B - 7.5 cM - Xbcd1231-2B/XAtPPr5/Xcsl107-2B/Cre1[10013].

**Cre2[238].** Derived from *Ae. ventricosa* 10[238,9991]. 6M[9991] v2: H-93-8 Cre6[238]. Although H-93-8 is a double M(5A), 7M(7D) substitution line, Cre2 was presumed to be located in a separate undetected translocated 6M segment[9991].

**Cre3.** [CcnD1[329],Ccn-D1[328]]. 2DL[328]. v: Synthetic hexaploids[329]. dv: *Ae. tauschii* accessions AUS 18912[328]; AUS 18913[328]; CPI 110809[329]; CPI 110810[328]. ma: Co-linearity with 2BL for Xcdo-36-2D and XAtPPr5/Xbcd1231-2D/G4/G12/Cre3 (see Cre1)[10013].

**Cre4.** [CcnD2[329],Ccn-D2[328]]. 2D[328]. dv: *Ae. tauschii* accessions AUS 18914[329]; CPI 110813[328].

**Cre5[0107].** Derived from *Ae. ventricosa* {0107,0009}. [CreX[0009,0183]]. 2AS[0107]=2A-2N’-6N’. v: VPM1[0107]; Many VPM1 derivatives[0107]; Notable exceptions of lines with Lr37, Srl38 and Yr17, but lacking Cre5 include Trident and Line L22[0107]; However a contribution of the Cre5 region was detected in Trident/Molineux [10343]. su: Moisson 6N’(6D)[0183]. dv: *Ae. ventricosa* 10[0183]. ma: Associated with the Xgwm359-2A (R²=8%) - Xwmc177-2A (R²=7%) region in Trident/Molineux [10343].

Two resistance gene analogues similar to the candidate gene Cre3 were isolated from the *Ae. ventricosa* segment carrying Cre5

**Cre6[0138].** Derived from *Ae. ventricosa* {0138}. 5N’{0138}. ad: Moisson + 5N’{0138}. v: H-93-35{0138}. v2: H-93-8 Cre2[0138].

**Cre7[0104].** Derived from *Ae. triuncialis* [0105]. [CreAet[0105]]. v: TR353 derivatives[0105].

**Cre8[0220].** [CreF[0012,0138]]. 6BL[0220], on basis of linkage with Xbcd11-6B and Xcdo347-6B[0220]. v: Barunga[0220]; Festiguay[0012,0220]; Frame[0138,0220]; Molineaux[0012,0220]. ma: Linked to RFLP loci Xbcd11-6B and Xcdo347-6B. The 6B location of the Xcdo347 probe used in this study was confirmed by nulli-tetrasomic analysis[0220]; Associated with the Xgwm147-6B (R²=24%) - Xcdo247-6B (R²=12%) region in Trident/Molineux [10343].

**CreR[0133,0318].** 6RL[0133]. ad: Wheat + 6R [0318]; Wheat + 6RL[0318]; Various deletion stocks[0318]. su: CS + 6R(6D)[0133]. al: Rye accession T701-4-6[0133]; Triticale T-701[0138]. ma: Cent......XksuF37 - 3.7 cM - CreR[0133]; Deletion mapping indicated CreR was located near Got-R2[0318].
**CREX** {10486}. Derived from *Ae. variabilis* 2AS or 2DS {10486}. **ad**: Line M {10487}. **v**: Line D {10486}. **ma**: RAPD markers Op02_{1000}, OpR4_{1600}, OpV3_{450} {10486}.

**Crey** {10486}. Derived from *Ae. variabilis* 3BL {590}. **v**: Line X {10487}. **ma**: Co-segregation with RAPD OpY16_{1065} which was converted to SCAR16 {10486}. May be the same gene as *Rkn-mn1* (see reaction to *Meloidogyne naasi*).

QTL: **Qcre.src-1B** was located to the Xwmc719-1B (R^2 = 12%) - Xgwm140-1B (R^2 = 12%) region in Trident/Molineux {10343}.

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**89. Reaction to Magnaporthe grisea** (Herbert) Barr

*M. grisea* is a pathogen of blast on many graminaceous species, the best known of which is rice. In Brazil it has become a pathogen of wheat. The wheat pathotype(s) is different from those attacking other species such as rice, oat, millets and weeping lovegrass.

**Rmg1** {0333,10462}. [Rwt4 {0302}]. 1D {10462}. **s**: CS (Cheyenne 1D) {10462}. **v**: Cheyenne {10462}; Norin 4 {0302}; Norin 26 {10462}; Shin-chunaga {10462}.

**Rmg2** {10461}. 7A {10461}. **i**: CS (Thatcher 7A) {10461}. **v**: Thatcher {10461}; CS (Thatcher 6B) {10461}. **v2**: Thatcher {10461}; CS (Red Egyptian 6D) {10639}. **s**: CS (Red Egyptian 6D) {10639}. **v**: Red Egyptian {10639}.

**Rmg3** {10461}. 6B {10461}. **i**: CS (Thatcher 6B) {10461}. **v**: Norin 4 {10639}; Norin 26 {10639}; Norin 29 {10639}; P168 {10639}; Shin-chunaga {10639}; T. compactum No. 24 {10639}.

A second gene designated *Rwt3* {0302} was present in CS and Norin 4. Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

**Rmg4** {10639}. 4A {10639}. **v**: Norin 4 {10639}; Norin 26 {10639}; Norin 29 {10639}; P168 {10639}; Shin-chunaga {10639}; T. compactum No. 24 {10639}.

**Mg5** {10639}. 6D {10639}. **s**: CS (Red Egyptian 6D) {10639}. **v**: Red Egyptian {10639}.

A second gene designated *Rwt3* {0302} was present in CS and Norin 4. Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

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**90. Reaction to Mayetiola destructor** (Say) (*Phytophaga destructor*) (Say)

Insect pest: Hessian fly.

**H1** {1087}. **i**: Dawson/3 Poso, 6179 {1087}. **v2**: Big Club 43 H2 {1441}; Dawson H2 {166,1087}; Poso 42 H2 {1441}.

**H2** {1087}. **i**: Dawson/3 Poso, 6232 {1087}. **v2**: Big Club 43 H1 {1441}; Dawson H1 {166,1087}; Poso 42 H1 {1441}.

**H3** {156}. **v**: Ac{426}; Arthur{426}; Becker{749}; Cardinal{750}; Dual{1273}; Franklin{341}; Georgia 1123 {426}; GR855 {751}; GR876 {753}; Ike{10252}; Ion{426}; Larned{824}; Logan{426}; Monon{157}; Norkan{904}; Ottawa{547}; Purdue B 36162 A13-12 {156}; PI 468960 {1439}; Redcoat{1273}; Reed{1273}; Riley{1273}; Roland{148}; Russell{426}; Shawnee{547}; Titan{747}; Todd{426}; W38 {156}. **ma**: Clara Fay {375}.

A second gene designated *Rwt3* {0302} was present in CS and Norin 4. Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

Allan et al. {019} considered that **H3** and **H4** may be allelic. Also suggested by Shands and Cartwright {1317}. Linkage of 10.5 +/- 2% involving **H3** and *Pm3a* in PI 468960 was attributed to a chromosome 1A/5A translocation {1437}.

**H4**. **v**: Dixon {1441}; Java {1441}.

**H5** {1317}. **s**: Ap{162}; Arthur 71 {162}; Beau{875}; Downy{1223}; Magnum{10252}; Oasis{1109}; Ribeiro{1317}; Sullivan{1110}. **tv**: Giorgio 331-4 {1090}; PI 94567-6 {1317}; PI 94571-14 {1317}. **ma**: Cosegregation of **H5** and two RAPDs {296}.
H6{019}.  5A{425}. Based on the location of H9 on chromosome 1AS, H6 may also be located on chromosome 1AS{10231,10252}.  i: Erin = Newton-207^7/Arthur 71{1107}; Flynn = Newton-207^7/Knox 62{1107}.  v: Adder{1319}; Benhur{426}; Caldwell{1421}; Compton{1318}; CI 12855{019}; Excel{752}; Fillmore{1106}; Knox 62{426}; Lathrop{426}.  v2: Clara Fay H3{375}.  tv: Purdue 4835 A4-6{1105}.  tv2: PI 94587 H11 H16{019}.  ma: Cosegregation with three RAPDs{296}.

H7 & H8{425}.  Duplicate factors.  H7 is located in chromosome 5D {026}.  v: Adena{748}; Seneca{026,425}.

H9{1420}.  5A{162}.1AS{10231,10252}.  i: Iris = Newton-207^7/Ella{1107}.  v: Ella{875}; Line 822-34{162}.  v2: Elva CI 17714 H10{162}; Line 812-24 H10{1421}; Line 817-2 H10{1421}; Stella H10{875}.  ma: Cosegregation with two RAPDs{296}; STS-Pm - 1.7 cM - SOP005909 - 0.6 cM - Xksu1I/Xcni76/Xgdm33-1A - 0.5 cM - Xgwm176/Xpsp2999/Xcfa2153-1A - 0.5 cM - Xbarc263-1A - 1.2 cM - H9 - Xwmc24-IA{10231}; Xcfa2153-1A - 0.5 cM - H9 - 0.3 cM - Xbarc263-1A{10252}.

H10{1104}.  May be identical to H9 {10252}.  5A{162}.1AS{10252}.  i: Joy = Newton-207^3/IN76529A5-3-3{1107}.  v: IN76529{875}.  v2: Elva CI 17714 H9{162}; Line 817-2 H9{162}; Stella H9{875}.  ma: Cosegregation with one RAPD and close linkage to another RAPD{296}; Xcfa2153-1A - 0.5 cM - H10 - 1.3 cM - Xbarc263-1A{10252}; Xrapd9-2-1000/Xpsp2999-1A/Xgps7072-1A - 2.2 cM - H10{10252}.

H11{1422}.  1A{1222}.1AS{10252}.  i: Karen = Newton-207^4/IN916-1-3-1-47-1{1107}.  v: Kay{875,375}; Line 916{1422}; Line 920{1422}; Line 941{1422}.  tv2: T. turgidum PI 94587 H6 H16{1422}.  ma: Cosegregation with two RAPDs{296}; Xcfa2153-1A - 0.3 cM - H11 - 1.7 cM - Xbarc363-1A{10252}.

H12{1092}.  5A{1098}.  i: Lola = Newton-207^4/Luso{1107}.  v: Luso{1092}.  ma: Cosegregation with one RAPD and close linkage of H12 to another RAPD{296}.

H13{1104}.  6DL{441}.6DS{10251,10388}.  i: Molly = Newton-207^7/KU221-19/Eagle/KS806{1107}.  v: KS81H1640HF{441}; PI 562619{10388}; SW34=Langdon/Ae. tauschii RL 5544{10388}; T. turgidum var. durum cv. Gulab KU 134/Ae. tauschii KU 2076, KU 221-19{525}; T. turgidum var. persicum straminium KU 138/Ae. tauschii KU 2076, KU 221-19{525}.  dv: Ae. tauschii KU 2076{525}.  ma: Cosegregation with a RAPD{296}; Xgdm36-6D - 2.7 cM - H13/Xcfd132-6D - 1.1 cM - Xcfd132-6D{10251}; Xcfd132-6D - 3.7 cM - H13{10388}.

H14{875}.  5A{875}.  tv: IN 81601A2-3-3{875}.  tv2: ELS 6404-160 H15{875}.  ma: Cosegregation with a RAPD{296}.

H15{875}.  5A{875}. Based on the location of H9 on chromosome 1AS, H15 may also be located on chromosome 1AS{10231}.  tv: IN81602C5-3-3{875}.  tv2: ELS 6404-160 H14{875}.

H16{1106}.  5A{1098}.  tv: IN 80164H5-2-9{1106}; N80164{1097}.  tv2: PI 94587 H6 H11{1106}.  ma: Cosegregation of H16 and a RAPD{296}.

H17{1090}.  5A{1090}.  tv: PI 428435{1090}.  ma: Cosegregation of H17 and a RAPD{296}.

H18{1090}.  v: Marquillo{426,874}; Redlant{10715}; Shield{198}.

H19{1089}.  tv: PI 422297{1089}; This germplasm possesses a second gene which is allelic or closely linked with H16{1089}; IN84702{1097}.  tv2: PI422297 H29{1097}.

H20{025}.  2B{025}.  tv: Jori{025}.

H21.  2B {383} = 2BS.2R#2L{389}.  v: Hamlet = KS89WGRC8{1312}; KSWR 69-2-4-3{383}; KS85HF01-5{383}.  ad: KSWR 297h-1-1-9{383}.  al: Chaupon rye{383}.  ma: A RAPD amplified by primer OPE-13 was shown to co-segregate with H21{9938}; A STS primer set SJ07 was developed to identify 2RL, and hence H21{0233}. 

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**143 PATHOGENIC DISEASE/PEST REACTION**

\(H22\) \{1199\}. 1D{1199}.1DS{10381}. \(v:\) KS8WGRC1{1199}; KS85WGRC01=Ae. tauschii TA1644/Newton/Wichita\{1199\}; PI 572542{10388}. \(ma:\) Xgdm33-1D - 1.0 cM - H22 - 0.3 cM - Xhor2KVG-1D - 0.5 cM - Xgwp7082-1D{10381}.

\(H23\) \{1199\}. 6D{442}.6DL{1199}.6DS{10251}. \(v:\) KS89WGRC03 = TA1642/2*Wichita{442,10251}; PI 535766{10388}. \(al:\) Ae. tauschii TA1642{10251}.

\(H24\) \{1199\}. 3D{442,1199}.6DL{861}. \(v:\) KS89WGRC6{442}; PI 535769{10388}. \(ma:\) H24 - 5.9 cM - Xbcd451 - 6D/Xcdo482 - 6D{861}.

\(H25\).

\(H26\). 4D\{217\}.3DL{10388}. \(v:\) KS92WGRC26{217}; SW8 = Langdon/Ae. tauschii Clae 25{10388}. \(dv:\) Ae. tauschii TA2473{217}. \(ma:\) Xcfd211 - 3D - 7.5 cM - H26 - 2.9 cM - H26 - 2.9 cM - Xwgc7330 - 3D - 4.0 cM - Xgwm3 - 3D\{10388\}.

\(H27\) \{235\}. 4M\{235\}. \(su:\) H-93-33\{235\}. \(al:\) Ae. ventricosa No. 10\{235\}; Ae. ventricosa No. 11\{235\}.

\(H28\) \{171\}. 5A\{171\}. \(tv:\) PI 59190\{171\}.

\(H29\) \{1097\}. [\(H27\)] \{171\}. 5A\{1097\}. \(tv:\) PI422297 H19\{1097\}.

\(H30\) \{0256\}. Derived from Ae. triuncialis \{0256\}. \(v:\) TR-3531\{0256\}. \(al:\) Ae. triuncialis\{0256\}.

\(H31\) \{0332\}. 5BS\{0332\}. \(v:\) P961696\{0332\}. \(tv:\) CI 3984\{0332\}. \(ma:\) STS marker Xupw4148-5B - 3 cM - H31\{0332\}.

\(H32\) \{10137\}. 3DL{10137}. \(v:\) Synthetic W7984\{10137\}. \(ma:\) Xgwm3-3D - 1.7 cM - H32 - 1.7 cM - Xcfd-3D\{10137\}.

\(Hdic\) \{10262\}. 1AS\{10262\}. \(v:\) KS99WGRC42\{10262\}. \(tv:\) T. dicoccum PI 94641\{10262\}. \(ma:\) Xcfa2153-1A - 1.4 cM - Hdic - 0.6 cM - Xgwm33-1A\{10262\}.

\(H WGRC4\) \{10251\}. 6DS\{10251\}. \(v:\) KS89WGRC04 = TA 1695/3*Wichita\{10251\}. \(ma:\) Allelic with H31\{10251\}.

A recombination value of 12.0% between leaf-rust reaction \{possibly Lr10\} and Hessian-fly reaction in Selection 5240 was reported \{018\}.

91. Reaction to Meloidogyne spp.

Root rot nematode, root knot eelworm

\(Rkn\{632\}. \(dv:\) Ae. squarrosa G3489. \(v:\) Prosquare, a synthetic hexaploid of Produra/Ae. squarrosa G3489\{632\}.

\(Rkn-mm1\) \{1621\}. Derived from Ae. variabilis\{1621\}. 3B\{590\}. \(v:\) X8 = CS/Ae. variabilis No. 1/Rescler/3/Lutin\{1620\}; X35\{1620,1621\}. \(ma:\) Co-segregation with RAPD OpY16\{1065\} and close linkage with several markers including Est-B5\{0103\}; converted to SCAR Y16\{10486\}; May be the same as CreY (see reaction to Heterodera avenae).

92. Reaction to Mycosphaerella graminicola (Fuckel) Schroeter

Disease: Septoria tritici blotch

\(Stb1\) \{1586\}. 5BL\{10123\}. \(v:\) Bulgaria 88\{1586\}; Oasis\{1586\}; P881072-75-1\{10123\}; SO852\{10123\}; Sullivan\{1586\}. \(ma:\) Located in FL 5BL-11 - 5BL-14\{10123\};
Close linkage with 2 RAPD markers at >0.68 and 1.4 cM in P881072-75-1\{10123\}; Cent.....Xbarc74-5B - 2.8 cM - Stb1\{10123\}.

Stb2. [Stb2\{1586\}]. 3BS\{10105\}. v: Nova Prata\{1586\}; Veranopolis\{1586\}. ma: Xgwm389-3B/Xgwm533-3B - 1.0 cM - Stb2 - 3.7 cM - Xgwm493-3B\{10105\}.

Stb3. [Stb3\{1586\}]. 6DS, according to \{10556\} this location is not correct\{10105\}. 7AS\{10556\}. v: Israel 493\{1586\}. ma: Stb3 - 3.0 cM - Xgdm132-6D\{10105\}.

Stb4\{1410\}. 7D\{0326\}.7DS\{10140\}. v: Cleo\{1410\}; Gene\{10010\}; Tadinia\{1410,10140\}; Tadorna\{1410\}. ma: XAGG/CAT10 - 4.0 cM - Stb4 - 0.7 cM - Xgwm111-7D - 1.4 cM - XATCG/CAA5 ......Cent\{10140\}; Stb4 - 0.7 cM - Xgwm111-7D\{10140\}.

Stb4 segregated independently of Stb1 but its relationship with Stb2 and Stb3 is unknown.

Genetic analysis of Tadinia indicated single gene segregation (assumed to be Stb4) with a Californian culture but a different single gene segregated with South American isolates \{10140\}.

Stb5\{0186\}. Identified using M. graminicola IPO94269\{0186\}. Derived from Ae. tauschii accession 37-1 \{0186\}. 7DS\{0186\}. v: Bezostaya\{0187\}; Hereward\{0187\}; Sears’ Synthetic\{0186\}; Shafir\{0187\}; Vivant\{0187\}. su: CS’8/S\{Syn7D\}\{0186\}. dv: Ae. tauschii 37-1\{0186\}. ma: Rc3 - 6.6 cM - Stb5 - 7.2 cM - Xgwm44-7D - Centromere\{0186\}; Stb6 - 2 cM - Xgwm369-3A\{0187\}.

Stb6\{0187\}. Confers resistance to M. graminicola isolate IPO323 but not to isolate IPO94269 \{0187\}. 3AS\{0187\}. v: Amigo\{10448\}; Arina\{10448\}; Amada\{10448\}; Atlas 66\{10448\}; Ble Seigle\{10448\}; Bon Fermier\{10448\}; Chinese Spring\{10448\}; Bezostaya 1\{10495\}; Flame\{0187\}; Gene\{10448\}; Heines Kolben\{10448\}; Hereward\{10448\}; Poros\{10448\}; Senat\{10448\}; Shafir\{10448\}; Tadinia\{10448\}. v2: Bulgaria 88 Stb1\{10448\}; Israel 493 Stb3\{1048\}; Kavkaz-K4500 Stb7 Stb10 Stb12\{10101\}; TE9111 Stb7 Stb11\{10102\}; Veranopolis Stb2\{1048\}. ma: A resistance gene from Senat located at or near the Stb5 locus was mapped 5 cM from microsatellite Xgwm369-3A on chromosome arm 3AS\{10067\}.

Stb7\{0311\}. 4AL\{0311\}. v: ST6 = Estanzuela Federal\{0310, 0311\}. v2: Kavkaz-K4500 Stb6 Stb10 Stb12\{10011\}; TE9111 Stb6 Stb11\{10102\}. ma: Xwmc219-4A - 0.8 cM - Xwmc4A - 0.3 cM - Stb7\{0311\}; Stb7 was closer to Xwmc313-4A than to Xwmc219-4A\{10011\}.

Stb8\{0326\}. 7BL\{0326\}. v: Synthetic hexaploid W7984 (parent of ITMI population)\{0326\}. ma: Xgwm146-7B - 3.5 cM - Stb8 - 5.3 cM - Xgwm577-7B\{0326\}.

Stb9\{10027\}.

Information withheld until publication

Stb10\{10011\}. Confers resistance to cultures IPO94269 and ISR8036, but not to IPO87019 \{10011\}. 1D\{10011\}. v2: Kavkaz-K4500 L.6.A.4 Stb6 Stb7 Stb12 = JIC.W9995\{10111\}. ma: Associated with Xwmd848-1D\{10111\}.

Stb11\{10012\}. Confers resistance to isolate IPO90012 \{10012\}. 1BS\{10012\}. v: JIC W 9996; TE9111. v2: TE9111 Stb6 Stb7\{10012\}. ma: Distal to Xbarc008-1B\{10012\}.

Stb12\{10011\}. Confers resistance to cultures ISR398, ISR8036 and IPO87019 \{10011\}. 4AL\{10011\}. v2: Kavkaz-K4500 Stb6 Stb7 Stb10\{10011\}. ma: Stb12 was closer to Xwmc219-4A than to Xwmc313-4A\{10011\}.

Stb13\{10347\}. Confers resistance to Canadian cultures MG96-13 and MG2 \{10347\} 7BL\{10347\}. v: DH line 90S05B*01\{10347\}; DH line 98S08C*03\{10347\}. v2: Salamouni Stb14\{10347\}. ma: Xwmc396-7B - 9 cM - Stb13\{10347\}; Xwmc396-7B - 7 cM - Stb13\{10347\}.
**Stb14**{10348}. Confers resistance to Canadian isolate MG2 but not to MG96-13 {10347} 3BS{10348}. v: DH line 98S08A*09{10348}. v2: Salamouni Stb13{10347}. ma: Xwmc500-3B - 2 cM - Stb14 - 5 cM - Xwmc623-3B{10348}.

