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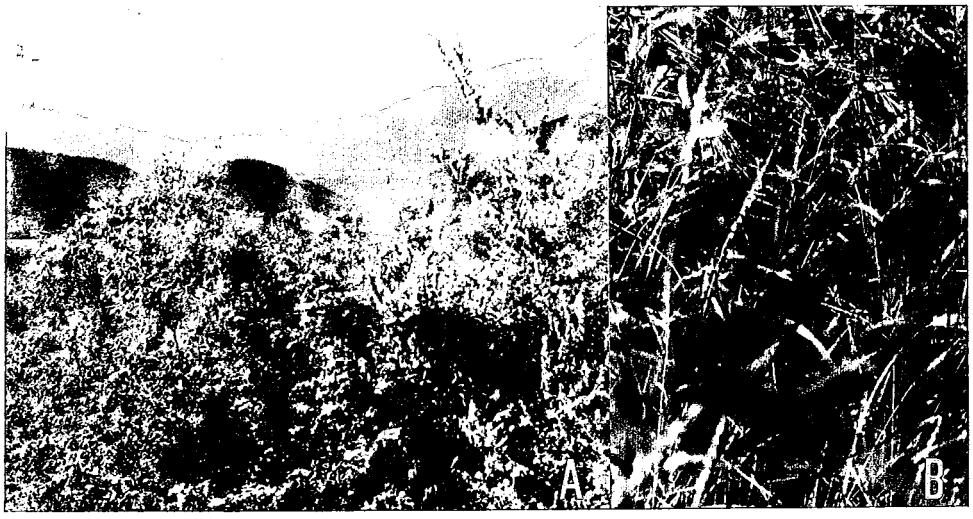

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Review

A review on amphiploids in the *Triticeae*, obtained in Bulgaria during 1950–1990

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Twenty amphiploids in the tribe *Triticeae*, obtained in Bulgaria for a period of 40 years (1950–1990) have been summarized and listed here. They are arranged according to their chromosome number: four are tetraploids, eight-hexaploids, three-octoploids, one possesses 64 chromosomes, and four with 70 chromosomes. Almost all of them are synthetic forms that are induced by chromosome doubling of sterile interspecific or intergeneric hybrids.

Amphiploids provide a starting point for the production of alien additions, substitutions and interspecific transfers in wheat. Emphasis is made on their meiotic stability, seed setting, disease resistance and some other characters that are of importance for wheat breeding. Genome formulae and seed availability from developer are also presented.

The artificial doubling of chromosome numbers has been used as an efficient method for overcoming the sterility of intergeneric F_1 plants. In Bulgaria, Doncho Kostoff initiated experiments to apply suitable techniques for doubling the chromosome number in sterile interspecific hybrids, especially for the cross *Triticum timopheevi* × *T. monococcum*. He named this amphiploid *T. timococcum*, showing resistance to fungal pathogens (after Tsikov and Stoilov 1959).

After the intensive work of D. Kostoff on wide hybridization (Kostoff 1937, Kostoff and Arutiunova 1937, Kostoff 1940, 1941), many intergeneric hybrids and amphiploids were obtained by crossing cultivated wheats with alien species. In general, natural or synthetic amphiploids are easier to use for transferring desired alien genes to common wheat than are sterile hybrids from direct crosses between alien species and wheat.

The present review aims to group together and list all amphiploids obtained in Bulgaria during 1950–1990, and to briefly consider their important characters for wheat breeding. Origin, valuble features and seed availability of amphiploids are given in Table 1.

1. Amphiploids with 2n = 28

Aegilops squarrosa var. *strangulata* × *T. boeoticum* No. 1

Savov and Panayotov (1989) describe two forms of the amphiploid with either *T. boeoticum* No. 1 or No. 3, both collected in Bulgaria. Plants having *T. boeoticum* No. 1 as the parent are highly viable and more fertile than those with *T. boeoticum* No. 3. The amphiploid is fully resistant to fungi irrespective of the aneuploid variation that is induced by the *T. boeoticum* form used in the cross.

Table 1 Origin, characteristics and seed availability of amphiploids in the *Triticeae*, obtained in Bulgaria from 1950–1990.

Pedigree	Genome constitution* (n)	Valuable characters for plant breeding	Seed availability from:
1. 2n=28			
Ae. squarrosa var. *strangulata*×*T. boeoticum* No. 1	AD	Resistance to fungi, tough rachis	IWS M. Savov
Ae. squarrosa var. *strangulata*×*T. boeoticum* No. 3	AD	Resistance to powdery mildew, tough rachis	IWS M. Savov
Ae. squarrosa var. *strangulata*×*H. villosa*	DV	Resistance to fungi	IWS M. Savov
Triticale (2n=42)×*S. cereale* (2n=28)	?	High protein content and tillering, short stem	IG Z. Sabeva
2. 2n=42			
T. boeoticum No. 1×*T. dicoccum* Khapli-III**	AAB	Resistance to fungi, large grain size	IWS M. Savov
T. dicoccum Khapli-III×*Ae. squarrosa* var. *strangulata*	ABD	Resistance to fungi	IWS M. Savov
T. timopheevi var. *typica*×*Ae. squarrosa* var. *strangulata*	AGD	Resistance to fungi, cold resistance	IWS M. Savov
T. timopheevi M-1×*Ae. squarrosa* var. *strangulata*	AGD	Resistance to fungi, winter hardness, high tillering	IWS M. Savov
T. polonicum×*T. boeoticum*	AAB	Resistance to powdery mildew, large grain size	IWS M. Savov
T. durum×*S. cereale*	ABR	Short stem, high productivity, fungal resistance	IWS S. Tsvetkov
T. durum×*Ae. speltoides*	ABS		P. Spetsov
T. turanicum×T. timopheevi	?	Fungal and winter resistance, large grain	M. Savov
3. 2n=56			
T. aestivum×*S. cereale*	ABDR	Short stem, early maturity, fungal and cold resistance	V. Baichev
T. sphaerococcum×*S. cereale*	ABDR	Resistance to powdery mildew high protein content	IIPR I. Stankov
T. aestivum×*Ae. speltoides*	ABDS	Resistance to powdery mildew	IWS P. Spetsov
4. 2n=64			
Ae. squarrosa var. *strangulata*×*H. villosa*×*T. palaeocolchicum*×*E. giganteus*×*T. dicoccum* Khapli-III	?	Resistance to fungi, high protein content, vegetative propagation	IWS M. Savov
5. 2n=70			
T. aestivum×*Ae. variabilis*	ABDUS	Resistance to powdery mildew	P. Spetsov
T. aestivum×*Ae. kotschyi*	ABDUS	Resistance to powdery mildew, high tillering	P. Spetsov
T. aestivum×*Ae. ovata*	ABDUM	High protein content, fungal resistance	IG B. Bochev
T. aestivum×*Ae. columnaris*	ABDUM	High protein content, fungal resistance	IG B. Bochev

*, Genome symbols after Kimber and Tsunewaki (1988, Proc. 7th Int. Wheat Genet. Symp., Cambridge, UK);
**, Seeds available from reciprocal combination;
IG, Acad. Doncho Kostoff, Institute of Genetics, Sofia 1113;
IWS, Institute for Wheat and Sunflower, General Toshevo 9520;
IIPR, Institute of Introduction and Plant Resources, Sadovo 4122

The rachis and spikelets of the two F_1 hybrids and amphiploids are non-fragile and free threshing. Breaking at different parts of the rachis is pronounced in the parents. This shows that strength of rachis and grain separation from the husks in *Triticum* species may be a result not only of mutation but also of gene interaction.

