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I. Article

Dosage effect of the *kr* genes on preventing crossability of Chinese Spring wheat with *Dasypyrum villosum* (L.) Candargy

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Summary

The crossabilities of monosomic and disomic Chinese Spring wheat with *D. villosum* have been tested. Monosomics of the homoeologous group 5 showed a significantly higher seed set than disomic Chinese Spring, whereas the other monosomics do not exhibit remarkable differences when they were crossed with *D. villosum*. The results indicated dosage effects of the three pairs of *kr* genes on preventing crossability between Chinese Spring and *D. villosum*. A gene or genes on D genome chromosome(s) was observed, which inhibits the development of the seed endosperm after hybridization, resulting in shrivelling seeds. The genetic mechanism of crossability of Chinese Spring wheat with *D. villosum* was suggested.

Introduction

Many wild relatives of common wheat, *Triticum aestivum* (genomically AABBDD), are reported to carry desirable genes which might be useful in broadening the genetic variability of cultivated wheat. Wide hybridization is considered by plant breeders as an important method to transfer these useful germplasm from wild species into hexaploid wheat (Sharma and Gill 1983).

Dasypyrum villosum (L.) Candargy ($2n=2x=14$, VV genomes, Syn. *Haynaldia villosa* (L.) Schur.), an annual, allogamous grass distributed in Mediterranean and Caucasus regions, is an important potential source of alien genes for wheat improvement. It possesses many useful characteristics including resistance to several wheat disease, such as powdery mildew, stem and leaf rust, and take-all fungus, and tolerance to adverse environmental conditions

(Blanco et al. 1983a, b; Jan et al. 1986) and favorable protein composition (Montebove et al. 1987)

Hybrids between diploid, tetraploid wheat and *D. villosum* have been readily achieved in a range of crossable rates (see review of von Bothmer and Claesson 1990). However, direct hybridization of hexaploid wheat with *D. villosum* has been more difficult. Successful crosses have been obtained, but usually with an extremely low percentage of seed set (Chen and Liu 1982; Jan et al. 1986; von Bothmer and Claesson 1990). Despite most of the possible chromosome addition lines of *D. villosum* to hexaploid wheat, *T. aestivum* L. cv. Chinese Spring, have been produced by a species-bridging method (Sears 1953; Hyde 1953), the direct cross between hexaploid wheat and *D. villosum* is beneficial to study the evolutionary and homoeologous relationships of the genus *Dasypyrum* with hexaploid *Triticum*, because of the *Dasypyrum* chromosomes in a pure hexaploid wheat background, while the addition lines achieved by a species-bridging procedure may contain either the genes or chromosomes of the bridging species. In this paper we report the results of an attempt to make cross between hexaploid wheat and *D. villosum*.

Materials and methods

Triticum aestivum L. cv. Chinese Spring, monosomics of Chinese Spring and *Dasypyrum villosum* (L.) Candargy from E. R. Sears were employed in the present study. All materials were grown in the field at Sichuan Agricultural University, Yaan city, Sicuan province, China. *Dasypyrum villosum* was planted normally at beginning of November in 1993. It is necessary that Chinese Spring and all its monosomics were sowed after a month to meet the flowering with *D. villosum*.

Chinese Spring and its monosomics, except the monosomics of 2D and 7B, were crossed as female with *D. villosum*. The Chinese Spring monosomic parents were selected from the selfed progenies of monosomic plants by means of root-tip mitosis analyses. No special aids and techniques were adopted in those crosses except to put newly mature anthers on just maternal stigma in profuse quantities. Well-developed caryopses were harvested after a month of pollination. Identifications of hybrid plants were carried out by the mitosis analyses. In the meanwhile, we examined whether the embryos were present for the non-germinating seeds or not. Thus the crossable percentage of this cross was estimated as the ratio of number of seeds with embryo to the number of pollinated florets. A Student's statistical t-test was applied to detect the crossability difference between a monosomics of Chinese Spring wheat and the control (normal Chinese Spring). The results of crossabilities of Chinese Spring wheat with *D. villosum* in two years were also used to control the crossable reliability.

Results and discussion

Pollination of 143 emasculated Chinese Spring florets by *D. villosum* yielded 1 seed, a ca. 0.7% seed set in 1993, whereas of 102 florets pollinated, 3 seeds were obtained, seed set was 2.9% in 1994. The t-test indicates there is no significant difference in two years, which inferred the crossing rates were identical in this study.

The results of cross were listed in Table 1, including the pollinated florets and percentages of seed set. The percentage of seed set varies between 0.0% and 22.6%. With regard to the female parents of monosomics, two distinct classes were found when *D. villosum* was used as pollinator. In the combinations with homoeologous group 5 of monosomics (5A, 5B and 5D) 17.1%, 22.6% and 10.8% of seed set were obtained, which demonstrated significantly higher seed set than that in cross with normal Chinese Spring by t-test, whereas in those with other homoeologous groups of monosomics, the percentages of seed set were below 10%, which did not exhibit remarkable differences in comparison to that with normal Chinese Spring. These results suggested the important role of maternal genotypes in wheat-*D. villosum* hybridization. We have known that three *kr* genes, which located on chromosomes 5A, 5B and 5D, respectively, control crossability between Chinese Spring wheat and rye species. The crossabilities of Chinese Spring with other wild species controlled by the *kr* genes have been reported in *Elymus giganteus* (Mujeeb-Kazi et al. 1983), *Hordeum vulgare* (Fedak and Jui 1982), and *Hordeum bulbosum* (Falk and Kasha 1981). Dai et al. (1988) investigated the relationship between the crossability of common wheat cultivars with *D. villosum* and rye, *Secale cereale*, by using common wheat cultivars having high and low crossable rates with rye, and found that the crossabilities of common wheat cultivars with *D. villosum* and rye are controlled by the same genetic system. Koba and Shimada (1993) reported the similar result using *Aegilops squarrosa* and *Secale cereale*. These findings support the traditional concept that the crossability between Chinese Spring wheat with wild species was suppressed by *Kr* genes, while was promoted by the recessive loci. Halloran (1966) reported a 1.2% seed set in his work using the monosomic 5B of Chinese Spring as female parent crossed with *D. villosum*, while using Chinese Spring as female parent, no seed was obtained. He has suggested that there might be a gene(s) on chromosome 5B of Chinese Spring which prevented successful cross in disomic condition, but in monosomic state, was ineffective. In the present study, it was found a high percentage of seed set in the cross between monosomic lines of 5A, 5B and 5D and *D. villosum*. With the results in the present study, we suggested that the three pairs of *kr* genes for crossability would be the recessive mutants of *Kr* gene, which expressed as reducing the effect on preventing cross between wheat and its wild species. Different *kr* gene would exhibit different degree of effect on reducing to prevent wide cross. The *kr1* gene is the strongest

Table 1. Seed set (%) and seedling produced from crosses between monosomics of Chinese Spring and *Dasypyrum villosum*

Monosomic for	No.florets pollinated	No.seeds with embryo	%	t-value	No. seedlings	% to florets pollinated
1A	108	8	7.8	1.22	1	1.0
1B	90	7	7.8	1.18	3	3.3
1D	40	4	10.0	1.82	0	0.0
2A	78	1	1.4	0.17	0	0.0
2B	107	1	0.9	0.55	0	0.0
2D	—	—	—	—	—	—
3A	87	6	6.9	0.93	2	2.3
3B	92	4	4.4	0.14	0	0.0
3D	158	4	2.5	0.19	0	0.0
4A	92	0	0.0	1.08		
4B	84	2	2.4	0.22	0	0.0
4D	108	0	0.0	0.51		
5A	76	13	17.1	3.00***	3	3.9
5B	106	24	22.6	4.02*****	3	2.8
5D	111	12	10.8	1.97*	0	0.0
6A	49	0	0.0	0.59		
6B	113	2	1.8	0.12	0	0.0
6D	61	1	1.6	0.00	0	0.0
7A	45	2	4.4	0.03	0	0.0
7B	—	—	—	—	—	—
7D	73	1	1.4	0.17	0	0.0
Normal C.S.	102	3	2.9	—	2	2.0

—: no cross made. *, ***, *****: significant at 5%, 0.5% and 0.1% level of probability, respectively.

mutant to reduce the effect of preventing wide cross and *kr3* is the weakest one. The results would have demonstrated the dosage effect of *kr* genes on preventing wide cross. The lack of *kr* genes in monosomics resulted in a higher seed set in their crosses with *D. villosum*.

Many obtained hybrid seeds failed to germinate on moist paper in petri dishes in the laboratory due mainly to their extremely shrivelling endosperm. Chen et al. (1982) and Dai

et al. (1988) found that the percentages of seed set in crossing *T. tauschii* as female parent, with *D. villosum* were considerably high (up to 80%), but the hybrid seeds almost did not germinate due to the lack of endosperm. *T. tauschii* is the donor species of D genome in hexaploid wheat. These facts may provide an evidence that a gene(s), carried on a certain D genome chromosome in *T. tauschii* and hexaploid wheat, refrains from development of endosperm in the process of seed formation after hybridization.

Table 1 shows the seedling frequencies per 100 florets pollinated is relatively low. For obtaining more hybrid plants, it is necessary to employ the cultural embryo rescue technique in the cross as von Bothmer and Claesson (1990) did in their work.

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Influence of the semidwarf genes, *Rht1* and *Rht2*, upon embryoid induction from anther culture of wheat

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Summary

To determine whether the semidwarf genes *Rht1* and *Rht2* influence on embryoid induction from anther culture, ditelosomic Chinese Spring for chromosomes 4B and 4D, and two sets of semidwarf isolines differing with the alleles at the *Rht1* and *Rht2* loci were compared. The absence of chromosome arms of 4B and 4D little affected embryoid induction. The *Rht1* and *Rht2* genes did not reduce embryoid induction in both sets. These results made it clear that there are no problems to improve cultivars carrying these semidwarf genes by means of anther culture method in a doubled haploid breeding program.

Key words: anther culture, embryoid induction, DH breeding, *Rht1* and *Rht2*, *Triticum aestivum* L.

Introduction

The semidwarf character has played an important part in crop production of major cereals. In common wheat (*Triticum aestivum* L.), twenty semidwarf genes, *Rht* (reduced height), have been identified. Of them, the genes commercially acceptable and successfully utilized are only *Rht1*, *Rht2* and *Rht8*. It is sure that these three genes will play a pivotal role in the future breeding programs. The *Rht1* and *Rht2* genes on the short arms of chromosomes 4B and 4D, respectively, are insensitive to gibberellic acid (GA) (Gale and Marshall 1976). In contrast, the *Rht8* gene on the short arm of chromosome 2D is responsive to it (Worland and Law 1980).

Application of doubled haploid (DH) breeding by anther culture is very promising and has many advantages, such that, short breeding period, easy detection of a character controlled by

recessive alleles, and so on. Despite significant improvements of anther culture technique, some genotypes show only weak response to current techniques (Andersen et al. 1987; Foroughi-Wehr and Zeller 1990).

Genotypic differences in anther culture response consist of at least three factors, embryoid induction, green plant regeneration and albino frequency (Henry and De Buyser 1985; Ekiz and Konzak 1994a). There are significant differences among genotypes in embryoid induction and albino frequency compared to plant regeneration (Ekiz and Konzak 1994b). Effects of the D genome on anther culture response has been demonstrated in recent studies (Shimada et al. 1991; Ghaemi and Sarrafi 1994). Foroughi-Wehr and Zeller (1990) assumed that the increased regeneration frequency by a substitution of chromosome 4B may result from a shift in hormone metabolism, which reduces the sensitivity of the cells to exogenous hormones. Mathias and Atkinson (1988) suggested that allelic variation at the *Rht1* and *Rht2* loci affect callus growth, somatic embryogenesis and plant regeneration, via an effect on the GA metabolism. Although genes that control somatic embryogenesis appear to be independent of those that control anther culture response (Agache et al. 1988), influences of the *Rht1* and *Rht2* genes on anther culture response have never been examined.

This study was intended to determine effect of chromosomes 4B and 4D using ditelosomic lines (Experiment 1) and of the *Rht1* and *Rht2* genes in isolines (Experiment 2) upon embryoid induction ability in wheat anther culture.

Materials and methods

Plant materials

Experiment 1: Chinese Spring (CS) and its four ditelosomic lines (DT) for chromosomes 4B and 4D were used. The lines were kindly presented by Prof. Y Furuta, Gifu University, Haruyutaka, which has a high embryoid induction ability, was used as a check cultivar.

Anther donor plants were grown in two replicates. The first replicate consisted of plants grown from April to July 1994 at the experiment field of Obihiro University and the second from June to August 1994 at a glasshouse.

Experiment 2: Three isolines of spring wheat Triple Derk (TD) and four of winter wheat Itana were used. They differ from each other in the alleles at the *Rht1* and *Rht2* loci. The TD and Itana isolines were kindly given by Dr. M.J. Dalling, University of Melbourne, and Dr. R.E. Allen, Washington State University, respectively.

TD and its semidwarf isolines had three replicates. The first replicate consisted of anther donor plants grown from April to July at the experiment field, the second and the third from March to May and June to August, respectively at a glasshouse. In the Itana set, anther donor plants were raised in two replicates. The first was from September 1993 to June 1994 at the

experiment field. Seeds of the second replicate were vernalized for 40 days at 5°C in a refrigerator, then they were grown from May to August 1994 in a growth cabinet (22, 18°C/day, night).

Anther culture

Spikes were collected when the microspores were estimated to be at the mid- to late-uninucleate stages, and were subjected to cold pretreatment for about 1 week at 4°C. Anthers of the primary and secondary florets from the middle of each spike were inoculated on the C17 medium (Wang and Chen 1986) with 0.9% sucrose and 0.7% agar (pH 5.6). Spikes were sterilized with 70% ethanol, and 12 anthers were placed in each ϕ 18 × 105 - mm test tube containing 5 ml medium under aseptic condition. All cultures were maintained at 29°C in the dark. The number of induced calli and embryoid were surveyed after about 40 days of incubation.

For the statistical analysis, all data were transformed by arcsine. Analysis of variance (ANOVA) was performed to evaluate effects of genotypes and environments.

Results

Experiment 1

Effect of the absence of 4B and 4D chromosome arms is given in Table 1. The number of cultured anther per line was about one thousand, except for DT 4BS and DT4DS. In these two DT lines, the removal of the long arms resulted in poor growth and small number of tillers. Embryoid induction frequency in Haruyutaka was 37.8% in the first replicate and 14.8% in the second replicate. CS euploid showed the induction frequency of 6.1% and 4.8%, in the first and second replicates, respectively. DT 4DL produced 7.6% embryonic structures which was the highest among the lines. On the contrary, DT 4DS had a low induction response with the mean of below 3%. However, the ANOVA indicated that all DT lines were not different from CS and there was a significant difference between replications ($p < 0.01$), because all lines in the first replicate showed higher induction frequency than in the second replicate. Consequently, it was found that the absence of chromosome arms of 4B and 4D had no significant effect on embryoid induction from anther culture.

Experiment 2

Effect of the *Rht1* and *Rht2* genes on embryoid induction in the TD set is shown in Table 2. The number of cultured anther of each line is about one thousand. In the TD set, the control TD carrying the *rht1* + *rht2* alleles had the mean induction frequency of 8.3%. There was no line that inferior induction response to the control, while the *Rht1* + *rht2* and *rht1* + *Rht2* lines had slightly high induction frequencies. The first replicate promoted a markedly high induction response over 20% in all lines. The ANOVA shows no significant differences among

Table 1. Anther culture response of the CS DT lines and ANOVA of embryoid frequency

Genotype	Replicate	No. of cultured anther	No. of calli + embryoid	% of calli + embryoid
CS (<i>rht1</i> , <i>rht2</i>) ^a	1	540	33(11) ^b	6.1
	2	456	22(3)	4.8
	Total	996	55(14)	5.5
DT 4BS (4BS; <i>rht1</i> , <i>rht2</i>)	1	312	26(4)	8.3
	2	192	5(1)	2.6
	Total	504	31(5)	6.2
DT 4BL (4BS; -, <i>rht2</i>)	1	540	46(15)	8.5
	2	480	12(1)	2.5
	Total	1020	58(16)	5.7
DT 4DS (4DL; <i>rht1</i> , <i>rht2</i>)	1	600	27(3)	4.5
	2	168	2(1)	1.2
	Total	768	29(4)	3.8
DT 4DL (4DS; <i>rht1</i> , -)	1	468	50(6)	10.7
	2	468	21(0)	4.5
	Total	936	71(6)	7.6
Haruyutaka ^c	1	540	204(22)	37.8
	2	480	73(8)	14.8
	Total	1020	277(30)	27.2

Factor	d.f	Mean square	F-value
Genotypes, G	4	10.61	3.35
Replications, R	1	88.51	28.01 ^{**}
G × R	4	3.16	

^a Missing chromosome arm and the allele at the *Rht* locus are present in parentheses.

^b The number of calli is given in parentheses.

^c Used as a check cultivar with a high response.

^{**} P=0.01~0.001.

lines but a significant difference among replications ($p < 0.01$).

In the Itana set shown in Table 3, the control Itana carrying the *rht1* + *rht2* alleles and the semidwarf *Rht1* + *Rht2* line had similar induction frequency around 4.5%. The *Rht1* + *rht2* line had a slightly high response. However, differences between genotypes were not larger than the variation due to genotype × replication interaction.

Table 2. Anther culture response of the Triple Derk set and ANOVA of embryoid frequency

Genotype	Replicate	No. of cultured anther	No. of calli + embryoid	% of calli + embryoid
Control, TD (<i>rht1</i> , <i>rht2</i>) ^a	1	216	43(8) ^b	19.9
	2	396	20(8)	5.1
	3	372	19(1)	5.1
	Total	984	82(17)	8.3
Semidwarf (<i>Rht1</i> , <i>rht2</i>)	1	156	31(4)	19.9
	2	288	19(9)	6.6
	3	540	54(9)	10.0
	Total	984	104(22)	10.6
Semidwarf. (<i>rht1</i> , <i>Rht2</i>)	1	324	67(14)	20.7
	2	384	36(19)	9.4
	3	480	19(3)	4.0
	Total	1188	122(36)	10.3

Factor	d.f	Mean square	F-value
Genotypes, G	2	4.36	0.59
Replications, R	2	141.69	19.17**
G × R	4	7.39	

^a Alleles at the *Rht* locus are present in parentheses.

^b The number of calli is given in parentheses.

** P=0.01~0.001.

Discussion

Embryoid induction from anther culture of the DT lines for chromosomes 4B and 4D was not significantly differed from CS euploid. Only DT 4DL showed a comparatively high response in the first replicate, suggesting a suppressing effect of the short arm of chromosome 4D. Shimada et al. (1991) found that a removal of either 4DS or 4DL of CS largely promoted embryoid induction. In the present study, embryogenesis of CS euploid was similar (about 6–7%) but no lines with remarkably increased response were detected. Thus, factor on chromosome 4D influencing embryogenesis in anther culture should be further examined.