**Stb15**{10341}. Confers resistance to Ethiopian culture IPO88004 {10341} 6AS{10341}. v: Stb15 - 14 cM - Xpsr904-6A{10341}.

**QTL:** Four QTLs for resistance to Mycosphaerella graminicola were identified in replicated field experiments in a double haploid population from Savannah (susceptible)/Senat(resistant). Senat contributed all the alleles providing resistance {10067}

**QStb.riso-2B** was mapped on chromosome arm 2BL linked to SSR marker Xwmc175-2B (LOD>5, R²>17%) {10067}.

**QStb.riso-3A.2** was mapped on chromosome arm 3AS linked to SSR markers Xwmc489-3A, Xwmc388-3A and Xwmc505-3A (LOD>4, R²>18%). Also detected at the seedling stage {10067}. Xgwm369-3A is present on chromosome arm 3AS {0187}. A resistance gene from Senat located at or near the Stb6 locus was mapped 5 cM from microsatellite Xgwm369-3A on chromosome arm 3AS {10067}.

**QStb.riso-6B** was mapped on the centromeric region between SSR markers Xwmc494-6B and Xwmc341-6B (LOD>16, R²>68%). Also detected at the seedling stage {10067}.

**QStb.riso-7B** was mapped on chromosome 7B close to SSR marker Xwmc517-7B (LOD>4, R²>11%) {10067}.

ITMI Population: Three QTL, **QStb.ipk-1DS, QStb.ipk-2DS** and **QStb.ipk-6DS** conferred seedling-stage resistance to 2 isolates, whereas 2 QTL **QStb.ipk-3DL** and **QStb.ipk-7BL** conferred separate adult-stage resistances to each isolate {10151}.

A weak QTL, **QStb.psr-7D.1**, giving partial resistance to Portuguese isolate IPO92006, was detected in the Xcdo475b-7B - Xswm5-7B region in chromosome 7DS {10341}.

**93. Reaction to Phaeosphaeria nodorum** (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

Disease: Septoria nodorum blotch, Stagonospa nodorum blotch.

**93.1. Genes for resistance**

**Snb1**{856}. 3AL{856}. v: Red Chief{856}. v2: EE8 Snb2{856}.

**Snb2**{856}. 2AL{856}. v2: EE8 Snb1{856}.

**Snb3**{1594}. 5DL{1594}. s: CS/Synthetic 5D{1594}. v: Synthetic{1594}. dv: Ae. tauschii{1594}.


**UBC521_650** was converted to a SCAR marker{0212}.

Allelism of the hexaploid wheat gene and the T. timopheevii SnbTM was suspected but not confirmed.
QTL
A QTL analysis of SNB response in the ITMI population found significant effects associated with chromosome 1B (probably \textit{Snn1}) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B \{10009\}. An additional QTL on 7BL was effective at a later stage of disease development \{10009\}.

Four QTLs, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B and 5D, were mapped in a Liwilla / Begra doubled haploid population. Longer incubation period and lower disease intensity were contributed by Liwilla \{10045\}.

Two QTLs for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in Arina / Forno RILs \{10065\}. The 3BL QTL, designated \textit{QSng.sfr-3BS}, was associated with marker \textit{Xgwm389-3B} and explained 31.2% of the variation. The resistance was contributed by Arina \{10065\}. The 4BL QTL, \textit{QSng.sfr-4BL}, was associated with \textit{Xgwm251-4B} and explained 19.1% of the variation. Resistance was contributed by Forno \{10065\}. A QTL on 5BL, \textit{QSng.sfr-5BL}, overlapped with QTLs for plant height and heading time \{10065\}. \textit{QSng.sfr-3BS} peaked 0.6 cm proximal to \textit{Xsun2-3B} \{10465\}. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes \{10465\}.

A QTL, \textit{QSnl.ihar-6AL}, identified in DH lines of Alba (R) / Begra (S) accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period \{10143\}.

Forno (S) / Oberkulmer spelt (R). Among 204 RILs leaf and glume response were genetically different but correlated ($R^2=0.52$). Ten QTLs for glume blotch (SNB) resistance were detected, 6 from Forno. A major QTL ($R^2=35.8\%$) was associated with \textit{q}. Eleven QTLs (4 from Forno) affected leaf blotch; 3 of these (chromosome 3D, 4B and 7B) with $R^2>13\%$ were considered potential candidates for MAS \{10250\}.

ITMI population: A major QTL, coinciding with \textit{Snn1}, was located in chromosome 1BS ($R^2 = 0.58$, 5 days after inoculation), minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL \{10009\}.

Br34 / Grandin: Three QTLs with resistance effects from BR34; \textit{Qsnb.fcu-5BL.1} (\textit{Tsn1}), $R^2 = 0.63$, \textit{Qsnb.fcu5BL.2}, $R^2 = 0.06$, and \textit{Qsnb.fcu-1BS} (vicinity of \textit{Snn1}), $R^2 = 0.10$ \{10458\}. QTL analysis of the RIL population with Culture Sn6 revealed four QTLs, \textit{Qsnb.fcu-2DS} ($R^2 = 0.3 - 0.49$) associated with \textit{Snn2}, \textit{Qsnb.fcu-5BL} ($R^2 = 0.14 - 0.2$) associated with \textit{Tsn1}, \textit{Qsnb.fcu-5AL} ($R^2 = 0 - 0.13$) associated with \textit{Xfcp13-5A}, and \textit{Qsnb.fcu-1BS} ($R^2 = 0 - 0.11$) associated with \textit{Xgdm125-1BS} \{10507\}.

P91193D1 (partially resistant) / P92201D5 (partially resistant) RIL populations were tested in Indiana and Western Australia for glume resistance. Two QTL were identified: \textit{Qng.pur-2DL.1} from P91193D1 ($R^2 = 12.3$ in Indiana and 38.1% in WA, respectively; \textit{Xgwm526.1-2D - Xcfd50.2-2D}) and \textit{Qng.pur-2DL.2} from P99201D5 ($R^2 = 6.9\%$ and 11.2\%, respectively; \textit{Xcfd50.3-2D - wPT9848}) \{10471\}.

HRWSN125(R)/WAWHT2074(S): Constant detection of \textit{QSnl.daw-2DL} for flag leaf resistance, and \textit{QSng.daw-4BL} for glume resistance over two years \{10584\}.

Tetraploid wheat
Langdon/Langdon (T. turgidum ssp. dicoccoides Israel-A 5B): QSnb.ndsu-5B located 8.3 cM proximal to tsn1 for tan spot resistance; $R^2 = 0.38\{10597\}$.

93.2. Sensitivity to SNB toxin
Australian cultivars with Tsn1 and tsn1 are listed in {10540}.

Tetraploid wheat

In a reevaluation of this work Faris and Friesen {10688} attributed all of the variation in SNB response to the presence or absence of SnTox1.

ma: Xbcd183-5B - 1.2 cM - Tsn1/Xbcd1030-5B - 2.4 cM - Xrz5-5B \{10688\}.

Tsn1 \{10458, 346, 10207\}. Sensitive to SnToxA, which is functionally identical to Ptr ToxA {10459}. chevron: See reaction to Pyrenophora tritici repentis {10458}. Cheyenne{0007}; Hope{0007}; Jagger{0007}; Kulm{346,10030,10458}; ND495{0007}; Timstein{0007}; Trenton{0315}. tv: Langdon{10458}.

tsn1 \{346,10207\}. Insensitivity (disease resistance) is recessive {346}. 5BL{346}.

snn1tsn1. Atlas 66 \{10458\}; BR34 \{10458\}; Erik \{10458\}; Opata 85 \{10507\}; ND688 \{10458\}.

Snn1 \{10008\}. Sensitivity to SnTox1 is dominant \{10008\} 1BS{10008}.

Snn2 \{10507\}. Sensitivity to SnTox2 is dominant \{10507\} 2DS{10507}.

QTL: ITMI population: A major QTL, coinciding with Snn1, was located in chromosome 1BS (R$^2=0.58$, 5 days after inoculation), minor QTLs were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL \{10009\}.

94. Reaction to Pratylenchus spp.
Root lesion nematode; prats

94.1. Reaction to Pratylenchus neglectus

Rlnn1 \{0121\}. 7AL{0121}.

ma: Mapped between markers Xpsr121-7A and Xgwm344-7A and 9 cM proximal to Lr20{0374}.
94.2. Reaction to Pratylenchus thornei
QTLs were located on chromosomes 2BS and 6DS {0122}.

95. Reaction to Puccinia graminis Pers.
Disease: Black rust; black stem rust; stem rust.
Note: Some near-isogenic lines are based on Marquis. The genes present in the Marquis background are not listed for those NILs.

Sr1. Deleted - see Sr9d.

Sr2{38,677}. Recessive allele. Adult plant response. 3BS{499}. s: CS 6/Hope 3B{499}. v2: HD2009 Sr30{10632}; Warigo Sr7b Sr17{499}; Suneca Sr8a Sr17{485}; Hopp Sr9d{499}; Lancer Sr9d Sr17{679}; Scout Sr9d Sr17{679}; See also{499,1040}. ma: Xgwm389-3B - 2.7 cM - Sr2 - 1.1 cM - Xglk683-3B{0358}.....Xglk683(STS Xsun2-3B) - 0.5 cM - Xgwm533-3B{0358}; These SSR loci were located within FL 0.87 - 0.75{0358}; All 27 lines with Sr2 carried a 120 bp allele at Xgwm533-3B; A 120 bp allele in 4 cultivars lacking Sr2 differed from the Sr2 associated allele at 4 base positions{0358}; STMs for the Xgwm533-3B locus had increased specificity as markers for Sr2{10142}. Sr2 is associated with pseudo-black chaff{742,1102} and seedling chlorosis (see {149}) and occurs very frequently in commercial wheats, especially in germplasm produced and distributed by CIMMYT. Sr2 has probably remained effective since the 1920s.

Sr3 & Sr4{047}. v: Marquillo - based on early data. No stocks available.

Sr5{047}. 6D{939,1308,1626}.6DS{939}. i: I Sr5-Ra{828}; I Sr5-Rb{828}; Sr5/7 LMPG{685}; Thatcher/10 Marquis{686}. s: CS 6/Thatcher 6D{1308}. v: Admonter Fruh{072}; Dacia{979}; Dong-Fang-Hong 2{564}; Dong-Fang-Hong 6{564}; Feng-Kong{563}; Hochzucht{046}; Hybrid 80-3{072}; Jubilejna{068}; Juna{076}; Kanred{1308}; Ke-Fang 1{564}; Stabil{072}; Viginta{071}; Vrakunski{072}. v2: Amika Sr31{076}; An-Hewi II Sr8a{564}; Beijing 10 SrTmp{564}; Dong-Xie 3 Sr31{563}; Dong-Xie 4 Sr31{563}; Erythrospermum 974 Sr8a{072}; Glenlea Sr6 Sr9b{327}; Istra Sr31{076}; Jing-Hong Sr17{564}; Jing-Hong 2 Sr17{564}; N.P.789 Sr11{1555}; Qing-Chung 5 Sr6 Sr11{564}; Solaris Sr31{076}; Victor Sr6 Sr8a{979}.

Sr6{687}. [SrKai{1167}]. 2D{1293,1308,1577}.2DS{942}. bin: 2DS5 - 0.47 - 1.00{10714}. i: I Sr6-Ra{828}; Kenya 58/10 Marquis{468,675}; Sr6/9 LMPG{685}. s: CS 5/Red Egyptian 2D{1308}. v: Africa 43{669}; Eureka{468,844}; Kenya stocks{669,670,673,687,689,1167,1557}; McMurachy{679}; Shield{198}. v2: Bowie Sr8a{1553}; Eurga Sr11{1553}; Fortuna Sr7a{679}; Gamut Sr9b Sr11{1555}; Glenlea (heterogeneous) Sr5 Sr9b{327}; Kentana 52 Sr7a{678,1577}; Kiric 66 Sr7b{979}; Lerma Rojo 64 Sr7b Sr9a{979}; No. 466 Sr9b Sr10{689}; Red Egyptian Sr8a Sr9a{687,1308}; Siete Cerros Sr11{033}; Victor I Sr5 Sr8a{979}. ma: Sr6 - 1.1 cM - Xwmc453-2D - 0.4 cM - Xcfd43-2D{10714}. See also{1553}.

Sr7{830}. 4A{671,830,1293}.4AL{939,1308}.

Sr7a{830}. [Sr7{687}]. i: Egypt Na101/6 Marquis{468}; Kenya 117A/6 Marquis{468}; Sr7a9 LMPG{685}. s: CS 7/Kenya Farmer 4B{830}; CS 8/Sapporo 4B{830}. v: Egypt Na101{669}; Kenya stocks{669,670,673,687,689}; Sapporo Haru Komugi Ichigo{689}. v2: Egypt Na95 Sr9b Sr10{687}; Fortuna Sr6{679}; French Peace Sr9a Sr13{680}; Kentana 52 Sr6{689}; Khapstein Sr13 Sr14{674}; W3746 Sr12{1371}.

Sr7b{830}. i: I Sr7b-Ra{828}. v2: Warigo Sr2 Sr17{499}; Kiric 66 Sr6{979}; Roussalka Sr8a{979}; Red Bobs Sr10{308}; Nell Sr17{1565}; Spica Sr17{939}; Marquis Sr18 Sr19 Sr20{675,830}.
Sr8. 6A[1293,1308]. 6AS[929,1368].
Sr8a[1368]. [Sr8[687]]. i: 1Sr8a-Ra[828]; Red Egyptian/10' Marquis[686]; Sr8a9/9 LMPG[685]. s: CS'5/Red Egyptian 6A[1308]. v: Marimp 3[979]; Mentana[844]; Strampelli[979]. v2: An-Hewi II Sr5[564]; E-Gan-Zao Sr17[564]; Erythrospernum 974 Sr5[5072]; Frontana Sr9b[689]; Golden Valley Sr17[979]; Hartog Sr2 Sr12[127]; Magnif G Sr9b[689]; Pitic 62 Sr9b[033]; Red Egyptian Sr6 Sr9a[687]; Rio Negro Sr9b[689]; Roussalka Sr7b[979]; Suneca Sr2 Sr17[485]; Victor I Sr5 Sr6[979].


This could be the gene located on chromosome 6A in ST464-A1 {10473} and one of the genes present in ST464, a parent of Leeds.


Sr9b[468]. [Sr9[687], SrKb1[468]]. i: Kenya 117A/10 Marquis[686]; Sr9b10 LMPG[685]. s: CS'7/Kenya Farmer 2B[939]. v: Gamenya[844]; Kenya stocks[669,670,673,678,689,1557]. v2: Egypt Na95 Sr7a Sr10[636]; Festival Sr15[1553]; Frontana Sr9a[689]; Gamut Sr6 Sr11[1555]; Glenlea Sr5 Sr6 heterogeneous[327]; Kenora Sr15[1553]; Magnif G Sr9a[689]; No. 466 Sr6 Sr10[689]; Pitic 62 Sr8a[033]; Rio Negro Sr8a[689]; Robin Sr11[879]; Veadeira Sr10[687].

See also [1553].

Sr9c. Originally reserved for Sr36.

Sr9d[678,831]. [Sr1[947,676,677]]. i: Hope/10' Marquis[677]; H-44/10' Marquis[677]; I Hope 2B-Ra[828]; Sr9d/8 LMPG[685]. v: Hoppa Sr2[1040]. v2: Lancer Sr2 Sr17[679]; Scout Sr2 Sr17[679]. tv: Arnautka[939]; Mindum[939]; Spelmar[939].

Sr9e[951]. [Sr9i[642], Sr9[1391]]. v: SST 16[1324]; SST 33[785]; SST 66[785]; SST 3R[1324]; Vernstein[845]. tv2: Combination III Sr36[841]; Sunstar Sr8a Sr12[939]. tv: ST464-A2[10473]; Vernal emmer[1391]; CI 7778[845]; Sr9e occurs in many tetraploid wheats[939,1378]. tv2: Arrivato Sr8b Sr13[10607]; ST464 Sr13[10473]. ma: Xgwm191-2B - 5.5 cM - Sr9e - 0.2 cM - Xgwm47-2B[10607].

Sr9f[826]. v: Chinese Spring[826]; Not present in the near-isogenic I Sr9a-Ra[826].

Sr9g[965]. s: CS’7/Marquis 2B Sr16[965]; CS’4/Thatcher 2B Sr16[965]. v2: Celebration Sr12 Sr16[965]; Eagle Sr26[842]; Hochzucht Sr5 Sr12[965]; Lee Sr11 Sr16[965]. tv: Acme[965]; Iumillo[965]; Kubanka[965].

See also [504].


Sr11[468]. [Sr11[687], Sr12[687]]. 6B[671,1143,1293,1309]. 6BL[1297]. i: 1Sr11-Ra[828]; Lee10 Marquis[686]. s: CS’7/Kenya Farmer 6B[830]; CS’9/Timstein 6B[1308]. v: Charter[844]; Flevina[072]; Gabo[687]; Kenya stocks[670,673,844,1557]; Sonora 64[033]; Sylvia[071]; Timstein[687,1308]; Tobari 66[033]; Yalta[844]. v2: Eurga Sr6[1553]; Gamut Sr6 Sr9b[1555]; Lee Sr9g Sr16[687]; N.P.790 Sr5[1555]; Qing-Chung 5 Sr5 Sr6[564]; Robin Sr9b[879]; Prospect SrWld[197]; See also[1553].
A resistance gene allelic with Sr11 was found in Chinese Spring [938], but the P. graminis culture for its detection was lost.

**Sr12** [1332]. Recessive. 3B{1332,682}.3BS{968}. s: CS‘7/Marquis Selection 3B Sr16[1332]; CS‘5/Thatcher 3B Sr16[1332]. v: Marquillo[682]; Tincurrien[939]; Windebru[939]. \( v_2: \) W3746 Sr7a[1371]. \( tv: \) Postulated for several durums[1378]. Sr12 is more widespread and probably more effective in conferring resistance than is usually acknowledged [939].

**Sr13** [674]. 6AL[929]. i: Khpastein/10‘Marquis[686]; Sr13/9‘LMPG[685]. v: French Peace Sr7a Sr9a[680]; Khpastein Sr7a Sr13 Sr14[674]; Machete Sr[10607]. tv: ST464-C[10473]. \( tv_2: \) Arrivato Sr8b Sr9e[10607]; Khapli Sr14[674]; ST464 Sr9e[10473].

**Sr14** [674]. 1BL[933]. i: Khpastein/10‘Marquis[686]. v: Line A[933]. \( v_2: \) Khpastein Sr7a Sr13[674].

**Sr15** [1554]. 7A{1293,1554}.7AL[1305]. v: Present in stocks possessing Pm1 and Lr20[931,1554]; See Reaction to Blumeria graminis and Reaction to P. triticina. ma: Associated with clustered markers[0323].

**Sr16** [830]. \([Sr12[1238].2B[830,1308].2BL[1307]. i: I Sr16-Ra[828]; I Th3B-Ra[832]. s: CS‘7/Marquis 2B Sr9g[1581]; CS‘4/Thatcher 2B Sr9g[1308]; CS‘5/Thatcher 3B Sr12[832]. v2: Thacher Sr5 Sr9g Sr12[939]; Lee Sr9g Sr11[939]. Sr16 is allelic with a gene in Kota (SrKt2[932]) [939].

**Sr17**. Recessive. \([sr17[964].7B[771].7BL[964,10565]. s: CS‘6/Hope 7B[964]. v: Forno[10511,10565]. v2: E-Gan Zeo Sr8a[564]; Golden Valley Sr8a[979]; Jing-Hong 1 Sr5[564]; Jing-Hong 2 Sr5[564]; Lancer Sr2 Sr9d[679]; Nell Sr7b[1565]; Scout Sr2 Sr9d[679]; Suneca Sr2 Sr8a[485]; Present in many stocks possessing Pm5[964]; See Reaction to Blumeria graminis. ma: Xwmc273-7B - 15.3 cm - Sr17[10565].

**Sr18** [054]. \([SrG2[844].nr1l1[1238].Srmq1[099].SrPsI[1263].SrMn1[1263].1D[054,1308,1582]. i: I Hope 1D-Ra[828]; Sr18/8 LMPG[685]. s: CS‘6/Hope 1D[1308]. v: Present in the majority of wheat stocks[828]; Stocks not possessing Sr18: Brevii[054]; Chinese Spring[828]; Eureka[054]; Federation[054]; Gular[054]; Kenya C6042[054]; Koala[054]; Little Club[828]; Morocco[054]; Norka[054]; Prelude[828]; Yalta[054].


**Sr20** [029]. \([Srmq3[1238].Sr13[1238].2B[029]. v: Mq-C[029]; RI-C[029]. v2: Reliance Sr5 Sr16 Sr18[029]; Marquis Sr7b Sr18 Sr19[029].


**Sr23** [950]. The following chromosome locations are consitstant with the finding that the first location was based on Rescue monosomics. Rescue differs from CS by a 2B-4B reciprocal translocation [939]. 4B[950].2BS[939]. v: Exchange[950]; Warden[950]; Sr23 is always associated with Lr16[950]. v2: Etoile de Choisy Sr29[950].
**Sr24**{956}. Derived from *Thin. elongatum*. 3DL = T3DS.3DL-3Ae#1L{956,389}. i: Sr24/9 LMPG{685}; Sears’ 3D/Ag translocations{956,1300}. v: Agent{956}; Blueboy II{956}; Collin{901}; Cloud{956}; Cody{1284}; Fox{956}; Gamka{785}; Karee{785}; Kinko{785}; Palmiet{785}; Sage{825,1024}; SST 23{1324}; SST 25{785}; Torres{128}; Wilga{785}. v2: Siouxland Sr31{1283}; List of Australian genotypes{0340}. su: Chinese Spring + 7Ae#1L{1304}. Sr24 is completely linked in coupling with Lr24{956} and often with red grain colour. See Reaction to *P. triticina*. 