Ae. squarrosa var. *strangulata* × *T. boeoticum* No. 3

Due to the large aneuploid variation, seed-setting is decreased to about 60–65% compared to the first amphiploid which shows fertility of 75–90%. Powdery mildew resistance depends on the plant chromosome number.

Ae. squarrosa var. *strangulata* × *Haynaldia villosa*

The amphiploid shows a very high resistance to diseases. Its crossability to wheat is of a good level. The seed-setting varies from 15 to 60% in the reciprocal F_1 hybrids (Spetsov 1988a). Using the amphiploid in crosses to wheat, disomic addition lines ($2n = 44$) have been obtained. An alien addition pair of telocentric chromosomes produces high resistance to powdery mildew and does not affect the phenotype and fertility of plants.

Tetraploid triticale

The amphiploid has been obtained by crossing hexaploid triticale to tetraploid rye (Sabeva 1985). It shows a high level of meiotic stability (about 4–5% aneuploids in the progeny), high tillering, short stem and protein content of 22–24%. It is thought that this triticale possesses equal number of wheat and rye chromosomes.

No data are available for disease resistance.

2. Amphiploids with $2n = 42$

T. boeoticum No. 1 × *T. dicoccum* var. Khapli-III

T. dicoccum var. Khapli-III was obtained from the cross of *T. dicoccum* to tetraploid rye. It is assumed that some introgression occurred between them, because the Khapli-III line looks like *T. dicoccum*, but differs in its complicated spikelet that usually forms 3–4 seeds instead of two.

The amphiploid shows high self-fertility, large grain size, normal crossability to wheat, and resistance to fungal pathogens. The latter character dominates in F_1 hybrids with common wheat. Amphiploid seeds are available from the reciprocal cross-combination.

T. dicoccum var. Khapli-III × *Ae. squarrosa* var. *strangulata*

This looks like common wheat, having normal meiosis, self-fertility and crossability to wheat. When the amphiploid is pollinated by *T. aestivum* cv. 'Michigan Amber' and the alloplasmic line (*Ae. longissima*)-'Siete Cerros 66', the seed-setting is normal. No seeds have been obtained in the reciprocal combination where pollen comes from the amphiploid. Preliminary data show that pollen does not germinate on stigmas. The amphiploid possesses high levels of fungal resistance.

T. timopheevi var. *typica* × *Ae. squarrosa* var. *strangulata*

This is characterized by normal seed germination, winter hardness and high resistance to mildew and rusts (Savov 1978). The amphiploid is used in the wheat breeding programme at IWS-General. Toshevo for transferring disease resistance.

T. timopheevi M-1 × *Ae. squarrosa* var. *strangulata*

The amphiploid differs from the above mentioned one by the use of *T. timopheevi* mutant line (M-1). This line shows high fungal resistance and protein content (26.5%) in comparison to the normal *timopheevi* form. The M-1 is a free-threshing line, with a more productive spike and shorter, elastic stem.

The amphiploid shows high fungal and cold resistance. Under code number H-68/44, it was involved in crosses to wheat for incorporation the resistance to fungi, and showing high combining ability (Spetsov 1988a, Mihova et al 1990). The F_1 hybrids are fertile when the amphiploid is used as a pollen donor.

T. polonicum × *T. boeoticum*

This looks phenotypically like *T. polonicum*, showing high powdery mildew resistance. The grain is large and elongated.

Hexaploid triticale

The first hexaploid triticale in Bulgaria was created at IWS-General. Toshevo by crossing *T. durum* line No. 13 and a winter rye No. 58 (Popov and Tsvetkov 1970). Many triticale forms have been obtained later as initial material for triticale breeding. The first releasing of hexaploid triticale variety 'Perun' was in 1979 (Baeva 1981). In 1983-90 period, several varieties, 'Vihren' and 'Persenk' for grain production and 'Belitsa-1' for green crop were introduced into agriculture (Tsvetkov 1989).

T. durum × *Ae. speltoides*

This seems to be genetically unstable, showing a low spike fertility. A study is in progress to determine its resistance to fungi.

T. turanicum × *T. timopheevi*

The amphiploid is a free-threshing form, having long awned spikes with large and elongated grains. It possesses high fungal and cold resistance.

3. Amphiploids with 2n = 56

Octoploid triticale

The first octoploid triticale in Bulgaria was obtained by D. Kolev (1968). After that many octoploid forms have been realized and employed in the triticale breeding programme due to their short stems, spike productivity and increased winter hardness (Baeva 1981, Tsvetkov 1989).

T. sphaerococcum × *Secale cereale*

Popov and Stankov (1979) described this amphiploid, obtained by using two lines of *T. sphaerococcum* and a rye form C-2. Spike fertility is low (10–12 seeds per spike) and aneuploid variation in the progeny reaches 40%. The amphiploid shows high levels of powdery mildew resistance and high protein content.

T. aestivum × *Ae. speltoides*

This newly obtained amphiploid utilizes wheat cultivars 'Chinese Spring' and 'Trayana' (winter type form, IWS-General. Toshevo selection). The amphiploid having 'Trayana', includes *speltoides* cytoplasm, because the reciprocal F_1 hybrid did not survive after colchicine treatment. The fertility is very low (1–10 seeds per spike) and is genetically unstable. Powdery mildew attacks plants to varying degrees.

4. Amphiploids with 2n = 64

The amphiploid comprises species of *Aegilops* (*Ae. squarrosa* var. *strangulata*, as mother line), *Haynaldia* (*H. villosa*), *Triticum* (*T. dicoccum* var. Khapli-III and *T. palaeocolchicum*), and *Elymus* (*E. giganteus*). This shows resistance to fungi, high protein content, good crossability to common wheat, but the fertility is very low (0.5–1.0%).

Intraplant variability is observed for many morphological traits. The amphiploid is preferentially maintained through vegetative propagation.

5. Amphiploids with 2n = 70

T. aestivum × *Ae. variabilis*

This is genetically unstable, with fragile black spikes and low fertility. Some of the plants in progeny are sterile (Spetsov 1988b). Powdery mildew attacks plants to a lower degree compared to the common wheat cultivars 'Charodeika' and 'Roussalka'. A pair of *Ae. variabilis* chromosomes has been added to the genome of later variety, inducing high resistance to powdery mildew fungus (Spetsov and Iliev 1991).

T. aestivum × *Ae. kotschyi*

This is also unstable, but the fertility is better than the above mentioned line with *Ae. variabilis*. In the progeny plants vary mainly due to the glume pubescence, irrespective of their high level of powdery mildew resistance, high tillering and winter hardness. This amphiploid is now including in hybridization to wheat for incorporation the powdery mildew resistance in common wheat breeding (Spetsov 1990).