In experiment 2, there were no semidwarf lines that decrease embryoid induction. Moreover, the *Rht1* + *rht2* lines were superior to the tall controls in embryoid induction in both the TD and Itana set. This would be supported by the high response of Haruyutaka used

Table 3. Anther culture response of the Itana set and ANOVA of embryoid frequency

Genotype	Replicate	No. of cultured anther	No. of calli + embryoid	% of calli + embryoid
Control, Itana (<i>rht1</i> , <i>rht2</i>) ^a	1	430	16(5) ^b	3.7
	2	400	20(3)	5.0
	Total	830	36(8)	4.3
Semidwarf (<i>Rht1</i> , <i>rht2</i>)	1	444	34(8)	7.7
	2	492	40(2)	8.1
	Total	936	74(10)	7.9
Semidwarf (<i>rht1</i> , <i>Rht2</i>)	1	576	28(6)	4.9
	2	516	37(7)	7.2
	Total	1092	65(13)	6.0
Semidwarf (<i>Rht1</i> , <i>Rht2</i>)	1	577	31(8)	5.4
	2	492	17(2)	3.5
	Total	1069	48(10)	4.5

Factor	d.f	Mean square	F-value
Genotypes, G	3	8.34	2.97
Replications, R	1	0.70	0.25
G × R	3	2.81	

^a Alleles at the *Rht* locus are present in parentheses.

^b The number of calli is given in parentheses.

as a check because this cultivar has a semidwarf stature controlled by the *Rht1* gene (Miura, unpublished data). These results may lead to conclusion that there are no problems in improving cultivars carrying the *Rht1* and *Rht2* genes by means of anther culture in breeding programs.

In addition to genotype of the anther donor plants, the physiological stage or the growing conditions of donor plants is a major determinant of anther culture response (Duyang et al. 1987; Bjornstad et al. 1989). Three experiments in the present study were designed to have two or three replicates with different conditions. The first replicate in the CS DT lines and the TD experiments, in which plants were raised at the experiment field showed striking superior response to other replicates in a glasshouse or growth cabinet. These results confirm importance of environments in which donor plants grow.

Moreover, anther culture response consist of three different and independently inherited

traits: embryoid induction, regeneration capacity and albino frequency (Henry and De Buyser 1985; Ekiz and Konzak 1994a). Hence examinations for regeneration of green plant and albino frequency are indispensable for much more practical study to determine the influence of the *Rht1* and *Rht2* genes on the production of DH.

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Natural occurrence of *Fusarium* mycotoxins in wheat grain collected from Dobroudja, the biggest wheat-producing region in Bulgaria

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Summary

Natural occurrence of *Fusarium* mycotoxins in grain of bread wheat due to fusarium head blight was surveyed using samples collected from Dobroudja, the biggest wheat-producing region in Bulgaria. Deoxynivalenol (DON) was detected in more than 80 % of the samples, while nivalenol (NIV) was detected only in one sample. A large variability was observed in the amount of DON (5-137 ng/g dry weight of grain). Our result shows that DON predominates among the trichothecene mycotoxins naturally occurring in this region of Bulgaria.

Introduction

Fusarium head blight is a disease causing significant yield losses in wheat and other cereals. The disease is important because it causes mycotoxicoses in animals and human due to contamination in infected grain and chaff with highly toxic fungal metabolites, i. e. trichothecene mycotoxins, including deoxynivalenol (DON), nivalenol (NIV) and their derivatives (Marasas et al. 1984).

Problems of fusarium head blight have not been seriously considered in Bulgaria until recently. There is no systematic survey on the distribution of causal *Fusarium* species, the natural incidence of fusarium head blight or *Fusarium* mycotoxin contamination in wheat grain. In Bulgaria, as in neighboring countries, however, a slowly but progressively increasing incidence of this disease has been noticed recently. We therefore made a survey on the natural

occurrence of *Fusarium* mycotoxins in wheat grain collected from Dobroudja, the biggest wheat-producing region in Bulgaria.

Materials and Methods

Grain samples from forty-four breeding lines and cultivars of bread wheat (*Triticum aestivum* L.) were collected in the Experimental Fields and farmers' fields near the Institute of Wheat and Sunflower, Dobroudja, near General Toshevo, Bulgaria. Mycotoxin concentration in grain (10 g) was determined after extraction with acetonitrile-water (3:1) and purification by Florisil column and GC-MS according to the method by Luo et al. (1990). The determination was made in duplicate for all samples and mean values were presented.

Results and Discussion

A considerable amount of information is available on the natural occurrence of *Fusarium* mycotoxins in infected wheat grain in the central European countries, Canada, USA, China,

Table 1. Natural occurrence of *Fusarium* mycotoxins in grain of bread wheat collected from the region of Dobroudja, Bulgaria

Wheat line/cultivar	Origin	Mycotoxin(ng/g dry wt of grain)	
		DON	NIV
TR420-72IWS	Bulgaria	80	nd
TR880-58IWS	Bulgaria	103	nd
TR1020-75IWS	Bulgaria	80	nd
ID1052-4IWS	Bulgaria	nd	nd
TR880-152IWS	Bulgaria	nd	nd
AK302-1IWS	Bulgaria	11	nd
TR420-48IWS	Bulgaria	14	nd
IWWRN155/83P5052-53	Austria	15	nd
TRP859	England	70	nd
IWWPMP2022/85FR81-11	France	nd	nd
IWWPMP2116/85FR81-16	France	5	nd

(continued on the next page)

IWWPMP2119/85FR81-5	France	9	nd
IWWPMP2167/86FR84-3	France	83	nd
ARSLR62/87FR84-1	France	10	nd
ARSLR67/87FR84-6	France	112	nd
Roazon	France	80	nd
IWWRN105/84 Niavt 21	Hungary	nd	nd
FUS4/88	Hungary	nd	nd
FUS5/88	Hungary	91	nd
FUS6/88	Hungary	45	nd
FUS8/88	Hungary	67	nd
FUS9/88	Hungary	32	nd
5517A5-5-1P3	USA	43	nd
IWWRN144/83SC792197	USA	40	nd
IWWRN135/83SC783737	USA	nd	nd
IWWRN138/83SC790079	USA	nd	nd
IWWPMP2147/86SC820627	USA	8	nd
IWWRN145/85Zg37-82	Yugoslavia	26	nd
Sutjeska	Yugoslavia	20	nd
Bezostaya 1*	USSR	20	tr
Mironovskaya 61*	USSR	28	nd
Charodejka	Bulgaria	22	nd
Pliska	Bulgaria	28	nd
Pliska*	Bulgaria	68	374
Prjaspa	Bulgaria	13	nd
Prjaspa*	Bulgaria	17	nd
Prostor	Bulgaria	57	nd
Rusalka*	Bulgaria	13	nd
Sadovo 1*	Bulgaria	60	nd
Slavyanka 196*	Bulgaria	27	tr
Trakia*	Bulgaria	25	tr
Vratsa*	Bulgaria	92	nd
Yantar*	Bulgaria	137	nd
Zlatostrui*	Bulgaria	65	nd

nd: not detected; tr: traces (<1 ng/g dry wt).

* These samples were collected from farmers' fields and all others were from the Experimental Fields of the Institute of Wheat and Sunflower.

Korea and Japan (Trenholm et al. 1983, Eppley et al. 1984, Ueno et al. 1985, Visconti et al. 1986, Tanaka and Ueno 1989, Van Egmond 1989, Snijders 1990, Luo et al. 1992). On the other hand, there has been very little information in Bulgaria (Yoshizawa 1992). According to these reports, DON is distributed worldwide, while NIV is restricted only in western-Japan, Korea and England (Tanaka and Ueno 1989). In the present survey we studied 44 samples randomly collected in the region of Dobroudja and found that more than 80 % of them were contaminated with DON, while NIV was detected only in one sample (Table 1). A large variability was found in the amount of DON, ranging from 5 to 137 ng/g dry weight of grain. This level of DON contamination was similar to that already reported in the central and south-eastern European countries including Bulgaria (Yoshizawa 1992).

Among several *Fusarium* species causing fusarium head blight in wheat, *F. graminearum* was most frequently distributed in the humid and moderately humid regions in south-eastern Europe, e. g. in Rumania and Yugoslavia (Moldovan et al. 1981, Tomasovic and Koric 1991). In the north-eastern part of Bulgaria and especially in the region of Dobroudja, however, *F. culmorum* has been considered as the main pathogen. The occurrence of this species varied from 60 to 80 % depending on the year among *Fusarium* species recognized in infected wheat grain, followed by *F. graminearum* (Petkov unpublished). *F. equiseti* (Corda) Sacc. and *F. avenaceum* (Fr.) Sacc. are considered as semi-important pathogens infecting wheat spikes in this region (Petkov unpublished). A study on the mycotoxin productivity of *Fusarium* species collected from the infected wheat grain from Dobroudja showed that a majority of the isolates of *F. graminearum* and *F. culmorum* produced mainly DON and its derivatives on artificial "rice culture" (Yoshizawa in prep.). Our result at least shows that DON-producing strains are more important in epidemics of fusarium head blight than NIV-producing strains in Bulgaria. It was also noted that some cultivars that were widely cultivated in the region in the near past, such as Charodejka, Rusalka and Trakia, showed lower levels of mycotoxin contamination than the recently developed cultivars including Yanter and Prostor (Table 1). Among the latter group, only Prjaspa showed a low level of DON in the two samples examined. Since DON and related trichothecenes likely play a role as a virulence factor in the development of fusarium head blight (Atanassov et al. 1994), the above result might indicate higher susceptibility of some recent cultivars to this disease.

Our first survey of the natural occurrence of *Fusarium* mycotoxins in Bulgaria showed the importance of DON as a prominent trichothecene mycotoxin in this area. It is emphasized that this type of survey should be continued at least for some years using a larger number of samples.

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II. Research Information

Effect of heat stress on germinability of some wheat genotypes and their hybrids

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Wheat is primarily a cool season crop. Heat stress is known to affect coleoptile length as well as number of primary roots and eventually the germinability, in wheat. Rainfed wheat in India is required to be grown little early to take advantage of the preceding monsoon rains. This makes wheat germinate under relatively higher temperature conditions. The study under report made use of eight wheat purelines viz., Hindi 62, Narmada 4, Kalyansona, Kharchia 65, Sonalika, WH 283, DWR 39 and HI 1011, and their all possible 28 hybrids excluding reciprocals, to identify genotypes suitable for such heat stress conditions. A random sample of 12 well formed seeds was taken for each genotype for each of the three replications studied. Four seeds wrapped in water soaked germinating paper were kept in one petriplate. This was repeated for all the genotypes over the two temperatures of 20 and 35°C. After seven days, observations on coleoptile length, average number of radicals and total radical length were recorded.

Analysis of variance indicated significant differences among entries for all the characters (Table 1). Temperature \times entries interaction was found to be non-significant only for average number of radicals. Therefore, only pooled results are presented for this character. Mean, range and coefficients of variation for different characters over the two temperature regimes as also the genotypes least affected by heat stress are presented in Table 1. It can be seen from the table that genotypes viz. DWR 39, WH 283 and Kharchia 65 resisted the stress effect. Many hybrids involving Hindi 62 as one of the parents showed minimum change due to heat stress. These genotypes hold promise to serve as good starting material for any breeding work aiming at developing wheat genotypes tolerant to heat during germination and early post germination phase.

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Table 1. Analysis of variation (ANOVA) and the genotypes least affected by high temperature stress for different characters

Sl. No.	Parameter	Average number of radicals	Total radical length (cm)			Coleoptile length (cm)		
			20°C	35°C	Pooled	20 °C	35 °C	Pooled
A	ANOVA parameter	Pooled	20°C	35°C	Pooled	20 °C	35 °C	Pooled
A1	Mean	9.5	22.2	7.3	—	9.8	3.6	—
A2	Range	3.0 to 4.57	3.3 to 41.3	0.8 to 17.6	—	2.6 to 15.4	0.9 to 8.6	—
A3	Coefficient of variation	68.6	38.3	60.8	—	33.9	51.2	—
A4	Mean squares							
	-Entries	0.94**	222.4**	59.8**	110.4	33.4**	10.2**	33.6**
	Temperature × Entries	0.17	—	—	169.5**	—	—	10.7**
B.	Genotypes least affected by high temperature stress #		Hindi 62 × Somalika (-2.3) Kharchia (-8.8) DWR 39 (-11.8) Hindi 62 × WH 283 (-15.2) HI 1011 (-21.0) WH 283 (-26.9) Hindi 62 × Kalyansona (-28.0)			DWR 39(-15.4) Hindi 62 × Kalyansona (23.5) WH 283 (31.8) Hindi 62 × Kharchia 65 (-40.6) Hindi 62 × WH 283 (-45.3) Hindi 62 × HI 1011 (-50.9) Hindi 62 × Narmada 4 (-51.6)		

** Significant at 1% level of significance

Figure in parentheses indicates % change by 35°C over 20 °C.



***Triticum aestivum*—*Triticum araraticum* hybrids and their cytology**

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Triticum araraticum (wild form of *Triticum timopheevi*, $2n=4x=28$, AAGG) has been considered a valuable source of resistance to a number of wheat (*Triticum aestivum*, $2n=6x=42$, AABBDD) pathogens, particularly *Puccinia graminis tritici*, *P. recondita tritici*, *Erysiphe graminis tritici* and *Tilletia* species (McIntosh and Gyrfas 1971). However, poor crossability of *T. araraticum* with cultivated wheat is the main barrier which precludes the transfer of resistance gene(s) from the former to the latter species. Consequently, there are relatively few reports on the successful transfer of disease resistance from *T. araraticum* to common wheat (Allard and Shands 1954; Watson and Luig 1958; McIntosh and Gyrfas 1971).

In order to transfer useful genes from *T. araraticum* to common wheat, three wheat cvs. Chinese Spring (*ph 1b* mutant), C 306 and HB 208 were crossed as females with *T. araraticum* (Acc. No. 4697) under field conditions. Embryo culture or hormone application was not employed and the crossed seed were harvested at maturity. For meiotic studies, the spikes of the hybrids were fixed in aceto-alcohol (1:3 v/v) for 24 hours and then stored in 70% alcohol. The anthers were squashed in 2% acetocarmine and examined for metaphase-1 chromosome relationships.

The number of florets pollinated for the three crosses, viz., *ph 1b* mutant \times *T. araraticum*, C 306 \times *T. araraticum* and HB 208 \times *T. araraticum* (hereafter Hy-1, Hy-2 and Hy-3, respectively) were 40, 35 and 38, respectively and the per cent seed set 37.5, 34.3 and 31.6, respectively. Depending on the crossing directions and wheat genotypes with or without *kr1* gene, seed set ranging from 3.8 to 34.0% has also been reported by Farshadfar et al. (1994).

Hybrid plants derived from the three interspecific crosses were partially fertile and there were 8.0, 1.2 and 3.0 seeds per spike in Hy-1, Hy-2 and Hy-3, respectively. The pollination of over 35 florets of Hy-3 with wheat cv. RSP 122 produced 8 BC₁ seeds. The percentage germination of F₂/BC₁ seeds of Hy-1, Hy-2 and Hy-3, and that of Hy-3 \times RSP 122 was 13.3, 6.6, 8.0 and 12.5, respectively.

While Hy-3 and its backcross with RSP 122 await cytological analysis, the data of meiotic

Table 1. Meiotic chromosome pairing in F₁'s of interspecific cross of *T.aestivum* with *T. araraticum*

Cross	Chromosome number	No. of PMC's analyzed	Chromosome pairing			
			I	II		III
				Ring	Rod	
<i>ph 1b</i> mutant × <i>T. araraticum</i>	35	16	19.8 *(17-21)	7.9 (7-9)	—	—
C 306 × <i>T. araraticum</i>	35	29	28.1 (23-31)	1.5 (0-3)	1.9 (0-4)	0.03 (0-1)

*Figures in parentheses indicate range value.

chromosome pairing pertaining to Hy-1 and Hy-2 are presented in Table 1. The pentaploid hybrids ($2n=5x=35$, ABDAG) originating from *ph 1b* mutant × *T. araraticum* cross combination (Hy-1) showed univalents and bivalents without multivalent formation. While number of univalents and bivalents ranged from 17–21 and 7–9, respectively, the mean bivalent frequency was 7.9 per cell.

Hy-2, on the other hand, was characterized by the formation of 28.1 univalents, 3.3 bivalents and 0.03 trivalents per cell. Of the bivalents, 44.0% were ring and 56.0% rod configurations. Trivalent association was recorded in one cell (3.4%) only. Increased level of chromosome pairing in Hy-1 as compared with Hy-2 could be due to the absence of *Ph* gene.

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III. Gene Symbol

Catalogue of Gene Symbols for Wheat: 1995 Supplement

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The most recent edition of the Catalogue (9441) was published in the Proceedings of the 8th International Wheat Genetics Symposium held in Beijing, China, 1993 (1995 ZS Li & ZY Xin eds. pp.1333-1500). The revised Guidelines for Nomenclature of Biochemical/Molecular Loci in Wheat and Related Species (which include nomenclature guidelines for QTLs) were included with the 1994 Supplement. This Supplement has been offered to the editors of the Annual Wheat Newsletter and the Wheat Information Service for inclusion in their respective journals.

Genetic nomenclature proposal

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format 'XxyzAN1N2N3, where 'X' is the usual symbol for a DNA marker of unknown function; 'xyz' is the usual laboratory designator (e.g., kg for Keygene); A is a single upper-case letter denoting the rare-cutter enzyme used, e.g., P for PstI, etc.; N1 and N2 are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N3 is a three-digit number corresponding to the molecular weight of the fragment.

The foregoing should be considered only as a proposal at this time as no AFLPs yet appear in the catalogue. Comments regarding the proposal are welcomed and should be sent to the authors of the catalogue.

Additions and revisions to symbols list:

Aba	Abscisic acid-induced
C1	Coloured aleurone (maize clone)
Esi	Early-salt induced
Ger	Germin
G1b3	(1-3,1-4)- β -glucanase
G1b33	(1-3)- β -Glucanase isozyme G3
G1b35	(1-3)- β -Glucanase isozyme G5
Gli-1-1	Omega gliadins
Gli-1-2	Gamma gliadins
Glob	7S globulin
Ica	Chymotrypsin inhibitor
Isa	α -Amylase and subtilisin inhibitor
Lhcb	Light-harvesting antenna complex for photosystem II (CAB)
P	Long glumes (polonicum)
Pdk	Pyruvate orthophosphate dikinase (Pdk replaces Ppdk)
Phy	Phytochrome
Pki	Protein kinase inhibitor

Plc Plastocyanin
Ppc Phosphoenolpyruvate carboxylase (*Ppc* replaces *Pepe*)
Psif Protein synthesis initiation factor
Sus Sucrose synthase (maize clone)
vg Variegated red seed coat colour

Additions to Laboratory Designators list

A list of laboratory designators that have appeared in the literature, including those listed below, is available electronically via the Internet Gopher from host greengenes.cit.cornell.edu, port 70, menu "Grains files to browse" / "Reserved Laboratory Designators for DNA Probes, Primers and Markers".