**Sr25**{956}. Derived from *Thin. elongatum*. 7DL = T7DS.7DL-7Ae#1L{291,956,388,657}. i: Sears’ CS 7D/7Ag translocations{956,1300}; Sr25/9 LMPG{685}. v: Agatha Sr5 Sr9g Sr12 Sr16{956} = T4{1323}; Mutant 28{388}. 7AL = T7A-7Ae#1L{330}. v: Sears’ 7A/7Ae#1L No. 12{330,1304}; Sears’ 7D/7Ag#11 carries neither Sr25 nor Lr19{939}. su: Chinese Spring + 7Ae#1L(7D){1304}. See Lr19, reaction to *Puccinia triticina*. Sr25/Lr19 often show complete linkage in wheat {956}. Knott{681} obtained two mutants (28 and 235) of Agatha with reduced levels of yellow pigment in the flour. One of these mutants lacked Sr25. Marais{890} also obtained mutants with reduced yellow pigment in Indis derivatives and some of these lacked Sr25.

**Sr26**{956}. Derived from *Thin. elongatum*. 6AL{364} = T6AS.6AL-6Ae#1L{388,389}. i: Sr26/9 LMPG{685}. v: Avocet{364}; Flinders{1449}; Harrier{939}; Jabiru{956}; King{1451}; Kite{956}; Knott’s 6A-6Ae#1L translocation to Thatcher{672}; Takari{253}. v2: Bass Sr36{1450}; Eagle Sr9g{956}. ma: Detected with several RFLP probes{0138}; A PCR marker, Sr26#43 was reported in{10257}. Sr27. Derived from *S. cereale*. 3A(T3A-3R) = T3AS.3R#1S{003,896,389,10162}. i: Sr27/9 LMPG{685,10162}. v: WRT wheat-rye translocation, available in CS, Thatcher and Pembina backgrounds. Translocated from Imperial rye to Chinese Spring by Acosta{003,10162}; Widespread in triticale{966,1384,10162}. 3A = T3AL.3RS{896}. v: W964 = 3RS.3AL.1/4 Inia 66{896}; W968 = 3RS.3AL.1/5 Condr{896}; W970 = 3RS.3AL.88/5 SST3{896}; W966 = 3RS.3BL.26/4 Inia 66{896}. 3B = T3BL.3R#1S{896}. v: W966 = 3RS.3BL.26/4 Inia 66{896}. Sr30(688). [SrW]. 5DL{688}. i: Sr30/7 LMPG - Lines 1, 2, and 3{685}. v: Festiguay{688}; Mediterraneen W1728{1369}; Webster{688}. v2: HD2009 Sr2{10632}; Klein Cometa Sr8b{1368}; Relative common in Australian and Mexican wheats. Various unnamed accessions{208,1321}. Sr31. Derived from *S. cereale* cv. Petkus. See also Reaction to *P. striiformis*, Yr9: Reaction to *P. triticina*, Lr26 1B = T1BL.1RS = T1BL.1R#1S{389} or 1R(1B). i: MA1 and MA2 four-breakpoint double translocation lines 1RS-1BS-1RS.1BL in Pavon{0084}. v: Amika {heterogeneous} Sr5{076}; Cougar{0267}; Feng-Kang 2{563}; Feng-Kang 8{563}; Gamtoos{785};
Sr32. Derived from *Ae. speltoides*.  
2A [939,1304] = T2AL-2S#1L-2S#1S [389].  
2B [1304] = T2BL-2S#1S [389].  
2D [1304] = T2DL-2S#1L-2S#1S [389].  
Sr33. (linked with *Gli-D1*). [SrSQ(650)]. 1DL(650).1DS(620).  
Sr34[967]. Derived from *Ae. comosa*.  
2A [967] = T2AS-2M#1L-2M#1S [389].  
2D [967] = T2DS-2M#1L-2M#1S [389].  
Sr35[957]. [SrTml(1522)]. 3AL[957].  
Sr36[939]. [SrTil(949)]. 2BS[939].  
Sr37[939]. [SrT2(949)]. 4BL[939].  
Sr38[062]. Derived from *Ae. ventricosa*.  
2AS[062].6M=2MS-6MS.6ML or 2MS-6ML.6MS[0009].  
Sr39(646). Derived from *Ae. speltoides*. 2B[651].  
Sr5 (heterogenous). Derived from *Ae. speltoides*.
**Pathogenic Disease/Pest Reaction**

**Sr41** (1215). 4D{1215}. v: WDR-B1{1214}. v2: Waldron Sr5 (heterogeneous) Sr11 (heterogeneous).

**Sr42** (938). 6DS{938}. v: Norin 40{938}.

**Sr43.** Derived from *Thin. elongatum.*
7DL = T7DL-7Ae#2L.7Ae#2S{657,389}. tr: KS10-2{653}.
7D = T7DS.7Ae#2L{657,389}. tr: KS23-9{653}; KS24-1{653}; KS24-2{653}.

**Sr44** (389). Derived from *Thin. intermedium.*
T7DS - 7Ai#1L.7Ai#S 7Ai#1L{389}. v: Line 86.187{939}; Several 7A - 7Ai#1L translocations{0089}.
7Ai#2, 7Ai#2S. su: Group 7 alien substitution lines with 7Ai#1 and 7Ai#1S{939}. ad: TAF2 = L1{169}.

**Sr45** (894). [SrD {934}, SrX {1805}]. 1D{897}.1DS{894}. v: 87M66 -2{894}; 87M66 -6{897}; Thatcher + Lr21, RL5406[894,934]; Various backcross derivatives developed at PBI Cobbitty{1461}. dv: Ae. tauschii RL5289{894,934}. Tests of natural and induced mutants of *P. graminis* f. sp. *tritici* indicated that Sr45 has identical specificity to Sr21{934}.

**Sr46** (10538). 2DS{10538}. v: L-18913 / Meering selections R9.3{10538}; R11.4{10538}; R14.2{10538}. v2: L-18913 = Synthetic Langdon / Ae. tauschii var. *meyeri* AUS 18913 Sr9e {10538}. ma: Co-segregation with RFLP Xpsr649 -2DS at both the diploid and hexaploid levels{10538}; A PCR-based marker, csSC46 was developed from a BAC clone containing Xpsr649{10538}.

**Sr47** (10549). Derived from *Ae. speltoides.* 2B = 2BL - 2SS{10549}. tv: DAS15{10549}. al: Ae. speltoides PI 369590{10549}.

**Sr48** (10564). [SrAn1 {10565}]. 2AL{10564,10565}. bin: 2AL1 -0.85 -1.00{10564}. v: Arina{10511,10564,10565}. ma: Yr1 - 16.5 cM - Sr48 {10564}; Yr1 - 16.5 cM - Sr48{10564}; Sr48 is considerably distal to the most distal of published markers, all of which are proximal to Yr1.

**Sr49** (10704). 5BL{10704}. v: AUS 28011{10704}. ma: Sr49 - Xwmc471-5BL, 7.8 cM{10704}.

**SrA** (323). v: SW55-1{323}; SW56-1{323}. v2: SW33-5 Sr9a Sr13{323}; SW54-3 Sr9d Sr13{323}.

**SrR.** 1RS. ad: CS + Imperial 1R{0377}. v: 1DS-1RS translocation stocks{0377}. al: Imperial rye. ma: Several markers tightly linked with SrR were identified in{0377}.

**SrTmp** (1230). v: Bai-Yu-Bao{564}; Beijing 9{564}; Beijing 11{564}; Fertodi 293{977}; Martonvasari 5{977}; Mironovska = Mironovskaya 808{068,977}; Nung-Ta 139{564}; Parker{977}; Trison{1230}; Triumph 64{841,1230,977}; Xuzhou 14{564}; Yen-An 15{564}. v2: Beijing 10 Sr5{564}.

**SrWld** (1230). v2: Prospect Sr11{197}.

**SrZdar** (067). 1B{067}. v: Zdar{067}.

Additional temporary designations are listed in {1230}.
Genotype lists: {323,970,10270,10511,10697}.

Complex genotypes:

AC Taber: Sr2, Sr9b, Sr11, Sr12{9905}.

Centurk: Sr5 {979}, Sr6 {979}, Sr8a, Sr9a {979}, Sr17 {979}.

Chris: Sr5 {679,1371}, Sr7a {1371}, Sr9g {1371}, Sr12 {1371}.

Egret: Sr5 {939}, Sr8a {939}, Sr9b {939}, Sr12 {939}.

FKN: Sr2, Sr6, Sr7a, Sr8a {791}, Sr9b {791}.

H-44: Sr2, Sr7b {677}, Sr9d {677}, Sr17.
The image contains a page from a scientific document discussing pathogenic disease/pest reaction. The text is about various species and their susceptibility to disease, with a focus on resistance mechanisms. The text includes gene designations, bin locations, and the effects of different genes across various species. It also discusses QTLs (quantitative trait loci) and their contributions to disease resistance. The document provides a detailed list of species and their resistance traits, including gene numbers and specific resistance mechanisms.

For example, the text mentions the species **Arina**, associated with the gene **Qsr.sun-5BL**, and its contribution to disease resistance. The text also includes a section on QTLs, which are genetic markers associated with disease resistance traits. It states that three of several QTLs gave consistent effects across environments, with R² values indicating the percentage of phenotypic variance explained by the QTL. The text concludes with a discussion on the reaction to **Puccinia striiformis** Westend, noting that this fungus causes disease in several species, and the designated genes for resistance to stripe rust are listed.
S. spelta album, T. spelta album

v2: Avocet (U.K.) Yr1 Yr6[1459]; Brigand Yr14[083]; Cleo Yr3c[1457]; Cleo Yr3c Yr14[1431]; Fenman Yr1[1459]; Flamingo Yr6[1430]; Flevina Yr7[1430]; Galahad (heterogeneous) Yr1 Yr14[1459]; Garant Yr7[230]; Hardi Yr7[230]; Heines Kolben Yr6[611]; Heines Peko Yr6Yr25[746]; Heines VII Yr25[851]; Ibis Yr1[604]; Lely Yr7[1430]; Liberator Yr3c[1431]; Longbow Yr1 Yr6[083]; Mardler Yr1 Yr3a Yr4a Yr13[1459]; Maris Beacon Yr3b Yr4b[1459]; Maris Huntsman Yr3a Yr4a Yr13[604]; Maris Nimrod Yr13[1459]; Markman Yr1 (heterogeneous) Yr13[1459]; Mithras Yr1 Yr6[1459]; Nautica Yr9[1430]; Norman Yr6[083]; Rapier Yr4[083]; Rothwell Perdix Yr1[604]; Sonalika YrA[1352]; Stella Yr3[1430]; Sylvia Yr1[1430]; Tadorna Yr1[1431]; Viginta Yr3a Yr4a[073,071]; Wizard (heterogeneous) Yr14[1459]; Yamhill Yr3a Yr4a[181,182, see also, 184]; Zdar Yr4a[073].

Yr2 originally referred to a gene in Heines VII conferring resistance to European pathotypes. However, Heines VII possesses an additional resistance gene Yr2[1351] which can be detected with a geographically wider range of pathogen isolates. Yr2 is present in Kalyansona[1351] and a range of spring wheats distributed by CIMMYT.

Yr3. Undesignated allele. v: Enky[050]; Vilmorin 23; Staring[1430]. v2: Minister Yr2[1430]; Savannah Yr1 Yr2 Yr9 Yr32[10016]; Senat Yr32[10016]; Stella Yr2[1430].

Yr3a[851]. 1B[185,184].2B{10370}; i: Taichung 29*6/Vilmorin 23[10370]. v: Bon Fermier[1431]; nudif TP1[1431]; Stephens[182,184]. v2: Argent Yr1 Yr4a Yr6[1067]; Cappelle-Desprez Yr4a[851]; Druchamp Yr4a[185,182, see also, 184]; Hobbit Yr4a Yr14[604]; Kinsman Yr4a Yr6[604]; Mardler Yr1 Yr2 Yr4a Yr13[1459]; Maris Huntsman Yr2 Yr4a Yr13[604]; Maris Freeman Yr4a Yr6[604]; Maris Ranger Yr4a Yr6[604]; Nord Desprez Yr4a[182,184]; Top Yr4a[230]; Viginta Yr2 Yr4a; Yamhill Yr2 Yr4a[182]; Zdar Yr4a[073,071]. ma: Yr3(YrV23) - Xwmc356-2B, 9.4 cM[10370].

Yr3b[851]. Chen & Line[182] found that a second gene in Hybrid 46 - presumably this gene - was not located at the Yr3 locus v2: Hybrid 46 Yr4b[851].

Yr3c[851]. 1B[184]. v: Minister[851,182,184]. v2: Cleo Yr2[1430]; Maris Beacon Yr2 Yr4b[1459].

Yr4. Undesignated allele. [YrRub[10720]]. 3BS[10720]. bin: 3BS3 - 0.87 - 1.00[10720]. v: Avalon[10720]; Bolac; Emu S[10720]; Kenya Kubangu[050]; Rubric AUS33333[10720]. v2: Avalon Yr14[083]; Rapier Yr2 Yr14[083]. ma: Yr4 - 2.9 cM - Xcfr3530-3B - 2.4 cM - Xbarc75-3B[10720].

The conclusion that YrRub is Yr4 is based on specificity similarities and the presence of the Xcfr3530 and Xbarc75 alleles in the five genotypes listed above. The 3BS location is not consistent with that listed below for Yr4a and Yr4b.

Yr4a[851]. 6B[185,184]. v: Vilmorin 23[184]. v2: Argent Yr1 Yr3a Yr6[1067]; Cappelle-Desprez Yr3a[851]; Druchamp Yr3a[182]; Hobbit Yr3a Yr14[604]; Huntsman Yr2 Yr3a Yr13[604]; Kinsman Yr3a Yr6[604]; Maris Ranger Yr3a Yr6[604]; Maris Freeman Yr3a Yr6[604]; Mardler Yr1 Yr2 Yr3a Yr13[1459]; Nord Desprez Yr3a[182]; Top Yr3a[230]; Viginta Yr2 Yr3a[073,071]; Yamhill Yr2 Yr3a[182,185, see also, 184]; Zdar Yr3a[073,071].

Yr4b[851]. 6B[184]. v: Avalon[1160]; Opal[1431]; Staring[1430]. v2: Hybrid 46 Yr3b[851,182, see also, 184]; Maris Beacon Yr2 Yr3b[1160,1459]; nudif TP12 Yr3c[1431]; Stella Yr2[1430].

Yr5[877]. 2BL[034]. v: By 33[03102]; E5557[1267]; E8510[1267]; T. spelta album[877]; Seven spelt accessions from Europe and Iran[640]. ma: Yr5 - 10.5 & 13.3 cM - Xgwm501-2B[03102]; Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers Xwgp17-2B, Xwgp19-2B and Xwgp26-2B[10096]; Xwgp17-2B was later converted into a
simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker [10097]; Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310 [10435].

Yr6 [877]. 7B [1622]. 7B/46, 7BS [331]. v: Austerlitz [230]; Fielder [181]; Heines Kolben [1622]; Koga I [746]; Maris Dove [604]; Recital [230]; Takari [368]. v2: Argent Yr1 Yr3a Yr4a [1067]; Avocet (UK) Yr1 Yr2 [1459]; Flamingo Yr2 [1430]; Heines Peko Yr2 [746, 877]; Kinsman Yr3a Yr4a [604]; Kolben Yr2 [611]; Longbow Yr1 Yr2 [803, 1459]; Maris Freeman Yr3a Yr4a [604]; Maris Ranger Yr3a Yr4a [604]; Mithras Yr1 Yr2 [1459]; Norman Yr2 [803, 1459]; Nudif TP241 Yr7 [1431]; Nudif TP250 Yr7 [1431]; Orca Yr3c [1431]; Pavon 76 Yr7 [284]; Penjamo 62 (heterogeneous) Yr18 [1562]. tv: Duilio [192]; Latino [192]; Norba [192]; Quadrundo [192]; Rodeo (heterogeneous) [192].

Yr7 [877]. 2B [612, 1429]. 2BL [965]. i: Taichung 29*6/Lee [10371]. v: Present in many hexaploid wheats with Sr9g - see [965]; Brock [887]; Lee [877]; Nudif TP257 [1431]; PBW12 [1352]; Prinqual [230]; Renard [083]; Talent [230]; Tango [230]; Tommy [083]; WL2265 [1352]. v2: Donata Yr9 [1430]; Flevina Yr2 [1431]; Garant Yr2 [230]; Hardi Yr2 [230]; Lely Yr2 [1430]; Nudif TP241 Yr6 [1431]; Pakistan 81 = Veery#5 Yr9 [284]; Pavon 76 Yr6 [284]; Reichersberg 42 Yr25 [10010]; Thatcher [965]. tv: Iumillo [965]; but not present Acme and Kubanka which also carry Sr9g [965]. ma: Yr7 - Xgwm526-2B, 5.3 cM [10371].

Yr8 [1217, 1218]. Derived from Ae. comosa. 2D = T2D-2M [1218] = T2DS-2M#1L2M#1S [389]. tr: Chromosome 2D-2M translocations in Hobbit Sib and Maris Widgeon [1016]; Compair [1217, 1218]; CS 3D/2M 3/8 [967]; See also Sr34 and [967]. 2A = 2A-2M = T2AS-2M#1L2M#1S [389]. tr: CA 2A/2M 4/2 [967]. 2M-1. su: CS 2M#1(2A) [967].

Yr9 [878]. Derived from S. cereale. See also Reaction to P. graminis, Sr31: Reaction to P. triticina Lr26

1B=1BL.1RS. v: Almus [998]; Aurora [1623]. Chromosome status not specified. v: Baron [083]; Benno [998]; Bezostaya II [998]; Branka [071]; Clement [1430, 1532]; Cougar [0267]; Danubia [083]; GR876 [753]; Hammer [083]; Iris [068]; Kavkaz [1623]; Kromerzhizhskaya [1149]; Lyutestsens 15 [1149]; Lovrin 10 [998]; Lovrin 13 [998]; Mildress [1027]; Perseus [998]; Predgornaya [998]; Rawhide (heterogeneous) [0267]; Riebesel 47/51 [877, 1623]; Roxana [068]; Sabina [068]; Salmon [998]; Sarhad 82 [284]; Selektan [068]; Shtorm [1149]; Skorospelka 35 [998]; Sleipner [1038]; Solanis [068]; St 2153/63 [997]; Stuart [083]; Veery [986]; Weique [1627]; Winnetou [998]; Weihenstephan 1007/53 [1623]. v2: Agra Yr3 [968, 071]; Donata Yr7 [1430]; Haven Yr6 [10038]; Kauz and derivatives, Bakhtawar 94, WH452, Memof, Basribey 95, Seyhan 95 Yr18 Yr27 [10160]; Lynx Yr6 Yr17 [10038]; Nautica Yr2 [1430]; Pakistan 81 = Veery#5 Yr7 [284]; Savannah Yr1 Yr2 Yr3 Yr7 [10016]; Stetson Yr1 [083]; Sparta Yr3 [071]. tv: Cando’2/Veery, KS91WGRC14 [381].

1R(1B) [997, 1623]. su: Burgas 2 [998]; Clement [1160]; Lovrin 13 [998]; Mildress [998]; Mironovskaja 10 [998]; Neuzucht [1623]; Orlando [1623]; Roseana [068]; Saladin [997]; Salzmunder Bartweizen [1623]; St 14/44 [998]; Weique [1627]; Wentzel W [1623]; Winnetou [1027]; Zorba [998]; See also [050]. ma: Several markers tightly linked with Yr9 were identified in [0377]; Yr9 - 3.7 cM - Xgwm582-1BL [10365].

Stripe rust resistant wheat - S. africanum derivatives G17 (substitution line with 1R, 5.3 cM; 1B-1BL, 1RS and L2-20 (putative cryptic translocations) are reported in {10596}.

Yr10 [878]. Yr10av [0262]. 1B [641]. 1BS [1002]. v: Moro [878]; PI 178338 [878]; QLD709 = Janz’2/T. vavilovii [0262]; T. spelta 415 [641]; T. vavilovii AUS 22498 [0262]. ma: A SCAR marker was described in [0261]; QLD709 and T. spelta 415, both with white glumes, failed to amplify the SCAR sequence, but both carried unique alleles at the Gli-B1 and Xpsp3000-JB loci [0262]. These differed from the Moro source of Yr10. Yr10 - 1.5 cM -
Yr11. Adult plant resistance. [R11{1157}]. v: Joss Cambier{606}. v2: Heines VII Yr2 Yr25 see{970}.

Yr12. Adult plant resistance. [R12{1157}]. v: Fleurus{1158}; Frontier{1159}; Pride{1157}. v2: Armada Yr3a Yr4a{1160,081}; Mega Yr3a Yr4a{1157,1160}. v: Waggoner Yr3a Yr4a Yr6{1158}.

Yr13. Adult plant resistance. [R13{1157}]. v2: Bounty Yr1 Yr3a Yr4a{1459}; Brigand Yr2 Yr3a Yr4a Yr14{609}; Copain Yr3a Yr4a{1158}; Gawain Yr2 Yr3a Yr4a Yr14{081}; Guardian Yr2{082}; Hustler Yr1 Yr2 Yr3a Yr4a{083,1459}; Kinsman Yr3a Yr4a Yr6{1459}; Mardler Yr1 Yr2 Yr3a Yr4a{1459}; Maris Huntsman Yr2 Yr3a Yr4a{083,604,1459}; Maris Nimrod Yr2 Yr3a Yr4a{607,1157,1459}; Marksman Yr1{heterogeneous} Yr2 Yr3a Yr4a{1459}; Pageant Yr2 Yr3a Yr4a{082}; Professor Marchal Yr2 Yr3a Yr4a{607}; Sportsman Yr1 Yr3a Yr4a{1459}; Virtue Yr1 Yr3a Yr4a{083,1158,1459}.

Yr14. Adult plant resistance. [R14{1157}]. v: Kador{1158}; Score{1157}; Wembley{610}. v2: Avalon Yr3b Yr4b{083,1459}; Brigand Yr2 Yr3a Yr4a Yr13{083,609,1459}; Galahad Yr1 Yr2{heterogeneous} Yr3a Yr4a{083,1459}; Gawain Yr2 Yr3a Yr4a Yr13{081}; Hobbit Yr3a Yr4a{1459,1157}; Maris Bilbo Yr3a Yr4a{1157,1459}; Moulin Yr6{083}; Rapier Yr2 Yr3b Yr4b{083}; Wizard Yr2{heterogeneous} Yr3b Yr4b{083,1459}.