T. aestivum × *Ae. ovata*

A ditelocentric line of 'Chinese Spring' is used in crosses to *Ae. ovata*. The amphiploid is genetically unstable, with low fertility, but possessing fungal resistance and high protein content.

T. aestivum × *Ae. columnaris*

The variety 'Chinese Spring' is included in this amphiploid, showing the same genetic

properties as the above mentioned one (Bochev 1988).

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Structural alterations of chloroplast and mitochondrial DNA in progenies of the alloplasmic wheat with rye cytoplasm

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Summary

Comparative study of the mt and ct DNA digestion patterns with *Bam*HI and *Eco*RI was carried out in alloplasmic wheat with rye cytoplasm and its progenies produced from individual selfpollinated plants and hybrids with two wheat varieties using as males. Variations of organelle DNA from maternal ones were found in hybrid progeny of the alloplasmic lines with wheat varieties as following fasions: modification both in mt and in ct DNA; modifications only in mt DNA and ct DNA of wheat type; modified ct DNA and mt DNA of the rye type and both mt and ct DNA of the wheat type. Biparental inheritance of organelle DNA was supposed. The structural alterations provides the development of wheat lines with new combination of cytoplasmic genes.

Introduction

Investigations of alloplasmic wheat lines have shown the importance of cytoplasmic genes for plant productivity (Tsunewaki 1980, Ponayotov 1983, Maan 1979). Alloplasmic lines as model systems have some limitations both for more detail study on the nucleo-cytoplasmic interactions and for application of positive cytoplasmic effects in plant breeding. The limitations are; difficulties of distinguishing between chloroplast and mitochondrial gene effects on plant characters, and impossibility of new combinations or recombinations of organelle DNAs due to their strict uniparental plasmagene inheritance.

A part of these problems can be solved by somatic hybridization (Gleba et al 1985). However, researchers are limited by choosing agricultural crops in which protoplast fusion followed by regeneration is possible.

It is known some cases of biparental inheritance of plastid genes in *Antirrhinum majus* (Dier 1967) and *Secale cereale* (Frost et al 1970) or mt DNA barley and rye hybrids (Saliman et al 1987) although normally these species have maternal inheritance of plasmagenes.

The present study is conducted to determine polymorphism of mt and ct DNA among individual hybrids and selfpollinated progenies of the alloplasmic wheat with rye cytoplasm.

Materials and methods

The materials for the present study comprised alloplasmic wheat with genome of Lutescense 62 variety and rye cytoplasm of Viatka variety — (*cereale*)-Lt62, BC6, two selfpollinated

lines (92 and 96) received from this population, hybrid 555 — F_6 (*cereale*)-Lt62 × (10D2 × Lenigradka), three lines L1, L2 and L3 received from hybrid F_2 (*cereale*)-Lt62 × Leningradka, three lines Ld1, Ld2 and Ld3 received from hybrid F_2 (cereale)-Lt62 × Ledovka. F_6 seeds were used in L and Ld lines. Pedigrees of these lines described in Table 1. Seeds of rye (Vyatka, Chulpan, Polycrossnaja, Voskhod) and wheat (Lutescens 62, Leningradka, Ledouka) varieties including parental ones were used for comparison.

For isolation of mt DNA, 5-6 day old etiolated seedlings were used (Wilson and Chourey 1984), and for that of ct DNA, 7-10 day old seedlings grown under light (Bookjans et al 1984). Purified mt DNA and ct DNA were restricted by *Eco*RI and *Bam*HI, and their restriction patterns were analyzed after conducting gel-electrophoresis.

Results

Comparative analysis of mitochondrial DNA

Patterns of *Eco*RI and *Bam*HI restriction fragments are shown in Fig. 1. According to the obtained data mt DNA of the alloplasmic wheat (*cereale*)-Lt62 was similar to that of maternal rye var. Vyatka. Varieties of rye had shown different patterns of mt DNA (Fig. 1A). Differences between Lt62 and var. Vyatka concerned only the glow intensity of some fragments, but not their quantity. At least the majority of plants of this alloplasmic wheat is supposed to contain mt DNA of the maternal rye variety. Two selected lines 92 and 96 from this alloplasmic wheat Lt62 were investigated for heterogeneity in organelle DNA. The data had shown that the line 92 contained the typical rye mt DNA of Vyatka, while the line 96 differed from wheat and rye.

Mt DNA of the 555 hybrid was similar neither to wheat nor rye mt DNA. It had both unique and similar parental fragments. More probable explanation of these data is biparental inheritance of mt DNA and as a result of this the development of mt DNA diversity among hybrid plants, which contained molecules of both parents and recombinant ones.

The lines isolated from hybrids (*cereale*)-Lt62 × *T. aestivum* cv. Leningradka had differential mt DNA. L1 and L2 lines were similar to each other, but had mt DNA different from that of rye, wheat and hybrid 555. L3 lines had the same mt DNA as maternal lines as is shown by both restriction enzymes.

All three lines isolated from hybrid (*cereale*)-Lt62 × *T. aestivum* cv. Ledovka contained mt DNA pattern identical with male but not female parents.

Comparative analysis of chloroplast DNA

Patterns of restriction fragments of ct DNA are shown in Fig. 2. Ct DNA of alloplasmic wheat Lt62 with *S. cereale* cytoplasm was not different in number and distribution of their fragments from its female parent rye variety Vyatka. However, the lines isolated form this alloplasmic wheat differed from each other. The line 92 had rye ct DNA, the line 96 had

Table 1. Mt and ct DNA types in alloplasmic wheat, its selfpollinated and hybrid progenies

Investigated samples		DNA			
		Chloroplastic		Mitochondrial	
Line	Pedigree	*Eco*RI	*Bam*HI	*Eco*RI	*Bam*HI
Lt62	(*cereale*)–Lt62 BC_6	S	S	S	S
92	Selfpollinated line from (*cereale*)–Lt62	S		S	
96	Selfpollinated line from (*cereale*)–Lt62	T		M1	
555	F_6 (*cereale*)–Lt62 (♀)×(10D2×Leningradka) (♂)	C1		M2	
L1	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Leningradka (♂)	T	C2	M3	M4
L2	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Leningradka (♂)	T	C2	M3	M4
L3	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Leningradka (♂)	S	C3	S	S
Ld1	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Ledovka (♂)	T	T	T	T
Ld2	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Ledovka (♂)	T	T	T	T
Ld3	F_6 selfpollinated line from F_2 (*cereale*)–Lt62 (♀)×Ledovka (♂)	T	T	T	T

S: DNA rye type, T: wheat type, C1, C2, C3: changed (recombinant) type of ct DNA, M1, M2, M3, M4: changed (recombinant) type of mt DNA.