<p><i>abc</i> (Barley cDNA* clones) Kleinhofs, A. North American* Barley* Genome Mapping Project Dept. of Agronomy & Soils Washington State University Pullman, WA 99164 USA</p>	<p><i>cdo</i> (Oat cDNA clones) Sorrells, M.E. (see <i>bcd</i>)</p>
<p><i>ak</i> Kleinhofs, A.* (see <i>abc</i>)</p>	<p><i>csb</i> Appels, R. CSIRO*, Division of Plant Industry Institute of Plant Production and Processing GPO Box 1600 Canberra ACT 2601 Australia</p>
<p><i>bcd</i> (Barley cDNA clones*) Sorrells, M.E. Dept. of Plant Breeding & Biometry Cornell University 252 Emerson Hall Ithaca, NY 14853 USA</p>	<p><i>csc</i> Chandler, P.* CSIRO*, Division of Plant Industry Institute of Plant Production and Processing GPO Box 1600 Canberra ACT 2601 Australia</p>
<p><i>bgl</i> Lane, B.G.* Faculty of Medicine University of Toronto Dept. of Biochemistry Medical Sciences Building Toronto, Ontario M5S 1A8 Canada</p>	<p><i>csd</i> Dennis, L.* CSIRO*, Division of Plant Industry Institute of Plant Production and Processing GPO Box 1600 Canberra ACT 2601 Australia</p>
<p><i>bnl</i> Burr, B. Brookhaven National Laboratory* Biology Dept. Upton, NY 11973 USA</p>	<p><i>glk</i> (Wheat gDNA clones; 'glk' is lab designator for loci detected with 'Tag' clones) Appels, R. (see <i>csb</i>)</p>
<p><i>bzh</i> Dudler, R. Institut fur Pflanzenbiologie* Universitat Zurich Zollikerstrasse 107 CH-8008 Zurich Switzerland</p>	<p><i>hhu</i> Westhoff, P. Institut fur Entwicklungs- und Molekularbiologie der Pflanzen Heinrich-Heine-Universitat* Universitats strasse 1/Geb. 26.03.02 D-40225 Dusseldorf Germany</p>

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npi Grant, D.
Pioneer Hi-Bred
International
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php Grant, D. (see *npi*)

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UK

psr (Wheat clones)
Gale, M.D.
John Innes Centre
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Colney, Norwich NR4 7UH
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psp (PCR markers)
Gale, M.D. (see *psr*)

rgc (Rice cDNA* clones)
Sasaki, T.
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Tsukuba
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Japan

rgg (Rice gDNA* clones)
Sasaki, T. (see *rgc*)

rgr (Rice root* cDNA
clones)
Sasaki, T. (see *rgc*)

rgy (Rice YAC* end clone)
Sasaki, T. (see *rgc*)

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<p>wg (Wheat gDNA clones) Sorrells, M.E. (see <i>bcd</i>)</p>	

Organisation of the catalogue

4. Add **itv**: = Near isogenic tetraploid stocks.
ma: = Mapped in segregating populations.

Gross morphology

Add at the end of the section:

'Q has been mapped in the distal region of 5A, flanked by *Xrsq805(Embp)*-5A (proximal 4.6 cM) and *Xpsr370*-5A (distal 4.3 cM) (9542).'

Accumulation of abscisic acid (new section)

A quantitative trait locus (QTL) was mapped on 5AL between *Xpsr575*-5A (proximal) and *Xpsr426* (distal) (9544).

Anthocyanin Pigmentation

4. Purple Culm

Pc. **itv**: LD222*11/CS (Hope 7B) (9538).

Crossability with *rye* and *Hordeum* spp.

Insert: 'Crossability between wheat and *Aegilops squarrosa* is controlled by the Kr series of genes (9518).'

DNA Markers

See 'Genetic nomenclature proposal' above for a proposal for the naming of AFLP loci.

Delete the present preamble and substitute,

'The following list catalogues DNA-marker loci that (1) have been detected either by Southern hybridization of DNA restriction fragments or as sequence-tagged-sites by amplification of DNA fragments with primers and (2) have been localized to specific wheat chromosomes.

The list does not include the 5S-RNA or the 18S-5.8S-26S rRNA (*Nor*) loci, which are included elsewhere in the catalogue. No attempt has been made to list orthologous loci in related species, although many have been identified (e.g., 950,951).

The nomenclature used is that published in the 1994 Supplement, except for some loci detected with 'known-function' clones for which other nomenclature has been used in the publications cited. The reference(s) that follow the locus symbols designate the publication(s) in which the chromosomal locations or map positions of the loci were first reported. References that are in parentheses () contain the listed locus symbol, while the symbols for loci for which the references are in brackets [] were assigned by the curators in accordance with the current nomenclature guidelines. Symbols previously assigned to loci appear as synonyms in brackets. Symbols for a few DNA markers detected with known-function DNA probes are marked with an asterisk, *, ;these are temporary, pending assignment of the laboratory designator.'

Other chromosomes bearing markers detected with the same probe or the same primers are indicated in parentheses after the probe or the primers.

Locus Symbol	Identifying Probe or Primers
Group 1S	
Delete previous corresponding entries and substitute:	
<i>Xpsr11(Glu-3)-1A,B,D</i> [339].	[<i>XGli-1A,B,D</i> (9441)].pTag 544 (49).
<i>Xpsr13(Gli-1-1)-1A,B,D</i> [1130,1129].	[<i>XGli-A,B,D1-1</i> (9441)].
	pTag 1436 (49).
<i>Xpsr884(Ica1)-1A,B,D*</i> (1129).	[<i>XIca-1A,B,D</i> (1129)]. pcI-1-4 (1162).
Add:	
<i>Xpsp2999(Glu-3)-1A</i> (9540).	PSP2999F/PSP2999R.
<i>Xpsp3000(Gli-1-1)-1B</i> (9540).	PSP3000F.1,PSP3000F.2/ PSP3000R.
<i>Xpsr634-1A,B,D</i> (9546,9547).	PSR634.
<i>Xpsr937-1A,B,D</i> (9546,9547).	PSR937.
<i>Xpsr949-1A,B,D</i> (9546,9547).	PSR949.
<i>Xpsr1201-1A</i> (1179).	PSR1201 [a39(159)]. (5A,4D,5B).
Group 1L	
Delete previous corresponding entries and substitute:	
<i>Xcdo1312-1B</i> [24].	[<i>XcniCDO1312-1B</i> (9441)].
	CDO1312. (5A,4B,D).
<i>Xcsd19(Adh)-1A,B,D</i> [726].	[<i>XAdh-1A,B,D</i> (9441), <i>Adh-A,B,D2</i> (726), <i>Xadh3'</i> (309)]. p3NTR (726).
<i>Xhhul(Pdk1)-1A,B,D</i> [138].	[<i>XPpdk-1A,B,D</i> (9441)].
	PPDK4 (1152).
<i>Xmsu488(Lec)-1A,B,D</i> [1130,1129].	[<i>XLec-1A,B,D</i> (9441)].pNVR1 (835).
<i>Xpsr12(Glu-1)-1A,B,D</i> [1069,340].	[<i>XGlu-A,B,D1-1</i> , <i>XGlu-A,B,D1-2</i> (9441)].
	pTag1290 (1069).

Xpsr82 (Em)-1A,B,D* (269). [XEm-1A,B,D (9441)]. p10-15 (1161).
Xpsr121 (Glb3)-1A,B,D (342). [XGlb3-1A,B,D (9441)]. PSR121 (140). (7A,B,D).
Xpsr462 (Pgk1)-1A,B,D [138]. [XPgk1-1A,B,D (9441)]. P7 (606).
Xwia482 (Glb3)-1A,B,D [342]. [XGlb3-1A,B,D (9441)]. pLW2.1 (605). (7A,B,D).

Add:

XEsi47-1A,B,D (9583). pESI47 (9584).
XLhcb1-1A,B,D (9592). Primers for exon of wheat *Lhcb1*1*.
Xpsr78-1A,B,D (9546,9547). PSR78. (3A,B,D).
Xpsr313-1A,B,D (9546,9547). PSR313.
Xpsr601-1A,B,D (9546,9547). PSR601.
Xpsr941-1A,B,D (9546,9547). PSR941.
Xpsr946-1D (9547). PSR946. (2D, 5D, 7A,DL,DS).
Xpsr953-1A,B,D (9546,9547). PSR953.
Xpsr957-1A,B,D (9546,9547). PSR957.
Xwye838 (Adpg2)-1A,B,D (9546,9547). pSh2.25 (9555).

Group 1

Delete: *Xadh3'* (see '*Xcsd19(Adh)*-1A,B,D' in Group 1L)

Add:

Xnpi97-1A,B (9543). Npi97. (4B,D).
Xnpi293-1A,B,D (9543). Npi293.
Xrgc405-1D (9549). RGC405.
Xrgc424-1A,B,D (9549). RGC424.
Xrgc470-1A,B,D (9549). RGC470.
Xrgg1084-1A (9549). RGG1084.
Xrgr662-1A,B,D (9549). RGR662. (7A,B,D).
Xumc81-1B (9543). UMC81. (5A,B,D, 7A,B,D).

Group 2S

Revise: *Xpsr946-2D*; add '1D' in the last column.

Delete previous corresponding entries and substitute:

Xbzh834 (Per)-2A,B,D [186]. [XPer-2A,B,D]. POX375 (850).
Xpsr489 (Ss2)-2A,B,D* [186,127]. [XSs2-2A,B,D]. pST3 (643).
Xpsr801 (Rbcs)-2A,B,D* [138,293]. [Rbcs-2A,B,D (138), xbcs-2A,B,D (293)]. pW9 (109), pTS512 (1001). (5A,B,D).
Xpsr804 (Sbp)-2B(1) [183,182]. [XSbp-2B(1)]. S9.2 (837). (2BL,3A,B,D,7B).
XRbpα-2A,B,D (293)*. pSV10 (293).

Group 2L

Delete previous corresponding entries and substitute:

Xpsr471 (Gadp1)-2A, B, D* [138]. [XGadp1-2A, B, D]. pZm57 (108).
Xpsr804 (Sbp)-2B.2 [183, 186]. [XSbp-2B(2)]. S9.2 (837).
 (2BS, 3A, B, D, 7B).

Group 2

Add:

Xphp10005-2A, B, D (9543). Php10005. (7A, B, D).
Xpsr2019 (Aba8)-2A, B, D (323). ABA8
Xrgc12-2A, B, D [9549]. [XEif-2A, B, D]. RGC12. (5B).
Xrgc854-2B, D (9549). RGC854.
Xumc190 (Sus1)-2B, D (9543). UMC190. (7A, 4A, 7D).

Group 3S

Add:

Xppc-3A, B, D* (9592). pM52/SE3. (7A, B, D).
Xpsr1060-3A, B, D (185, 144). PSR1060.
Xrgc30-3A, B, D (9549). RGC30.
Xrgc146-3A, B, D (9549). RGC146.

Group 3LNote: *Xpsr1060* moved to 3S.

Delete previous corresponding entries and substitute:

Xcsc475 (Tlp)-3A, B, D [185]. [XTlp-3A, B, D]. pHv14 (137).
Xpsr804 (Sbp)-3A, B, D [183, 182]. [XSbp-3A, B, D]. S9.2 (837). (2BS, BL, 7B).
Xpsr833 (Per)-3A, B, D* [274]. [XPer-3A, B, D]. BP1 (847). (7A, 4A, 7D).
Xrsq805 (Emb)-3B [180]. [XEmb-3B]. pGC19 (322). (5A, B, D,
 6A, B, A^d, 7D).
Xwia483 (Cxp1)-3A, B, D [182]. [XCxp1-3A, B, D]. pλc.3 (188).
Xwia807 (Glb33)-3A, B, D [185]. [XGlb33-3A, B, D]. p7E (1128).
Xwia858 (Glb35)-3B, D [185]. [XGlb35-3B, D]. G5 (248).
 Add:
Xbcd115-3D [9589]. BCD115 (24, 9589).
Xbcd451-3D [9589]. [Xcn1BCD451 (9589)]. BCD451 (24, 9589).
Xcdo394-3D [9589]. [Xcn1BCD394 (9589)]. BCD394 (24, 9589).
Xcdo482-3D [9589]. [Xcn1CDO482 (9589)]. CDO482 (24, 9589).
XEsi48-3A, B, D (9583). pESI48 (9584).
XksuG48-3D [9589]. [XksuG48 (B) (9589)]. pTtksuG48 (309)
 [DGG48 (9589)].
Xpsr78-3A, B, D (182). PSR78. (1A, B, D).
Xrgc112-3A, B, D (9549). RGC112.

Group 3

Delete: Xp300-3D.

Add:

XksuG36-3D [9589].

pTtksuG36 (309).

[DG G36(9589)].

Group 4S (4AL:4BS:4DS)

Revise: Xpsr153-4A,B,D, Xpsr1206-4A and Xpsr1316-4A; add (9541) as reference.

Delete previous corresponding entries and substitute:

Xak466(Nra1)-4A [140].

[XNra-4B (140),
XNra-4A (9441)]. pNRp10 (142). (6A,B,D,
7A,D).Xpsr160(Plc)-4A [140]. [Xpsr160-4B (140),
Xpsr160-4A (9441)]. PSR160. (7A,D).Xpsr470(Wx)-4A* [140]. [XWx-4B (140),
XWx-4A (9441)]. pcwx27 (871).
(7A,D).

Xrsq808(Glob)-4A,B,D [718].

[XGlo-4A,B,D (9441)]. PSP511 (833).

Add:

Xabc310-4A (9541).

ABC310.

Xpsr332-4A,B,D (9541).

PSR332.

Xpsr392-4A (9543).

PSR392. (7A,D).

Xpsr573-4A (9541).

PSR573.

Xpsr584-4A,B,D (9541).

PSR584.

Xpsr604-4A (181,9541).

PSR604. (7A,D).

Xpsr833(Per)-4A* [181].

[XPer-4A].

BP1 (847). (3A,B,D,
7A,D).

Xpsr927-4A,D (9541).

PSR927. (7B).

Xpsr1206-4A (1179,9541).

PSR1206. (5B).

Xpsr1316-4A (1179,9541).

PSR1316
[L3-17(1131)].

(5B).

Xpsr1327-4A (9541).

PSR1327. (1A,D, 5D).

Xpsr1871(Pki)-4A,B,D* (9541).

pBT6-505T (9559).

Xucb821(PhyA)-4A,B,D (9541).

pZmP173.H3 (9560).

Xumc190(Sus1)-4A (9543).

UMC190. (2B,D, 7A,D).

Xwg622-4A,B (9541).

WG622.

Xwe835(Wx)-4A (9543).

pCSS22 (9555).

(7A,D).

Group 4L (4AS:4BL:4DL)

Note:

XPer-4A, Xpsr604-4A, Xpsr1206-4A and Xpsr1316-4A have been moved to 4AL.

Revise:

Xpsr59-4A,B,D; add (9541) as reference.

Xpsr164-4B,D; add (1189) as reference.

Xpsr563-4D; change reference to (342).

Xpsr567-4B,D; add '5A' in the last column.

Xpsr1051-4A,B,D; substitute (9541) for (869).

Delete previous corresponding entry and substitute:

Xpsr39(Fbp)-4A,B,D [138] (9541).

[XFbp-4A,B,D].

F16.1.

Xpsr484(Cat)-4B,D* [1179].

[XCat-4B,D].

pCat2.1c (83). (5A).

Add:

Xbg1485(Ger)-4A,B,D (9541).

Germin (5961). (3B).

Xbn15.09-4A,B,D (9543).

Bn15.09.

<i>XEsi3-4B,D</i> (9583).	pESI3 (9584).
<i>Xnpi209-4A,B,D</i> (9543).	Npi209.
<i>Xnpi403-4A,B,D</i> (9543).	Npi403.
<i>Xnpi427-4A,B,D</i> (9543).	Npi427.
<i>XPhy-4A,B,D*</i> (9592).	Primers for 3rd exon of oat <i>PhyA</i> .
<i>Xpsr648-4A</i> (9541).	PSR648. (1B, 7D).
<i>Xpsr860 (Uba)-4A,B,D</i> (9541).	pUBA1 (369). (5A,B,D).
<i>Xpsr914-4A,B,D</i> (869, 9541).	PSR914.
<i>Xpsr920-4A,B,D</i> (9541).	PSR920.
<i>Xpsr921-4A,B,D</i> (9541).	PSR921.

Group 4

Add:

<i>Xnpi97-4B,D</i> (9543).	Npi97. (1A,B).
<i>Xrgc225-4A,B,D</i> (9549).	RGC225.
<i>Xrgc454-4A,D</i> (9549).	RGC454. (5A,B).

Group 5S

Revise: *Xpsr326-5A,B,D*: add (9542) as reference.

Xpsr946-5D: add '1D' in the last column.

Delete previous corresponding entries and substitute:

Nor-D3 (See Nucleolus Organiser Regions). [*XNor-D3*].
pTA71 (301).

Xwaxc1 (Acl1.1)-5A,B,D [184].
[*XAcl1-5A,B,D* (9441)]. pACP11.

Group 5L

Revise:

Xpsr164-5A; add (1179) as reference.

Xpsr1206-5B and *Xpsr1316-5B*; add (9541)
as reference.

Xpsr567-5B,D; change to '*Xpsr567-5A,B,D*'.

Delete previous corresponding entries and substitute:

Xksu24-5A,B,D.1,.2 [453].
[*Xksu24-5(1)A,B,D*]. pHv24.

Xpsr14 (α-Amy3)-5A,B,D [1179].
[*Xα-Amy-5A,B,D* (1179), *αAmy3* (62)].
λAmy33 (62).

Xpsr120-5A,B,D.1,.2 (585, 1179).
[*Xpsr120-5A,B,D(1), (2)*].
PSR120.

*Xpsr484 (Cat)-5A** [1179].
[*XCat-5A*]. pCat2.1c (83). (4B,D).

*Xpsr801 (Rbcs)-5A,B,D** [293].
[*rbcs-5A,B,D* (293), *XRbcs-5A,B,D* (9441)].
pW9 (109), pTS512 (1001).
(2A,B,D).

Xrsq805 (Embp)-5A,B,D [180, 1179].
[*XEmbp-5A,B,D* (9441)]. pGC19 (322)
(3B, 6A, B, A^d,
7D).

*Xpsr819 (Adpg1)-5A,B,D** [1179].
[*XAdpg1-5A,B,D*]. WL:agal (774).

*Xpsr860 (Uba)-5A,B,D** [1179].
[*XUba-5A,B,D*]. pUBA1 (369). (4A,B,D).

Xwaxc2 (Acl1.3)-5B [184, 1179].
[*XAcl3-5B*]. pACP1 (336). (7A,B,D).

Xwaxc4 (Acl1.2)-5A,B,D [1179].
[XAc12-5A,B,D]. pACP11 (337).