Yr15[432,969]. 1BS{939,969}. v: Agrestis{0330}; Boston{0330}; Cortez{0330}; Legron{0330}; Hexaploid derivatives of T. dicoccoides G-25[432,466]; V763-2312[969]; V763-254[969]. tv: T. dicoccoides G-25[432,431,466]; D447 derivatives B1, B2, B9, B10{1434}. ma: Xgwm33-1B - 5 cM - Yr15[9904]; Xgwm33-1B - 4.5 cM - Yr15 - 5.6 cM - UBC199200 - 5.6 cM - Nor-B1{0110}; Gene order Yr15 - Yr24 - Xgwm11-1B{10112}. ma, tv: OPB131420 - 27.1 cM - Yr15 - 11.0 cM - Nor-B1{1434}.

Yr16[1598]. Adult plant resistance. 2D[1598]. v: Bersee{1604}; Cappelle-Desprez{1598}.

Yr17[062]. 2AS{062}. 2AS-6M'.6M' = 2MS-6MS.6ML of 2MS-6ML.6MS{0009}. v: Apache{10554}; See Lr37 (Reaction to P. triticina) and Sr38 (Reaction to P. graminis); Arche{0044}; Balthazar{0044}; Bill{10554}; Brigadier{0044}; Caphorn{10554}; Clever{10554}; Clarus{10554}; Cordial{0044}; Coraise{10554}; Eureka{0044}; Hussar{0044}; Kris{10283}; Pernel{0044}; Rapsodia{10554}; Renan{0044,10554}; Rheia{10554}; RL 6081[939]; Genotype list in{02105}. v2: Lynx Yr6 Yr9{0044,10038}; Savannah Yr1 Yr2 Yr2 Yr32{10016}; ma: Yr17 was closely linked to the SCAR marker SC-Y15, developed from RAPD marker OP-Y15580, and to Xpsr150-2N'{0044}; Characterized by null alleles for Xwmc382-2A and Xwmc407-2A{10283}. The 2NS translocated segment carrying Yr17 replaced the distal half of chromosome 2A (25-38 cm) from Xcmwg682-2A to XksuH9-2A. PCR markers were developed for the 2NS and 2AS alleles of Xcmwg682 {10073}.

Yr18[1362]. 7D{1362}. 7DS{324}. i: Thatcher near-isogenic lines with Lr34 including the 13 2-gene combinations reported in{434,937}. v: Jupateco 73R; Lerma Rojo 64{1375}; Nacazari 76{1375}; Tesia F 79{1375}; Tonichi S 81{1375}; Wheaton{1375}. v2: Parula Yr29{10281}; Penjamo 62 Yr6{heterogeneous}{1375}; Saar Yr29{10481}; Wheats with Lr34 (See Lr34); Others{1376}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Bascriebey 95, Seyhan 95 Yr9 Yr27{10160}. ma: Complete linkage with Lr34{937,1362}; Ltn{1361}; and Bdv1{1363}; Xgwm120-7D - 0.9 cM - Yr18 - 0.7 cM - Xgwm295-7D{10259}. c: See Lr34.

This gene is identical to Lr34, Pm38 and Ltn and confers stem rust resistance in some genetic backgrounds.

Yr19[183]. [YrCom{183}]. 5B{183}. v2: Compair Yr8{183}.

Yr20[183]. [YrFie{181}]. 6D{183}. v2: Fielder Yr6{183}. 

Gli-B1 - 1.1 cM - Xpsp3000-1B{0261}; Yr10 - 1.2 cM - Xpsp3000-1B - 4.0 cM - Gli-B1{0321}; Cosegregation between a RGA marker RgaYr10a and Yr10 was reported in{0376}.
**Yr21**{183}.  [YrLem{181}].  1B{183,10450}.  **v**:  Lemhi{183}.

A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei* {10450}. Both genes were mapped relative to RGAP markers. Yr21 - YrRpsLem, 0.3 cM {10450}.

**Yr22**{183}.  [YrLeL{183}].  4D{183}.  **v2**:  Lee Yr7 Yr23{183}.

**Yr23**{183}.  [YrLe2{183}].  6D{183}.  **v2**:  Lee Yr7 Yr22{183}.

**Yr24**{952}.  [YrCH42].  1BS{952}.  **v**:  Chuanmai 42{10339}; Meering*3/K733/Ae. tauschii AUS18911{952}; Synthetic 769{10339}.  **tv**:  Decoy 1{10339}; K733{952}.  **ma**:  Gene order Yr15 - Yr24 - Xgwm11-1B{10112}; Xbarc187-1B - 2.3 cM - Yr24 - 1.6 cM - Xgwm498-1B{10339}.

Yr24 is identical to Yr26 {10339, 939}.

**Yr25**{158}.  1D{158}.  **v**:  Carina{0010}; Hugenout{0010}; Strubes Dickkopf{158, 10016}; TPI295{158}; TP981{158}; Tugela{0314}; Tugela-DN{0010,0314}.  **v2**:  Carstens V Yr32{10016}; Heines Peko Yr2 Yr26{0010}; Reichersberg 42 Yr7{0010}; Spaldings Prolific YrSP{10016}.

Yr25 was predicted to be present in Strubes Dickkopf, Heines VII Yr2, Heines Peko Yr2 Yr6, Reichersberg 42 Yr7 and Clement Yr9 {158}. This prediction was confirmed for Heines VII, Heines Peko and Reichersberg 42 {0010} but the pathogen culture used in {0010} was not virulent on Clement(Yr9) or on Strubes Dickkopf where another, or a different gene, must be present.

**Yr26**{617}.  1BS{0285}. The earlier location of 6AS {6AL.6VS}{617} is not correct..1BL{10544}.  **bin**:  C-1BL-6-0.32{10544}.  **v**:  Nannong 9918{10544}; Nei 2938{10544}; Nei 4221{10544}; Neimai 9{10544}; Lines R43, R55, R64 and R77{0285}.  **tv**:  *T. turgidum* Gamma 80-1.  **tr**:  Yangmai-5{617}.  **ma**:  Yr26 - 1.9 cM - Xgwm11-1B/Xgwm18-1B{0285}; Xgwm11/18-1B - 1.1 cM - Xwe171/202/10-1B - 0.4 cM - Xwe177/201-1B - 0.3 cM - Xwe173-1B - 1.4 cM - Yr26 - 6.7 cM - Xbarc181-1BL - 3.0 cM - Xwmc419-1BL{10544}.

According to {10554} the markers most closely associated with Yr26 are actually located in chromosome 1BL.

Yr26 is identical to Yr24 {10339,939}.

**Yr27**{928}.  [YrSk{928}].  2BS{928}.  **v**:  Ciano 79{928}; Inquilab 91{928}; Kauz{928}; McMurchy{928}; McMurachy{928}; Opata 85{928}; PWB343{928}; Selkirk{928}; Webster{928}.  **v2**:  Attila Yr27{928}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 Yr9 Yr18{10160}.  **ma**:  When analysed as a QTL, variation associated with the Yr27 locus was associated with RFLP markers Xcdo152-2B and Xcdo405-2B{928}.

Many CIMMYT wheat lines {953}. Recombination Yr31 - Yr27, 0.148, Yr31 - Lr23, 0.295 {0325}.

**Yr28**{1377}.  4DS{1377}.  **v**:  Synthetic = Altar 84/Ae. tauschii W-219. Synthetic/Opata 85 SSD population. Genotype lists:{1325,970}.  **dv**:  Ae. tauschii W-219{1377}.  **ma**:  Close association with Xwmg634-4DS{1377}.

Yr22 was also reported for chromosome 4D, but in the absence of an appropriate single gene stock and the unavailability of avirulent cultures in most laboratories, tests of linkage with Yr28 are unlikely in the foreseeable future.

**Yr29**{0119}.  Adult plant resistance {0119}.  **s**:  Lalbahadur(Parula 1B){10281}.  **v2**:  Attila Yr27{10281}; Parula Yr18{10281}; Pavon F76 Yr6 Yr7 Yr30{0119}; Saar Yr18{10481}; Yr29 is completely linked with Lr46. See Lr46{0119}.  **ma**:  Xwmc44-1B - 1.4 cM - Xbac24prot - 9.5 cM - Yr29 2.9 cM - Xbac17R ....Xgwm140-1B{10281}; Xgwm44-1B - 3.6 cM - Yr29 - 2.1 cM - Xtg818/Xbac17R....Xgwm140-1B{10281}; Associated with Ltn2 and Lr46.

**Yr30**{0120}.  Adult plant resistance {0120}.  **s**:  Lalbahadur(Parula 1B){10281}.  **v2**:  Attila Yr27{10281}; Parula Yr18{10281}; Pavon F76 Yr6 Yr7 Yr29{0120}; Yr30 is closely linked with Sr2 and Lr27{0120}.
**Yr31**(0325). 2BS.  **v:** Pastor(0325).  **ma:** Recombination values:  *Yr31* - *Yr27*, 0.148; *Yr31* - *Lr23*, 0.295; *Yr27* - *Lr23*, 0.131(0325).

**Yr32**(10016).  [YrCV(939), YrCV(1430)]. 2AL(10016).  **i:** Avocet S*/4/Carstens V{970}; Cook/6/Carstens V{970}; CRW380 = Carstens V/3*/Avocet S{10016}; Tres/6*/Avocet S{10016}.  **v:** Anouska[1430]; Caribo[1430]; Consort[10016,10023]; Cyrano[1430]; Danis[10023]; Deben[10023]; Hereward[10021,10022]; Okapi[1430]; Oxbow[10021]; Senat[10016]; Solist[10016]; Stakado[10016]; Tres[10016]; Vivant[10023]; Wasmo[10016].  **v2:** Carstens V *Yr25*(10016); Felix *Yr3*(1430); Krakatoa *Yr1*(10021,10038); Savannah *Yr1* *Yr2* *Yr3* *Yr4* *Yr17*(10016); Senat *Yr3*(10016); Zdar *Yr3a* *Yr4a*(067).  **ma:** Xwmc198-2A - 2 cM - *Yr32*(10016); *Yr32* was coincident with one AFLP marker(10016).

**Yr33**(10039). More readily detected in seedling tests at elevated temperatures [10336]. 7DL(10039).  **v:** Batavia(10039).  **m:** Linkage with Xgwm111-7D and Xgwm437-7D(10039).

**Yr34**(10040). This gene confers a weak seedling resistance (IT 2C to 3C) and a strong adult plant resistance (0 to 10R) [10040] to Australian pathotype 134E16A+, but is not effective against Australian pathotype 110E14 [10040]. **v:** AUS22857(10040); WAWHT2046=AUS91389(10040).  **ma:** Xgwm410.2-5A - 8.2 cM - BJ - 12.2 cM - *Yr34*(10040).

**Yr35**(10203).  [Yr58{10204}]. 6BS(10203).  **v:** 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS*[10204].  **tv:** *T. dicoccoides* 479[10204].

**Yr36**(10138,10272). Adult plant resistance 6BS(10138).  **i:** Yecora Rojo NIL PI 638740[10138].  **v:** Glupro[10138]; UC1041+Yr36[10649].  **itv:** UC1113 NIL PI 638741[10138].  **tv:** RSL#65[623,10138,10649].  **T. dicoccoides** FA-15[10138].  **ma:** *Yr36* is between Xucw74-6B and Xucw77-6B and 3-7 cM proximal to Nor- *B2*(10138); *Yr36* is closely linked to the high grain protein locus of *T. turgidum* var. *dicoccoides* FA-15[10138]; Nor-B2 ....Xucw68-6B - Xucw69-6B/Xbarc101-6B/Yr36 - Xucw66-6B[10272]; *Yr36* is 2-4 cM proximal to Gpc-BJ[10272].  **c:** ACF33182; *Yr36* is wheat kinase-START[10649]; WK51 is absent in almost all modern tetraploid and common wheats[10649].

**Yr37**(10139). Derived from *Ae. kotschyi*. 2DL(10139).  **v:** Line S14[10139].  **ad:** Line 8078[10139].  **al:** Ae. kotschyi 617[10139].

**Yr38**(10224).  [Yr52{10204}]. 6A(6AL-6L*,6S*)[10224].  **v:** Line 0352-4 = *Ae. sharonensis*-174/9*CS/3*W84-17/3*CS/4/W84-17[10224]; Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 are reported in [10691].  **al:** Ae. sharonensis-174[10224].

**Yr39**(10416). HTAP resistance 7BL[10416].  **v:** Alpowa[10416].  **ma:** Closely linked to several RGAP markers[10416].

**Yr40**(10328). Derived from *Ae. geniculata* 5DS(5DL,5DS-T5MS*)[10328].  **v:** TA 5602[10328]; TA 5603[10328].  **al:** *Ae. geniculata* (=ovata) (U*U*M*MM*) TA10437[10328].  **ma:** Completely linked with distinctive alleles of Gsp, Xfbb276 and Xbcd873[10328]; Completely linked with *Lr57*[10328].

**Yr41**(10502).  [YrCN19(10228)]. 2BS[10228,10502].  **v:** AIM[10228]; AIM6[10228]; Chuanong 19[10228,10502].  **ma:** Complete linkage to a 391 bp allele of Xgwm410-2BS[10228]; Xgwm410-2B - 0.3 cM - *Yr41*(10502).

**Yr42**(10537). Derived from *Ae. neglecta* 6A = 6AL-6L*,6S*{10537}.  **v:** Line 03M119-7A{10537}.  **al:** *Ae. neglecta* 155[10537].

**Yr43**(10673). 2BL[10673].  **v:** ID0377s=PI 591045[10673]; Lolo[10673]; many ID0377s derivatives[10673].  **ma:** Xwms501-2B - 11.6 cM - Xwgp110-2B - 4.4 cM - *Yr43* - 5.5 cM - Xwgp103-2B - 12.8 cM - Xbarc139-2B[10673].

**Yr44**(10673).  [YrZak(10674)]. 2BL[10674].  **v:** Zak=PI 607839[10674].  **ma:** XSTS7/8/Yr5 - 12.7 cM - Yr44 - 3.9 cM - Xwgp100 - 1.1 cM - Xgwm501-2B[10674].
**Pathogenic Disease/Pest Reaction**

**Yr45** \[10677\]. 3DL \[10677\]. *v*: PI 181434 \[10677\]. *ma*: *Xbarc6-3D* - 0.9 cM - *Xwmc656-3D* - 6.9 cM - *Xwp118-3D* - 4.8 cM - *Yr45* - 5.8 cM - *Xwp115-3D* \[10677\].

This gene is highly effective and confers resistance to all North American *Pst* pathotypes.

**Yr46** \[10677\]. Adult plant resistance. 4D \[10677\]. *i*: RL6077=Thatcher*6/PI 250413 \[10677\]. *v*: PI 250413 \[10677\]. *ma*: Close linkage with Xcfd71-4D and Xbarc98-4D estimated at 4.4 cM, and Xcfd23-4D at 5.2 cM (all on the same side of Yr46) \[10677\].

**Yr47** \[10679\]. 5BS. *bin*: 5BS - 0.71 - 0.81. *v*: AUS28183 = V336 \[10679\]. *ma*: 5 +/- 2 cM proximal to Lr52 \[10679\].

This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of *Pst*. V336 is the original source of Lr52.

**Yr48** \[10705\]. Adult plant resistance. 5AL. *bin*: 5AL23. *v*: UC1110 (S)/PI 610750 RIL 167 (R) \[10705\]. *ma*: Co-segregated with Vrn2, Be495011, Xcfa2149-5AL, Xgpw2181a-5AL, Xwmc74-5AL, and Xwmc410-5AL \[10705\]; Xwmc727-5AL - 4.4 cM - Yr48 - 0.3 cM - Xwms291-5AL \[10705\].

PI 610750=Synthetic 205 (Crop 1 / *Ae. tauschii*) \[10705\].

Sources of additional genes for seedling (designated "12") and adult resistances ("13", "14", "15") are listed in \[1430\].

Genotype list: Chinese common wheats \{10369\}. European wheats \{10579\}. U.K. wheats \{10697\}. 96.2. Temporarily designated genes for resistance to stripe rust

North American workers \{181,186,184\} allocated a number of temporary designations to uncatalogued genes detected with North American *P. striiformis* accessions. Druchamp, Yamhill and Stephens were reported to carry 'Yr3a or Yr4a" because these genes could not be distinguished with the cultures that were used.

**YrA**. Refers to a phenotype specificity that appears to be controlled by complementary genes \{1563\}. *v*: Avocet \* (= heterogeneous); Anza = Karamu = Mexicani = T4 = WW1 = WW15; Banks; Condor*; Cocamba; Egret*; Inia 66; Lerma Rojo 64; Lerma Rojo 64A; Nainari 60; Nuri 70; Sanda 73; Sonalika; Zaminder 80. *v2*: Condor selection P44 Yr6*; Pari 73 Yr6; Saric 70 Yr6; Yecora 70 Yr6 \[1563\].

**YrAlp** \[10416\]. 1BS \[10416\]. *v2*: Alpowa Yr39 \[10416\]. *ma*: YrAlp - 15.2 cM - Xgwm18-1B - 1.1 cM - Xgwm11-1B \[10416\]; and more closely linked to RGAP markers \[10416\].

**YrC142** \[10667\]. 1BS. *v*: Synthetic CI142=Gaza/Boy\//*Ae. tauschii* 271 \[10667\].

*ma*: Located in the Yr24/Yr26 region close to Xbarc187-1B and Xgwm273-1B \[10667\].

Although postulated to be unique this gene is likely Yr24/Yr26.

**YrC591** \[10606\]. 7BL \[10606\]. *v*: C591 \[10606\]; Zhongzhi 1 \[10606\]. *ma*: Xcfa20-40-7B - 8.0 cM - YrC591 - 11.7 cM - SCP35M48 \[10606\].

**YrCle** \[186\]. 4B \[186\]. *v2*: Clement Yr9 \[186\].

**YrCK** \[10220\]. Temperature sensitive \{10219\}. 2DS \{10220\}. *v*: Cook Yr34 \[10219\]; Sunco Yr34 \[10220\].

**YrCN17** \[10562,10686\]. Derived from *S. cereale* 1B, 1BL, 1RS \[10562,10686\]. *v*: Chuannong 17 \[10686\]; CN12 \[10562\]; CN17 \[10562\]; CN18 \[10562\]. *dv*: *S. cereale* R14 \[10562\]. *al*: *S. cereale* L155 \[10562\].

**YrD** \[185\]. 6A \[185\]. *v*: Druchamp \[185,185\].

**YrDa1** \[186\]. 1A \[186\]. *v2*: Daws YrDa2 \[186\].

**YrDa2** \[186\]. 5D \[186\]. *v2*: Daws YrDa1 \[186\].

**YrDru** \[184,185\]. 5B \[184\]. 6B \[185\]. *v*: Druchamp \[184,185\].

**YrDru2** \[184\]. 6A \[184\]. *v*: Druchamp \[184\].
**YrExp1** \{10601\}. 1BL\{10601\}. **v2**: Express YrExp2\{10601\}. ma: Xwgp78-1B - 4.2 cM - YrExp1 - 3.4 cM - Xwmc631-1B\{10601\}.

**YrExp2** \{10601\}. 5BL\{10601\}. **v2**: Express YrExp1\{10601\}. ma: Xgwm639-5B - 9.2 cM - Xwgp81-5B - 1 cM - YrExp2 - 0.7 cM - Xwgp82-5B\{10601\}.

Based on the presence of the nearest flanking markers YrExp2 was postulated in Expresso, Blanca Grande, Buck Pronto and Jeff/Pronto \{10601\}.

**YrH46** \{184\}. 6A\{184\}. **v2**: Hybrid 46 Yr4b\{184\}.

Not the same gene as YrDru2 \{184\}.

**YrH52** \{10003\}. 1BS\{10003\}. tv: T. dicocoides H52\{10003\}. ma: distal ...Yr15 - 9.6 cM - YrH52 - 1.4 cM - Nor-B1 - 0.8 cM - Xgwm264a - 0.6 cM - Xgwm18\{10003\}; Xgwm273a - 2.7 cM - YrH52 - 1.3 cM - Xgwm413/Nor1...centromere\{0108\}.

**YrHVII** \{186\}. 4A\{186\}. **v2**: Heines VII Yr2 Yr25\{186\}.

**YrMin**. 4A\{184\}. **v**: Minister\{184\}.

**YrMor** \{186\}. 4B\{186\}. **v2**: Moro Yr10\{186\}. ma: The development of an STS marker, derived from an AFLP fragment, that co-segregates with YrMor was reported in \{0357\}.

**YrND**. 4A\{184\}. **v2**: Nord Desprez Yr3a Yr4a\{184\}.

May be the same as YrMin \{184\}.

**YrP81** \{10696\}. 2BS\{10696\}. **v**: P81\{10696\}; Xu29\{10696\}. ma: Xgwm429-2B - 1.8 cM - YrP81 - 4.1 cM - Xwmc770-2B\{10696\}.

**YrR212** \{10562\}. Derived from S. cereale 1B, 1BL1RS\{10562\}. **v**: R185\{10562\}; R205\{10562\}; R212\{10562\}. al: S. cereale R212\{10562\}.

**YrS** \{185\}. 3B\{185\}. **v**: Stephens\{185\}.

**YrS2199** \{10618\}. 2BL\{10618\}. **bn**: 2BL0.89-1.00\{10618\}. **v**: S2199\{10618\}. ma: Xgwm120-2B - 11.0 cM - YrS2199 - 0.7 cM - Xdp269-2B\{10618\}.

**YrSte** \{184\}. 2B\{184\}. **v**: Stephens\{184\}.

**YrSte2**. Stephens \{184\} 3B\{184\}.

**YrSP** \{10018\}. 2BS\{10018\}. **i**: Cx1=Avocet S*4/Spaldings Prolific\{10018\}. **v2**: Spaldings Prolific Yr25\{10018\}.

**YrS5** \{10352\}. [YrSp\{10353\}]. 2B\{10353,10352\}.probably 2BL. **i**: Avocet*3/Spaldings Prolific\{10353\}; Taichung*6/Spaldings Prolific\{10352\}. **v**: Spaldings Prolific\{10353,10352\}. ma: YrSp - Xwmc-2B, 12.1 cM\{10352\}.