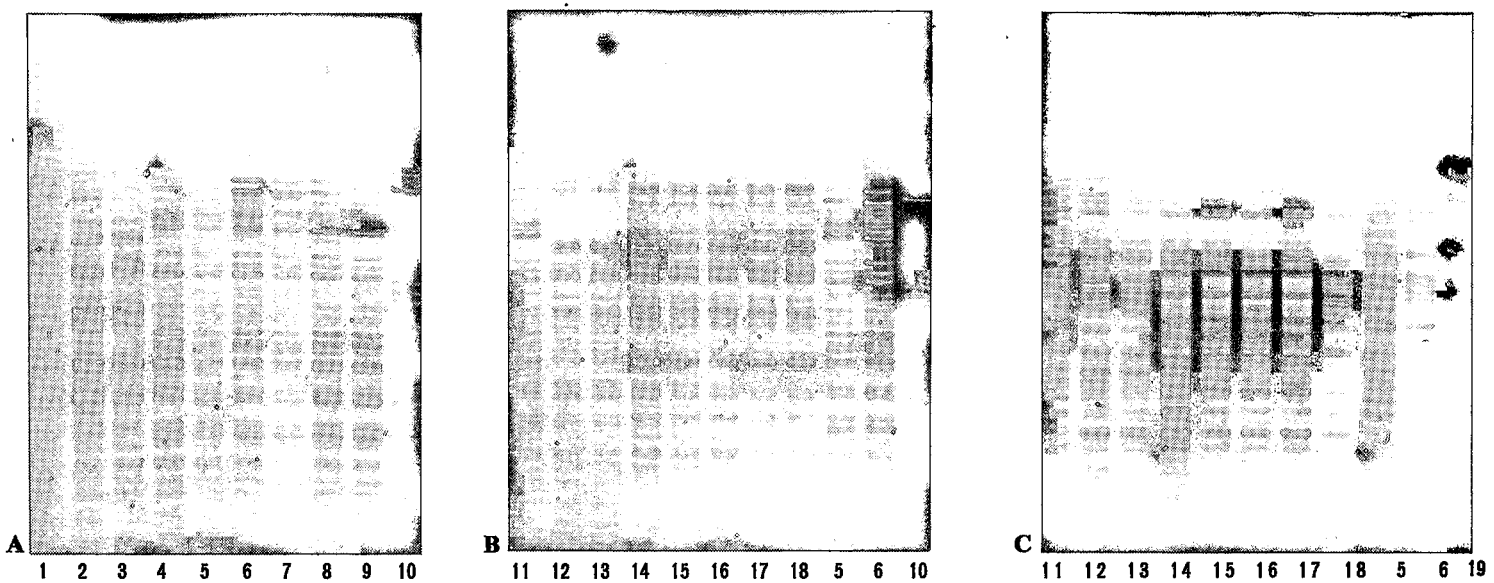

Fig. 1. *Eco*RI (A, B) and *Bam*HI (C) restriction fragment pattern of mitochondrial DNA.
1. *T. aestivum* var. Lutescens 62; 2. Hybrid 555; 3. 96 line; 4. 92 line; 5. (*cereale*)-Lt62; 6. *S. cereale* var. Vyatka; 7. *S. cereale* var. Chulpan; 8. *S. cereale* var. Polycrossnaja; 9. *S. cereale* var. Voskhod; 10. phage λ (*Pst*I); 11–13. L3, L2, L1 lines consequently; 14. *T. aestivum* var. Leningradka; 15–17. Ld3, Ld2, Ld1 lines consequently; 18. *T. aestivum* var. Ledovka; 19. phage λ (*Bam*HI).

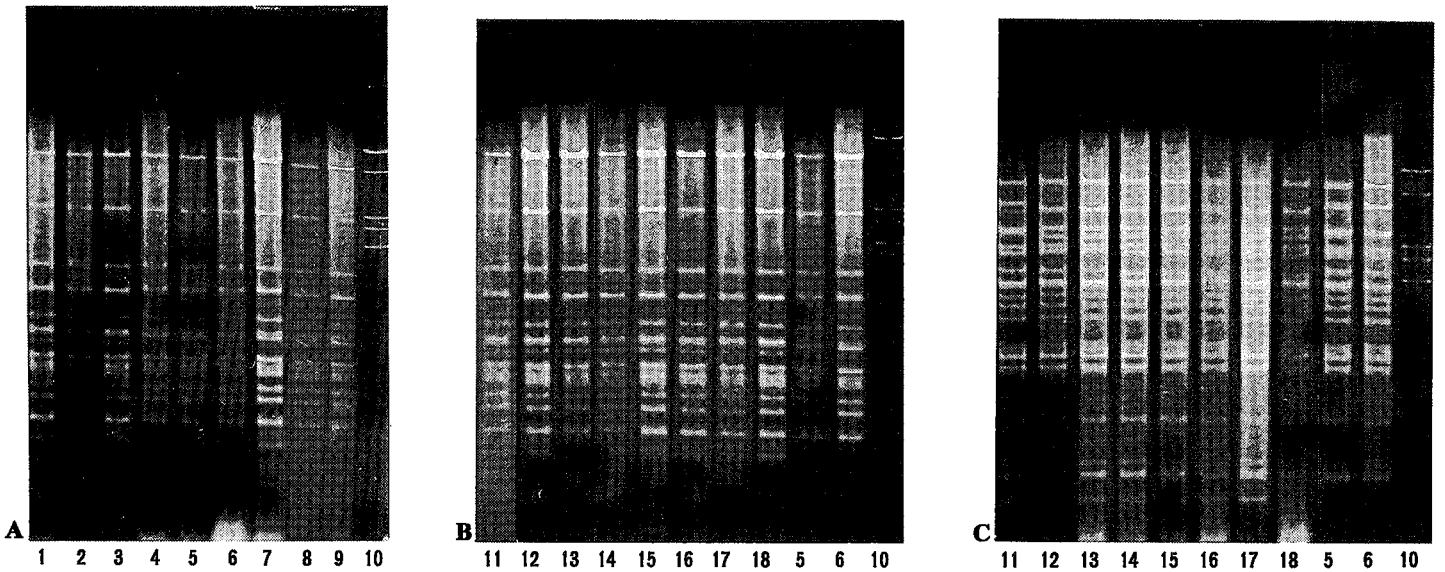

Fig. 2 *Eco*RI (A, B) and *Bam*HI (C) restriction fragment pattern of chloroplast DNA.
1. *T. aestivum* var. Lutescens 62; 2. Hybrid 555; 3. 96 line; 4. 92 line; 5. (*cereale*)-Lt62; 6. *S. cereale* var. Vyatka; 7. *S. cereale* var. Chulpan; 8. *S. cereale* var. Polycrossnaja; 9. *S. cereale* var. Voskhod; 10. phage λ (*Pst*I); 11–13. L3, L2, L1 lines consequently; 14. *T. aestivum* var. Leningradka; 15–17. Ld3, Ld2, Ld1 lines consequently; 18. *T. aestivum* var. Ledovka.

ct DNA similar to wheat.

Ct DNA of the hybrid 555 as its mt DNA was unique and probably a mixture of both parental DNAs and/or alternated molecules.

Three lines originated from hybrid (*cereale*)-Lt62 × Ledovka had ct DNA of wheat type (*Eco*RI and *Bam*HI), but three lines originated from hybrid (*cereale*)-Lt62 × Leningradka had ct DNA of an alternated type at least as is shown by *Bam*HI.