Add:
Xcdo504-5A (9542). CDO504.
XEsi4-5A,B (9583). pESI4 (9584).
XEsi14-5A,B,D (9583). pESI14 (9584).
XEsi28-5B,D (9583). pESI28 (9584).
XEsi32-5A,B (9583). pESI32 (9584).
Xpsb85-5A [9542]. [Xpsrb85]. PSB85.
Xpsb89-5A [9542]. [Xpsrb89]. PSB89.
Xpsr2021 (Aba2)-5A (9542). ABA2 (323).
Xsfri (9552). J13/1 / J13/2.
Xwg644-5A (9542). WG644.

Group 5

Delete: *Xpsr170-5B*.

Revise: *Xtam68-5A*; add '(6A^d,B^d)' in last column

Add:

Xpsr167-5B (950). PSR167. (6A,B,D).
Xrgc12-5B [9549]. [Xeif-5B]. RGC12. (2A,B,D).
Xrgc454-5A,B (9549). RGC454. (4A,D).
Xrgc975-5A,B,D (9549). RGC975. (7A,B,D).
Xrgg73-5A,B,D (9549). RGG73.
Xumc81-5A,B,D (9543). UMC81. (1B,7A,B,D).

Group 6S

Revise:

Xpsr167: Add (5B) in the last column.

Xtam6-6A,B (179), 6B^d (9596). TAM6 (179). (6A^d).
Xtam10-6A,B (179), 6B^d (9596). TAM10 (179). (6A^d).
Xtam31-6A,B,D (179), 6A^d,B^d (9596). TAM31 (179).
Xtam57-6A,B (179), 6B^d (9596). TAM57 (179). (6A^d,DL).
Xtam60-6B (179), 6A^d,B^d (9596). TAM60 (179).

Delete previous corresponding entries and substitute:

Xak466 (Nra1)-6A,B,D [140,475].
[XNra-6A,B,D(140),XNar-6A,B,D(475)].
bNRp10(142). (4A,7A,D).

Xpsr8 (Cxp3)-6A,B,D [60,429], 6A^d,B^d (9596).
[XCxp-6A,B,D(9441)]. 2437 (61).

Xpsr10 (Gli-2)-6A,B,D [339,429], 6A^d (9596).
[XGli-6A,B,D]. pTag53 (339,9599).
(6B^d).

Xpsr477 (Pgk2)-6A,B,D [138].
[XPgk2-6A,B,D]. p20 (606).

Xrsq805 (Embp)-6B [180,429].
[XEmbp-6B]. pGC19 (322). (3B,5A,B,D,
6AL,6A^d,7D).

Add:

Xbcd21-6D (9589). BCD21 (24,9589).
Xbcd342-6D (9589). BCD342 (24,9589).
XksuG8-6B^d (9596). pTtksuG8 (309). (6A^d,D).
XksuG48-6A^d,B^d (9596). pTtksuG48 (309).
XksuH11-6A^d (9596). pTtksuH11 (309).
Xmwg684-6B (9552). cMWG684.

Group 6L

Revise:

XksuF19-6B^d (9596). pTtksuF19 (309).

XksuF37-6A^d,B^d (9596). pTtksuF37 (309).

Xpsr463(Prk)-6A,B,D [138], *6A^d* (9596).
[*XPrk-6A,B,D* (138)].

Xtam9-6A,B,D (179), *6A^d* (9596). R6.1 (838).
TAM9 (179).

Xtam17-6A,B,D (179), *6A^d* (9596). TAM17 (179).

Xtam21-6A,B,D (179), *6B^d* (9596). TAM21 (179).

Xtam25-6A,B,D (179), *6A^d,B^d* (9596). TAM25 (179).

Xtam26-6A,B,D (179), *6A^d,B^d* (9596). TAM26 (179).

Xtam27-6A,B,D (179). TAM27 (179). (6A^d).

Xtam28-6B,D (179), *6A^d,B^d* (9596). TAM28 (179).

Xtam36-6A,B,D (179), *6A^d,B^d* (9596). TAM36 (179).

Xtam57-6D: Add '(6A^d,B^ds)' in last column.

Xtam74-6A,B,D (179), *6A^d* (9596). TAM74 (179). (6B^d).

Delete previous corresponding entries and substitute:

Xpsr463(Prk)-6A,B,D [138].

[*XPrk-6A,B,D*]. R6 (838).

Xrsq805(Embp)-6A [180,429].

[*XEmbp-6A*]. pGC19 (322). (3B, 5A,B,D,

6A^d,BS, 7D).

Xpsr815(α-Amy-1)-6A,B,D [566].

[*α-Amy1* (566), *Xα-Amy-6A,B,D* (9441)].

2128 (566).

Add:

Xak1220(Nra2)-6A,B,D [9585].

[*XNra-6A,B,D* (9585)]. pMJ4 (9586).

Xbcd1-6B^d (9596). BCD1 (24).

Xcsb112(Dhn5)-6A^d,B^d [9596].

[*XDhn5-6A,B* (9596)].

pHv5 (9599). (6D).

XESi18-6B,D (9583), *6B^d* (9596). pESI18 (9584). (6A,A^d).

XESi35-6A,B,D (9583). pESI35 (9584).

XksuE18-6B^d (9596). pTtksuE18 (309).

Xtam68-6A^d,B^d (9596). TAM68 (179). (5A,6D).

Xutal(Psif)-6B.1,.2 (9596) p26 (9598).

Group 6

Revise: *Xα-Amy-6D*; change reference for pHv10 to (744).

Delete previous corresponding entry and substitute:

Xcsb112(Dhn5)-6D [309].

[*Xhv5-6D* (309); *XDhn-6D* (9441)].

pTZ18R-DHN5 (161).

(6A^d,B^d).

Revise:

Xpsr563-6A; change reference to (342).

Xtam27-6A^d (9596). TAM27 (179). (6A,B,D).

Xtam68-6D (179). TAM68 (179). (5A, 6A^d,B^d).

Add:

XESi18-6A (9583), *6A^d* [9596]. pESI18 (9584).

(6B,D,B^d).

<i>XksuG8-6D</i> (9589), 6A ^d (9596).	<i>pTtksuG8</i> (309). [DG G8 (9589)]. (6B ^d).
<i>XksuG48-6D</i> (9589). [<i>XksuG48 (A)</i> (9589)].	<i>pTtksuG48</i> (309). [DG G48 (9589)].
<i>XksuH4-6D</i> (9589).	<i>pTtksuH4</i> (309). [DG H4 (9589)].
<i>Xnpi253-6A, B, D</i> (9543).	<i>Npi253</i> . (7A, B, D).
<i>Xpsr10 (Gli-2)-6B^d</i> (9596).	<i>pTag53</i> (339, 9599). (6A, B, D, A ^d).
<i>Xpsr2020 (ABA3)-6A, B, D</i> (323).	ABA3.
<i>Xrgc597-6A, B, D</i> (9549).	RGC597.
<i>Xrgy341-6B</i> (9549).	RGY34L.
<i>Xrsq805 (Embp)-6A^d</i> (9596).	<i>pGC19</i> (322). (3B, 5A, B, D, 6A, B, 7D).
<i>Xtam10-6A^d</i> (9596).	TAM10 (179). (6A, B, B ^d).
<i>Xtam57-6A^d</i> (9596).	TAM57 (179). (6A, B, B ^d).
<i>Xtam74-6B^d</i> (9596).	TAM74 (179). (6A, B, D, A ^d).
<i>Xumc114-6A, B, D</i> (9543).	UMC114. (7A, B, D).
<i>Xwg933-6A</i> (9596).	WG933 (24).

Group 7S

Revise: *Xpsr563-7A, D*; change reference to (342).
Xpsr567-7B; add '5A' in the last column.
Xpsr604-7A, D; add (9541) as reference.

Delete previous corresponding entries and substitute:

<i>Xak466 (Nra1)-7A, 7D</i> [140].	[<i>XNra-7A, D</i> (140)].	<i>bNRp10</i> (142). (4A, 6A, B, D).
<i>Xpsr160 (Plc)-7A, 7D</i> [140].	[<i>Xpsr160-7A, D</i> (140)].	PSR160. (4A).
<i>Xpsr470 (Wx)-7A, 7D*</i> [140].	[<i>XWx-7A, D</i>].	<i>pcwx27</i> (871). (4A).
<i>Xpsr490 (Ss1)-7A, B, D*</i> [342].	[<i>XSs1-7A, B, D</i> (342), <i>Ss1</i> (643)].	<i>pST8</i> (643).
<i>Xpsr833 (Per)-7A, D*</i> [181].	[<i>XPer-7A, D</i>].	<i>BP1</i> (847). (3A, B, D, 4A).
<i>Xpsr946-7D.1</i> (186).	[<i>Xpsr946-7D (1)</i>].	<i>PSR946</i> . (1D, 2D, 5D 7AL, DL).
<i>Xwaxc2 (Acl1.3)-7A, B, D</i> [184].	[<i>XAcl3-7A, B, D</i>].	<i>pACP1</i> (336). (5B).
Add: <i>XEsi2-7A, D</i> (9583).		<i>pESI2</i> (9584). (7AL, BL). (6A, B, D).
<i>Xnpi253-7A, B, D</i> (9543).		<i>Npi253</i> . (2A, B, D).
<i>Xphp10005-7A, B, D</i> (9543).		<i>Php10005</i> . (4A).
<i>Xpsr392-7A, D</i> (9543).		<i>PSR392</i> . (4A).
<i>Xumc105-7A, B, D</i> (9543).		UMC105.
<i>Xumc190 (Sus1)-7A, D</i> (9543).		UMC190. (2B, D, 4A).
<i>Xwye835 (Wx)-7A, D</i> (9543).		<i>pCSS22</i> (9555). (4A).

Group 7L

Revise: *Xpsr340-7A,B,D* and *Xpsr350-7B,D*; change reference to (342).

Delete previous corresponding entries and substitute:

Xhhu2(Ppc1)-7A,B,D [139,140].

[*XPepc-7A,B,D* (139,140),

XPpc-7A,B,D (9592)].

SORCO (1152).

(3A,B,D).

Xpsr3(α-Amy-2)-7A,B,D (566,139,140).

[*α-Amy2* (566), *Xα-Amy-7A,B,D* (566,139,140)].

4868 (61), *Amy2/46* (410).

Xpsr121(Glb3)-7A,B,D (9543).

PSR121 (140).

(1A,B,D).

*Xpsr476(Gapd2)-7A,B,D** [138].

[*XGapd2-7A,B,D*].

p2m9 (108).

*Xpsr803(Fed)-7A,B,D** [148,342].

[*XFed-7A,B,D*].

pFed (148).

Xpsr804(Sbp)-7B [183,182].

[*XSbp-7B*].

S9.2 (837). (2B,3A,B,D).

Xpsr946-7A,7D.2 [186].

[*Xpsr946-7A,7D(2)*].

PSR946.

(1D, 2D, 5D,
7DS).

Xrsq805(Embp)-7D [180,344].

[*XEmbp-7D*].

pGC19 (322). (3B, 5A,B,D,

6A,B,A^d).

Xwia482(Glb3)-7A,B,D [181,342].

[*XGlb3-7A,B,D*].

pLW2.1 (605).

(1A,B,D).

Add:

XEsi2-7A,B (9583).

pESI2 (9584).

(7AS,DS).

Xnpi454-7A,B,D (9543).

Npi454.

Xumc114-7A,B,D (9543).

UMC114.

(6A,B,D).

Group 7

Add:

Xnpi416-7A (9543).

Npi416.

Xpsr487(C1)-7D (9543).

pEco1.0 (9562).

Xrgc975-7A,B,D (9549).

RGC975. (5A,B,D).

Xrgr662-7A,B,D (9549).

RGR662. (7A,B,D).

Xumc81-7A,B,D (9543).

UMC81. (1B,5A,B,D).

Xumc113-7A,B,D (9543).

UMC113.

Xumc207(Ss1)-7A,B,D (9543).

UMC207(Sh1).

Frost resistance

Add: 'Frl has been mapped to the mid-region of 5AL, 2.1 cM distal from *Xcdo504-5A* and *Xwg644-5A* and proximal to *Xpsr426-5A* (9542).'

Glaucousness

W₁^I.

itv: LD222*11/*T.turgidum* var.

pyramidale recognitum

(9538).

Grain Hardness/Endosperm Texture (revised)

Grain hardness or endosperm texture significantly influences flour milling extraction, flour properties and end use. Using a Brabender

laboratory mill to produce bran samples, Law et al. (560) showed that grain hardness was controlled by alleles at a single locus. The dominant allele *Ha* controlling softness was present in Chinese Spring and the allele for hardness, *ha*, was present in Hope. More recently, it was shown that soft wheat possesses greater levels of a 15,000kD starch granule protein, friabilin, than hard wheats (9520).

Ha (560). 5DS (560). **v**: Chinese Spring (560); Cappelle Desprez (9520); Heron (1052,9520).
ha (560). **v**: Falcon (1052,9520); Holdfast (9520).
 s: CS*6/Cheyenne 5D (655); CS*6/Hope 5D (560). Cappelle Desprez*/Besostaya 5D (9520).

The addition of King II rye chromosome 5R converted Holdfast wheat from hard to soft (9520). A 14,500kD rye analogue was also isolated from 6x triticales which have soft texture (9520). All ryes have soft texture.

Two genes for grain hardness were reported in (43).

Hairy Glume

Hg. **itv**: LD222*11/*T. turgidum* var. durum melanops (9538).

Height

Rht12. 5A (9531).
 Rht12 delayed ear emergence by 6 days (9531).

Long Glume

P (9537). 7A or 7B (based on linkage of 0.2 with a gene for red coleoptile (9537)).
 itv: LD222*11/*T. turgidum* var. polonicum (9538).

Meiotic Characters

2. Pairing homoeologous

Ph1a. Not applicable - see *ph2b* (9516).

Insert after *ph1c*: The mutant lines with *ph1b* and *ph1c* carry deletions of the chromosome segment possessing *Ph1* in the respective parent lines (424,9517).

Ph2b (9516).

Nucleolus Organiser Regions

Nor-A1: Add '**dv**: *T. monococcum* (9587)' and add '167,252,607,720' as references for *T. spelta*.

Nor-A3: Add '9587' as reference after 5AS and add '*T. monococcum*' after '**dv**:'

Nor-A7 (9502). 5AL (9502). v: CS; Cheyenne; Wichita.
tv: Langdon.
Nor-B6 (9502). 1BL (9502). v: CS; Cheyenne, Wichita.
tv: Langdon.
Nor-D8 (9502). 3DS (9502). v: Wichita.

Two sites designated temporarily as Nor-Ax and Nor-Ay were identified in *T. monococcum* ssp. *boeoticum*, but were absent in ssp. *urartu*.

Proteins

2. Enzymes

I. Acid phosphatase

AcpH-M^V1 [9591]. [Aph-v (9591);
AcpH-M^V1 (9590)]. 4M^V (9591).
tr: H-93-33 (701).

Add comment 'Also, Wehling (9594) identified four acid phosphatase loci in *S. cereale*, three of which are located in 7R.'

II. Alcohol dehydrogenase (Aliphatic)

Adh-C1 [9595]. G (9595).
ad: *T. aestivum* cv. Alcedo/ *Ae.*
caudata line G.

Adh-M^V1: Add synonyms '[ADH₁ (701); Adh-M^V1 (9590)].'

III. Aminopeptidase

Amp-C1 [9595]. D (9595). ad: *T. aestivum*
cv. Alcedo/
Ae. caudata line D.

Amp-R2: Add comment

'Linkage data indicating that Amp-R2 is in 4RS has been reported (9582).'

V. β -Amylase

β -Amy-C1 [9595]. B (9595). ad: *T. aestivum*
cv. Alcedo/
Ae. Caudata line B.

Immediately prior to β -Amy-Agⁱ1, insert

'Two β -Amy-D^c1 alleles were predominant in 60 accessions of *T. tauschii* (9593).'

After β -Amy-Agⁱ1, add:

β -Amy-E^b1 (9588). 5E^bL (9588). tr: 5AS.5E^bL.

Revise the α -Amy1 listing as follows:

α -Amy1 [761,9519]. [Amy 6B2 (761), Amy-B2 (9519)].
6BL (761,9519). v: CS.
 α -Amy1a [9519]. [α -Amy-B1a]. v: CS.
 α -Amy1b [9519]. [α -Amy-B1b]. v: Jones Fife.
 α -Amy1c [9519]. [α -Amy-B4]. v: *T. durum ssp.*
georgicum

The presence of α -Amy1 reported in (761) was confirmed by segregational tests in a CS x Jones Fife population and in a population derived from a tetraploid cross (9519). The recombination with α -Amy-B1 was 9.3 % and 22.3 %, respectively.

VI. Endopeptidase

Ep-M^V1 [9590]. [*Ep-M^V1* (9590)]. *7M^VL. s:* *7M^V* (7D).

VII. Esterase

Immediately prior to *Est-A1*, insert:

'Genetic control of esterases [carboxylic ester hydrolases (E.C.3.1.1.1)], has recently been the subject of a comparative study (9554).'

EST-1 is a dimeric enzyme that electrofocuses around pH 4.0 and is expressed in all tissues except endosperm (9554).'

Est-H1; change reference to (9554).

Add:

Est-S¹1 (9554). *3S¹* (9554).
ad: CS/ *Ae. longissima*.

Immediately prior to *Est-A2*, insert: '*EST-2* is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.'

Immediately prior to *Est-A3*, insert: '*EST-3* is a monomeric enzyme that is expressed in young seedlings (this enzyme was not observed in 9554).'

Add:

Est-H3 (361). *7H* (361). ad: CS/Betzes.

Immediately prior to *Est-A4*, insert:

'*EST-4* is a monomeric, leaf-specific enzyme that electrofocuses around pH 4.5.'

Immediately prior to *Est-A5*, insert:

'*EST-5* consists of 20 or more monomeric, grain-specific isozymes that electrofocus between pH 5.6 and 7.0.'

Modify the sentence immediately prior to *Est-A6* to:

'*EST-6* is a dimeric enzyme that electrofocuses around pH 7.6 and is specific to endosperm.'

Modify the sentence that begins, "Three alleles at *Est-D^t5* , to 'Three and six alleles at *Est-D^t5* (in *T. tauschii*) were reported in 546 and 9593, respectively.'

Add:

Est-R6 (9546). *2RS* (9546). ma: DS2 x RxL10.

Modify the sentence immediately prior to *Est-A7* to:

'EST-7 is a monomeric enzyme that electrofocuses in the same region as EST-6 but is specific to green tissues.'

Add:

'EST-8 consists of about 10 isozymes that electrofocus 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 659 and 449.'

<i>Est-A8</i> [449] (9554).	[<i>Est-A6</i> (449)].	3AL (449).	▼: CS.
<i>Est-B8</i> [440] (9554).	[<i>Est-B6</i> (449)].	3BL (449).	▼: CS.
<i>Est-D8</i> [440] (9554).	[<i>Est-D6</i> (449)].	3DL (449).	▼: CS.
<i>Est-R8</i> [440] (9554).		6RL (9554).	

ad: CS/Imperial, King
II.

EST-9 is a monomeric enzyme that electrofocuses around pH 5.0 and is expressed only in embryos.

<i>Est-A9</i> (9954).	3AS (9954).	▼: CS.
<i>Est-B9</i> (9554).	3BS (9954).	▼: CS.
<i>Est-D9</i> (9554).	3DS (9954).	▼: CS.'