**YrTye** \{186\}. 6D\{186\}. **v**: Tyee\{186\}.

**YrTrl** \{186\}. 6D\{186\}. **v2**: Tres YrTr2\{186\}.

**YrTr2** \{186\}. 3A\{186\}. **v2**: Tres YrTr2\{186\}.

**YrYam** \{184,185\}. 4B\{185\}. **v2**: Yamhill Yr2 Yr3a Yr4a\{185\}.

**YrZH84** \{10331\}. 7BL\{10331\}. **v**: Anong 7959\{10331\}; Zhoumai 11\{10331\}; Zhoumai 12\{10331\}. **v2**: Zhou 8425B Yr9\{10331\}. ma: Xwmc276-7B - 0.6 cM - Xcfa2040-7B - YrZH84 - 4.8 cM - Xbarc32-7B\{10331\}.

**YrV23** \{10370\}. Presumed to be Yr3a 2B\{184\}. **v**: Vilmorin 23\{10370\}; Vilmorin\{184\}. Allelic but not the same as YrSte \{184\}.

**Yrms-B1** \{10033\}. 3BS\{10033\}. **v**: Lgst.79-74\{0033\}. ma: Xgwm493 (distal) - 21 cM - Yrms-B1\{10033\}. As a QTL, Yrms-B1 was located in a 3 cM interval between Xgwm493-3B and Xgwm1329-3B\{10383\}.

### 96.3. Stripe rust QTLs

Two QTLs in Camp Remy/Michigan Amber were located on chromosome 2BL \{QYR1, LOD score 12\} and 2AL \{QYR2, LOD 2.2\} \{0287\}. Four QTLs were scored in the ITMI population. The most effective \{QYR3, LOD 7.4\} on chromosome 2BS was probably Yr27, the others were located in 7DS \{QYR4, LOD 3.4\}, 5A \{QYR5, LOD 2.8\}, 3D \{QYR6, LOD
Camp Remy/Recital: 217 RILs. Six QTLs for APR were detected over 4 years. *Qyr.inra-2BL* (R²=0.42-0.61) corresponded largely to seedling resistance gene *Rsp* and possibly *Yr7*. The other genes were *Qyr.inra-2AL*, *Qyr.inra-2BL*, *Qyr.inra-2DS* (perhaps *Yr16*), *Qyr.inra-5BL.1* and *Qyr.inra-5BL.2* [10279].

Seven QTLs were identified for stripe rust severity in a joint analysis of five datasets from a Fukuhokomugi/Oligoculm doubled haploid population [10060]. Their location, associated marker, percentage variation explained, and genotype contributing to enhanced resistance at that locus, are listed below.

3BS; Xgwm389-3B; 0.2-4.9%; Oligoculm [10060].
4BL; Xgwm538-4B; 1.8-12.3%; Oligoculm [10060].
4DL; Xwmc399-4D; 2.5-8.0%; Oligoculm [10060].
5BL; Xwmc415-5B; 2.4-16.1%; Oligoculm [10060].
6BS(cenromeric); Xgwm935-6B; 0.5-3.8%; Oligoculm [10060].
7BS; Xgwm935-7B; 1-5.2%; Oligoculm [10060].
7DS; Xgwm295-7D; 10.7-23.7%; Fukuhō [10060]; the 7DS QTL was probably *Yr18* [10060].

Four QTLs were identified for stripe rust infection in a joint analysis of three datasets from a Fukuhokomugi/Oligoculm doubled haploid population [10060]. Their location, associated marker, percentage variation explained and parent contributing to enhanced resistance at that locus are listed below.

2DL; Xgwm349-2D; 6.5-9.6%; Fukuhō [10060].
3BS; Xgwm389-3B; 15.1-24.5%; Oligoculm [10060]. The 3BS QTL may be *Yr30* [10060].
5BL; Xwmc415-5B; 6.4-12.7%; Oligoculm [10060].
7BL; Xwmc166-7B; 2.5-9%; Oligoculm [10060].

Otane (R)/Tiritea (S) DH population: QTL in 7DS (probably *Yr18*), 5DL (from Otane) and 7BL (Tiritea) [10150]. Interval mapping of 7DS indicated that the presumed *Yr18* was 7 cM from Xgwm44-7D [10150].

Kariega/Avocet S DH population: Two QTLs *QYrs.gsi-7D* (probably *Yr18*) and *QYrs.gsi.2B.1* accounted for 29 and 30%, respectively, of the phenotypic variation for stripe rust response. The nearest marker to the latter was Xgwm148-2B [10184].

Four QTLs were detected in a multiple cross analysis [10283]: Chromosome 2AL (probably *Yr32* in Deben, Kris and Soloist), 2AS (probably *Yr17* in Kris), 2BL (Xwmc149-2B - Xwmc317a-2B in Deben) and 6BL (Xwmc397-6B - Xwmc105b-6B in Soloist and Kris).

Avocet S/Pavon 76: QTL identified in 1BL (Xgwm259), 3BS (PstAATMseCAC2), 4BL (Xgwm495), 6AL (Xgwm617), 6BL (PstAAGGMseCGA1) [10443].

*T. monococcum* PAU14087 (resistant)/*T. boeoticum* PAU5088 (resistant): RIL population: One adult plant resistance QTL identified in each parent and named *QYrmt.pau-2A* (in a 3.6 cM interval between Xwmc407-2A and Xwmc170-2A; R² = 0.14) and *QYrth.pau-5A* (in a 8.9 cM interval between Xbarc151-5A and Xcfdl2-5A; R² = 0.24) [10518].

Luke (R)/Aquileja (R): Two QTLs for high-temperature adult plan resistance, *QYRLu.cau-
2BS.1 (distal, flanked by Xwmc154-2B and Xgwm148-2B, $R^2 = 0.366$) and QYrl.cau-2BS.2 (proximal, flanked by Xgwm148-2B and Xbarc167-2B, $R^2 = 0.415$) from Luke, and QYrag.cau-2BL (flanked by Xwmc175-2B and Xwmc332-2B, $R^2 = 0.615$) in Aquileja for stripe number {10582}.

Acocet S / Attila: QTLs were located on chromosomes 2BS (probably Yr27), 2BL (a race-specific effect) and 7BL (XP32/M59 - Xgwm344-7B {10586}).

Guardian / Avocet S: F3 lines. One major QTL, QPst.jic-1BL (Xgwm818-1 - Xgwm259-1B, $R^2$ up to 0.45), and two minor resistance QTLs on chromosomes 2D and 4B originating from Guardian {10589}. The major QTL was in the region of Yr29.

Stephens / Michigan Amber: Two QTLs for high temperature APR were located in chromosome 6BS: QYrst.wgp-6BS.1 located in a 3.9 cM region flanked by Xbarc101-6B and Xbarc136-6B and QYrst.wgp-6BS.2 located in a 17.5 cM region flanked by Xgwm132-6B and Xgdm113-6B {10602}.

Pingyuan 50 (R) / Mingxian 169 (S): DH population: APR: QYrcaas-2BS (Xbarc13-2BS) - Xbarc230-2BS, $R^2$=0.05-0.09, QYr.caas-5AL(Xwmc410-5AL - Xbarc261-5AL, $R^2$=0.05-0.2), QYrcaas-6BS(Xgwm361-6BS - Xbarc136-6BS, $R^2$=0.05-0.08) {10693}.

Renan (R) / Recital (S) RIL population: Tested for AUDPC in 1995/6 and 2005/6 with pathogen isolates avirulent and virulent, respectively, for Yr17:Yr.inra-2AS.2, (=Yr17), $R^2$=0.45, 1995/6; Yr.inra-2AS.1, $R^2$=0.9, 2005/6; Yr.inra-2BS, $R^2$=0.11 & 0.13, Yr.inra-3Bcent, $R^2$=0.06 in 2005/6; Yr.inra-6B, $R^2$=0.04 & 0.06; from Renan; and Yr.inra-2AS.1, $R^2$=0.09; Yr.inra-3DS, $R^2$=0.08 & 0.12 from Recital. Other QTLs were effective only at certain growth stages {10689}.

Express / Avocet S: RIL population: Relative AUDPC for high temperature APR was controlled by QYrex.wgp-6AS, $R^2$=0.326, interval Xgwm334-6A - Xgwp56-6A; QYrex.wgp-3BS, $R^2$=0.274, interval Xgwm299-3B - Xwgp66-3B, QYrex.wgp.1BL, $R^2$=0.094, interval Xwmc631-1B - Xwgp78-1B {10672}. When rust phenotyping was based on infection type only the 6S and 3B L QTLs were evident {10672}.

97. Reaction to *Puccinia triticina*

Disease: Brown rust, leaf rust.

97.1. Genes for resistance

_Lr1_ {1047}. 1B{1409}.5D{954}.5DL{945}. i: Centenario/6 5Thatcher{317}; Malakoff/6 Prelude{317}; Wichita 4/Malakoff{613}. v: Line 87E03-S2B1{10561}; Centenario{317}; Chicora 'S'{143}; Daws (heterogeneous){1019}; Dirkinw{1019}; Glenlea{1255,976}; Halle 9H37{074}; Hyslop{1019}; Luke {heterogeneous}{1019}; Malakoff{047}; McDermid{1019}; Mexico 120{933}; Newton{143,1024,1023}; Norco{1019}; Shabat Sonora{842}; Sonora 64{842}; Tarsa{842}; Uruguay{954}; Walliday{1019}. v2: Blueboy *Lr*10{143}; Blueboy II *Lr*10 *Lr*24{143}; Erythruspermum 142 and 953 *Lr*3{074}; Laura *Lr*10 *Lr*34{712}; Norka *Lr*20{1552}; Plainsman V *Lr*3{1024}; Suneca *Lr*13{485}. dv: Several _Ae. tauschii_ accessions{10191}. ma: Co-seg. with _Xpsr567-5D_ and _Xglk621-5D_ in a Frisal/Lr1 resistant line. pTAG621 was converted to a diagnostic STS{354}. Terminally located{10189}; In _Ae. tauschii_ recombination in the region was 5-10X that in common wheat, gene order _Xpsr567-5D - Lr1 - Xabc718-
5D{10191}; Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat{10408}; A candidate gene for *Lr1, Lr1RGA1*, encoding a CC-NBS-LRR protein, cosegregated with *Lr1*{10408}; Co-segregation with RGA567-5{10561}. *c* *Lr1* is a member of a multigene family (PSR567), has a CC-NBS-LRR structure, and produces a protein of 1,344 aa, EF567063{10561}.

**Lr2.** 1B{1409}.2DS{843,942}.

**Lr2a**{320}. [Lr2{047}].  
- Prelude*6/Webster{320}; Red Bobs*6/Webster{320}; Webster/6'Thatcher{306}; Wichita 4/Webster{613}.  
- Eureka CI 17738{143}; Festiguay{843}; Webster{047}.  
- 1: Alex *Lr10*{976}; Ck 9385 *Lr9*{10146}; Ck 9663 *Lr2 Lr10*{10146}; Guard *Lr10*{976}; James *Lr10*{976}; Len *Lr10*{976}; Marshall *Lr10*{976}; Mediterranean W1728 *Lr3*{1369}; Shield *Lr3 Lr10*{198}; Waldron *Lr10*{143}.

**Lr2b**{320}.  
- Brevit{320}; Loros{320}; Wichita/4{613}.  
- All three Thatcher NILs with named alleles carried the STS marker {10469}. Resistance in Storlom cosegregated with an STS derivative of *Xmgw798-6B*. All three Thatcher NILs named *Lr3* alleles carried the STS marker {10469}.

**Lr3**{047}. Because *Lr3* appears to be a complex locus {486} Democrat and Democrat/6b *Thatcher should be accepted as standards. There is evidence to suggest that the allele in Mentana, and therefore many derivatives, is *Lr3b* {939}. If this is correct, many genotypes listed under *Lr3a* are likely to be *Lr3b*.

Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmgw798-6B*. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

**Lr3a**{10028}. [Lr3{047}]. 6B{549}.6BL{939}.  
- Wichita 4/Mediterranean{613}.  
- Belocerkovskaja 289{074}; Bennett{1024}; Democrat{047}; Fertodi 293{074}; Gage{1024}; Hana{068}; Homestead{1024}; Ilyitchovka{075}; Juna{075}; Jubilejne{068}; Kawvale{143}; Lancota{1024}; Mara{068}; Mediterranean{047}; Mediterranean W3732{1369}; Mentana{842}; Mironovskaya 264 & 808{074}; Odra{075}; Osetinskaya{074}; Ottawa{143}; Pawnee{1408}; Ponca{143}; Rannaja 12{074}; Shawnee{143}; Shirahada{842}; Skorospelka 3b{074}; Sledkovicova K1004{074}; Viginta{068}; Warrior{143,1024}; Yubileynaya{075}.  
- Amika *Lr26*{076}; Bezostaya 1 *Lr34*{074}; Bowie *Lr14b*{319}; Erythromercurium 142 & 953 *Lr1*{074}; Istra *Lr26*{076}; Mediterranean W1728 *Lr2a*{1369}; Plainsman V *Lr1*{1024}; Shield *Lr2a Lr10*{198}; Solaris *Lr26*{076}; See also{069}.  
- *Thatcher* 6/Bage; RL6094 = Tc 6/T6{307}.  
- Bage{486}.  
- Storlom{10469}.  
- *Ma*: Co-segregation with *Xmgw798-6B*{9921,10469}; cDNA marker TaR16 was completely linked to *Lr3* in a population of 109 gametes{10058}; *UBC840*{549} - *Lr3a*, 6 cM{10263}.

**Lr3b**{486,10028}. [Lr3b{486}].  
- Tc 6/Bage; RL6094 = Tc 6/T6{307}.  
- Bage{486}.  
- T6 *Lr16*{307}.

**Lr3c**{486,10028}. [Lr3c{486}].  
- Tc 6/Klein Aniversario.  
- Blava{10345}; Klein Aniversario{486}.

**Lr4, Lr5, Lr6, Lr7, Lr8**{365}.  
- Purdue Selection 3369-61-1-10 = Waban{365}; Not available as separate single-gene lines.

**Lr9**{1408}. Derived from *Ae. umbellulata*. 6B{954,1296,1299}.6BL = T6BS.6BL-6U4L1{389}.  
- T47 = Transfer = CS + *Lr9*{1408}; Thatcher 6/Transfer; Wichita*4/Transfer{613}; Lines listed in{10244}.  
- Abe{143}; Arthur 71{1320,1024}; Clemson 201{465}; McNair 701 & 2203{143}; PI 468940{1439}; Riley 67{1320,1024}; Sullivan{1110}; Transfer{1296}.  
- Ck 9835 *Lr2a*{10146}; Ck 9663 *Lr2a Lr10*{10146}.
Lockett *Lr24*{1046}; Oasis *Lr11*{1109}. **ma:** Co-seg with *XksuD27-6B*{048}; co-seg with *Xmgw684-6B* and STS *Xsfr1*{1272}; *Lr9* - 8 cM - *Xpsr546-6B*{1272}; SCAR markers were developed in {10244}. The structures of additional translocations are given in {389}.

**Lr10**{199}. *LrL*{031}. 1A{312,546}.1AS{939}. **i:** Exchange/6 *Thatcher*{306}; Gabo/6 *Thatcher*{306}; Lee/6 *Thatcher*{306}; Selkirk/6 *Thatcher*{306}; Timstein/6 *Thatcher*{306}. **s:** CS*5/Timstein 1A{939}; CS/7 Kenya Farmer 1A{939}. **v:** Centurk{1024}; Centurk 78{1024}; Concho{143}; Federation{939}; Mayo 52{031}; Mayo 54{031}; Parker{546,1024}; Rocky{1024}; Scout 66{02101}; Sinton{1256}; Tascosa{143}; TAM-105{055}; Unknown accessions{208}; See also {0337}. **v2:** Alex *Lr2a*{976}; Blueboy *Lr1*{143}; Blueboy II *Lr1 Lr24*{143}; Ck 9663 *Lr2a Lr9*{10146}; Era *Lr13*{143}; Exchange *Lr12 Lr16*{031}; Gabo *Lr23*{031}; Guard *Lr2a*{976}; James *Lr2a*{976}; Kenya Farmer *Lr23*{939}; Laura *Lr1 Lr34*{712}; Lee *Lr23*{031}; Len *Lr2a*{976}; Marshall *Lr2a*{976}; Parker 76 *Lr24*{143}; Selkirk *Lr14a Lr16*{031,199}; Shield *Lr2a Lr3*{198}; Timstein *Lr23*{031}; Waldron *Lr2a*{143}; Warden *Lr16*{031}. **ma:** Xedo426-1A - 5.1 cM - *Lr10*{1058}; *Lr10* - 8 cM - Glu-A3{355}; cosegregation with *Xsfr1(Lrk10-1A)* and *Xsfr1(Lrk10-1A)*{1270}; complete linkage with *Xsfr1(Lrk10-1A)*, which encodes a protein kinase{639}; *Lr10* was cloned - it has a CC-NBS-LRR structure, syn, *Tl10rgal* GenBank AY270157{10442}. **c:** *Lr10* (*Tl10rgal*, GenBank AY270157) encodes a CC-NBS-LRR protein of 919 aa{10033}.

**Lrk10.** A receptor-like kinase. The locus *Xsfr1(Lrk10)-1A*, detected by the probe Lrk10, is completely linked with *Lr10* in chromosome 1AS {356}. The gene encodes a receptor-like kinase with extracellular and kinase domains {0297}. Using probe pLrk10-A, developed from the extracellular domain, 6 homologues were found in chromosomes 1A (1), 1B (3) and 1D (2) as well as group 1 chromosomes of *T. monococcum*, *Ae. tauschii* and barley {0296,0294}. Probes based on the kinase domain identified further homologues in chromosomes 3AS and 3BS as well as the corresponding regions in rice and maize {0294}. Both orthologous and paralogous evolution were suggested.

**Lr11**{1409}. 2A{1409}. **i:** Thatcher 6/Hussar{306}; Wichita 4/Hussar{613}. **v:** Bulgaria 88{142}; Hart{1024}; Hazen{049}; Hussar{1409}; Pioneer 2850{0523}; Pocahontas{1046}; Saluda{10146,10699}. **v2:** Ck9803 *Lr18*{10595}; FFR 524 *Lr18*{10595}; Karl 92 *Lr3 Lr10*{02101}; Oasis *Lr9*{143}; Pioneer 2684 *Lr18*{10595}; SS520 *Lr18*{10595}.

**Lr12**{326}. Adult plant reaction. 4B{312}. **i:** Exchange/6 *Thatcher*{306}. **v:** Opal{306}. **v2:** AC Domain *Lr10 Lr34*{0228}; Chinese Spring *Lr34*{301}; Exchange *Lr10 Lr16*{326}; Sturdy *Lr13*{301}; Unknown accessions{208}.

**Lr13**{326}. Although originally described as a gene for adult plant reaction {032,326}, *Lr13* can be detected at the seedling stage especially at high temperatures {939,1156}. **BS**{939}. **i:** TC*7/Frontana = RL4031{306}; fifteen Thatcher lines with 2-gene combinations{711}. **v:** This gene is very widespread{939}; Hereward{0288}; Hustler{608}; Kinsman{608}; Kenya Plume{1370}; Manitou{326}; Mardler{608}; Maris Huntsman{608}; Moulin{0288}; Napayo{070}; Neepawa{143}; Norman{608}; Pastiche{0288}; Polk{143}; Virtue{608}. **v2:** AC Barrie *Lr6*{10178}; Beaver *Lr26*{1032}; BH1146 *Lr34*{0268}; Biggar *Lr14a*{712}; Chris *Lr34*; Columbus *Lr16*{1258}; Cumpas 88 *Lr26*{1373}; Era *Lr10*{143}; Frontana *Lr34*{032,326,1374}; Genesis *Lr14a*{712}; Hartog *Lr1 Lr46*{127}; Hobbit *Lr17a*{608}; Hobbit Sib *Lr17a*{1350}; Inia 66 *Lr14a Lr17*{1373}; Klein Aniversario *Lr3ka*{032}; Kenyon *Lr16*{300}; Lerma Rojo 64 *Lr17a Lr34*{1373}; Oasis 86 *Lr19*{1373}; Parula *Lr34 Lr46*{1374}; Suneca *Lr1*{485}; Yecora *Lr1*{1374}. **ma:** *Xpsr912-2B* - 9.1 cM - *Lr13* - 7.9 cM - *Xbcd1709-2B* - 9.8 cM - Cent.{0088}; *Lr13* - 10.7 and 10.3 cM - *Xgwm630-2BS*{10463}; *Xbarc163-2B* - 5.1 cM - *Lr13* - 8.7 cM - *Xstm773b-2B*{0329}.

**Lr14.**
**Pathogenic Disease/Pest Reaction**

**Lr14a**{[319,964]}. \([LrLu{[10520]}]\). 7B{[964]}7BL{[770]}. \(i:\) Selirk/6'Thatcher{[319]}. \(s:\) CS*6/Hope 7B{[964]}. \(v:\) Aotea{[964]}; Brigand{[608]}; Gala{[964]}; Glenwari{[964]}; Hofed{[964]}; Hope{[964]}; H-44{[964]}; Lawrence{[964]}; Redman{[964]}; Regent{[964]}; Renown{[964]}; Spica{[964]}. \(v2:\) Biggar Lr3{[712]}; Brambling Lr23 Lr34{[10563]}; Genesis Lr13{[712]}; Inia 66 Lr13 Lr17a[939]; Selkirk Lr10 Lr16[319]. \(tv:\) Lloreta INIA{[10520]}; Somateria{[10520]}. \(ma:\) Xwmc273-7B - 13 cM - Lr14a - 10 cM - Xgwm344-7B{[10520]}.

**Lr14b**{[319]}. \(i:\) Maria Escobar/6'Thatcher{[319]}. \(v:\) Weebill 1{[10571]}. \(v2:\) Bowie Lr3{[9226]}; Maria Escobar Lr17{[319]}; Rafaela Lr17{[314]}.

**Lr14ab**{[843]}. 2DS{[843,942]}. \(i:\) Lr14a/6'Thatcher/Lr14b/6'Thatcher Seln{[319]}.

**Lr15**{[843]}. 2DS{[843,942]}. \(i:\) Thatcher*6'Kenya W1483{[306]}.. \(v:\) Kenya W1483{[843]}.

Probably allelic with Lr2.

**Lr16**{[318]}. The following chromosome locations are consistent with the finding that the first location was based on the use of a Rescue monosomic series. Rescue differs from CS by a 2B-4B translocation {939}. Lr16 is always associated with Sr23. \([LrE{[031]}]\). 4B{[312]}2BS{[939,10170]}. \(i:\) Exchange/6'Thatcher{[306]}; RL6096 = Tc*6'T6{[307]}.