Discussion

The results of organelle DNA analyses are summarized in Table 1. According to the obtained data sex crosses between wheat with rye cytoplasm, and wheat varieties can result in the production of new combinations of cytoplasmic genes:

1. Wheat ct DNA, but alternated mt DNA (line 96)
2. Ct and mt DNA of an alternated type (hybrid population 555, L1 and L2 lines)
3. Ct DNA of an alternated type, but mt DNA of rye type (L3)
4. Paternal inheritance of ct and mt DNA (Ld1, Ld2 and Ld3 lines).

Paternal inheritance of organelle DNAs was a strange fact of the present study. The explanation of this phenomenon is not clarified until more detail analysis of a great number of lines isolated from hybrids or alloplasmic lines with rye cytoplasm is carried out. A preliminary hypothesis could be drawn at present time as follows; mainly the progenies of plants having wheat organelle DNA or plant with wheat organelle DNA restriction sites were selected for the analyses because such plants had more vigour as result of the interactions between the nucleus and cytoplasmic genes.

This hypothesis was confirmed by our observations of the alloplasmic line and its hybrids under field conditions. The plants of (*cereale*)-Lt62 had shorter stems, smaller ears and fewer seeds to propagate than the euplasmic line. However, the majority of plants from F_2 hybrids had the vigor similar to wheat varieties used as pollinators. Not only "powerful", but "weak" plants were used for developing lines. However, it was very difficult to get enough seeds from "weak" plants for the analysis.

Although reasons of mt and ct DNA alterations are not known the present study had demonstrated the possibility to develop wheat lines with new combination of organelle DNAs.

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Cytogenetic study on the origin of some special Chinese landraces of common wheat

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Summary

Tibetan Weedrace, Yunnan Hulled Wheat, Sichuan White Wheat complex (including Chinese Spring) and Xinjiang Rice Wheat are four special landraces of *Triticum aestivum* L. which were found in China. Genomic analysis showed that they were different from *T. aestivum* L. var. *spelta* by one to two pairs of chromosomes. These four Chinese landraces could be classified into two groups, with the Xinjiang Rice Wheat in one group and all the remaining in the other. These two groups were found to be distinguished by two pairs of chromosomes and one of them was identified as chromosome 6B. Cytogenetic analysis showed that these two groups of common wheat landraces might be independently originated in China via pollination of different accessions of the cultivated wheat tetraploid by the *Aegilops tauschii* accessions which has been discovered as a native species in the northwestern China and as a weed in the central China as well.

Introduction

The Xinjiang Rice Wheat (XR) is a Polish-wheat-like landrace collected from Xinjiang. The Tibetan Weedrace (TW) is a brittle-rachis weedrace in barley field found in Tibet and the nearby northwestern Sichuan as a weed. The Yunnan Hulled Wheat (YH) is a glume-hulled landrace growing in Yunnan. The Sichuan White Wheat complex (SW) are a group of cultivated common wheat with multifloret spikelets, rounded glume and lemma. All these four special wheat landraces have been so far only found in China. Morphological and cytogenetic studies showed that they all had the AABBDD genome (Chen 1980; Lu and Zhang 1983; Yao 1983; Chen et al 1988; Yen et al 1988). However, these Chinese landraces have some primitive traits that distinguish them from *T. aestivum* var *spelta* (SP) and the common wheat of the East Mediterranean origin (Yao 1983; Chen et al 1988; Yen et al 1988). Based on these evidences, they were considered to be originated in China (Riley et al 1967; Chen 1985; Chen et al 1988; Yen et al 1988). However, the problems of how and where they originated still remain unanswered.

In this paper, we describe the results of the cytogenetical analysis of these four special Chinese common wheat landraces. The origin of these four landraces are also discussed.

Table 1. Plant materials used in this study

Material	Genome	Note
Aegilops tauschii Cosson	DD	Collected from Xinjiang, Shaanxi, Henan and Iran
Triticum aestivum L. var. *spelta* (SP)	AABBDD	From Dr. S. Sakamoto and Chinese Academy of Agric. Sci.
Triticum aestivum L.	AABBDD	
Tibetan Weedrace (TW)		From Dr. P. D. Chen and Dr. Y. S. Ma
Yunnan Hulled Wheat (YH)		From Dr. Y. C. Dong
Chinese Spring (CS)		From Dr. E. R. Sears
Sichuan White Wheat complex (SW)		From Sichuan Academy of Agric. Sci.
Chengdu-guang-tou		
Pen-an White Wheat		
Xinjin White Wheat		
Langzhong White Wheat		
Xinjiang Rice Wheat (XR)		From Chinese Academy of Agric. Sci. and Xinjiang Academy of Agric. Sci.

Materials and methods

The plant materials used in this study are listed in Table 1. They are all maintained in Triticeae Research Institute, Sichuan Agricultural University.

Interspecific hybrids were obtained by the conventional crossing method through immature hybrid embryo culture on N6 medium. The hybrid plants were moved to Barkam, Sichuan in August to survive the summer and moved back and grown in Triticeae Research Institute of Sichuan Agricultural University at Dujiangyan City in October.

Mitotic analysis were made in root-tip cells fixed in the 3 : 1 ethanol(95%)-glacial acid solution and stained by the Feulgen procedure. Meiotic analysis were done in pollen mother cells (PMCs) fixed and stained as the root-tip cells.

Results

The D genome in the special Chinese hexaploid landraces

Table 2 shows the meiotic configurations at MI in the PMCs of the hybrids involving *Aegilops tauschii*. The chromosome pairing at MI of the PMCs of the F_1 hybrids of *Ae. tauschii* with the TW, SW (including CS, Chengdu-guang-tou, Pen-an White, Xinjin White Wheat and Langzhong White Wheat) were all normal (Table 2 and Fig. 1a and b): Seven