Add the following comments at the end of the Esterase section:

'EST-2, EST-5 and EST-8 are controlled by genes on 3L and where a recombination test was possible between *Est-D5* and *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 apply to the EST-1 and EST-6 genes located in the 3S arms (9554).

The *Est-6* gene of rye has been mapped (181) and the *Est-6* genes of wheat were mapped comparatively in the proximal region of 2S (186). The *Est-2*, *Est-5*, *Est-8* loci were mapped to the extreme distal region in the 3L arms (185).'

VIII. Glucosephosphate isomerase

Immediately prior to *Gpi-Agⁱ1*, insert:

'No allelic variation at *Gpi-D^t1* was found in 60 accessions of *T. tauschii* (9593).'

IX. Glutamate oxaloacetate transaminase

<i>Got-C3</i> [9595].	F (9595).	ad: <i>T. aestivum</i> cv. Alcedo/ Ae. caudata line C.
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Got-R2: Add synonym '[*Got3* (9594)].'

Got-R3: Add synonym '[*Got4* (9594)].'

Got-R4: Add synonym '[*Got2* (9594)].'

Add comment 'Wehling (9594) has identified a GOT locus designated *Got1* in 4RL of *S. cereale*.'

XVII. Shikimate dehydrogenase

Skdh-M^V1 [9590]. [Skdh-M^V1 (9590)].
5M^V. s: 5M^V(5A), 5M^V(5D).

XX. Aromatic alcohol dehydrogenase

Aadh-C1 [9595]. C (9595). ad: *T. aestivum* cv.
Alcedo/ Ae.
caudata line C.

XXI. Aconitase

Aco-M^V2 [9590]. [Aco-M^V2 (9590)].
5M^V. s: 5M^V(5A), 5M^V(5D).

XXV. Adenylate kinase

Adk-M^V1 [9590]. [Adk-M^V1 (9590)].
7M^VL. s: 7M^V(7D).

3. Endosperm storage proteins

I. Glutenins

Seven transfers of *Glu-D1a* and 10 of *Glu-D1d* (5 + 10) from chromosome 1D to chromosome 1A in triticale were described (9521).

4. Protease inhibitors

Add:

III. Inhibitors of α -amylase and subtilisin

<i>Isa-A1</i> (9553).	2AL (9553).	v: CS.
<i>Isa-A1a</i> (9553).		v: CS.
<i>Isa-A1b</i> (null) (9553).		v: Cajenne 71.
<i>Isa-B1</i> (9553)	2BL (9553).	v: CS.
<i>Isa-B1a</i> (9553).		v: CS.
<i>Isa-B1b</i> (9553).		v: Bihar.
<i>Isa-D1</i> (9553).	2DL (9553).	v: CS.

Orthologous genes were identified in *Ae. speltoides* and *T. timopheevi* (9553). All durum wheats investigated had the genotype *Isa-A1b*, *Isa-B1b*.

Red Grain Colour

The Red grain colour section has been considerably revised following a proposal for renaming the genes in set nomenclature (9558) and the availability of isogenic lines (9556) and mapping data (9551). The section is reproduced here in its entirety.

Gene symbols have been reassigned as proposed at the 8th International Wheat Genetics Symposium (9557), with the former R2 = R-A1, the former R3 = R-B1, and the former R1 = R-D1.

R-AI [389].[R2].	3AL (680, 714).	i: Novosibirskaya 67*9/Solo (9556).
R-BI [389].R3]	3BL (714, 9551).	i: Novosibirskaya 67*9/k-28536 (9556).
R-DI [390].[R1]	3DL (917, 919).	i: Novosibirskaya 67*9/CS (9556).
R-NI (9557).	3N (9557).	su: CS/Ae. uniaristata.
R-RI (9558).	6RL (9558).	ad: Holdfast/King II.
R-VI (1111).	3VL (1111).	tvad: Creso/D. villosum.

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-3Ag translocations (660).

Red colour is dominant to white; at each locus the white allele is assigned a and the red b. White-grained *T. aestivum* and amber-grained *T. durum* cultivars 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-DI.

Numerous genetic studies have identified hexaploid varieties carrying specified one, two, or all three R alleles:

R-A1b R-B1a R-D1a	Diamant 2 (11); ; Norin 10 -Brevor 14 (20); Red Bobs (714); Sapphire; Wembley (9551); Baron; Hustler; Maris Widgeon; Mercia; Motto; Slejpner; Talent (9546).
R-A1a R-B1b R-D1a	Dollar (9551); Canon; Grana; Supreme (9546).
R-A1a R-B1a R-D1b	Chinese Spring; Pawnee (390); Alexandria; Jerico; Minaret (9551); Apollo; Axona; Dwarf A; Fortress; Longbow; Luna; Mardler; Maris Huntsman; NFC 75/93/27A; Rapler; Voyage; Vuka (9546).
R-A1b R-B1b R-D1a	Red Chief (389); Avalon; Bersée; Cappelle Desprez; Feuvert; Mission; Parade; Rendezvous; Yuri (9551).
R-A1b R-B1a R-D1b	Broom (9551); Bezostaya 1; Brigand; Brock; Kronjuwel (9546).
R-A1a R-B1b R-D1b	Kharkov (714); Fenman; Norman; Pastiche; Riband; Sperber; Squadron; Urban (9546).
R-A1b R-B1b R-D1b	Arin; Banco; Joel; Koga; Vilmorin 5917 (473); Bowie; Frondoso (816); Frontiera (305); Hope (157,158); Japanese Bearded (1134); Kanred (760, 1027); Lin Calel (760); Neepawa; Park; RL 4137 (44); PI 178383 (709); Renown (303); Thatcher (694); Cub; Tonic (9551); Ambassador; Boxer; Brimstone; Carmen; Cheyenne; Dauntless; Drum; Durin; Favorits; Fresco; Galahad; Haven; Hornet; Kador; NFC 70/84C; Probus; Rannyaya 12; Rektor; Sentry; Soleil (9546).

Other studies identified wheats carrying either one or two, unidentified *R-1* alleles: (44, 305, 390, 451, 472, 473, 760, 816, 955, 967, 1054, 9551).

The *R-1* loci were mapped to the distal regions of the long arms of group 3, *R-A1* between flanking markers *Xpsr483(Cxpl)*-3A (28 cM proximal) and *Xpsr904*-3A (7 cM distal) (9551), *R-B1* between *Xbcd131-3B* (5 cM proximal) and *Xabc174-3B* (5 cM distal), *R-D1* between *Xbod131-3D* (cosegregant) and *Xabc174-3D* (15 cM distal) (9546).

Response to vernalization

Add the following comment immediately prior to *Vrn2*:

'*Vrn1* was mapped to the mid region of 5AL, cosegregating with *Xcdo504-5A*, *Xwg644-5A* and *Xpsr426-5A* (9542).'

Restorers for *T. timopheevii* cytoplasm

Rf1. 1AS (9511).

Rf4. 1BS (9511).

Rf6 (9523). 6AS [T6AL.6AS-6U] (9522).

tr: Line 2114 (9522).

6BS [T6BL.6BS-6U] (9522).

tr: Lines 040-5, 061-4 (9522).

Ribosomal RNA

5S rRNA genes

5S-Rrna-A1: Add '9587' as reference for 1AS.

5S-Rrna-A2: Add '9587' as reference for 5AS, add '208' as reference for CS and '208' and '9587' as references for *T. monococcum*.

Variegated Red Seed Coat

vg (9512).

v: Line 10859 (9512).

vgvg genotypes in Line 10859 are variegated. The *Vg/vg* locus was independent of the single red gene locus in Line 10859. In a cross to Selkirk (*R1R1 R2R2 R3R3*), *vgvg* was expressed only in plants with one *R* gene (9512).

Reaction to Pests and Diseases

Reaction to Barley Yellow Dwarf Virus

Bdv1 (977,981).

i: Jupeteco 73R (compared to Jupeteco 73S) (977).

v: Many CIMMYT genotypes, see *Lr34/Yr18/Ltn*.

Reaction to *Erysiphe graminis*

Pm7. Revised to: T4BS.4BL-5RL (9506), but more recently shown to be T4BS.4BL-2RL (9539).

Pm20. 6RL. v: KS93WGRC28 = P1 (9402,9528).
su: 6R(6D) (9506).
ad: 6R addition (9506).

Pm21 (9501). 6AS (T6AL.6VS). v: 5 independent translocations (9501).

Reaction to *Diuraphis noxia*

Dn1. 7D (9526).

Reaction to *Heterodera Avenae*

Cre1. Cre (996).

Cre2 (9510). v: H93-8 (9510).
Derived from Ae. ventricosa (9510).

Cre3. CcnD1 (9513), Ccn-D1 (9514).
2DL (9514). v: Synthetic hexaploids (9513).
dv: *T. tauschii* accessions AUS 18912 (9514); AUS 18913 (9514); CPI 110809 (9513); CPI 110810 (9514).

Cre4. CcnD2 (9513), Ccn-D2 (1914).
2D (9514). dv: *T. tauschii* accessions AUS 18914 (9513); CPI 110813 (9514).

Resistance to *Puccinia graminis*

Sr25. 7DL[T7DS.7DL-7Ae#1L (9508, 9509)].
v: Mutant 28 (9508).

Sr26. 6AL [T6AS.6AL-6Ae#1L (9508)].

Sr33. 1DS (9505).

Sr42 (9529). 6DS (9525) v: Norin 40 (9525).

Sr43. 7DL [T7DL-7e12L.7e12S] (9509).
tr: KS10-2 (471).
[T7DS.7e12L] (9509).
tr: KS23-9; KS24-1; KS24-2 (471).

Reaction to *Puccinia recondita* Rob. ex Desm.

Lr1. v: Laura Lr10 Lr34 (9530).

Add the following comment at the end of the Lr9 listing:
'Lr9 allele was mapped in the distal region of 6BL, cosegregating with Xmgw684-6B and the STS Xsfr1, 8 cM from Xpsr546-6B (9552).'

Lr10. v: Laura Lr1 Lr34 (9530).

Lr13. v: Biggar Lr14a (9530); Genesis Lr14a (9530). Kenyon Lr16 (9533).

Lr14a. v: Biggar Lr13 (9530); Genesis

Lr13 (9530).

Lr16. v: Kenyon Lr13 (9533).

Lr19. 7DL [T7DS.7DL-7Ae#1L (9508,9509)].
v: Mutant 28 (429).
[T7DS.7DL-7Ae#1-7DL (9508)].
v: Mutant 238 (489).

Lr25. Revised to T4BS.4BL-5RL (9506), but more recently shown to be T4BS.4BL-2RL (9539).

Lr34. 7DS (9532). v: Laura Lr1 Lr10 (9530).
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 (9432).

Lr37. Recessive (9529).

Lr43. 7D (9504).

Lr45 (9524). 2A [T2AS-2RS.2RL] (9524).
i: RL6144 = Thatcher*7/ST-1 (9524).
v: ST-1 (9524). Various Australian backcross derivatives (9524).

Complex genotype: Buck Manantial Lr3 Lr13 Lr16 Lr17 Lr34? (9533).
Pasqua Lr11 Lr13 Lr14b Lr30 Lr34 (9534).

Temporary designation: LrW2 (9503).

Genotype lists: Add: 9515 (U.S.A. cultivars).

At the end of the 'Reaction to *Puccinia recondita*' section, add the following comment:

'A gene, identified only as Lr, was transferred to wheat chromosome 2AS from 6M^V (9545). Cosegregating markers are Xpsr933-2A and Xpsr150-2A.'

Reaction to *Puccinia striiformis*

Yr6. v: Penjamo 62 (heterogeneous) Yr34 (9536).

Yr18. 7DS (9532 - complete association with Lr34).
v: Lerma Rojo 64 (9535);
Nacarzari 76 (9535); Tesia 79 (9535); Tonichi 81 (9535);
Wheaton (9535). Penjamo 62 Yr6 (heterogeneous) (9535).

Yr19 (9527). YrCom (9527).
5B (9527). v: Compair Yr8 (9527).

Yr20 (9527). YrFie (141).
6D (9527). v: Fielder Yr6 (9527).

Yr21 (9527). YrLem (141).
1B (9527). v: Lemhi (9527).

Yr22 (9527). YrLel (9527).
4D (9527). v: Lee Yr7 Yr23 (9527).

Yr23 (9527). YrLe2 (9527).
 6D (9527). v: Lee Yr7 Yr22 (9527).

Genetic Linkages

Chromosome 1D

1DS	<i>Gli-D1</i>	-	<i>Sr33</i>	5.6 ± 2.4%	9505
				7.6 ± 2.8%	9505
		-	Centromere	37.3 ± 5.1%	9505
		-	<i>Glu-D1</i>	44.3 ± 5.2%	9505
				47.2 ± 5.2%	9505
				47.2 ± 5.2%	9505
	<i>Sr33</i>	-	Centromere	29.6 ± 4.8%	9505
		-	<i>Glu-D1</i>	40.9 ± 5.2%	9505
				39.5 ± 5.1%	9505
1DL	<i>Glu-D1</i>	-	Centromere	16.5 ± 3.8%	9505

Chromosome 6A

6AS

Line 2114 Xbcd342-6U (*Rf6*)-cent 31.4 cM 9522

6AL

cent	-	<i>α-Amy-A1</i>	3.8%	9505
<i>B1</i>	-	<i>Rht12</i>	<2.5cM	9531
	-	<i>Ibf-A1</i>	0	9531*

* considered to be an anomolous result.

Chromosome 6B

6BL	cent	-	<i>α-Amy-B1</i>	13.8 ± 2.6%	9519
		-	<i>α-Amy-B3</i>	5.5 ± 1.7%	9519
	<i>α-Amy-B1</i>	-	<i>α-Amy-B3</i>	9.3 ± 2.2%	9519
durum					
	<i>α-Amy-B1</i>	-	<i>α-Amy-B5</i>	< 1.0%	9519
	<i>α-Amy-B1</i>	-	<i>α-Amy-B4</i>	22.3 ± 3.5%	9519
	cent	-	<i>α-Amy-B5</i>	2.1 ± 1.1%	9519
	cent	-	<i>α-Amy-B1</i>	13.2 ± 3.5%	9519
	cent	-	<i>α-Amy-B4</i>	26.1 ± 5.0%	9519

Chromosome 7D

7DS. This chromosome arm is physically longer than the arm designated 7DL, but is homoeologous to those arms designated 7AS and 7BS (9507,9508).

Bdv1 - *Lr34/Yr18/Ltn* 0 977

7DL. Physically shorter than 7DS; see note for 7DS above.

7DS	<i>Lr34</i>	-	<i>Lr29</i>	0	9432
	<i>Lr34</i>	-	<i>Rc3</i>	30.25 ± 2.88%	9432

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Amendments

323. Replace: Gulli M, Maestri E, Hartings H, Raho G, Perrotta C, Devos KM, & Marmiroli N Isolation and characterization of abscisic acid inducible genes in barley seedlings and their responsiveness to environmental stress. *Life Science Advances - Plant Physiology* (In Press).
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IV. Proposal

Suggested guidelines for the nomenclature and abbreviation of the genetic stocks of wheat, *Triticum aestivum* L. em Thell., and its relatives¹

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The current nomenclature for describing the aneuploids of common wheat was introduced by Sears in 1954 and described in detail by Kimber and Sears in 1968. This nomenclature can be lengthy, and its use in manuscripts and descriptive figures cumbersome. Additionally, the needs of computerized databases require a shortening of these terms to save time and storage space. The ability to search lists of stocks suggests the need for succinct, descriptive abbreviations for the genetic stocks in wheat. GrainGenes, the wheat genome database, is no exception as search criteria can yield several screens of data. The purpose of this communication is to provide a list of recommended abbreviations for the aneuploid lines and genetic stocks in wheat.

Several recommended guidelines presented by Kimber and Sears (1968) will be used. These include designating:

- i) telocentric chromosomes with the letter "t",
- ii) isochromosomes with the letter "i",
- iii) the ability of chromosomes to pair with superscripts following the chromosome symbols. The actual pairing may vary considerably from cell to cell. The idealized pairing configuration is indicated in all cases even though it may rarely form,
- iv) chromosome status shown by the chromosome number followed by symbols indicating the configuration,
- v) chromosome arms by S (genetically short) or L (genetically long), and
- vi) substituted chromosomes by the homoeologous group number and genome designation. The designation of the chromosome that was replaced follows in parentheses.

Publications by Gill (1986) and Gill et al. (1991) added additional descriptors for wheat genetic stocks. The symbols were based on suggestions by the Chicago (1966) and Paris Conferences (1971) for Standardization in Human Cytogenetics. Where applicable, these conventions will also be used:

- vii) single and three letter designations specify rearranged chromosomes, such as "del" for deletion and "r" for ring chromosome,
- viii) the short system for defining translocation lines includes only the break points and the following punctuation: "." indicates a break at the centromere, a dash "-" indicates an interstitial breakpoint, and a slash "/" indicates an unknown breakpoint,
- ix) the detailed system describes translocation lines by defining their band composition and the additional symbols, ":" break (terminal deletion), "::" break and join, and
- x) a translocation chromosome is indicated by a "T" preceding a description of the translocation. Further descriptions of translocated chromosomes are given in Gill et al. (1991) and will be described as needed.

A brief survey of the literature published in the proceedings of the International Wheat Genetics Symposia (I through VII), as well as later issues of the journal GENOME, indicate that the choice of

¹ This is contribution 95-541-J from the Kansas Agricultural Experiment Station, Manhattan.

terminology is left to the authors. However, it seems that over time, some conventions were standardized. These are the designation of:

- xi) nullisomic lines with an "N" followed by the designated chromosome and genome,
- xii) monosomic lines with an "M" followed by the designated chromosome and genome,
- xiii) the disomic condition with a "D" followed by the designated chromosome and genome,
- xiv) the trisomic condition with "Tri" followed by the designated chromosome and genome,
- xv) tetrasomic lines with a "T" followed by the designated chromosome and genome. A "T" is also the designator for translocation lines to be consistent with current literature,
- xvi) nullisomic-tetrasomic lines with an "N" followed by the number and genome of the nullisomic chromosome and a "T" followed by the same for the tetrasomic chromosome, as in N1A T1B,
- xvii) monosomic and disomic additions by "MA" and "DA", respectively, and
- xviii) monosomic and disomic substitutions as "MS" and "DS", respectively, followed by chromosome designation as indicated in rule vi, and
- xix) abbreviations for wheat cultivars according to "Wheat Cultivar Abbreviations", 1985, Special Report 749, Agricultural Experiment Station, Oregon State University, Corvallis. This publication is currently under revision by CIMMYT.

Rules of hierarchy, established to ensure consistency in the naming of stocks, include that:

- xx) the short arm is listed before the long arm,
- xxi) the monosomic condition (either for the whole chromosome, chromosome arms, or parts thereof) is listed before the disomic condition except in cases where it is superceded by rule xxii,
- xxii) telosomic chromosomes are listed before isosomic chromosomes,
- xxiii) in translocation chromosomes, the common wheat chromosome regardless of arm, is listed before the alien chromosome segment, and
- xxiv) in translocation chromosomes between two alien chromosomes where the breakpoint is unknown, the order is according to homoeologous group.