AC Domain{[10170]}; AC Foremost{[10170]}; Arapahoe{[20101]}; Brule{[20101]}; Ciano 79{[1373]}; Etoile de Choisy{[074]}; Imuris 79{[1373]}; McKenzie{[10170]}; Millenium{[02101]}; Papago 86{[1373]}; Redland{[02101]}; Vista{[02101]}.

\(v2:\) AC Barrie Lr3{[10178]}; Columbus (heterogeneous) Lr13{[1258]}; Exchange Lr10 Lr12{[031]}; Kenyon Lr13{[300]}; Selkirk Lr10 Lr14a{[031]}; T6 Lr3b{[307]}; Warden Lr10{[031]}.

**Lr17**{[318]}. \(Lr17a\{[318],[1350]\}. \([LrL\beta{[10520]}]\). 2A{[314]}2AS{[062]}.

\(bin:\) 2AS-5{[10572]}.

\(i:\) Klein Lucero/6 Prelude{[318]}; Klein Lucero/6 Thatcher{[318]}; Maria Escobar/4'Thatcher{[318]}.

\(v:\) EAP 26127{[314]}; Jagger{[1350]}; Jupateco{[939]}; Klein Lucero{[318]}; TAM11{[10595]}; Trego{[10572]}.

\(v2:\) Fuller Lr39{[10699]}; Inia 66 Lr13 Lr14a{[9010]}; Lerma Rojo 64 Lr13 Lr34{[1373]}; Maria Escobar Lr14b{[318]}; Rafaela Lr14b{[314]}.

\(ma:\) Xbarc123-2A - 4.8 cM - Xgwm636-2A - 4.0 cM - Lr17a{[10571]}; Xgwm614-2A - 0.7 cM - Lr17a - Xwmc407-2A{[10572]}.

**Lr17b**{[1350]}. \([LrH{[970]},WRB2{[615]}]\). 2A{[1350]}.

\(v:\) Brock{[0260]}; Harrier{[1350]}; Maris Fundin{[1350]}; Norin 10-Brevor, 14{[1350]}; Norman{[1350]}.

\(v2:\) Contra Lr13{[10345]}; Hobbit Sib = Dwarf A Lr13{[1350]}; Kalasz Lr13{[10345]}; Riband Lr13{[10345]}; Sarka Lr13{[10345]}; Tarso Lr26{[0229]}.

**Lr18**{[318]}. Derived from *T. timopheevii*. Independently derived lines with Lr18 possess a unique N band terminally located in chromosome 5BL {[1614]}.

Low seedling responses conferred by Lr18 are most effective at 15-18C. With increasing temperatures the response becomes less effective and ineffective at 25-27C {[935], see also, 1614]}.

5BL {[935]} = T5BS.5BL-5G#1L{[389]}.

\(i:\) Africa 43/7'Thatcher{[318]}; Red Egyptian PI 170925/6'Thatcher{[318]}.

\(v:\) Africa 43{[318]}; Red Egyptian PI 170925{[318]}; Red Egyptian PI 17016-2c{[318]}; Sabikei 12{[935]}; Timvera{[935]}; Timvera Derivative{[935]}; Certain WYR accessions{[935]}; FTF{[1614]}; Several Sabikei lines including Sabikei 12{[1614]}.

\(v2:\) Ck9803 Lr11{[10595]}; FFR 524 Lr11{[10595]}; Pioneer 2684 Lr11{[10595]}; SS520 Lr11{[10595]}. 

**Lr19**{[140]}. Derived from *Th. elongatum*.

7DL = T7DS.7DL-7Ac#1L{[291,956,1323,388,657,389]}. \(i:\) Agatha = T4 – TC + Lr19{[956,1323]}; Sears trasfer 7D-7Ag no.1{[10255]}.

\(v:\) L503{[1346]}; L513{[1346]}; Mutant 28{[598]}; Sunnan{[684]}; See Sr25.

7AL. \(v:\) Lines I-22 and I-23{[10255]}.

\(v2:\) Oasis 86 Lr13{[1373]}.

7AL. \(tv:\) This translocation was transferred to durum wheat and engineered to produce...
normally inherited secondary recombinants with smaller alien segments, such as R1{10633}. **ma:** Located in the Xwmg420-7Ag - Xwmg2062-7Ag interval{10255}; RAPD, SCAR and SSR markers co-inciding with, or flanking, Lr19 in a derivative of Knott's Agatha Mutant 28 (C80.1) were reported in{10379}. **c:** A candidate sequence, AG15, with a 1,258 amino acid sequence and a CC-NBS-LRR structure was reported in{10575}.

The chromosome with Lr19 in Indis is probably identical to that in Agatha {1162}. Lr19 is usually associated with Sr25. Sears' transfer 7D-7Ag No. 11 carries neither Lr19 nor Sr25. See Lr29.

Knott {681} obtained two mutants (28 and 235) of Agatha possessing Lr19, but with reduced levels of yellow pigment in the flour. Marais {890,892} obtained mutants and recombined lines with intermediate levels of, or no, yellow pigment. It was shown that recombinant line 88M22-149 lacked yellow pigment {1163}.

Secondary translocation line I-96 derived from Sears' 7D-7Ag no.1 involved Lr19 being located in an intercalary segment with low yellow pigment and lacking Sd1 {10255}. Lr19 in lines I-22 and I-23 retaining yellow pigment but lacking Sd1 was transferred to durum chromosome 7BL {10255}. One of the lines with the shortest 7Ag segment, Lr19-I49-299, was used in a further cycle of recombination {10278}.

**Lr20**{140}. 7AL{1305.1554}. **s:** CS’5/Axminster 7A{1293}. **v:** Axminster{348,1175,1305}; Birdproof{1554}; Bonus{1554}; Converse{1554}; Festival{1554}; Kenora{1554}; Kenya W744{1554}; Maris Halberd{608}; Normandie{348,1554}; Sappo{608}; Sicco{310}; Thew{140,1552}; Timmo{608}. **v2:** Norka Lr1{1554}; See Pm1 (Reaction to Blumeria graminis) & Sr15 (Reaction to Puccininia graminis) with which Lr20 is always associated. Lr20 in Sicco appears to differ from that in Sappo, Timmo and Maris Halberd{310}; Lr20 in Norka (Lr1+Lr20) may differ from that in Thew{939}. **ma:** Complete cosegregation of several markers including Xedo347-7A, Xpsr1217A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A and Xsts638-7A with Pm1 and Lr20 was reported in {0323}; Lr20 -STS638, 7.1 cm{10263}.

**Lr21**{1241}. [Lr40{1200,10415}]. 1D{650}.1DL{1241}.1DS{448}. **i:** Thatcher’6/Tetra Canthatch/Ae. tauschii var. meyeri RL 5289{306}. **v:** Tetra Canthatch/Ae. tauschii var. meyeri RL 5289, RL 5406{648}; McKenzie{0228}; WGRC2 = TA1649/3* Wichita{0299}; WGRC7 = Wichita/TA1649/2*Wichita{0299}. **v2:** AC Cora Lr13{713}; WGRC16 = TAM107*3/Ae. tauschii TA 2460 Lr39{220,10415}. **dv:** Ae. tauschii accessions: RLS289 = TA1599{1241}; Ae. tauschii TA2460 Lr39{220,10415}; TA1649{0299}; TA1691{0299}; TA2378{0299}; TA2470{0299}; TA2483{0299}; TA2495{0299}; TA2527{0299}; TA2528{0299}. **ma:** All members of the Lr21 family carry a STS derivative of XksuD14-1D that has a resistance gene analogue structure{0299}; XksuD14-1D was reported to map 1.8 cm proximal to Lr21 in{0375}; Lr21 - 0 cm - rgaYr10b - 0.6 cm - Xgdm33-1D{0360}; Xksu-1D is part of Lr21{10420}; Lr21 was cloned and shown to have a NBS-LRR structure{10420}.

A reconstituted effective Lr21 allele (designated Lr21-b) was obtained as a rare (1/5,872)
recombinant (accession TA4446) between Lr21 pseudogenes in common wheat cultivars Fielder and Wichita {10620}.

**Lr22.** 2DS{1241}. Adult plant reaction. i: Neepawa*6/RL5404, RL4495{10467}; Thatcher 3/Tetra Canthatch/Ae. squarrosa var. *strangulata* RL 5271{306}; Thatcher 7//Tetra-Canthatch/RL5271, RL 6044{10467}. v: Tetra Canthatch/Ae. squarrosa var. *strangulata* RL 5271, RL 5404{311}. v2: AC Minto Lr11 Lr13{713}. 

dv: Ae. squarrosa var. *strangulata* RL 5271. ma: Xgwm296-2DS - 2.0 cM - Lr22a{10446}; Xgwm455-2D - 1.5 cM - Lr22a - 2.9 cM - Xgwm296-2D{10467}.

**Lr22b**{298}. Adult plant reaction. v: Canthatch{298}; Marquis{970}; Thatcher{298}.

This gene will be present in near-isogenic lines based on Thatcher.

**Lr23**{948}. [LrG{951}]. 2BS{948}. i: Lee FL 310/6 Thatcher{948}. s: CS*7/Kenya Farmer 2B{948}; CS*6/Timstein 2B {948}. v: Cranbrook{02119}; Grim{1091}; Hope/Timstein{1091}; I 310678{1091}; 1 310685{1091}; I 349162{1091}; IWP94{10569}; K 45973{1091}; K 51070{1091}; Rocta{1091}. v2: Gamynia Lr3{1552}; Gabo Lr10(1552); Kenya Farmer Lr10{1552}; Lee Lr10{1552}; Timstein Lr10{1552}; Bramling Lr14a Lr3{10563}. tv: Altar 84{1058}. ma: associated with Xksu904(Per2)-2B{0090}. A QTL, which is likely to correspond to Lr23, was identified in the Opatia 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by W-7974{0090}.

**Lr24.** Derived from *Thin. elongatum*.

Always present with Sr24 {956}. See Sr24 (Reaction to *P. graminis*). [LrAg{141}]. 3DL{956,1389}. v: Cody{1284}; Cutter{10595}; Jagalene{10595}; McCormick{10595}; Ogallala{10595}; Osage{143}; Payne{1390,1024}; SST 23{1324}; SST 44 = T4R{1324}; Timpaw{1255}; Torres{128}; Wanken{1255}; Australian genotypes{10340}. v2: Blueboy II Lr1 Lr10{141}; Lr10{1552}; Lee Lr10{1552}; Timstein Lr10{1552}; Bramling Lr14a Lr3{10563}. tv: Altar 84{1058}. ma: Co-seg of Lr24 in Agent with 8 RFLP markers; segment in Sears' 3D-3Ag#1 is shorter than in Agent{048}; Tagged with Xpsr1203-6B{1271}; cosegregation with RAPD marker that was converted to a SCAR{231}; Linked with SCAR marker SCS7719 earlier thought to tag Lr19{10147}.

1BL{185} = T1BL.1BS-3Ae#1L{600}. v: Amigo{1463,630,185}; Teewon{600}. ma: SCAR markers were developed in {10368}.

A PCR marker, Sr24#12, was confirmed across all sources of Lr24 {10257}.

**Lr25.** Derived from *S. cereale* cv. Rosen. 4BS{270,271,380,389}. v: Transec{273}; Transfed{269}; Always present with *Pm7*. ma: Cosegregation with a RAPD{1165}. Revised to T4BS.4BL-5RL {543} and later to T4BS.4BL-2R#1L.

**Lr26.** Derived from *S. cereale*. See also Reaction to *P. graminis*, Sr31; Reaction to *P. striiformis*, Lr26. 1R (1B),T1BL.1RS. i: MA1 and MA2 four breakpoint double translocation lines 1RS-1BS-1RS-1BS.1BL in Pavon{0084}. v: AGS 2000{10595}; Derivatives of Petkus rye - see Yr9 (Reaction to *P. striiformis*) & Sr31 (Reaction to *P. graminis*); Bacanora 88{1373}; Cougar{0267}; Pioneer 26R61{10595}; Rawhide (heterogeneous){0267}; GR876{753}; Iris{075}; Sabina{075}. v2: Beaver Lr13{10687}; Cumpas 88 Lr13{1373}; Istra Lr3{076}; Siouxland Lr24{1283}; Solaris Lr3{076}; Many wheats with Lr26 also carry Lr3. Amika (heterogeneous) Lr3{076}; See also{310}. tv: Cando’2/Veery; KS91WGRC14{381}. ma: Several markers tightly linked with Lr26 were identified in {0377}.

1BS/1RS recombinants 4.4 cM proximal to Gli-B1/Glu-B3 {0084}. Hanusova *et al*. {492} identified 127 wheats with Lr26 but only 16 of them were listed.

**Lr27**{1367}. One of two complementary genes; the second gene, Lr31, is located in chromosome 4BS {1367}. The following wheats have both Lr27 and Lr31. Lr27 is present in wheats with Sr2, but is not expressed in the absence of the complementary factor {1366}. [LrGt{1366},A{1058,1366}]. 3BS{1367}. s: CS 6/Ciano 3B{1366}.

**Lr28**[967]. Derived from *Ae. speltoides*. 4AL[967] = T4AS.4AL-7S#2S[389]. i: CS 2A/2M 4/2[967]; CS 2D/2M 3/8[967]. ma: Lr28 was tagged using STS primer OPJ-01378[1052]; A linked RAPD marker, S421640 was converted to a TPSCAR, SCS421570[10236].

**Lr29**[939]. Derived from *Th. elongatum*. 7DS[939] = T7DL-7Ae#1S[389]. i: Sears’ CS 7D/Ag#11[939,1300]; RL6080 = Tc’6/Sears’ 7D/Ag#11[316]. ma: Co-segregation with two RAPDs[1165].


**Lr33**[325]. 1BL[325]. i: RL 6057 = Tc’6/PI 58548[297,325,321]. v: PI 268454a[297]; PI 58548[297,325]. v2: PI 268316 Lr2c Lr34[297]; Others[1322].

**Lr34**[297,299]. In addition to conferring seedling and adult plant resistance, *Lr34* responds in a complementary manner when combined with either *Lr33* or *LrT3* [321]. In the Thatcher background, *Lr34* is associated with increased resistance to stem rust [299,321]. Although the resistance gene in the near-isogenic Thatcher line, RL6077, was considered to be *Lr34* on the basis of disease response, leaf tip necrosis and its association with resistance to stripe rust, a cross with RL6058 segregated for two genes. A translocation to another chromosome was suggested [324]. [LrT2[321]]. 7D[299].7DS[324,1058]. i: Arina + Lr34[10648]; Lalbahadar + Lr34[10648]; Line 897[321]; Line 920[321]. Selections Jupateco 73R Lr17a Lr27 + Lr31 and Jupateco 73S Lr17a Lr27 + Lr31 and Cocoraque 75 Lr13 Lr17a Lr27 + Lr31 and Anhuac 75 Lr13 Lr17a Lr27 + Lr31, can be considered near-isogenic for the presence and absence, respectively, of Lr34[1361]. v: Ardito[10648]; Arina*3/Forno[10380]; Bezostaya[10387,10648]; Condor[10387,10648]; Cook[10387]; Forno[1066,10380,10387]; Fukuho-Komugi[10387,10648]; Kavkaz[10648]; Lantian 12[10682]; Libellula[10682]; Otane[10387]; Pegaso[10648]; Penjamo 62[10648]; RL 6058 = Tc’6/PI 58548[297]; PI 268454[297]; 268454[297]; Westphal 12[0268]; Others[299,321,1322,1376]; See[1362]. v2: Anza = WW15 Lr13 heterogenous[10648]; Bramling Lr14a Lr23[10563]; BH1146 Lr13; Chinese Spring Lr12 Lr31[301,10648]; Chris Lr13[10648]; Frontana Lr13[1374]; Glenlea Lr1[327,10648]; Jupateco R Lr17a, Lr27 + Lr31[10648]; Lageadinho LrT3[321]; Laura Lr1 Lr10[712]; Mentana Lr3b[10493,10648]; Parula Lr13 Lr46[1374]; PI 58548 Lr33[297,321]; RL 6059 = Tc’6/Terenzio Lr33[297]; RL 6069 = Tc’6/Lageadinho LrT3[321]; RL 6070 = Tc’5/PI 321999 LrT3[321]; RL 6050 = Tc’6/Terenzio LrT3[321]; Saar Lr46[10481]; Sturdy Lr12 Lr13[301]; Terenzio Lr3 Lr30 LrT3[321]; Thirteen Thatcher lines with 2-gene combinations[434]. ma: Complete linkage with *Ltn* (leaf tip necrosis)[1361]. *Yr18* (Reaction to *P. striiformis*)[1362,937] and *Bdv1* (Reaction to barley yellow dwarf virus) and *Pm38* (Reaction to *B. graminis*)[0090]; association with Xwg834-7D[0268]; Xgwm120-7D - 0.9 cM - Lr34 - 2.7 cM - Xgwm295-7D[10259]; Lr34 … XsfrBF473324 - 0.5 cM - Xsfr.cdo475-7D - 0.7 cM - Xswm10-7D[10387]; A 150 bp allele (b) of STS csLV34, derived
from wEST BQ788742 was identified in most wheats with \textit{Lr34}; \textit{CsLV34a} - 0.4 cM - \textit{Lr34}{10387}; STS marker \textit{csLV34} was used to confirm or postulate the presence of \textit{Lr34} in Australian cultivars {10493} and Hungarian materials {10701}. c: \textit{Lr34} spanning 11,805 bp and producing a 1,401 aa protein belongs to the drug resistance subfamily of ABC reporters {10648}; contained within FJ436983 {10648}. A QTL, which is likely to correspond to \textit{Lr34}, was identified in the Opata 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by Opata 85 {0090}. 

This gene is identical to \textit{Yr18}, \textit{Pm38} and \textit{Ltn} and confers stem rust resistance in some genetic backgrounds.

Diagnostic markers based on the gene sequence are reported in {10713}; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry \textit{Lr34} {10713}. 

\textbf{\textit{Lr35}}{651}. Derived from \textit{Ae. speltoides}{651}. Adult plant resistance {651}. 2B{651}. v: RL 5711{651}. ma: \textit{Ae. speltoides} Popn. 2. 

\textbf{\textit{Lr36}}. Derived from \textit{Ae. speltoides}. 6BS{292}. v: Line 2-9-2; Line E84018. al: \textit{Ae. speltoides} Popn. 2. 

\textbf{\textit{Lr37}}{062}. Derived from \textit{Ae. ventricosa}. Recessive {667}. \textit{Lr37} can be recognised in seedlings at low temperatures (17°C) and is effective in adult plants under field conditions. See also \textit{Sr38} (Reaction to \textit{P. graminis}) and \textit{Yr17} (Reaction to \textit{P. striiformis}) 2AS{062}.6M = 2MS-6M.6MSL or 2MS-6ML.6MS{0009}. VPM1 and derivatives: 2AS{062} = 2AL.2AS-2N'S{0213}. i: RL 6081 = Tc/VPM1{939}; RL6081 = Tc/8/VPM1{316}; various NILs listed in {0213}. v: Hyak{021}; Madsen{020}; Rendezvous{062}; VPM1{062}; VPM1 derivatives{939}; see also Reaction to \textit{P. striiformis tritici} \textit{Yr17}. 

A resistance gene analog containing an NBS-LRR R gene sequence was isolated from the \textit{Ae. ventricosa} segment carrying \textit{Lr37} {0183}. The 2NS translocated segment carrying \textit{Lr37} replaced the distal half of chromosome 2A (25-38 cM) from \textit{Xcmwg682-2A} to \textit{XksuH-9-2A}. PCR markers were developed for the 2NS and 2AS alleles of \textit{Xcmwg682} {10073}. 


\textbf{\textit{Lr39}}{1200,02100}. Derived from \textit{Ae. tauschii} {02100}. \textit{Lr41} {215}. 2DS{02100}. v: Fuller{10595}; KS90WGRC10 = TAM107^3/Ae. tauschii TA2460{220}; Overley{10595,10699}; TA4186 = TA1675^2/Wichita{02100}; Thunderbolt{02100}. v2:
Fuller Lr17α[10699]; WGRC16=TAM107*3/ Ae. tauschii TA2460[220]. dv: Ae. tauschii TA 1675[02100]; Ae. tauschii TA2460 Lr21[220,10415]; Lr21[220,10415]. ma: 10.7 cM distal to Xgwm210-2D[02100].

Lr40[1200,10415]. Deleted, see Lr21

Lr41[215]. Deleted, see Lr39


Lr43[218]. Deleted, wrongly based on a gene combination


Lr46[1364]. Completely linked with Yr29[0119]. Adult plant resistance.

1B[1346].1BL[0119]. s: Lalbahadur(Pavon 1B) Lr1[1364]; Lalbahadur(Parula 1B)[10281]. v: Attila[10281]. v2: Pavon F76 Lr1 Lr10 Lr13[1364,0119]; Parula Lr13 Lr34[10281]; Saar Lr34[10481]. ma: An RFLP marker associated with Lr46 with a recombination value of about 10% was identified in[0119]; Xwmc44-1B - 1.4 cM - Xbac24prot - 9.5 cM - Lr46 - 2.9 cM - Xbac17R......Xgwm140[10281]; Xwmc44-1B - 3.6 cM - Lr46 2.1 cM - Xg818/Xbac17R......Xgwm140[10281]; XSTS1BL2 - 2.2 cM - Lr46/XSTS1BL9 - 2.2 cM - XSTS1BL7[10326].

Associated with Ltn2 and Yr29.

Lr47[9901]. Derived from Ae. speltoides[9901].

7AS = Ti7AS-7S#S.7S#L[9901]. v: Pavon derivative PI 603918[9901].

7A = T7AS-7S#S.7S#I[389]. v: CI 17882, CI 17884, CI 17885, KS, 90H450[9901].

7AL = Ti7AS.7AL-7S#1L[9901]. v: Pavon derivative PI 603919[9901]. ma: Lr47 was located in the distal one-third of 7AS, 2-10 cM from the centromere and within a 20-30 cM segment[9901]. Complete linkage with several RFLP markers[9901] and PCR specific markers[0126].