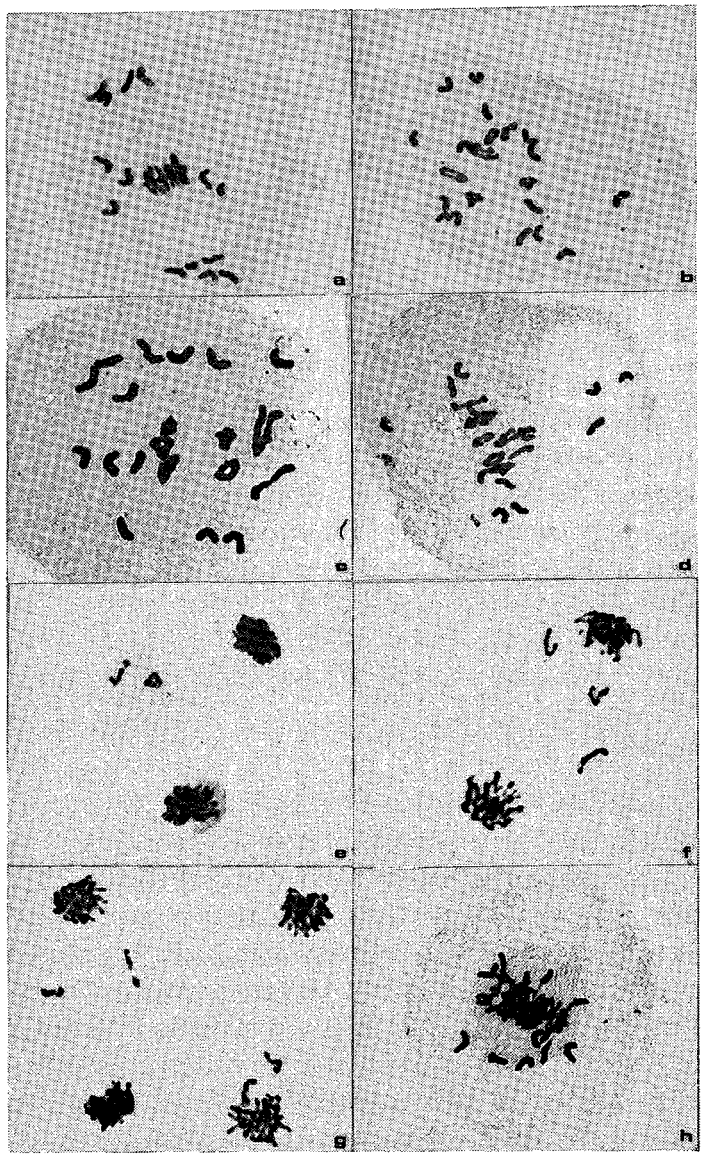

Fig. 1 Meiotic Configuration of the PMCs in the F_1 hybrids. a: TW×*Ae. tauschii* at MI, 14 I and 7 ring II. b: CS×*Ae. tauschii* at MI, 14 I, 2 rod II and 5 ring II. c: SP×*Ae. tauschii* at MI, 13 I, 1 rod II, 5 ring II and 1 III. d: SP×*Ae. tauschii* at MI, 11 I, 2 rod II, 3 ring II, 1 III and 1 IV. e: CS×XR at A I, showing lagging chromosome 6B. f: YH×XR at A I, showing lagging chromosome 6B. g: TW×XR at A II, showing lagging chromosome 6B. h: SP×XR at MI, 8 I.

Table 2. Meiotic configurations at MI in the PMCs of the F_1 intergeneric hybrids

Combination	Cells observed	Univalents	Bivalents			Trivalents	Quadri-valents
			Rod	Ring	Total		
T. aestivum var. *spelta*	207	13.84	1.58	5.39	6.97	0.04	0.01
×*Ae. tauschii*		11-14	0-4	3-7			
Tibetan Weedrace	195	14	0.51	6.49	7.00	0	0
×*Ae. tauschii*		14	0-1	6-7			
Chinese Spring	413	14	1.09	5.91	7.00	0	0
×*Ae. tauschii*		14	0-3	4-7			
Chengdu-guang-tou	300	14	1.13	5.87	7.00	0	0
×*Ae. tauschii*		14	0-4	5-7			
Xinjin White Wheat	200	14	1.18	5.82	7.00	0	0
×*Ae. tauschii*		14	0-3	4-7			
Langzhong White Wheat	200	14	1.20	5.80	7.00	0	0
×*Ae. tauschii*		14	0-4	5-7			
Pen-an White Wheat	100	14	1.22	5.78	7.00	0	0
×*Ae. tauschii*		14	0-3	4-7			

bivalents, most of which were ring, and no multivalent was observed in these hybrids. These results suggested that TW and SW had a quite primitive D genome which were structurally unchanged in comparison with the D genome of *Ae. tauschii.* In comparison with the F_1 hybrids of the SW with *Ae. tauschii,* the number of rod bivalents were reduced 50% in the F_1 hybrid of TW × *Ae. tauschii.* Therefore, the D genome in the TW might be closer to the genome of the *Ae. tauschii* than the D genome of the Sichuan Wheat complex was.

In the F_1 hybrid of SP×*Ae. tauschii,* 0.04 trivalents and 0.01 quadrivalents were observed. Cells which had both trivalent and quadrivalents were also observed (Fig. 1c and d). These results might indicate pairing between the D genome chromosomes and the A or B genome chromosomes and, therefore, confirm the translocation between these chromosomes in SP reported by Riley et al (1967). Our results suggested that one to three D genome chromosomes might be involved in these translocation.

Chromosome pairing in the hybrids involving the special Chinese hexaploid wheat landraces

The four special Chinese hexaploid wheat landraces were crossed with each other and with SP. Meiotic configurations at MI of the PMCs varied among these F_1 hybrids (Table 3, Fig. 1e-h). Pairing in the CS × Chengdu-guang tou was nearly normal. No multivalents were observed in this hybrid and the numbers of univalents and rod bivalents were very close to those observed in CS. It seems that there is no constructive difference between these two landraces. Since these two landraces are morphologically alike, CS is certainly a strain of the Chengdu-guang-tou landrace. In this study, the CS × Chengdu-guang-tou hybrid was used as a check.

Table 3. Meiotic configurations at MI in the PMCs of the F_1 hybrids

Combination	Cells observed	Univalents	Bivalents			Trivalents	Quadri-valents
			Rod	Ring	Total		
Chinese Spring × Chengdu-guang-tou	74	0.22 0–2	1.58 0–4	19.31 17–21	20.89	0	0
Chinese Spring × Yunnan Hulled Wheat	100	0.36 0–2	2.25 0–4	18.47 17–21	20.87	0.01 0–1	0 0
Chinese Spring × Tibetan Weedrace	100	0.45 0–4	2.42 0–4	18.24 15–21	20.66	0.01 0–1	0 0
Chinese Spring × *T. aestivum* var. *spelta*	100	1.47 0–6	3.28 0–7	16.90 14–21	20.18	0.06 0–1	0
T. aestivum var. *spelta* × Yunnan Hulled Wheat	100	1.56 0–6	4.03 0–9	16.08 12–21	20.11	0.05 0–1	0.02 0–1
T. aestivum var. *spelta* × Tibetan Weedrace	100	1.61 0–8	4.44 2–8	15.73 13–19	20.13	0.02 0–1	0.02 0–1
Chinese Spring × Xinjiang Rice Wheat	102	2.16 0–8	4.62 1–10	15.03 10–19	19.65	0.16 0–1	0
Yunnan Hulled Wheat × Xinjiang Rice Wheat	95	2.22 0–8	3.52 0–6	16.75 14–20	20.17	0.04 0–1	0
Tibetan Weedrace × Xinjiang Rice Wheat	100	2.55 0–14	4.30 0–10	14.73 8–20	19.03	0.11 0–1	0
T. aestivum var. *spelta* × Xinjiang Rice Wheat	103	3.07 0–12	5.32 2–11	13.82 11–18	19.14	0.21 0–1	0.01 0–1
Chinese Spring *	204	0.11	1.55	19.42	20.97	0	0

* : From P. D. Chen et al (1988).

In comparison with their meiotic configurations at MI of the PMCs to those of the check, the remaining nine hybrids can be grouped into three types. Type 1 consists the hybrids of CS with YH and TW. In these hybrids, the numbers of univalents and rod bivalents were a little bit higher than those in the check and only few multivalents were observed (Table 3). These results indicated that the genomes of TW and YH are very similar to that of CS though small differentiation has occurred.

Type 2 contains the hybrids of SP with CS, TW and YH. Two univalents were usually observed at MI of the PMCs of the hybrids in this group. The number of multivalents in the hybrids of this group were higher than the check (Table 3). This means that SP differs from CS, TW and YH by two chromosomes.