Some stocks require abbreviations or symbols that were previously neither required nor based on the guidelines presented here. These include:

- xxv) "Mt" and "Dt" indicate monotel- and ditelosomic lines following rules i (for telochromosomes), xii, and xiii,
- xxvi) the doubled condition is indicated with a "d" followed by the designated chromosome and genome, and
- xxvii) the number sign " # " is used to distinguish different chromosomes belonging to the same homoeologous group of chromosomes within accessions, between accessions of the same nondomesticated species, or between homologous chromosomes within a cultivar.

Finally, certain symbols for use in computer databases, where some text styles are not available, include that:

- xxviii) the symbol " ^ " encloses characters to be superscripted, and
- xxix) the symbol " ` " encloses characters to be subscripted.

The following is a list of each aneuploid type or genetic stock, with an example of how the data would be displayed in each of the GrainGenes model fields for germplasm. For simplicity, chromosome 1A of wheat is used along with a homoeologue in rye (*Secale cereale*) or *Triticum longissimum* where needed. All of the chromosome stocks are represented to appear in the cultivar "Chinese Spring", hereafter designated by the abbreviation CS. The first column lists the variable name from the GrainGenes germplasm model (see Appendix I for a list of all variables available in this model). The second column lists the actual data that will appear in the database next to the variable name. Chromosome configuration is included with respect to item iii above. Finally, a comment is included where required.

NULLISOMIC N -
 Germplasm Chinese Spring Nullisomic 1A
 Abbreviation CS N1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+0"1A
 Chromosome_number 40

MONOSOMIC M
 Germplasm Chinese Spring Monosomic 1A
 Abbreviation CS M1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1A
 Chromosome_number 41

TRISOMIC Tri
 Germplasm Chinese Spring Trisomic 1A
 Abbreviation CS Tri1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1A
 Chromosome_number 43
 Comment The abbreviation "Tri" was selected because the letter "T" already indicates tetrasomy and translocation lines. The other choice "Tr" might cause confusion with translocation line nomenclature.

TETRASOMIC T
 Germplasm Chinese Spring Tetrasomic 1A
 Abbreviation CS T1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1A
 Chromosome_number 44

NULLISOMIC-TETRASOMIC NT
 Germplasm Chinese Spring Nullisomic 1B-Tetrasomic 1A
 Abbreviation CS N1B-T1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 19"+1"1A(1B)
 Chromosome_number 42
 Comment Using rule vi, this could be abbreviated "CS NT1B(1A)", but we believe the above to be more easily read.

MONOTELOSOMIC Mt
 Germplasm Chinese Spring Monotelosomic

1AS
 Abbreviation CS Mt1AS
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+t"1AS
 Chromosome_number 41t

DITELOSOMIC Dt
 Germplasm Chinese Spring Ditelosomic 1AS
 Abbreviation CS Dt1AS
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+t"1AS
 Chromosome_number 42tt

DOUBLE MONOTELOSOMIC dMt
 Germplasm Chinese Spring Double Monotelosomic 1A
 Abbreviation CS Mt1AS-Mt1AL
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+t"1AS+t"1AL
 Chromosome_number 42t+t

Comment The use of a "+" in the chromosome_number field will distinguish this line from ditelosomic lines since both lines have two telochromosomes.

DOUBLE DITELOSOMIC dDt
 Germplasm Chinese Spring Double Ditelosomic 1A
 Abbreviation CS dDt1A
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+t"1AS+t"1AL
 Chromosome_number 44tt+tt

DITELO-MONOTELOSOMIC Dt Mt
 Germplasm Chinese Spring Ditelosomic 1AS-Monotelosomic 1AL
 Abbreviation CS Dt1AS-Mt1AL
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+t"1AS+t"1AL
 Chromosome_number 43tt+t
 Comment The ditelosomic chromosome is listed first regardless of arm, thus the abbreviation for the line ditelosomic 1AL-monotelosomic 1AS lists the long arm first.

MONO-ISOSOMIC **Mi**
 Germplasm Chinese Spring Mono-isosomic 1AS
 Abbreviation CS Mi1AS
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+i"1AS
 Chromosome_number 41i

DI-ISOSOMIC **Di**
 Germplasm Chinese Spring Di-isosomic 1AS
 Abbreviation CS Di1AS
 Species *Triticum aestivum*
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 20"+i"1AS
 Chromosome_number 42ii

MONOSOMIC ADDITION **MA**
 Germplasm Chinese Spring-Imperial Monosomic Addition 1R
 Abbreviation CS-I MA1R
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 21"+1"1R
 Chromosome_number 43
 Comment Where duplicate lines from the same cultivar are available, it may be necessary to add a number or symbol to distinguish them.

DISOMIC ADDITION **DA**
 Germplasm Chinese Spring-Imperial Disomic Addition 1R
 Abbreviation CS-I DA1R
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 21"+1"1R
 Chromosome_number 44

Germplasm Chinese Spring-*T. longissimum* Disomic Addition 1S¹A¹
 Abbreviation CS-TLON DA1S¹A¹
 Species *Triticum aestivum*
 Donor_species *T. longissimum*
 Donor_ID Texas A&M, accession #2
 Type Aneuploid
 Derived_from Chinese Spring
 Chromosome_configuration 21"+1"1S¹A¹
 Chromosome_number 44

Developed_by N. A. Tuleen
 Development_site Texas A&M University, College Station
 Comment The genome for *T. longissimum* is S superscript "1".

MONOSOMIC SUBSTITUTION **MS**
 Germplasm Chinese Spring-Imperial Monosomic Substitution 1R(1A)
 Abbreviation CS-I MS1R(1A)
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Substitution
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1R(1A)
 Chromosome_number 41

DISOMIC SUBSTITUTION **DS**
 Germplasm Chinese Spring-Imperial Disomic Substitution 1R(1A)
 Abbreviation CS-I DS1R(1A)
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Substitution
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1R(1A)
 Chromosome_number 42

INTERVARIETAL DISOMIC SUBSTITUTION **DS**
 Germplasm ChineseSpring-Wichita Disomic Substitution 1A WI(1A CS)
 Abbreviation CS-WI DS1A
 Species *Triticum aestivum*
 Type Substitution
 Donor_species Wichita
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"1A WI(1A CS)
 Chromosome_number 42
 Comment The substituting chromosome is part of the name, the substituting chromosome named in parentheses. For abbreviations, when cultivars substitute same chromosome, it need only be listed once.

TRANSLOCATION CHROMOSOMES **T**
TERMINAL TRANSLOCATION WITH CENTROMERIC BREAKPOINT
 Germplasm ChineseSpring-Imperial Translocation T1AS · 1RL
 Abbreviation CS-I T1AS · 1RL
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Translocation
 Translocation_description Terminaltranslocation with centromeric breakpoint

Derived_from Chinese Spring
 Chromosome_configuration 20"+1"T1AS · 1RL
 Chromosome_number 42
 Comment · indicates a break at the centromere. In the example above, the translocation chromosome consists of the short arm of chromosome 1A translocated to the long arm of 1R with the breakpoint at the centromere.

The following example is of an actual translocation line of this type and is how it appears in GrainGenes.

Germplasm Chinese Spring-*A. intermedium*
 Translocation T4DL · 4Ai#2S
 Abbreviation CS-AGAI T4DL · 4Ai#2S
 Species *Triticum aestivum*
 Donor_species *Agropyron intermedium*
 Type Translocation
 Translocation_description Terminal translocation with centromeric breakpoint

Derived_from Chinese Spring
 Chromosome_configuration 20"+1"T4DL · 4Ai#2S
 Chromosome_number 42
 Developed_by D. Wells
 Development_site South Dakota State University, Brookings

Comment The number sign (#) is used to distinguish between different chromosomes belonging to the same homoeologous group of chromosomes within accessions, as well as between accessions of the same species or cultivar. In this example, the long arm of *T. aestivum* chromosome 4D (4DL) is translocated with a centromeric breakpoint (·) to the short arm (S) of an *A. intermedium* chromosome (4Ai#2S)

TERMINAL TRANSLOCATION WITH NON-CENTROMERIC BREAKPOINT

Germplasm Chinese Spring-Imperial
 Translocation T1AS · 1AL-1RL
 Abbreviation CS-I T1AS · 1AL-1RL
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Translocation
 Translocation_description Terminal translocation with non-centromeric breakpoint
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"T1AS · 1AL-1RL
 Detailed_abbreviation CS-I1AS · 1AL1.4::1.21RL
 Chromosome_number 42

Comment - and :: indicate a break and rejoining within the arm. In the example

above, the translocation chromosome consists of the short arm of wheat chromosome 1A, a segment of the long arm of 1A with the breakpoint in band 1AL1.4 and a distal segment derived from 1RL with the breakpoint in band 1RL1.2.

INTERCALARY TRANSLOCATION WITH NON-CENTROMERIC BREAKPOINT

Germplasm Chinese Spring-Imperial
 Translocation T14AS · 4AL-6RL-4AL
 Abbreviation CS-I T14AS · 4AL-6RL-4AL
 Species *Triticum aestivum*
 Donor_species *Secale cereale* cv. Imperial
 Type Translocation
 Translocation_description Intercalary translocation with non-centromeric breakpoint
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"T14AS · 4AL-6RL-4AL
 Detailed_abbreviation CS-I T14AS4AL1.2::6RL-2.7::4AL
 Chromosome_number 42
 Comment T1 = an intercalary translocation.

TRANSLOCATION WITH UNKNOWN BREAKPOINT

Germplasm *Triticum araraticum* Translocation
 T4G/5G
 Abbreviation CS-TARA T4G/5G
 Species *Triticum aestivum*
 Donor_species *Triticum araraticum*
 Type Translocation
 Translocation_description Translocation with unknown breakpoint
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"T4G/5G
 Chromosome_number 42
 Comment /= unknown breakpoint

DELETION CHROMOSOMES del

Germplasm Chinese Spring Deletion 1AS-1
 Abbreviation CS del1AS-1
 Species *Triticum aestivum*
 Type Deletion
 Derived_from Chinese Spring
 Chromosome_configuration 20"+1"del1AS-1
 Detailed_abbreviation CS del1AS-1(S1.2,0.17)
 Chromosome_number 42
 Comment : = terminal deletion.

Numbers in detailed abbreviation indicate C-band where deletion occurs and fraction length of chromosome remaining.

References

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- Gill BS (1986) A proposal for wheat chromosome band nomenclature. In: North American Wheat Genetic Mapping and Cytogenetic Stocks Workshop, April 17-19, 1986, University of Missouri, Columbia. Ed: Qualset CO and McGuire PE. The National Association of Wheat Growers Foundation, Washington, D.C. 11-15.
- Gill BS, Friebe B, and Endo TR (1991) Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat (*Triticum aestivum*). Genome 34: 830 - 839.
- Kimber G and Sears ER (1968) Nomenclature for the description of aneuploids in the Triticinae. In: Proc 3rd Int Wheat Genet Symp, Ed: Findlay KW and Shepherd KW. Canberra, Australia. 468-473.
- Paris Conference (1971) Standardization in Human Cytogenetics. Birth Defects: Original Article Series, VIII:7 1972. The National Foundation, New York.
- Sears ER (1954) The aneuploids of common wheat. Research Bull. 572, Missouri Ag. Exp. Sta. 57 p.

Appendix I. GRAINGENES ?Germoplasm model

The following fields are currently available for use in the germplasm model for the description of genetic stocks.

?Germplasm
Other_name ?Germplasm XREF Other_name // Put data in only one.
Species UNIQUE ?Species
Donor_species ?Species //For addition chromosomes
Type #Germplasm_type
Collection_and_ID ?Collection ?Germplasm XREF Other_name
Cross_number ?Text //Identifier used by CIMMYT
Chromosome_configuration ?Text
Abbreviation ?Germplasm XREF Full_name
Full_name ?Germplasm XREF Abbreviation
Pairing_configuration ?Text
Chromosome_number ?Text //Not Int. "42tt" = ditelosomic substn.
Female_Parent UNIQUE ?Germplasm
Male_Parent UNIQUE ?Germplasm
Pedigree UNIQUE ?Text
Market_Class ?Text
Trait_study ?Trait_Study
Pathology ?Pathology XREF Resistant_line
Allele ?Allele //No XREF
Gene ?Gene //No XREF
Rearrangement ?Rearrangement XREF Germplasm
Derived_from ?Germplasm
Developed_by ?Text
Development_site ?Text
Date_of_release ?Text
Registration_No ?Text
Remark ?Text
Reference ?Reference XREF Germplasm
Mapping_data ?Map_Data
Image ?Image XREF Germplasm
Data_source ?Colleague ?Text //Text is date, e.g. 93.08.27
Polymorphism ?Polymorphism
Trait_scores ?Trait_scores//could be a long list.
Coefficient_of_parentage ?Germplasm Float //Must be at end of
//model; this could be a Long list.



V. Recent publications on wheat genetics

Following references are selected from the original database, *Life Sciences Collection of Cambridge Scientific Abstracts*, using key words, WHEAT AND GENETICS. The present list is continued from that in the last issue of WIS. The editor thanks CSA for authorizing WIS to publish the database.

1994

(25)

ACCN:001399614 CTLN:3649708
ABSJ:G (Genetics Abstracts);
K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)
AUTH:Pretorius, Z.A.;Kloppers,F.J.;
Drijepondt, S.C.
AFFN:Dep. Plant Pathol., Univ. Orange
Free State, Bloemfontein 9300, South
Africa
TITL:Effects of inoculum density and
temperature on three components of
leaf rust resistance controlled by Lr34
in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 91-96

(26)

ACCN:001399615 CTLN:3649709
ABSJ:G (Genetics Abstracts);
K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)
AUTH:Zwer, P.K.;Qualset, C.O.
AFFN:Oregon State Univ., Columbia Basin
Agric. Res. Cent., P.O. Box 370,
Pendleton, OR 97801, USA
TITL:Genes for resistance to stripe rust
in four spring wheat varieties. 2. Adult
plant responses
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 109-115

(27)

ACCN:001402169 CTLN:3652384
ABSJ:G (Genetics Abstracts)
AUTH:Sarrafi, A.;Amrani, N.;Alibert, G.
AFFN:Lab. Biotechnol. et Amelior.
Plantes, Equipe d'Accueil, Dir. Rec. et
Etd. Doct., 832, Inst. Natl.
Polytech., Ec. Natl. Super. Agron.
Toulouse, 145, Ave. Muret, 31076

Toulouse, France

TITL:Haploid regeneration from tetraploid
wheat using maize pollen
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 1, pp. 176-178

(28)

ACCN:001402173 CTLN:3652388
ABSJ:G (Genetics Abstracts);
K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)
AUTH:Bai, D.;Scoles, G.J.;Knott, D.R.
AFFN:Dep. Crop Sci. and Plant Ecol., Univ.
Saskatchewan, SK S7N 0W0, Canada
TITL:Transfer of leaf rust and stem rust
resistance genes from Triticum
triaristatum to durum and bread wheats
and their molecular cytogenetic
localization
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 3, pp. 410-418

(29)

ACCN:001402174 CTLN:3652389
ABSJ:G (Genetics Abstracts);
K(Microbiology Abstracts C:Algology,
Mycology & Protozoology)
AUTH:Shiwani,;Saini, R.G.
AFFN:Dep. Genet., Punjab Agric. Univ.,
Ludhiana-141 004, India
TITL:Genetics of adult-plant leaf-rust
resistance in four Indian and two
Australian bread wheat cultivars
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 3, pp. 436-439

(30)

ACCN:001402203 CTLN:3652418
ABSJ:G (Genetics Abstracts)

AUTH:Cadle, M.M.;Rayfuse, L.M.;Walker-Simmons, M.K.;Jones, S.S.*

AFFN:USDA, ARS, Wheat Genet., Qual., Physiol. and Dis. Res., Washington State Univ., Pullman, WA 99164-6420, USA

TITL:Mapping of abscisic acid responsive genes and vpl to chromosomes in wheat and *Lophopyrum elongatum*

HTIL:GENOME

HSSN:0831-2796

HYER:1994

HCOL:vol. 37, no. 1, pp. 129-132

(31)

ACCN:001402217 CTLN:3652432

ABSJ:G (Genetics Abstracts)

AUTH:O'Donoghue, L.S.;Bennett, M.D.

AFFN:Cambridge Lab., IPSR, Colney Lane, Norwich NR4 7UJ, UK

TITL:Comparative responses of tetraploid wheats pollinated with *Zea mays* L. and *Hordeum bulbosum* L.

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 87, no. 6, pp. 673-680

(32)

ACCN:001402275 CTLN:3652493

ABSJ:G (Genetics Abstracts)

AUTH:Nieto-Taladriz, M.T.;Branlard,G.; Dardevet, M.

AFFN:INRA-Stn. Amelior. Plantes, F-63039 Clermont-Ferrand, France

TITL:Polymorphism of omega-gliadins in durum wheat as revealed by the two-step APAGE/SDS-PAGE technique

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 87, no. 8, pp. 1001-1005

(33)

ACCN:001402285 CTLN:3652503

ABSJ:G (Genetics Abstracts)

AUTH:Xu, Jie;Conner, R.L.;Laroche, A.

AFFN:Dep. Plant Breed. and Blom., Cornell Univ., 252 Emerson Hall, Ithaca, NY 14853-1902, USA

TITL:C-banding and fluorescence in situ hybridization studies of the wheat-alien hybrid 'Agrotana'

HTIL:GENOME

HSSN:0831-2796

HYER:1994

HCOL:vol. 37, no. 3, pp. 477-481

(34)

ACCN:001402320 CTLN:3652538

ABSJ:G (Genetics Abstracts)

AUTH:Dubcovsky, J.;Galvez, A.F.;Dvorak, J.*

AFFN:Dep. Agron. and Range Sci., Univ. California, Davis, CA 95616, USA

TITL:Comparison of the genetic organization of the early salt-stress-response gene system in salt-tolerant *Lophopyrum elongatum* and salt-sensitive wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 87, no. 8, pp. 957-964

(35)

ACCN:001402483 CTLN:3652745

ABSJ:G (Genetics Abstracts)

AUTH:Schmid, J.E.;Winzeler, M.;Winzeler, H.

AFFN:Swiss Fed. Inst. Technol. (ETH), Inst. Plant Sci., Experimental Stn., CH-8315 Lindau, Switzerland

TITL:Analysis of disease resistance and quality characters of F sub(1) hybrids of crosses between wheat (*Triticum aestivum*) and spelt (*Triticum spelta*)

HTIL:EUPHYTICA

HSSN:0014-2336

HYER:1994

HCOL:vol. 75, no. 1-2, pp. 105-110

(36)

ACCN:001402490 CTLN:3652752

BSJ:G (Genetics Abstracts)

AUTH:Tsegaye, S.;Becker, H.C.;Tesemma, T.