Lr51[0308]. 1BL[0308]. i: Express’7/T1[0308]; Kolin’7/T1[0308]; UC1037’7/T2[0308]. v: Neepawa 6/Ae. speltoides F-7, selections 3 and 12[0306]; Interstitial translocations T1AS.1AL-1S#F7-12L-1AL[0308] = T1; T1BS.1BL-1S#F7L-1BL[0306]. al: Ae. speltoides F-7 selections 3 and 12[0306]. ma: Linked with RFLP markers Xmsg710-1B and Xaga7-1B[0308]; A CAPS marker was developed from XAg7-1B[0308].


**Pathogenic Disease/Pest Reaction**

*Lr55* \(10180\). Derived from *Elymus trachycaulus* \(10180\). 1B (1BL.1HS \(10180\). **ad**: CS + 1H \(10180\). **v**: KS04WGRC45 = Heyne*3/TA5586.

*Lr56* \(10224\). [Lr512 \(10204\)]. 6A (6AL-6S* \(10204\). 6S* \(10204\)). **v**: Line 0352 = *Ae. sharonensis* -174/9*CS/3*W84-17/3/CS/4/W84-17 \(10224\). Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 - are reported in \(10224\). **al**: *Ae. sharonensis* -174 \(10224\).

*Lr57* \(10328\). Derived from *Ae. geniculata*. 5DS (5DL.5DS-T5MS \(G\) \(10328\). **v**: TA5602 \(10328\); TA5603 \(10328\); Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry *Lr13*. **al**: *Ae. geniculata* (=ovata) (U\(^6\)S\(^M\)G \(G\) \(10328\). **TA10437** \(10328\). **ma**: Completely linked with distinctive alleles of Gsp, Xfbb276 and Xbcd873 \(10328\). Completely linked with *Yr40* \(10328\).

*Lr58* \(10375\). Derived from *Ae. triuncialis* = 2BL \(10375\). = T2BS.2BL-2L \(0.95\). **v**: TAT505 = WL711 \* 4/ *Ae. triuncialis* TA10438 *Lr13* \(10375\). **al**: *Ae. triuncalis* TA10438 \(10375\). **ma**: TA5605 possesses *Ae. triuncialis* alleles of RFLP markers XksuH16, XksuF11 and Xbg123 and SSR marker Xcfd \(50\) in the terminal region of chromosome 2BL \(10375\).

*Lr59* \(10399\). Derived from *Ae. peregrina* 1A, probably 1AS. alien centric fusion \(10399\). **v**: Line 0306 \(10399\) = *Ae. peregrina*-680/2*CS/5*W84-17 \(10399\). **al**: *Ae. peregrina* (USS, 2n = 28) \(600\) \(10399\).

*Lr60* \(10400\). [LrW2 \(10305\)]. 1DS \(10400\). **v**: RL6172 \(10305\) = Thatcher*3/V860. **ma**: *Lr60* - 8.4 cM - Xbarc149-1D/Lr21 \(10400\). *Lr60* - 13 cM - Lr21 \(10400\).

*Lr61* \(10485\). 6BS \(10485\). **tv**: Guayacan 2 \(10485\); Guayacan INIA \(10485\). **ma**: *Lr61* - 2.2 cM - P81/M70-260/P87/M75-131 - 4.6 cM - P87/M76-149 - 21.7 cM - Xwmc487-6B \(10485\).

*Lr62* \(10537\). Derived from *Ae. neglecta* 6A = 6AL-6\(^{AE}\) = 6S* \(10537\). **v**: Line 03M119-71A \(10537\). **al**: *Ae. neglecta* \(10537\).

*Lr63* \(10550\). Derived from *T. monococcum* 3AS \(10550\). **i**: RL 6137 = Thatcher*6/TMR5-J14-12-24 \(10550\). **v**: TMR5-J14-12-24 \(10550\). **dv**: *T. monococcum* \(10546\). **ma**: Very closely linked to Xbarc321-3A \(10550\).

*Lr64* \(10550\). 6A \(10550\). **i**: RL 6149 = Thatcher*6/T. dicoccoides* 8404 \(10550\). **tv**: *T. dicoccoides* 8404 \(10550\). **ma**: Xbarc104-6A - 13.9 cM - Lr64 - 21.9 cM - Xgwm427-6A \(10550\).

*Lr65*.

Tentatively approved subject to an alellism test and acceptance by a journal.

*Lr66* \(10591\). *LrS13* \(10592\). 3A \(10591\). **3A = 3AS*. **v**: Line 07M127-3 = *Ae. speltoides* / 5*CS // 2*CSph1b mutant /3/2 * W84-17/4/CSN3AT3B \(10591\). **al**: *Ae. speltoides* Accession 691 \(10591\). **ma**: Most user-friendly marker, SCAR S15-t3 \(10591\).

*Lr67* \(10675\). Adult plant resistance 4DS \(10675\). **i**: RL6077 = Thatcher*6/P1 250413 \(10675\). **PI**: 250413 \(10676\). **ma**: Associated with Xcfd71-4D \(10675\); Pleiotropic with *Yr46*; Close linkage with Xcfd71-4D and Xbarc98-4D estimated at 4.4 cM, and Xcfd23-4A at 5.2 cM (all on the same side of Lr67/Yr46 \(10678\).

*LrKr1* \(10233\). **v**: Thatcher \(10233\). **v2**: Kanred *LrKr2* \(10233\).

*LrKr2* \(10233\). **v2**: Kanred *LrKr1* \(10233\).

*LrMq1* \(10233\). **v**: Marquis \(10233\).

*LrTb* \(820\). Adult plant resistance \(820\). **v2**: AC Taber *Lr13 Lr14a* \(820\).

*LrTm* \(2027\). **dv**: *T. monococcum* **ma**: Linked to microsatellite locus Xgwm136 \(2027\).

*LrTr* \(2027\). **v**: *Ae. triuncialis* derivatives \(2027\). **ad**: *WL711 BC2F5 addition lines* \(2027\). **al**: *Ae. triuncalis* Acc. 3549 \(2027\). **ma**: Lines with *LiTr* possessed a homologue of Xgwm368-4B \(2027\).

*LrTt1* \(10031\). Recessive allele \(10031\). [LrTt1 \(10031\)]. **2A** \(10031\). **v**: Line 842 = Saratovskaya*2/T. timopheevii spp. viticulosum \(10031\). **ma**: Xgwm812-2A - 1.5 cM - LrTt1 \(10031\).

*LrVPM* \(1603\). 7DL \(1603\).
**LrW2**{305}. A gene, identified only as *Lr*, was transferred to wheat chromosome 2AS from 6M' {113}: cosegregating markers were *Xpsr933-2A* and *Xpsr150-2A*.

**LrZH84**{10581}. 1BL{10581}. *v*: Zhoumai 11{10682}. *v2*: Predgornaia 2 *Lr26*{10581}; Zhou 8425B *Lr26*{10581}. *ma*: *Xbarc8-1B* (cent) - 5.2 cM - *LrZh84* - 3.9 cM - *Xgwm582-1B*{10581}.

A series of temporary designations for seedling and adult plant resistance genes in six durums is given in {1648}. A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* - 8.9 cM - *Lr* - 2.3 cM - STS *Xtxw200* {10253}.

Complex genotypes:

AC Domain: *Lr10 Lr16 Lr34* {820}.

Alsen: *Lr2a Lr10 Lr13 Lr23 Lr34* {10223}.

Benito: *Lr1 Lr2a Lr12 Lr13* {1256}.

Buck Manantial: *Lr3 Lr13 Lr16 Lr17 Lr34?* {300}.

Era: *Lr10 Lr13 Lr34* {342}.

Grandin: *Lr2a Lr3 Lr10 Lr13 Lr34* {821}.

Mango: *Lr1 Lr13 Lr26 Lr34* {1374}.

MN7529: *Lr1 Lr2a Lr10 Lr16* {976}.

Opata 85: *Lr10 Lr27+Lr31 Lr34* {1058}.

Pasqua: *Lr11 Lr13 Lr14b Lr30 Lr34* {304}.

Prospect: *Lr1 Lr2a Lr10 Lr13* {197}.

Roblin: *Lr1 Lr10 Lr13 Lr34* {303,713}.

Trap: *Lr1 Lr3 Lr10 Lr13 Lr34* {1374}.

AC Splendor: *Lr1 Lr16 Lr34* {10179}.

AC Teal: *Lr1 Lr13 Lr16* {821}.

Alsen: *Lr2a Lr19 Lr13 Lr23 Lr34* {10152}.

Norm: *Lr1 Lr10 Lr13 Lr16 Lr23 Lr34* {10152, 10223}.

Genotype lists: Australian cultivars {0288}; Chinese cultivars {0013, 10682}; Combinations with *Lr34* {1361}; Cultivars from the former USSR {1380}; Czechoslovakian cultivars {855,0102}; European cultivars {0229,0260,0288,0337,10345}; Indian cultivars {1365,1345}; Indian Subcontinent {1365}; Mexican cultivars {1373}; U.S.A. cultivars {1219,978,0334,10111,10146,10152}, see also {970}.

### 97.2. Suppressor of genes for resistance to *P. triticina*

**SuLr23**{1058}. Suppressing allele. 2DS{1058}. *v*: Altar 84/Ae. *tauschii* 219{1058}.

**suLr23**{1058}. Non-suppressing allele *v*: Opata 85{1058}.

See also evidence for specific suppression in {948}.

### 97.3. QTLs for reaction to *P. triticina*

Two QTLs, located distally on chromosome arm 1BL and on chromosome 7DS, were mapped for leaf rust severity in a Fukuho-komugi/Oligoculm doubled haploid population {10060}. The resistance on 1BL was contributed by Oligoculm and explained 15% of the variation. The 1BL QTL may correspond to *Lr46* and was associated with marker *Xwmc44-1B* {0460}. The resistance on 7DS was contributed by Fukuho-komugi and explained 41% of
the variation. The 7DS QTL corresponds to Lr34 and was associated with marker Xgwm295-7D (10060).

Two major QTL, located on chromosomes 7D and 1BS, for leaf rust resistance were mapped in an Arina/Forno RIL population (10066). The resistance on 7D was contributed by Forno and explained 32% of the variation. This QTL most likely corresponds to Lr34 (10066). The resistance on 1BS (QLr.sfr-1BS) was associated with Xgwm604-1B and was contributed by Forno (10066). Additional minor QTLs were identified on chromosome arms 2DL, 3DL, 4BS and 5AL (10066).

QTLs for leaf rust resistance were identified in (0050) and were named by the catalogue curators as follows:

**Beaver/Soissons DH population**: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B(1BL.1RS), 4BS (proximal to Xbarc20-4B) and 5AS (QLTBvr5AS, proximal to Xbarc10-5A) and in the vicinity of wPt-8756 and wPt-1931 (10687).

QLr.sfr-1B (0050). 1B(0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xpsr949-1B and Xgwm18-1B (0050).


QLr.sfr-3A (0050). 3A(0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xpsr570-3A and Xpsr543-3A (0050).

QLr.sfr-4B (0050). 4B(0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xpsr921-4B and Xpsr593-4B (0050).

QLr.sfr-4D (0050). 4DL(0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xglk302-4D and Xpsr1101-4D (0050).

QLr.sfr-5D (0050). 5DL(0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer(0050). ma: Associated with Xpsr906-5D and Xpsr580-5D (0050).

QLr.sfr-7B.I (0050). 7B (0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xpsr593-7B and Xpsr129-7B (0050).

QLr.sfr-7B.2 (0050). v: Forno/T. spelta cv. Oberkulmer mapping population; the resistance was contributed by Forno(0050). ma: Associated with Xglk750-7B and Xmwg710-7B (0050).

QTLs: Two QTLs for slow leaf rusting, located on chromosomes 2B and 7BL, were mapped for final severity, area under disease progress curve, and infection rate in a CI 13227 (resistant)/Suwon (susceptible) SSD population (10211). QLr.osu-2B was associated with microsatellite markers Xbarc18-2B and Xbarc167-2B (R² = 9-18%). QLr.osu-7BL was associated with microsatellite marker Xbarc182-7B (R² = 12-15%) (10211). CI 13227 contributed the resistant alleles for both QTLs. QLrid.ocu-2D, linked to Xgwm261-2D, affected the duration of infection (10211).

Avocet S/Pavon 76: QTL identified included: 1BL (PstAFAMseCAC1&2), 4BL (Xgwm368), 6AL (Xgwm617), 6BL (PstAGGMseCGA1) (10443).
Avocet S/Attila: At least two additive genes for slow rusting \textsuperscript{10586}. In addition to \textit{Lr46} there were small effects on chromosomes 2BS, 2BL and 7BL \textsuperscript{10586}.

\textbf{Tetraploid wheat}

Colosseo/Lloyd: A major QTL, \textit{QLr.ubo-7B.2}, for seedling and adult plant resistance from Colosseo, was located between \textit{Xgwm344.2-7B} and DART 378059, bin 7BL 10-0.78-1.00 \textsuperscript{10600}.

TA4152-60/ND 495 DH population: Four QTLs for APR, \textit{QLr.fcu-3AL}(Xcfa2183-3AL - \textit{Xgwm666-3AL}, R\textsuperscript{2}=0.18), \textit{QLr.fcu-3BL}(Xbarc164-3BL - Xfcp544-3BL, R\textsuperscript{2}=0.19), \textit{QLr.fcu5BL}, and \textit{QLr.fcu-6BL}(Xbarc5-6BL - \textit{Xgwm669.2-6BL}, R\textsuperscript{2}=0.12) were from TA4152-60 and \textit{Xlr.fcu-4DL}(Xgdm61-4DL - Xcfa2173-4DL, R\textsuperscript{2}=0.13) was from ND495 \textsuperscript{10717}. The 3AL QTL conferred seedling resistance to all 3 races, and the 3BL gene gave race-specific seedling resistance to one race. \textit{Xlr.fcu-3BL} was effective only in the presence of an allele associated with \textit{Xgwm359} \textsuperscript{10717}.

98. Reaction to \textit{Pyrenophora tritici-repentis} (anomorph: \textit{Drechlera tritici-repentis})

\textbf{Disease: Tan spot, yellow leaf spot.}

Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, \textit{Ptr ToxA}, \textit{Ptr ToxB} and \textit{Ptr ToxC} have been identified (see \textsuperscript{10153}). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved.

A review is provided in \textsuperscript{10690}.

98.1. Insensitivity to tan spot toxin (necrosis)

\textit{tsn1} \textsuperscript{346,10207}. Insensitivity (disease resistance) is recessive \textsuperscript{346}. \textit{Tsr1} \textsuperscript{10508}, see Resistance to tanspot. 5BL\textsuperscript{346}. \textbf{v}: AC Barrie\textsuperscript{10153}; AC Cadillac\textsuperscript{10153}; AC Elsa\textsuperscript{10153}; Atlas 66\textsuperscript{10458}; BR34\textsuperscript{0007,10458}; CEP17\textsuperscript{0007}; Chinese Spring\textsuperscript{0007,10458}; Erik\textsuperscript{0007,10030,10458}; IA807\textsuperscript{0007}; IA905\textsuperscript{0007}; Laura\textsuperscript{10153}; ND688\textsuperscript{10458}; Opata 85\textsuperscript{10458}; Synthetic W-7976 = Cando/R143/Mexicali ‘S’/3/Ae. squarrosa C122\textsuperscript{346,10207,10458}; Synthetic W-7984 = Altar 84/Ae. tauschii CI 18\textsuperscript{0007,10458}. \textbf{tv}: Altar 84\textsuperscript{0007}; D87450\textsuperscript{0007}; \textit{T. dicoccoides} Israel A\textsuperscript{10506}. \textbf{ma}: Xbcd1030-5B - 5.7 cM - \textit{tsn1} - 16.5 cM - Xwg583-5B\textsuperscript{346}; \textit{tsn1} - 3.7 cM - Xbcd1030-5B\textsuperscript{0007}; Xfcp9-5B - 0.4 cM - Ts1/Xfcp17-5B - 0.2 cM - Xfcp9-5B\textsuperscript{10207}; Xfcp17-5B - 0.2 cM - \textit{Tsn1} - 0.6 cM - Xfcp9-5B\textsuperscript{10207}; Xfcp1-5B and Xfcp2-5B delineated \textit{Tsn1} to an interval of about 1 cM\textsuperscript{10337}; \textit{Tsn1} was placed in a 2.1 cM region spanned by XBF483506 and XBF138151.1/XBE425878/Xfsc1/XBE443610\textsuperscript{10413}. According to \textsuperscript{10030} the same dominant allele, presumably \textit{tsn1}, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

\textit{Tsn1}. Sensitive to \textit{Ptr ToxA}. \textbf{v}: Bobwhite\textsuperscript{10458}; Cheyenne\textsuperscript{0007,10458}; Glenlea\textsuperscript{10458}; Grandin\textsuperscript{10458}; Hope\textsuperscript{0007,10458}; Jagger\textsuperscript{0007}; Katepwa\textsuperscript{10458}; ND2709\textsuperscript{10458}; ND495\textsuperscript{0007}; Sumai 3\textsuperscript{10458}; Timstein\textsuperscript{0007,10458}. \textbf{v2}: Kulm \textit{Tsc1} \textsuperscript{346,10030,10458}; Trenton \textit{Tsc1} \textsuperscript{0315}. \textbf{tv}: Langdon\textsuperscript{10458}.

In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected by 4-5 genes \textsuperscript{10030}.

\textit{Ptr ToxA} is functionally identical to \textit{S. nodorum} ToxA but has two predicted amino acid
differences \textit{[10459]}. See Reaction to \textit{Phaeosphaeria nodorum}. Australian cultivars with \textit{tsn1} and \textit{Tsn1} are listed in \textit{[10540]}. \textit{Tsn2} \textit{[10344]}. Conditions resistance to race 3 \textit{[10344]} 3BL \textit{[10344]}. \textit{sv}: LDN(DIC-3B) \textit{[10344]}. \textit{tv}: \textit{T. turgidum} no. 283, PI 352519 \textit{[10344]}; \textit{T. dicoccoides} Israel-A \textit{[10344]}. \textit{ma}: Identified as a QTL in region \textit{Xgwm285-3B - Xwmc366.2-3B} (R \textit{= 91\%}) \textit{[10344]}; Also classified as a single gene: \textit{Xgwm285-3B - 2.1 cM - tsn2 - 15.2 cM - Xwmc366.2-3B} \textit{[10344]}. In Kulm/Erik, toxin response accounted for 24\% of the variation in disease response, which was affected by 4-5 genes \textit{[10030]}. 

98.2. Insensitivity to tan spot toxin (chlorosis) \textit{Tsc1} \textit{[344]}. Sensitivity to Ptr ToxC \textit{[344]}. 1AS \textit{[344]}. \textit{v}: 6B365 \textit{[0315]}; Opata 85 \textit{[344]}. \textit{v2}: Kulm \textit{Tsn1} \textit{[0315]}; Trenton \textit{Tsn1} \textit{[0315]}. \textit{ma}: \textit{Gli-A1 - 5.7 cM - Tsc1 - 11.7 cM - XksuD14-1A} \textit{[0315]}. According to \textit{[10376]} the same allele, presumably \textit{tsc1}, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN2137 in crosses with 6B-365. \textit{tsc1} \textit{[344]}. Insensitivity is recessive. \textit{QTsc.ndsu-1A} \textit{[9924]}. \textit{v}: Katepwa \textit{[0315]}; Opata 85 \textit{[0315, 10015]}. \textit{tsc2} \textit{[10344]}. Insensitivity allele \textit{[10015]}. \textit{v}: Opata 85 \textit{[0315, 10015]}. \textit{QTsc.ndsu-4A} \textit{[0090]}. \textit{v}: Opata 85/Synthetic W-7984 \textit{[0090]}. Resistance was contributed by W-7976/Trenton resistance was contributed \textit{[10344]} by \textit{W-7976/Trenton} there was association with \textit{Xwg622-4A} \textit{[0264]}; Minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants \textit{[0264]}. QTLs: 'ITMI population': In addition to \textit{tsc2} which accounted for 69\% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (\textit{Xksu916(Oxo)}-4AS \textit{W-7948}) accounted for 20\% of the phenotypic variation \textit{[10015]}. Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in \textit{[10153]}. Grandin(S)/BR34(R) RILs: QTL in 1BS, \textit{QTs.fcu-1BS}, (13-29\% of variation depending on race) and 3BL, (13-41\%) were involved in resistance to 4 races. Five other QTL showed race specific responses \textit{[10248]}. 

98.3. Resistance to tan spot \textit{Tsr1}. \textit{[tsn1} See: Insensitivity to tanspot toxin]. Resistance is recessive. 5BL. \textit{v}: Genetic stocks that do not have \textit{Tsn1} and other genes that respond to toxins produced by the pathogen. The gene in Erik was allellic with resistance in a diverse set of genotypes including spelt and durum derivatives \textit{[10557]}. \textit{Tsr2}. Resistance is recessive. Confers resistance to race 3 \textit{[10344]}. \textit{tsn2} \textit{[10344]}. \textit{sv}: LDN (DIC-3B) \textit{[10344]}. \textit{tv}: \textit{T. dicoccoides} Israel-A \textit{[10344]}. \textit{tv2}: \textit{T. turgidum} no. 283, PI 352519 \textit{Tsr5} \textit{[10344]}. \textit{ma}: Identified as a QTL in region \textit{Xgwm285-3B - Xwmc366.2-3B} (R \textit{= 91\%}) \textit{[10344]}; Also classified as a single gene: \textit{Xgwm285-3B - 2.1 cM - tsn2 - 15.2 cM - Xwmc366.2-3B} \textit{[10344]}. \textit{Tsr3}. \textit{[tsn3} \textit{[10394]}]. 3D \textit{[10394]}. 3DS \textit{[10419]}. \textit{v}: XX41 = [Langdon/Ae. tauschii CI 00017] \textit{[10394]}; XX45 \textit{[10394]}; XX110 \textit{[10394]}. \textit{dv}: Ae. tauschii CI 00017 \textit{[10394]}. \textit{ma}: \textit{Xgwm2a - tsn3}, 15.3 cM, 14.4 cM and 9.5 cM in CS/XX41, CS/XX45 and CS/XX110,
respectively\{10419\}. Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant - all three were hemizygous-effective \{10394\}. The genes were given different temporary designations \{10394, 10419\}, but all will be considered to have a common gene until they are shown to be different.

**Tsr4.** Resistance is recessive. Resistance to race 1 (culture ASC1a) \{10350\}. \[tsn4\{10350\}\]. 3A\{10350\}. \textit{v:} Salamouni\{10350\}.