Type 3 includes the hybrids of XR with CS, TW, YH and SP. At the MI of PMCs of the hybrids in this group, 3–4 univalents were usually observed, and the number of multivalents were also higher than the check. This result indicated that XR differs from CS, TW, YH and SP by 3–4 chromosomes. Univalents were observed to be formed usually by

satellite chromosomes in the hybrid of XR with CS, TW and YH (Fig. 1e-g). This kind of univalents were found in 53.3%, 45.2% and 55.1% of the PMCs observed in the hybrids involving CS, TW and YH, respectively. Morphologically, these satellite chromosomes seem to be chromosome 6B.

Discussion

As described above, *T. aestivum* var. *spelta* differs from the four special Chinese hexaploid wheat landraces by one to two pairs of chromosomes, and the D genome in these four Chinese landraces were more primitive than the D genome of *T. aestivum* var. *spelta*. These results reveal that the four special Chinese hexaploid wheat landraces may originate independently and later than this *T. aestivum* var. *spelta*.

Based on the results of this study, the four special Chinese landraces may be classified into two groups. The first group is composed of TW, YH and SW (which is represented by CS). Members in this group have similar genomes. Riley et al (1967) discovered that the A, B and D genomes of CS were structurally unchanged relative to A and B genomes of *T. turgidum* var. *dicoccoides* and the D genome of *Ae. tauschii* Cosson respectively. The present study showed that the A, B and D genomes in TW, YH and SW were as primitive as those of CS. Therefore, they might be derived from the same progenitor and thus may be grouped together and called "Chinese Spring group". In this group, TW has some wild, primitive characters such as fragile spike, and its D genome is closer to the D genome of *Ae. tauschii* Cosson than the D genomes of other members. Therefore, TW might originate from cross between *T. turgidum* and *Ae. tauschii* at the middle portion of the Yellow River Valley and thus be the progenitor of this group. It is possible that the ancestor hybrid derivatives were later introduced into Sichuan, Yunnan and Tibetan area and envolved into YH and SW through natural and human selection.

Xinjiang Rice Wheat composes the second group. The present study showed that XR differs from the CS group by two pairs of chromosomes. Our observation also indicated that one of the two chromosomes may be chromosome 6B. In their analysis of XR with CS ditelosomics, Chen et al (1988) pointed out that it was the B genome that differed between these two landraces. It seems that it is not the D genome chromosome, as suggested by Yao et al (1983), but the B genome chromosomes that differ between these two landraces. XR also differs from SP by two chromosomes. Chen et al (1988) reported that there was little difference between the D genomes of XR, TW, YH and CS. It might indicate that the D genome of XR may also be primitive. The present study reconfirmed the results of Riley et al (1967) that SP differed from *Ae. tauschii* by one pair of D genome chromosome. The present study also showed that XR differs from SP by one to two pairs of chromosomes. Therefore, XR might not originate from a hybrid between *T. turgidum* L. var. *polonicum* and the Chinese Spring group nor evolve from *T. aestivum* var. *spelta* as suggested by Chen (1985). Instead, XR might be derived from a hybrid between *Ae. tauschii* and an emmer

wheat in which the B genome had changed. From the viewpoint of morphology, this emmer wheat may be *T. turgidum* L. var. *polonicum*.

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An attempt to transferring stem solidity of *Triticum aestivum* to triticale ($2n=6x=42$). I. Investigations in F_1

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Summary

The stem solidity in wheat appears an decisive factor for the resistance to damages by wheat stem sawflies. A transfer of the solid stem from *Triticum aestivum* in triticale ($2n=6x=42$) was conducted through the use of the wide hybridization methods in a breeding way by application of simple and complex crosses. The solid stem of MBX-11-7 winter soft wheat was inherited dominantly in F_1 crossing with the 42-chromosome triticale T-AD-17-B (with hellow stem). The hybrid plants in F_1 with solid stem are distinguished for a lot of high meiotic disturbances reaching 96.80% compared to 46.36% for the male parent from ♂ T-AD-17-B and 2.22% for the female parent form ♀ MBX-11-7.

Introduction

Today it is known that the stem solidity, both in wheat and triticale, appears as decisive factor for their resistance to damages by European wheat stem sawfly *Cephus pygmaeus* L. (Yamashita 1937; Platt and Larson 1944; Larson 1959; McKenzie 1965; Tsvetkov 1973). According to Holmes and Peterson (1958, 1960, 1961) and Roberts (1954) the resistance in wheat, as related to the sawfly, can be divided into three categories: (1) lack of appeal to the ovipositing female and resistance to oviposition, (2) suppression of egg hatching or larval tunneling, and (3) nutritional requirement of larval. Holmes and Peterson (1962) established that the largest larval mortality occurs in solid stemmed wheat. The triticale varieties distributed now, similar of wheat and rye, are distinguished for hollow stem and poor resistance to the basic wheat pest.

In the literature there are no cases indicating the solid stem transfer from *T. aestivum* in triticale ($2n=42$) with the aim to develop forms with a solid stem resistance to *Cephus pygmaeus* L.

Materials and methods

The method of hybridization *T. aestivum* (solid stem) × Triticale ($2n=42$, hollow stem) was used. Winter common wheat MBX-11-7 (Bulgaria, solid stem), and triticale T-AD-17-B (Bulgaria, hollow stem) and AD-No. 11 (Maya II-ARM"S", Mexico, hollow stem) were used as components for crossing.

Stem solidity was determined by three cross sections in the first top (ear-next) internode

and by a cross section in the middle of every next (2nd, 3rd, 4th). The cross section of the first top internode were made 2.5 cm below ear, in the middle of the internode and 2.5 cm above the base (McNeal 1961). Degree of stem solidity was determined by the scale of Sapegin (1938) and that of Larson (1959): 1 = hollow stem (thin walls); 2 = hollow stem (thick walls); 3 = intermediate stem solidity; 4 = solid stem with extremely opening; 5 = solid stem.

The analyses of the meiosis in PMC was conducted on preparations through squeezing of the object (Nikolov 1966).

Results and discussion

A. First hybrid generation (F_1)

The winter common wheat MBX-11-7 (Bezostaya 1 × No. 13) with a solid stem and possessing high resistance to *Cephus pygmaeus* L. (Tsvetkov 1973) developed by us was used in the transfer of the solid stem from *T. aestivum* in triticale ($2n = 42$).

In our investigation the winter common wheat MBX-11-7 was crossed with the short-stemmed triticale T-AD-17-B, a hollow stemmed line. Only one hybrid plant was produced in F_1 with indication No.477 (MBX-11-7 × T-AD-17-B) because of the high inviability of the hybrid seed, due to the common wheat mother component. The hybrid plant had a height of 104.0 cm (degree of dominance of +1.17) and very long spikes (incomplete dominant inheritance +0.69) (Table 1).