AFFN:Swedish Univ. Agric. Sci., Dep. Plant Breed. Res., S-26831, Svaloev, Sweden

TITL:Isozyme variation in Ethiopian tetraploid wheat (*Triticum turgidum*) landrace agrotypes of different seed color group

HTIL:EUPHYTICA

HSSN:0014-2336

HYER:1994

HCOL:vol. 75, no. 1-2, pp. 143-147

(37)

ACCN:001402501 CTLN:3652763

ABSJ:G (Genetics Abstracts)
AUTH:Brown, T.A.;Allaby, R.G.;Brown,K.A.;
O'Donoghue, K.;Sallares, R.
AFFN:Dep. Biochem. and Appl. Mol. Biol.,
UMIST, Manchester M60 1QD, UK
TITL:DNA in wheat seeds from European
archaeological sites
HTIL:EXPERIENTIA
HSSN:0014-4754
HYER:1994
HCOL:vol. 50, no. 6, pp. 571-575

(38)
ACCN:001402532 CTLN:3652794
ABSJ:G (Genetics Abstracts)
AUTH:Mashiringwani, N.A.;Mashingaidze,K.;
Kangai, J.;Olsen, K.
AFFN:Dep. Res. and Specialist Services,
P.O. Box 550 CY, Causeway Harare,
Zimbabwe
TITL:Genetic basis of grain filling rate
in wheat (*Triticum aestivum* L. emend.
Thell.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1994
HCOL:vol. 76, no. 1-2, pp. 33-44

(39)
ACCN:001402534 CTLN:3652796
ABSJ:G (Genetics Abstracts);
W2(Agricultural and Environmental
Biotechnology Abstracts); K
(Microbiology Abstracts C: Algology,
Mycology & Protozoology)
AUTH:Bariana, H.S.;McIntosh, R.A.
AFFN:Univ. Sydney Plant Breeding Inst.,
107 Cobbitty Rd, Cobbitty, NSW 2570,
Australia
TITL:Characterisation and origin of rust
and powdery mildew resistance genes in
VPm1 wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1994
HCOL:vol. 76, no. 1-2, pp. 53-61

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ACCN:001402554 CTLN:3652816
ABSJ:G (Genetics Abstracts)
AUTH:Harris, J.D.;Taylor, G.A.;Blake,
T.K.;Sands, D.C.
AFFN:Central Agricultural Res. Cent.,
Moccasin, MT 59462, USA

TITL:A fluorimetric assay for determining
variation of lysine in wheat gliadin
proteins
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1994
HCOL:vol. 76, no. 1-2, pp. 97-100

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ACCN:001402731 CTLN:3652999
ABSJ:G (Genetics Abstracts); Z (Entomology
Abstracts)
AUTH:Schroeder-Teeter, S.;Zemetra,R.S.;
Schotzko, D.J.;Smith, C.M.;Rafi, M.
AFFN:Dep. Plant, Soil and Entomol. Sci.,
Univ. Idaho, Moscow, Idaho 83844, USA
TITL:Monosomic analysis of Russian wheat
aphid (*Diuraphis noxia*) resistance in
Triticum aestivum line PI137739
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993-1994
HCOL:vol. 74, no. 1-2, pp. 117-120

(42)
ACCN:001406119 CTLN:3656867
ABSJ:G (Genetics Abstracts)
AUTH:Ogihara, Y.;Hasegawa, K.;Tsujiimoto,
H.
AFFN:Kihara Inst. Biol. Res., Yokohama
City Univ., Nakamura-cho 2-120-3,
Minami-ku Yokohama 232, Japan
TITL:High-resolution cytological mapping
of the long arm of chromosome 5A in
common wheat using a series of deletion
lines induced by gametocidal (Gc) genes
of *Aegilops speltoides*
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1994
HCOL:vol. 244, no. 3, pp. 253-259

(43)
ACCN:001415265 CTLN:3665506
ABSJ:G (Genetics Abstracts)
AUTH:Gornicki, P.;Podkowinski, J.;
Scappino, L.A.;DiMaio, J.;Ward, E.;
Haselkorn, R.*
AFFN:Dep. Mol. Genet. and Cell Biol.,
Univ. Chicago, 920 E. 58th St., Chicago,
IL 60637, USA
TITL:Wheat acetyl-coenzyme A carboxylase:
cDNA and protein structure
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424

HYER:1994
HCOL:vol. 91, no. 15, pp. 6860-6864

(44)

ACCN:001415568 CTLN:3665810
ABSJ:G (Genetics Abstracts);
W2(Agricultural and Environmental
Biotechnology Abstracts)
AUTH:Vega, J.M.;Abbo, S.;Feldman,M.;
Levy, A.A.
AFFN:Dep. Plant Genet., Weizmann Inst.
Sci., Rehovot 76100, Israel
TITL:Chromosome painting in plants: In
situ hybridization with a DNA probe
from a specific microdissected
chromosome arm of common wheat
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1994
HCOL:vol. 91, no. 25, pp. 12041-12045

(45)

ACCN:001418856 CTLN:3669290
ABSJ:G (Genetics Abstracts)
AUTH:Jiang, J.;Gill, B.S*
AFFN:Wheat Genet. Resour. Cent. and Dep.
Plant Pathol., Kansas State Univ.,
Manhattan, KS 66506-5502, USA
TITL:New 18S-26S ribosomal RNA gene loci:
Chromosomal landmarks for the evolution
of polyploid wheats
HTIL:CHROMOSOMA
HSSN:0009-5915
HYER:1994
HCOL:vol. 103, no. 3, pp. 179-185

(46)

ACCN:001418905 CTLN:3669339
ABSJ:G (Genetics Abstracts)
AUTH:Maan, S.S.
AFFN:Dep. Crop and Weed Sci., North
Dakota State Univ., Fargo, ND 58105, USA
TITL:Interactions between the scs and Vi
genes in alloplasmic durum wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 2, pp. 210-216

(47)

ACCN:001418906 CTLN:3669340
ABSJ:G (Genetics Abstracts)
AUTH:Song, Jiasheng;Hedgcoth, C.*
AFFN:Dep. Biochem., Willard Hall, Kansas

State Univ., Manhattan, KS 66506-3702,
USA

TITL:Influence of nuclear background on
transcription of a chimeric gene(orf256)
and coxI in fertile and cytoplasmic male
sterile wheats

HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 2, pp. 203-209

(48)

ACCN:001420282 CTLN:3670791
ABSJ:V (Virology & AIDS Abstracts);
N(Biochemistry Abstracts 2: Nucleic
Acids); G (Genetics Abstracts)
AUTH:Chen, J.;MacFarlane, S.A.;Wilson,
T.M.A.*
AFFN:Dep. Virol., Scottish Crop Res.
Inst., Invergowrie, Dundee DD2 5DA, UK
TITL:Detection and sequence analysis of a
spontaneous deletion mutant of soil-
borne wheat mosaic virus RNA2 associated
with increased symptom severity
HTIL:VIROLOGY
HSSN:0042-6822
HYER:1994
HCOL:vol. 202, no. 2, pp. 921-929

(49)

ACCN:001420707 CTLN:3671216
ABSJ:W2(Agricultural and Environmental
Biotechnology Abstracts); G (Genetics
Abstracts)
AUTH:Song, J.;Hedgcoth, C.*
AFFN:Dep. Biochem., Willard Hall, Kansas
St. Univ., Manhattan, KS 66506-3702, USA
TITL:A chimeric gene (orf256) is expressed
as protein only in cytoplasmic male-
sterile lines of wheat
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1994
HCOL:vol. 26, no. 1, pp. 535-539

(50)

ACCN:001426875 CTLN:3676800
ABSJ:Z (Entomology Abstracts)
AUTH:Belzunce, L.P.;Lenfant, C.;
Di Pasquale, S.;Colin, M.-E.
AFFN:INRA Stn. Phytopharm., BP 91, 84143
Montfavet Cedex, France
TITL:In vivo and in vitro effects of wheat
germ agglutinin and Bowman-Birk soybean
trypsin inhibitor, two potential

- transgene products, on midgut esterase and protease activities from *Apis mellifera*
- HTIL:COMP. BIOCHEM. PHYSIOL., B
HSSN:0305-0491
HYER:1994
HCOL:vol. 109B, no. 1, pp. 63-69
-
- (51)
ACCN:001432731 CTLN:3683290
ABSJ:G (Genetics Abstracts)
AUTH:McNeil, D.;Lagudah, E.S.;Hohmann,U.; Appels, R.
AFFN:CSIRO, Div. Plant Ind., P.O. Box 1600, Canberra, ACT 2601, Australia
TTIL:Amplification of DNA sequences in wheat and its relatives: The Dgas44 and R350 families of repetitive sequences
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 2, pp. 320-327
-
- (52)
ACCN:001436085 CTLN:3686960
ABSJ:Z (Entomology Abstracts); D (Ecology Abstracts); G (Genetics Abstracts)
AUTH:De Barro, P.J.;Sherratt,T.N.; Carvalho, G.R.;Nicol, D.;Iyengar,A.; Maclean, N.
AFFN:Dep. Biol., Univ. Southampton, Bassett Crescent East, Southampton SO9 3TU, UK
TTIL:An analysis of secondary spread by putative clones of *Sitobion avenae* within a Hampshire wheat field using the multilocus (GATA) sub(4) probe
HTIL:INSECT MOL. BIOL.
HSSN:0962-1075
HYER:1994
HCOL:vol. 3, no. 4, pp. 253-260
-
- (53)
ACCN:001439347 CTLN:3689574
ABSJ:G (Genetics Abstracts)
AUTH:Miyashita, N.T.;Mori, N.;Tsunewaki, K.
AFFN:Lab. Genet., Fac. Agric., Kyoto Univ., Sakyo-ku, Kyoto 606-01, Japan
TTIL:Molecular variation in chloroplast DNA regions in ancestral species of wheat
HTIL:GENETICS
HSSN:0016-6731
- HYER:1994
HCOL:vol. 137, no. 3, pp. 883-889
-
- (54)
ACCN:001439368 CTLN:3689595
ABSJ:G (Genetics Abstracts)
AUTH:Devos, K.M.;Chao, S.;Li, Q.Y.; Simonetti, M.C.;Gale, M.D.
AFFN:John Innes Cent., Norwich Res. Park, Colney, Norwich NR4 7UH, UK
TTIL:Relationship between chromosome 9 of maize and wheat homeologous group 7 chromosomes
HTIL:GENETICS
HSSN:0016-6731
HYER:1994
HCOL:vol. 138, no. 4, pp. 1287-1292
-
- (55)
ACCN:001441730 CTLN:3692059
ABSJ:G (Genetics Abstracts)
AUTH:Luthra, O.P.;Saharan, R.P.;Kumar, J.
AFFN:Dep. Genet., CCS Haryana Agric. Univ., Hisar-125 004, India
TTIL:Genetics of synchrony of ear emergence in wheat
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1994
HCOL:vol. 10, no. 1, pp. 125-127
-
- (56)
ACCN:001448028 CTLN:3699007
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); N(Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Tsuchiya, K.;Nagashima, T.;Yamamoto, Y.;Gomi, K.;Kitamoto, K.*;Kumagai,C.; Tamura, G.
AFFN:Natl. Res. Inst. Brew., 2-6-30, Takinogawa, Kita-ku, Tokyo 114, Japan
TTIL:High level secretion of calf chymosin using a glucoamylase-prochymosin fusion gene in *Aspergillus oryzae*
HTIL:BIOSCI., BIOTECHNOL., BIOCHEM.
HSSN:0916-8451
HYER:1994
HCOL:vol. 58, no. 5, pp. 895-899
-
- (57)
ACCN:001448890 CTLN:3699999
ABSJ:Z (Entomology Abstracts)
AUTH:Nieto-Lopez, R.M.;Blake, T.K.*
AFFN:Dep. Plant and Soil Sci., Montana

State Univ., Bozeman, MT 59717-0312,
USA

TITL:Russian wheat aphid resistance in
barley: Inheritance and linked
molecular markers

HTIL:CROP SCI.

HSSN:0011-183X

HYER:1994

HCOL:vol. 34, no. 3, pp. 655-659

(58)

ACCN:001461974 CTLN:3713480

ABSJ:G (Genetics Abstracts)

AUTH:Redaelli, R.;Metakovsky,E.V.;

Davidov, S.D.;Pogna, N.E.*

AFFN:Ist. Spec. Cerealicoilt., Sect. Appl.

Genet., Via Cassia 176, 00191 Roma,

Italy

TITL:Two-dimensional mapping of gliadins
using biotypes and null mutants of
common wheat cultivar Saratovskaya 29

HTIL:HEREDITAS

HSSN:0018-0661

HYER:1994

HCOL:vol. 121, no. 2, pp. 131-137

(59)

ACCN:001461976 CTLN:3713482

ABSJ:G (Genetics Abstracts);

K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)

AUTH:Ma, Z.Q.;Sorrells, M.E.*;Tanksley,
S.D.

AFFN:Dep. Plant Breed. and Biom., Cornell
Univ., Ithaca, NY 14853, USA

TITL:RFLP markers linked to powdery
mildew resistance genes Pm1, Pm2, Pm3,
and Pm4 in wheat

HTIL:GENOME

HSSN:0831-2796

HYER:1994

HCOL:vol. 37, no. 5, pp. 871-875

(60)

ACCN:001461977 CTLN:3713483

ABSJ:G (Genetics Abstracts);

K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)

AUTH:Tosa, Y.

AFFN:Kochi Univ., Fac. Agric., Nankoku,
Kochi 783, Japan

TITL:Gene-for-gene interactions between
the rye mildew fungus and wheat
cultivars

HTIL:GENOME

HSSN:0831-2796

HYER:1994

HCOL:vol. 37, no. 5, pp. 758-762

(61)

ACCN:001461987 CTLN:3713493

ABSJ:G (Genetics Abstracts);

K(Microbiology Abstracts C: Algology,
Mycology & Protozoology);

W2(Agricultural and Environmental
Biotechnology Abstracts)

AUTH:Innes, R.L.;Kerber, E.R.

AFFN:Agric. Canada, Res. Stn., 195 Daffoe
Rd., Winnipeg, MB R3T 2M9, Canada

TITL:Resistance to wheat leaf rust and
stem rust in Triticum tauschii and
inheritance in hexaploid wheat of
resistance transferred from T. tauschii

HTIL:GENOME

HSSN:0831-2796

HYER:1994

HCOL:vol. 37, no. 5, pp. 813-822

(62)

ACCN:001462030 CTLN:3713536

ABSJ:G (Genetics Abstracts)

AUTH:Cai, Xiwen

AFFN:Dep. Crop and Soil Sci., USDA-ARS,
Washington State Univ., Pullman, WA
99164-6420, USA

TITL:Chromosome translocations in the
common wheat variety 'Amigo'

HTIL:HEREDITAS

HSSN:0018-0661

HYER:1994

HCOL:vol. 121, no. 2, pp. 199-202

(63)

ACCN:001466048 CTLN:3716711

ABSJ:G (Genetics Abstracts)

AUTH:Miller, T.E.;Reader, S.M.;Purdie,
K.A.;King, I.P.

AFFN:John Innes Cent., Colney, Norwich NR4
7UJ, UK

TITL:Determination of the frequency of
wheat-rye chromosome pairing in wheat x
rye hybrids with and without chromosome
5B

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 2-3, pp. 255-258

(64)

ACCN:001466493 CTLN:3717156

ABSJ:G (Genetics Abstracts)
 AUTH:Henry, Y.;Marcotte, J.-L.;De Buyser, J.
 AFFN:Lab. Biol. Mol. Veg., Bt 630, URA
 CNRS 1128, Univ. Paris XI, 91405 Orsay, France
 TITL:Chromosomal location of genes controlling short-term and long-term somatic embryogenesis in wheat revealed by immature embryo culture of aneuploid lines
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 2-3, pp. 344-350

 (65)
 ACCN:001466496 CTLN:3717159
 ABSJ:G (Genetics Abstracts)
 AUTH:Miura, H.;Tanii, S.;Nakamura, T.; Watanabe, N.
 TITL:Genetic control of amylose content in wheat endosperm starch and differential effects of three Wx genes
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 2-3, pp. 276-280

 (66)
 ACCN:001466497 CTLN:3717160
 ABSJ:G (Genetics Abstracts)
 AUTH:Pijnaacker, L.P.;Ferwerda, M.A.
 AFFN:Dep. Genet. Univ. Groningen, Cent. Biol. Sci., P.O. Box 14, NL-9750 AA Haren, Netherlands
 TITL:Sister chromatid exchanges in cultured immature embryos of wheat species and regenerants
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 2-3, pp. 287-292

 (67)
 ACCN:001470041 CTLN:3721071
 ABSJ:G (Genetics Abstracts)
 AUTH:Yamamori, M.;Nakamura, T.;Endo, T.R.; Nagamine, T.
 AFFN:Okinawa Sub-trop. St., Japan Int. Res. Cent. Agric. Sci., Ishigaki, Okinawa 907, Japan
 TITL:Waxy protein deficiency and chromosomal location of coding genes in common wheat
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 2-3, pp. 179-184

 (68)
 ACCN:001470404 CTLN:3721440
 ABSJ:G (Genetics Abstracts)
 AUTH:Chen, Z.;Devey, M.;Tuleen, N.A.;Hart, G.E.*
 AFFN:Dep. Soil and Crop Sci., Texas A&M Univ., College Station, TX 77843-2474, USA
 TITL:Use of recombinant substitution lines in the construction of RFLP-based genetic maps of chromosomes 6A and 6B of tetraploid wheat (*Triticum turgidum* L.)
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 6, pp. 703-712

 (69)
 ACCN:001470406 CTLN:3721442
 ABSJ:G (Genetics Abstracts)
 AUTH:Hyne, V.;Kearsey, M.J.;Martinez, O.; Gang, W.;Snape, J.W.
 AFFN:Cambridge Lab., John Innes Cent. Plant Sci. Res., Colney Lane, Norwich NR4 7UJ, UK
 TITL:A partial genome assay for quantitative trait loci in wheat (*Triticum aestivum*) using different analytical techniques
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 89, no. 6, pp. 735-741

 (70)
 ACCN:001474201 CTLN:3725661
 ABSJ:G (Genetics Abstracts)
 AUTH:Ogihara, Y.;Shimizu, H.;Hasegawa, K.; Tsujimoto, H.;Sasakuma, T.
 AFFN:Kihara Inst. Biol. Res., Yokohama City Univ., Nakamura-cho 2-120-3, Minami-ku, Yokohama 232, Japan
 TITL:Chromosome assignment of four photosynthesis-related genes and their variability in wheat species
 HTIL:THEOR. APPL. GENET.
 HSSN:0040-5752
 HYER:1994
 HCOL:vol. 88, no. 3-4, pp. 383-394

(71)
ACCN:001480323 CTLN:3731401
ABSJ:G (Genetics Abstracts)
AUTH:Belay, G.;Merker, A.;Tesenma, T.
AFFN:Dep. Plant Breed. Res., Swedish
Univ. Agric. Sci., Box 7003, S-750-07
Uppsala, Sweden
TTTL:Cytogenetic studies in Ethiopian
landraces of tetraploid wheat (*Triticum
turgidum* L.) I. Spike morphology vs
ploidy level and karyomorphology
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1994
HCOL:vol. 121, no. 1, pp. 45-62