**Tsr5.** \[tsn\{10509\}\]. 3BL\{10509\}. \textit{tv2:} \textit{T. turgidum} no. 283, PI 352519 \textit{Tsr2}\{10509\}. \textit{ma:} \textit{Tsr5} - 8.3 cM - \textit{Xgwm285-3B} - 2.7 cM - \textit{Tsr2}\{10509\}.

**Tsr6\{10668\}.** Resistance is recessive. 2BS\{10668\}. \textit{v:} ND-735\{10668\}. \textit{ma:} \textit{Xwmc382-2B} - 15.3 cM - \textit{wPt-0289} - 4.6 cM - \textit{Tsr6} - 18.7 cM - \textit{Xwmc-2B}\{10668\}.

According to \{10668\} \textit{Tsr6} should be identical to \textit{tsc2} (see Insensitivity to tan spot toxin (chlorosis)).

**TsrHar\{10590\}.** 3B\{10590\}. \textit{v:} Dashen\{10590\}; HAR 604\{10590\}; HAR 2562\{10590\}. Effective against races ASC1a (race 1) and DW-16 \{10590\}.

**QTL**

\textit{QTsc.ndsu-1A} \{9924\}. Resistance is likely recessive \{344\}. \[Tsc1 \{344\}\]. 1AS \{344\}. \textit{v:} Synthetic W7984 \{344\}. \textit{ma:} Association with Gli-1 \{344, 0040, 0264\}. \textit{QTsc.ndsu-1A}, or a closely associated gene, confers insensitivity to \textit{Ptr} ToxC, see \{0315\}. Inoculation with purified toxin \textit{Ptr} ToxC was used to map this locus. \textit{QTsc.ndsu-1A} confers resistance in both seedlings and adult plants.

\textit{QTsc.ndsu-4A}. 4AL \{0090\}. \textit{v:} Opata 85/W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984 \{0090\}; In W-7976/Trenton resistance was contributed by W-7976 \{0264\}. \textit{ma:} Association with \textit{Xksu916(Oxo)-4A} and \textit{Xksu915(4-3-3a)-4A} \{0090\}; In W-7976/Trenton there was association with \textit{Xw622-4A} \{0264\}; Minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants \{0264\}.

QTLs: ITMI population: In addition to \textit{tsc2} which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL \(\textit{Xksu916(Oxo)-4AS}, W-7948\) accounted for 20% of the phenotypic variation \{10015\}.

Grandin (S) / BR34 (R) RILs: QTL in 1BS, \textit{QTs.fcu-1BS}, (13-29% of variation depending on race) and 3BL, \textit{QTs.fcu-3BL}, (13-41%) were involved in resistance to 4 races. Five other QTLs showed race specific responses \{10248\}.

Introgressions of genes for insensitivity to \textit{Ptr} ToxA and \textit{Ptr} ToxB are outlined in \{10153\}. QTL:

\textit{TA4152-60(R)/ND495(S)DH} population. Five QTLs for resistance, all from \textit{TA4152-60} \{10580\}, viz., \textit{QTs.fcu-2AS} and \textit{QTs.fcu-5BL} L conferring resistance to all races used, \textit{QTs.fcu-5AL} conferring resistance to races 1, 2 and 5, \textit{QTs.fcu-5B.2} conferring resistance to races 1 and 2, and \textit{QTs.fcu-4AL} conferring resistance to race 3.

\textit{WH542(R)/HD29(S)} RIL population: SIM indicated QTL on chromosomes 1B, 3AS, 3BL, 5B and 6BS, but only two were confirmed by CIM, \textit{Qts.ksu-3AS} flanked by \textit{Xbarc45-3A} and \textit{Xbarc86-3A} (LOD 5.4, \(R^2 = 0.23\)) and \textit{Qts.ksu-5BL} (probably \textit{Tsn1}) flanked by \textit{Xgwm499-5B} and \textit{Xest.stsbe968-5B} (LOD 6.5, \(R^2 = 0.27\)) \{10552\}.
99. Reaction to *Sitodiplosis mosellana* (Gehin)

Insect pest: Orange blossom wheat midge. Wheat midge. This pest should not be confused with *Contarinia tritici*, the yellow blossom wheat midge.

*Sml* [0218]. 2B[0218]. *v*: Augusta[0218]; Blueboy[0218]; Caldwell[0218]; Clark[0218]; FL302[0218]; Howell[0218]; Knox 62[0218]; Mono[0218]; Seneca[0218]. *ma*: Linked to a SCAR marker[0223]. *Sml* was mapped to a 2.5 cM interval on chromosome 2BS flanked proximally by AFLP-derived SCAR marker *WM1* and distally by SSR *Xgwm210-2B* [10291].

100. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Insect pest: Greenbug

*Gb1* [1514]. Recessive. *[gb1][222]*. *v*: CI 9058[222]; Dickinson Selection 28A[222].

*Gb2* [1313,1514]. 1A [554] = TIAL.1R#2S[389]. *v*: Amigo CI 17609[1313]; Century[0008]; TAM107[0008]; TAM200[0008]; TAM202[0008]. *ma*: 2.7 cM proximal to *Sec1* in 1RS, but co-segregated with *Sec-1P* [10167].

*Gb3* [624,1514]. Resistance in Largo and derivatives was controlled by multiallelic complementary genes [783]. *Gb3* was postulated to be one of the loci concerned.

7D[554].7DL[0319]. *v*: Largo CI 17895[622]; TAM110[0319]; TXGBE373[0319]. *ma*: Completely associated with 2 AFLP markers [0319]. These were also present in germplasm line KS9WGRC4, implying the likely presence of *Gb3* or a closely linked resistance gene [0319]: *Xgwm037* [7D] - 0.4 cM - *Gb3/Xwmc634* - 7D - 0.8 cM [10169].

*Gb4* [523,1514]. 7DL[10267]. *v*: CI 17959[903].

*Gb4* is either closely linked or allelic to *Gb3* [10267].

*Gb5* [1514,1515]. 7S(7A)[391]. *su*: CI 17882; CI 17884; CI 17885[1515].

*Gb6*. 1A = TIAL.1R#2S[1151]. *v*: GR51201[1152]; GR51202[1152]; GR51203[1152]; GR51204[1152]; GR51205[1152]; see also *Pm17* (Reaction to *Blumeria graminis*). *su*: Tx4386[1150]. *ad*: Tx4333[1150]. *al*: Insave rye.


*Gba* [10267]. 7DL[10267]. *v*: TA4152L94 = CETA/Ae. tauschii Wx1027[10267]. *ma*: *Xwmc671* - 7D - 34.3 cM - *Gba* - 20.7 cM - *Xbarc53* - 7D[10267].

*Gbb* [10267]. 7DL[10267]. *v*: TA452L24 = CROC 1/Ae. tauschii Wx224[10267]. *ma*: *Xwmc671* - 7D - 5.4 cM - *Gbb* - 20.2 cM - *Xbarc53* - 7D[10267].

*Gbc* [10267]. 7DL[10267]. *v*: TA4063.1 = 68111/Rugby/Ward/Ae. tauschii TA2477[10289]. *ma*: *Xgwm671* - 7D - 13.7 cM - *Gbc* - 17.9 cM - *Xgdm150* - 7D[10267].

*Gbd* [10267]. *v*: TA4064.1 = Altar 84/Ae. tauschii TA2841[10267]. *ma*: *Xgwm671* - 7D - 7.9 cM - *Gbd* - 1.9 cM - *Xwmc157* - 7D[10267].


*Gbx2* [10267]. *[Gbx][10267]*. *v*: W7984[10267]. *ma*: *Gbx2* was located 8.8 cM from *Gb3* [10267].


*Gbz* [10171]. 7DL[10171]. *v*: KSU97-85-3[10171]. *tv*: Ae. tauschii TA1675[10171]. *ma*: *Xgdm46* - 7D - 9.5 cM - *Xwmc157* - 7D - *Gb3* - 5.1 cM - *Xbarc53* - 7D[10171]; *Xwmc671* - 7D - 3.9 cM - *Gbz/Xwmc157* - 7D - 5.1 cM - *Xbarc53* [10267].
QTL: Antibiosis was associated with several markers, including Rc3 (7DS) in chromosome 7D {10167}. $QGb$.unlp.6A, for antixenosis was associated with Xgwm1009-6A and Xgwm1185-6A in a CS/CS(Synthetic 6A) DH population {10216}.

101. Reaction to Soil-Borne Cereal Mosaic Virus
Syn.: Soilborne wheat mosaic. Vectored to the roots by the fungus, Polymyxa graminis
$Sbm1$[10614]. [SbmCz1][10132]. 5DL[10614]. $v$: Cadenza{10132}; Tonic{10614}. $ma$: Xbarc110-5D - 14.7 cM - $Sbm1$ - 2.1 cM - Xwmc765-5D - 3.1 cM - Xbarc144-5D/Xwmc443-5D/RRES01-5D[10614]; Caps marker RRES01 was developed from an AFLP fragment[10614].

$Sbm1$ was identified in a DH population of Avalon (susceptible)/Cadenza {10132}.


A major QTL, $QSbv.ksu-5D$, (R$^2$=0.38) was found in Karl 92*2/TA4152-4 {10273}; the resistance was contributed by Karl 92.

102. Reaction to Tapesia yallundae. (Anomorph: Pseudocerosporella herpotrichoides (Fron) Deighton)
Disease: eyespot, strawbreaker footrot.
$Pch1$. [Pch[261]]. 7D{591,592}.7DL{708,1603}. $s$: Courtot*/Roazon 7D{592}; Hobbit Sib*/VPM1 7D{591}. $v$: Ae ventricosa derivative[261]; Coda{10513}; H-93-70{236,1521}; Hyak{021}; Madsen{020}; Rendezvous{1603}; Roazon{591}; 5L 219{1521}. 7A{0224}. $tv$: Five recombinant lines{0224}. $al$: Ae. ventricosa{261}. $ma$: $Pch1$ was linked to Ep-D1 and mapped 2 cM from microsatellite marker XustSSR2001-7D{10070}; Ep-d1b was a more reliable marker than the STS for selecting $Pch1$ {10238}; Leonard et al. {10513} predicted that Ep-D1 might encode an oligopeptidase B, and by comparative genetics, developed primers to a wheat oligopeptidase B-encoding wheat EST BU1003257. Complete linkage occurred for a derived STS marker Xorw1 and $Pch1$ in a Coda/Brundage RIL population and the marker identified the presence or absence of $Pch1$ among 44 wheat accessions{10513}.

$Pch1$ is closely linked with Ep-V1 {973}. Delibes et al. {236} concluded that $Pch1$ was not located in chromosome 7D whereas Law et al. {776} found that H-93-70 possessed a unique allele, Ep-D1b, in common with VPM1 and its derivatives. Eyespot resistance and Ep-A1b in chromosome 7A were genetically associated {704}.

$Pch2$[228]. 7A{704}.7AL{228,229}. $s$: CS*/Cappelle Desprez 7A{704,228}. $v$: Cappelle Desprez{704,228}. $ma$: Xcdo347-7A (distal) - 11 cM - Pch2 - 18.8 cM - Xwgl380-7A (proximal){229}. According to {0380}, this gene is not effective at the adult plant stage. Instead, the adult resistance of Cappelle-Desprez was controlled by a gene on chromosome 5A with the possibility of two less effective genes on 1A and 2B.

$Pch3$[616]. $ad$: CS + 4V{1050}.

$PchDv$[618]. 4VL{618}. $ad$: Wheat + 4V{618}. $su$: Wheat 4VL(4D), Yangmai 5{618}. $ma$: Distally located; Cent...Xcdo949-4V - 16 cM - $PchDv$ - 17 cM - Xbcd588-4V{618}. 
103. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Disease: Bunt, dwarf smut, stinking smut.

*Bt1*. [M1{135}]. 2B{1310}. s: CS/7/White Federation 38{1304}. v: Albit{129}; Banner Berkeley{129}; Federation 41{137}; Regal{129}; Sherman{137}; White Federation 38{1166}; White Odessa{137}. v2: Columbia Bt6{1005}; Hussar Bt2{135}; Hyslop Bt4{733}; Martin Bt7{135}; McDermid Bt4{734}; Odessa Bt7{137}; Tyee Bt4{022}.

*Bt2*. [H{129}]. v: Canus{137}; Selection PS60-1-1075{551}; Selection 1403{137}. v2: Hussar Bt1{135}.

*Bt3*. v: Florence{202,203}; Ridit{152,1000,1395}.

*Bt4*. Since Bt4 and Bt6 are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of Bt4, and Rio should be used as the source of Bt6. [T{136}]. 1B{1005,1274,1285}. v: Bison{1285}; Kaw{1285}; Nebred{1285}; Omaha{1285}; Oveson{1235}; Tres {heterogeneous}{023}; Turkey 1558{137}; Turkey 2578{137}. v2: Hyslop Bt1{733}; McDermid Bt1{734}; Martin Bt1{734}; McDermid Bt1{734}; Odessa Bt1{137}; Sherman Bt1{022}.

*Bt5*. 1B{1001}. v: Hohenheimer{397}; Selection R60-3432{551}.

*Bt6*. Since Bt4 and Bt6 are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of Bt4, and Rio should be used as the source of Bt6. [R{1418}]. 1B{1005}. v: Rio{1418}; Turkey 10095 & 10097{053}. v2: Columbia Bt1{1005}.

*Bt7*. [M2{1275}]. 2D{1000}. s: CS7/Cheyenne 2D{1000}. v: Baart{1275}; Cheyenne{1000}; Federation{1275}; Gallipoli{1000}; Onas{1275}; Ranee{1000}; Selection 1833{556}. v2: CI 7090 Bt9{1000}; Martin Bt1{137}; Odessa Bt1{137}; Oro Bt4{1000}; Turkey 3055 Bt4{1000}.

*Bt8*. [1558]. v: HY476{10181}; PI 178210{1558}; Yayla 305{1558}.

*Bt9*. [1006]. v: PI 166910{1006}; PI 166921{1006}; Selection M69-2073{551}. v2: CI 7090 Bt9{1000}; Jeff Bt10{1436}; PI 178383 Bt10{1006}; Ranger Bt10{1438}.

*Bt10*. [1004]. 6DS{10721}. i: BW553 = Neepawa*6//Red Bobs/PI 178383{10475}. v: AC2000{10181}; AC Cadillac{10181}; AC Carma{10181}; AC Crystal{10181}; AS Foremost{10181}; AC Taber{10181}; AC Vista{10181}; Fairview{1183}; PI 116301{1004}; PI 116306{1004}; Selection M69-2094{551}. v2: Jeff Bt9{1436}; PI 178383 Bt9{1000}; Ranger Bt9{1438}; Others{239,0128}. ma: Bt10 was completely linked with a 590 bp fragment produced by UBC primer 196{239}; RAPD - 1.5 cM - Bt10{763}; Bt10/FSD_RSA - 19.3 cM - Xgwm469-6D - 1.8 cM - Xwmc749-6D. The RAPD fragment was sequenced and converted to a diagnostic PCR marker for Bt10 in {0128}.

104. Reaction to *Tilletia indica* Mitra

Disease: Karnal bunt.

*Kb1*{394}. v: Chris{394}; CMH77.308 Kb2{394}.

*Kb2*{394}. v: PF7 113{394}; CMH77.308 Kb1{394}; Shanghai #8 Kb4{394}.

*Kb3*{394}. v: Amsel{394}.

*Kb4*{394}. v: Shanghai #8 Kb2{394}.

*Kb5*{394}. Recessive {394} v: Pigeon Kb6{394}.

*Kb6*{394}. Recessive {394} v: Pigeon Kb5{394}.

*Qkb.cnl-3B*{9956}. ma: Located in the interval XATPase-3B - Xcd1164-3B.

*Qkb.cnl-5A.1*{9956}. ma: Located in the interval Xmwg2112-5A - Xcd20-5A.

*Qkb.cnl-5A.2*{9956}. ma: Located in the interval Xabg391-5A - Xfba351-5A.
**Pathogenic Disease/Pest Reaction**

**Qkb.ksu-4BL.1.** WL711/HD29 (R) RILs: $R^2 = 0.25$, associated with Xgwm538-4B {10498}. WH542/W485 (R) RILs: $R^2 = 0.15$, Xgwm6-4BL - Xwmc349-4BL interval {10499}.

**Qkb.ksu-5BL.1.** WH542/HD29 (R) RILs: $R^2 = 0.19$, Xgdm116-5BL - Xwmc235-5BL {10499}.

**Qkb.ksu-6BS.1.** WH542/HD29 (R) RILs: $R^2 = 0.13$, Xwmc105-6BS - Xgwm88-6BS {10499}.

105. **Reaction to Ustilago tritici (Pers.) Rostrup**

Disease: Loose smut.

**Ut1** {1073}. **v:** Florence/Aurore {1073}; Renfrew {1073}; Red Bobs {1074}.

**Ut2** {1073}. **v:** Kota {1073}; Little Club {1073}.

**Ut3** {1074}. **v:** Carma {1074}.

**Ut4** {1074}. **v:** Thatcher/Regent {1074}.

**Utd1** {10684}. **5BS** {10684}. **tv:** D93213 {10684}; P9163-BJ08* B {10684}; VIR {10684}.

**Ut-x** {1164}. **v:** Biggar BSR {1164}.

Resistance to race 19 was associated with chromosome 6A of Cadet, Kota, Thatcher and TD18 {0208}. In the case of Cadet, resistance was localized to 6AS {0208}.

106. **Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)**

QTL: 79% of the variation between Geneva (resistant) and Augusta (susceptible) was associated with markers Xbcd1095-2D and Xcdo373-2D located 12.4 cM apart in chromosome 2DL {0131}. WSSMV is soil-borne and vectored by the fungus Polymxa graminis. This virus has some sequences similarity to Wheat Yellow Mosaic {10285}.

**Wss1** {10271}. Derived from Haynaldia villosa 4D(4DL.4VS) {10271}. T4VS.4DL {10271}. **tr:** NAU413 {10271}. **su:** Yangmai#5 4V(4D) {10271}.

107. **Reaction to Wheat Streak Mosaic Virus**

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be see-borne.

**Wsm1** {379,440}. Derived from *Th. intermedium*. **4A** {800} = T4AL.4Ai#2S {391}.4D = T4DL.4Ai#2S {391}.4D + T6AL.4Ai#2S {389}. **i:** Karl 4/C1 17884 = PI 583794 = KS93WGRC27 {440}. **v:** CI 17766 = B-6-37-1 {391}.800.1543; CI 17884 {391}; KS90H445 {391}; KS90H450 {391}; Mace {10694}. **ad:** CI 17881; CI 17883 {389}; CI 17886 {391}. **su:** 4Ai#2(4A):CI 15092 {391}; 4Ai#2(4D):CI 17882 & CI 17885 {391}.

**ma:** Wsm1 cosegregated with a STS amplified by the primer set STSJ15 {1456}.

Wsm1 is located in 4Ai#2S, CI 17882, CI 17884, CI 17885 and KS90H445 also carry a 7S chromosome substituting for 7A (See Reaction to *Schizaphis graminum*)

108. **Reaction to Xanthomonas campestris pv. undulosa**

Disease: Bacterial leaf streak

**Bls1** {244}. **v:** Pavon **Bls2** {244}; Mochis T88 Bls3 Bls4 {244}; Angostura F88 Bls5 {244}.

**Bls2** {244}. **v:** Pavon **Bls1** {244}.

**Bls3** {244}. **v:** Mochis T88 Bls1 Bls4 {244}.

**Bls4** {244}. **v:** Mochis T88 Bls1 Bls3 {244}.

**Bls5** {244}. **v:** Turnco F88 {244}; Angostura F88 Bls1 {244}.

**Bls1 bls2 bls3 bls4 bls5:** Alondra {244}.
109. Resistance to Colonization by *Eriophyes tulipae* (*Aceria tulipae*)

Mite pest: Wheat curl mite.

*Eriophyes tulipae* is the vector of wheat streak mosaic virus (WSMV) and the wheat spot mosaic agent (WSpM).

- **Cmc1**\{1467\}. 6DS\{1576\}. i: Norsa*5/Cmc1\{10166\}. v: *Ae. squarrosa*

  C14/Novamichurinka (= AC PGR 16635)\{1467\}; Norstar derivative\{0222\}.

- **Cmc2**\{1573\}. Derived from *Th. elongatum*. 6A = T6AS.6Ae#2S\{389\}.5B = T5BL.6Ae#2S\{389\}.6D \{1575\} = T6DL.6Ae#2S\{1575,389\}. i: Norstar*5/Cmc2\{10166\}. v: 875-94-2\{389\}. tr: Rescue Derivative\{1575\}. su: Cadet 6Ae#2(6A)\{1575\}; Cadet 6Ae#2(6D)\{1574\}; Rescue 6Ae#2(6A)\{1574\}; Rescue 6Ae#2(6B)\{1574\}; Rescue 6Ae#2(6D).

  ad: Cadet + mono-6Ae#2\{1574\}; Rescue + 6Ae#2\{1574\}.

- **Cmc3**\{0222\}. 1A = 1AL.1RS. i: Norstar*5/Cmc3 \{10166\}. Need to confirm relationship of 1RS segment in Amigo and Salmon as this NIL was derived from KS80H4200 a Chinese Spring Salmon line\{10166\}. v: Amigo; TAM107\{0222\}. v2: KS96GRC40 *Cmc4*\{0222\}.

  ma: Wheat lines with the 1RS segment and hence *Cmc3* can be selected with the rye-specific SSR Xscm09-1R\{0222\}.

- **Cmc4**\{0222\}. 6DS\{0222\}. v2: KS96WRC40 *Cmc3*\{0222\}. dv: *Ae. tauschii* accession\{0222\}.

  ma: XksuG8-6D - 6.4 cM - *Cmc4* - 4.1 cM - Xgdm141-6D\{0222\}.

110. Reaction to Wheat Yellow Mosaic Virus

WYMV is soil-borne and vectored by the fungus *Polymxa graminis*. This virus has some sequence similarity to Wheat Spindle Streak Mosaic \{10258\}.

- **YmYF**\{10258\}. 2DL\{10258\}. v: Yangfu 931\{10258\}. ma: Xpsp3039-2D/Xwmc181-2D - 0.7 cM - Xwmc41-3D - 8.1 cM - Xgwm349-2D\{10258\}.