(72)
ACCN:001480351 CTLN:3731429
ABSJ:G (Genetics Abstracts)
AUTH:Lukaszenwski, A.J.
AFFN:Dep. Bot. Plant Sci., Univ.
California, Riverside, CA 92521-0124,
USA
TTTL:Genetic mapping in the 1R.1D wheat-
rye translocated chromosomes
HTIL:GENOME
HSSN:0831-2796
HYER:1994
HCOL:vol. 37, no. 6, pp. 945-949

(73)
ACCN:001480976 CTLN:3732055
ABSJ:G (Genetics Abstracts)
AUTH:Nieto-Taladriz, M.T.;Perretant,M.R.;
Rousset, M.
AFFN:INRA, Stn. Amelior. Plantes, 63039
Clermont Ferrand Cedex, France
TTTL:Effect of gliadins and HMW and LMW
subunits of glutenin on dough
properties in the F sub(6) recombinant
inbred lines from a bread wheat cross
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1994
HCOL:vol. 88, no. 1, pp. 81-88

(74)
ACCN:001480981 CTLN:3732060
ABSJ:G (Genetics Abstracts)
AUTH:Pfeil, U.;Van der Kuip, H.;Hesemann,
C.-U.*
AFFN:Inst. Genet., Univ. Hohenheim, D-
70593 Stuttgart, FRG
TTTL:Non-radioactive organization and

transcript analysis of the ATPase
subunit 6 gene region in the
mitochondrial genome from fertile and
sterile (CMS) forms of wheat and
triticale
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1994
HCOL:vol. 88, no. 2, pp. 231-235

(75)
ACCN:001481049 CTLN:3732128
ABSJ:G (Genetics Abstracts)
AUTH:Somers, D.J.;Filion, W.G.
AFFN:J. Tuzo Wilson Res. Lab., Dep. Bot.,
Erindale Campus, Univ. Toronto, 3359
Mississauga Rd. N., Mississauga, ON L5L-
1C6, Canada
TTTL:The influence of the rye genome on
the accumulation of HSP18 and HSP70
transcripts in a wheat genetic
background
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1994
HCOL:vol. 88, no. 3-4, pp. 298-304

(76)
ACCN:001482507 CTLN:3733633
ABSJ:G (Genetics Abstracts)
AUTH:Paull, J.G.;Pallotta, M.A.;Langridge,
P.;The, T.T.
AFFN:Dep. Plant Sci., Waite Campus, Univ.
Adelaide, Glen Osmond, SA 5064,
Australia
TTTL:RFLP markers associated with Sr22 and
recombination between chromosome 7A of
bread wheat and the diploid species
Triticum boeoticum
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1994
HCOL:vol. 89, no. 7-8, pp. 1039-1045

(77)
ACCN:001482509 CTLN:3733635
ABSJ:G (Genetics Abstracts);
K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)
AUTH:Yamamori, M.
AFFN:Okinawa Sub-trop. Stn., Japan Int.
Res. Cent. Agric. Sci., Ishigaki,
Okinawa 907, Japan
TTTL:An N-band marker for gene Lr18 for
resistance to leaf rust in wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 5, pp. 643-646

(78)

ACCN:001482547 CTLN:3733673

ABSJ:G (Genetics Abstracts)

AUTH:Knox, R.E.;Howes, N.K.

AFFN:Agric. Canada, Res. Stn., P.O. Box
1030, Swift Current, SK S9H 3X2, Canada

TITL:A monoclonal antibody chromosome
marker analysis used to locate a loose
smut resistance gene in wheat
chromosome 6A

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 6, pp. 787-793

(79)

ACCN:001482548 CTLN:3733674

ABSJ:G (Genetics Abstracts)

AUTH:Chen, Qin;Lu, Y.L.;Jahier, J.*;
Bernard, M.

AFFN:Natl. Inst. Agron. Res., Stn.
Improv. Plants, BP 29, 35650 Le Rheu,
France

TITL:Identification of wheat-Agropropyron
crisatum monosomic addition lines by
RFLP analysis using a set of assigned
wheat DNA probes

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 1, pp. 70-75

(80)

ACCN:001483385 CTLN:3734522

ABSJ:G (Genetics Abstracts)

AUTH:Chen, P.D.;Tsujiimoto, H.;Gill, B.S.*

AFFN:Wheat Genet. Resour. Cent., Dep.
Plant Pathol., Throckmorton Hall,
Kansas State Univ., Manhattan, KS
66506-5502, USA

TITL:Transfer of Ph super(I) genes
promoting homoeologous pairing from
Triticum speltoides to common wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 88, no. 1, pp. 97-101

(81)

ACCN:001483399 CTLN:3734536

ABSJ:G (Genetics Abstracts)

AUTH:Liu, Z.-W.;Wang, R.R.-C.;Carman, J.G.

AFFN:USDA-ARS, For. and Range Res. Lab.,
Utah State Univ., Logan, UT 84322-6300,
USA

TITL:Hybrids and backcross progenies
between wheat (*Triticum aestivum* L.) and
apomictic Australian wheatgrass [*Elymus*
rectisetus (Nees in Lehm.) A. Loeve &
Connor]: Karyotypic and genomic analyses

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 5, pp. 599-605

(82)

ACCN:001483405 CTLN:3734542

ABSJ:G (Genetics Abstracts)

AUTH:Yen, Y.;Baenziger, P.S.

AFFN:Dep. Agron., Univ. Nebraska, P.O. Box
830915, Lincoln, NE 68583-0915, USA

TITL:Wheat chromosome 2D carries genes
controlling the activity of two DNA-
degrading enzymes

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 88, no. 1, pp. 30-32

(83)

ACCN:001483410 CTLN:3734547

ABSJ:G (Genetics Abstracts)

AUTH:Williams, K.J.;Fisher, J.M.;
Langridge, P.*

AFFN:Dep. Plant Sci., Univ. Adelaide,
Waite Campus, Urrbrae 5064, Australia

TITL:Identification of RFLP markers linked
to the cereal cyst nematode resistance
gene (Cre) in wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 927-930

(84)

ACCN:001483419 CTLN:3734556

ABSJ:G (Genetics Abstracts);

K(Microbiology Abstracts C: Algology,
Mycology & Protozoology)

AUTH:Schachermayr, G.;Siedler, H.;Gale,
M.D.;Winzeler, H.;Winzeler, M.;Keller,
B.*

AFFN:Dep. Plant Breed., Swiss Fed. Res.

Stn. Agron., Zuerich-Reckenholz,

Reckenholzstr. 191, Zuerich, Switzerland

TITL:Identification and localization of
molecular markers linked to the Lr9
leaf rust resistance gene of wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 88, no. 1, pp. 110-115

(85)

ACCN:001483428 CTLN:3734565

ABSJ:G (Genetics Abstracts)

AUTH:Borghini, B.;Perenzin, M.

AFFN:Ist. Spe. Cerealicolt., Via Mulino
No. 3, 20079 S. Angelo Lodigiano (MI),
Italy

TITL:Diallel analysis to predict
heterosis and combining ability for
grain yield, yield components and
bread-making quality in bread wheat (*T.
aestivum*)

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 975-981

(86)

ACCN:001483437 CTLN:3734574

ABSJ:G (Genetics Abstracts)

AUTH:Martinez, I.;Bernard, M.;Nicolas,
P.; Bernard, S.

AFFN:INRA, Stn. Amelior. Plantes, Domaine
Crouelle, 63039 Clermont-Ferrand Cedex,
France

TITL:Study of androgenetic performance
and molecular characterisation of a set
of wheat-rye addition lines

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 982-990

(87)

ACCN:001483439 CTLN:3734576

ABSJ:G (Genetics Abstracts)

AUTH:Aksel, R.

AFFN:Dep. Genet., Univ. Alberta,
Edmonton, AB T6G 2E9, Canada

TITL:Quantitative-genetic analysis of
reciprocal crosses between a winter and
a spring cultivar of common wheat
(*Triticum aestivum* L.)

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 1032-1038

(88)

ACCN:001483443 CTLN:3734580

ABSJ:G (Genetics Abstracts)

AUTH:Jiang, J.;Friebe, B.;Gill, B.S.*

AFFN:Dep. Plant Pathol. and Wheat Genet.
Resour. Cent., Kansas State Univ.,
Manhattan, KS 66506-5502, USA

TITL:Chromosome painting of Amigo wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 811-813

(89)

ACCN:001483468 CTLN:3734605

ABSJ:G (Genetics Abstracts)

AUTH:Quarrie, S.A.;Gulli, M.;Calestani, C.;
Steed, A.;Marmirolì, N.

AFFN:John Innes Cent., Norwich Res. Park,
Colney, Norwich NR4 7UH, UK

TITL:Location of a gene regulating
drought-induced abscisic acid production
on the long arm of chromosome 5A of
wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 6, pp. 794-800

(90)

ACCN:001483491 CTLN:3734628

ABSJ:G (Genetics Abstracts)

AUTH:O'Donoghue, L.S.;Bennett, M.D.

AFFN:Agric. Canada, Res. Branch, Cent.
Exp. Farm, Build. 50, Ottawa, ON K1A
0C6, Canada

TITL:Durum wheat haploid production using
maize wide-crossing

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 5, pp. 559-566

(91)

ACCN:001483493 CTLN:3734630

ABSJ:G (Genetics Abstracts)

AUTH:Morere-Le Paven, M.C.;De Buyser, J.;
Henry, Y.;Hartmann, C.;Rode, A.*

AFFN:Inst. Biotechnol. Plantes, URA CNRS
D-1128, Bat. 630, Univ. Paris XI, 91405,
Orsay, France

TITL:Unusual inheritance of the
mitochondrial genome organization in
the progeny of reciprocal crosses

between alloplasmic hexaploid wheat
regenerants

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 5, pp. 572-576

(92)

ACCN:001483514 CTLN:3734651

ABSJ:G (Genetics Abstracts); Z

(Entomology Abstracts)

AUTH:Dweikat, I.;Ohm, H.;Mackenzie, S.;
Patterson, F.;Cambron, S.;Ratcliffe, R.
AFFN:Dep. Agron., Purdue Univ., W.

Lafayette, IN 47907, USA

TITL:Association of a DNA marker with
Hessian fly resistance gene H9 in wheat

HTIL:THEOR. APPL. GENET.

HSSN:0040-5752

HYER:1994

HCOL:vol. 89, no. 7-8, pp. 964-968

(93)

ACCN:001489226 CTLN:3741001

ABSJ:G (Genetics Abstracts)

AUTH:Hang, A.;Tsuchiya, T.;Stanwood, P.C.;
Roos, E.E.

AFFN:USDA-ARS Natl. Small Grains

Germplasm Res. Facil., P.O. Box 307,
Aberdeen, ID, USA

TITL:Mitotic analysis of root tips from
cryopreserved and artificially aged
seeds of wheat

HTIL:CYTOLOGIA

HSSN:0011-4545

HYER:1994

HCOL:vol. 59, no. 1, pp. 125-133

(94)

ACCN:001493317 CTLN:3744417

ABSJ:G (Genetics Abstracts)

AUTH:Aggarwal, K.;Sharma, S.K.;Tripathi,
I.D.

AFFN:Dep. Genet., CCS Haryana Agric.

Univ., Hisar-125 004, India

TITL:Studies on isoenzyme patterns of
wheat varieties and induced mutants

HTIL:ANN. BIOL.

HSSN:0970-0153

HYER:1994

HCOL:vol. 10, no. 2, pp. 236-239

(95)

ACCN:001493318 CTLN:3744418

ABSJ:G (Genetics Abstracts)

AUTH:Dhanda, S.S.;Sharma, S.C.;Yunus,
M.;Karwasra, S.S.

AFFN:Dep. Plant Breed., CCS Haryana Agric.
Univ., Hisar-125 004, India

TITL:Evaluation of wheat germplasm for
yield, its components and morphological
traits

HTIL:ANN. BIOL.

HSSN:0970-0153

HYER:1994

HCOL:vol. 10, no. 2, pp. 232-235

(96)

ACCN:001496606 CTLN:3747902

ABSJ:G (Genetics Abstracts)

AUTH:Nakamura, C.;Ohtani, K.;Mori, N.;
Panayotov, I.;Kaneda, C.

AFFN:Lab. Genet., Fac. Agric., Kobe Univ.,
1 Rokkodai-cho, Nada-ku, Kobe 657, Japan

TITL:Physical mapping of chloroplast DNAs
of *Agropyron glaucum*, *Ag. trichophorum*
and *Haynaldia villosa* using alloplasmic
common wheat with cytoplasms of
respective species

HTIL:JAP. J. GENET.

HSSN:0021-504X

HYER:1994

HCOL:vol. 69, no. 6, pp. 645-655

(97)

ACCN:001504162 CTLN:3756275

ABSJ:G (Genetics Abstracts);

W2(Agricultural and Environmental
Biotechnology Abstracts); Z (Entomology
Abstracts)

AUTH:Cox, T.S.;Hatchett, J.H.

AFFN:USDA-ARS and Dep. Agron., Kansas
State Univ., Manhattan, KS 66502, USA

TITL:Hessian fly-resistance gene H26
transferred from *Triticum tauschii* to
common wheat

HTIL:CROP SCI.

HSSN:0011-183X

HYER:1994

HCOL:vol. 34, no. 4, pp. 958-960

1995

(1)

ACCN:001461105 CTLN:3712591

ABSJ:G (Genetics Abstracts)

AUTH:Bucholc, M.;Buchowicz, J.*

AFFN:Inst. Biochem. and Biophys., Polish
Acad. Sci., 5a Pawinskiego, 02-106
Warsaw, Poland

TITL:An extrachromosomal fragment of
telomeric DNA in wheat

HTIL:PLANT MOL. BIOL.

HSSN:0167-4412

HYER:1995

HCOL:vol. 27, no. 2, pp. 435-439

(2)

ACCN:001466865 CTLN:3717528

ABSJ:V (Virology & AIDS Abstracts);

N(Biochemistry Abstracts 2: Nucleic

Acids); W2(Agricultural and

Environmental Biotechnology Abstracts)

AUTH:Chen, Jianpeng;MaoFarlane,S.A.;

Wilson, T.M.A.*

AFFN:Dep. Virol., Scottish Crop Res.

Inst., Invergowrie, Dundee DD2 5DA, UK

TITL:Effect of cultivation temperature on

the spontaneous development of

deletions in soilborne wheat mosaic

virus RNA 2

HTIL:PHYTOPATHOLOGY

HSSN:0331-949X

HYER:1995

HCOL:vol. 85, no. 3, pp. 299-306



VI. Editorial Remarks

As you have already realized when you saw the cover illustration of the present issue, Wheat Information Service has changed its style and system. Since WIS had been established in 1954, four decades has passed. We are now in new era for wheat researches. Information exchange becomes quick and easy through computer systems, molecular approaches for the research are realistic, and genetic stocks have been accumulated for basic researches and breeding. However, demand for food production is still large, especially for fear of food shortage in the early stage of the 21st century, and we are faced to overcome the worldwide devastation of the earth land. Wheat researchers are asked to devote themselves on further development of scientific research in wheat as one of major crops.

Nevertheless to say the importance of genetic resources and genetic stocks for the bases of scientific and original researches, wheat has advantages of abundant information and materials in comparison to other plant studies. Wheat Information Service is willing to function as the international information distributor.

The essences of new editorial and managing policies are as follows:

(1) WIS should be an international journal for wheat genetics and breeding, not for regional report of agricultural performances.

(2) WIS publishes research articles with reviewer's judge. At the same time, research information, proposal for nomenclature, and announcement of meeting or book publication are successively accepted under consideration by editorial board.

(3) WIS is not the commercial journal for economic benefit. Donation system is introduced to ask subscribers to support continuous publication. This is a kind of worldwide cooperation among wheat researchers, some of who are trying to continue to study under severe social circumstance. Kihara Memorial Foundation will keep supporting financially, but beneficiary should pay for the part. Please understand this philosophy.

For the detail regulation, refer to the description on the cover-back page.

Further support to WIS is appreciated.



PR

A NEW BOOK PUBLISHED !

Plant Genome and Plastome: Their Structure and Evolution

In Commemoration of Professor Hitoshi Kihara's Centennial

Edited by Koichiro Tsunewaki

Kodansha Scientific Ltd., Tokyo, 1995

(See next page for the contents)

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- Hitoshi Kihara: The Golden Foundation *G. Kimber*
Prof. H. Kihara's contribution to plant genetics *K. Tsunewaki*

Part II. Genome Structure

- Molecular cytogenetics: an integrated approach for evolutionary, structural and functional analysis of plant chromosome *B. S. Gill*
Deletion stocks as the basic material for molecular cytogenetics *T. R. Endo*
Molecular-cytogenetic analysis of plant chromosomes by *in situ* hybridization *Y. Mukai*
Molecular cytogenetics and the wheat genome *J. S. Heslop-Harrison and T. Schwarzacher*
High resolution of genetic map of rice and the conserved colinearity between rice and wheat genomes *N. Kurata et al.*
The North American barley genome map on the cross HT and its comparison to the map on the cross SM *K. J. Kasha et al.*
Localization of genes and marker sequences on the isolated and fractionated plant chromosomes *I. Schubert et al.*
Molecular genetic analysis of rice bacterial blight resistance locus, *Xa21* *P. C. Ronald et al.*

Part III. Genome Evolution

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Genomic relationships and phylogeny in wheat obtained by RFLP analysis of nuclear DNA. *K. Tsunewaki and H. Nakamura*
The hybrid origin hypothesis of cultivated rice (*Oryza sativa*) explains some of the gaps in its RFLP maps and suggests an efficient mapping population for useful genes and QTLs *G. Second et al.*

Part IV. Plastome Structure and Evolution

- Replication slippage as a molecular mechanism for evolutionary variation in chloroplast DNA due to deletions and insertions *B. B. Sears et al.*
Chloroplast gene organization and phylogenetic relationships in green algae *M. Turmel et al.*
Structure and evolution of the chloroplast genomes in seedless land plants *L. A. Raubenson et al.*
Chloroplast genome evolution in conifers *V. D. Hipkins and S. H. Strauss*
Structure and evolution of chloroplast DNA in monocots *Y. Ogihara*

This book that is 190 pages plus 16 extra pages in length, including 4 color plates, may be recommended for researchers, teachers in higher educational institutions, graduate students, having a special interest in recent advances in plant genetics and evolution. Also recommended are libraries of universities and plant research institutions.

Copies of this books are distributed by the followings:

**Kozo Nishikawa, Director, Kihara Memorial Foundation
641-12 Maoika-cho, Totsuka-ku, Yokohama 244, Japan
FAX: +81-45-825-3307, e-mail: tsujimot@yokohama-cu.ac.jp.**

Price is 6,000 Japanese Yen (ca. \$ 60.00 US) per copy. Credit card (Master or Visa card only) or International Postal Money Order is acceptable at this price. If remittance is made by check, 3,000 Japanese Yen will be charged in extra per check to cover bank's handling charge.

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