The most valuable quality of the hybrid plant of the cross No. 477 was the solid stem in all internodes of the tillers. It was found that the solid stem of MBX-11-7 winter soft wheat was inherited dominantly in F_1 crossing with the 42 - chromosome triticale T-AD-17-B (Fig.1). In concerning of wheat Putnam (1942) also found that the solid stem was determinated by one dominant gene in tetraploid crosses. From other side Goytia Y Angulo et al (1935) discovered that this character was inherited by two recessive genes. Specially in wheat almost all attempts with the aim of transferring stem solidity of *T. durum* to *T. aestivum* evoked great difficulties. Yamashita (1937) and later Matsumura (1947) and Larson (1952) found a gene on chromosome XX (2D), which depressed genes for solid stem in A and B genomes. Platt and Larson (1944) did not succeed to transfer completely the solid stem from *T. durum* (cv. Golden Ball) into *T. aestivum*. They explained this with the gene O_D, which inhibit the genes, responsible for the solid stem. The monosomic analysis, made by Larson and McDonald (1959) found that the gene O_D was located on the chromosome XX (2D).

Investigations showed that the hybrid plant with solid stem from the cross No. 477 (MBX-11-7 × T-AD-17-B) were distinguished for a lot of high meiotic disturbances F_1 reaching 96.80% compared to 43.96% for the male parent from ♂ T-AD-17-B and 2.22% for the female parent from ♀ MBX-11-7.

With the aim to improve the fertility and earliness of the hybrid plant with a solid stem

Table 1. Degrees of stem solidity of the parental varieties and their F_1 hybrids

Parents and hybrids	No. of plants tested	Degree of stem solidity by internodes*						Plant height (cm)	Main spike		
		First top internode			Lower internode				Length	No. of spikelets	No. of grains
		2.5 cm below ear	middle	2.5 cm above base	2nd	3rd	4th				
I. Simple crossing											
♀ MBX-11-7 (*T. aestivum*)	20	1.0	5.0	4.2	4.9	3.9	4.4	101.7	13.1	21.2	52.8
♂ T-AD-17-B (Triticale, $2n=42$)	20	1.9	1.7	2.0	1.0	1.1	1.7	75.0	15.7	33.1	96.6
MBX-11-7 × T-AD-17-B (F_1)	1	5.0	5.0	4.0	4.0	3.0	4.0	104.0	15.3	27.0	10.0
II. Complex crossing											
♂ AD-No. 11 (Triticale, $2n=42$)	20	1.0	1.4	1.9	1.1	1.3	1.7	93.3	9.3	19.3	69.5
(MBX-11-7 × T-AD-17-B) × AD-No. 11 (F_1)	1	1.0	5.0	5.0	5.0	5.0	4.0	82.0	19.0	28.0	39.0

*: 1 = hollow stem; 5 = solid stem; from 1.1 to 4.9 = medial degrees from hollow to solid stem.

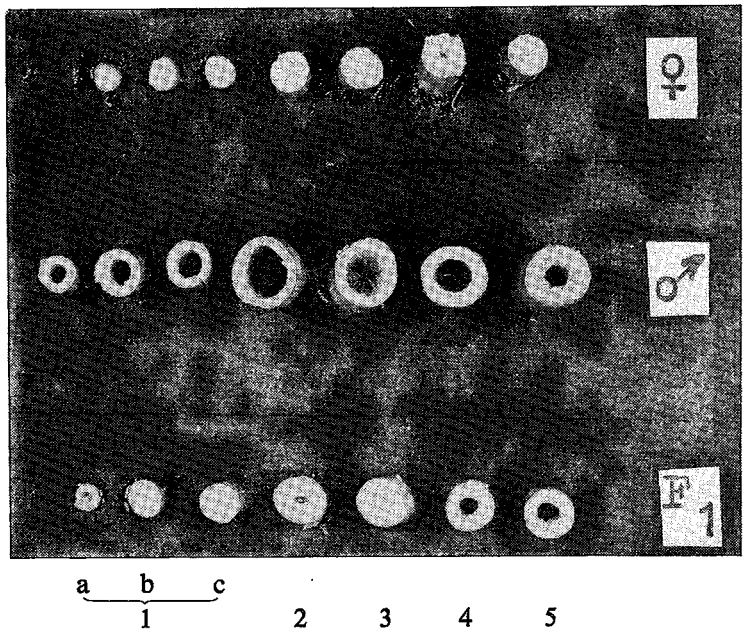

Fig. 1. Pieces demonstrating stem solidity internodes from top to bottom of the parental forms and F_1 hybrid: ♀ MBX-11-7 (*T. aestivum*) with a solid stem, ♂ T-AD-17-B (Triticale, $2n=42$) with a hollow stem, F_1 (MBX-11-7 × T-AD-17-B) with a solid stem. 1a. 2.5 cm below ear; 1b. in the middle of the topmost internode; 1c. 2.5 cm above the base of the topmost internode; 2, 3, 4, 5 pieces in the middle of the next internodes from top to bottom.

from the cross No. 477 (MBX-11-7 × T-AD-17-B) a repeated crossing already was done with the Mexican high-fertile triticale AD-No. 11 (Maya II-ARM"S") with a hollow stem and high resistant to rust and powdery mildew. Again only one normal hybrid plant was produced in F_1. The same had a comparatively short stem, very long spikes, improved fertility and a high resistance to rust and powdery mildew. The hybrid plant from the repeated crossing of F_1 was registered with the breeding number T-AD-592. One of its valuable quality was the solid stem in the all internodes. Ninety hybrid grains were obtained which were planted for a further breeding work (Table 1).

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An attempt to transferring stem solidity of *Triticum aestivum* to triticale ($2n = 6x = 42$). II. Analysis in F_2 - F_4

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Summary

New winter triticale forms with solid stem were found in F_2-F_4 generations from the hybridization of the winter common wheat (solid stem) and triticale ($2n = 42$) with hollow stem. This new developed triticale (2n = 42) showed high resistance to *Cephus pygmaeus* L.

Introduction

The possibility of blocking of the parasite penetration to the hostplant (Wallace and McNeal 1966) is proved by the development of winter triticale forms derived from a cross of T-AD-592 with a solid stem. By this breading program, lines with a high ento-immunity to the wheat stem fly *Cephus pygmaeus* L. will be bred, and the costs on the chemical control will be also saved (Tsvetkov 1982).

Materials and methods

One of the basic purposes of the complex cross T-AD-592 (MBX-11-7 × T-AD-17-B) F_1 × AD-No. 11 is the acquirement of hexaploid triticale with a solid stem as well as a short stem and high productivity at F_2 - F_4 generations of this cross. For this purpose the selection in F_2 was conducted on the solid stem.

The methods used to determine the degree of solidness of the stem and the analyses of the meiosis in PMC were mentioned in the previous paper (Tsvetkov 1992). All plants at F_2 - F_4 populations and parents were grown under isolator for guaranteeing trueness of materials.

Results and discussion

A. Second hybrid generation (F_2)

A transfer of the solid stem of *Triticum aestivum* into triticale ($2n = 6x = 42$) was carried out by interspecific hybridization (simple and complex cross). An interest in this project is how to combine the solid stem with plant height and the spike grain number. A number of F_2 plants derived from the interspecific cross T-AD-592 (MBX-11-7 × T-AD-17-B) F_1 × AD-No. 11 had solid stem in all internodes and were from 50 to 110 cm in plant height (Fig. 1). Most valuable plants are the hybrid with a solid stem and 61–80 grains per spike.

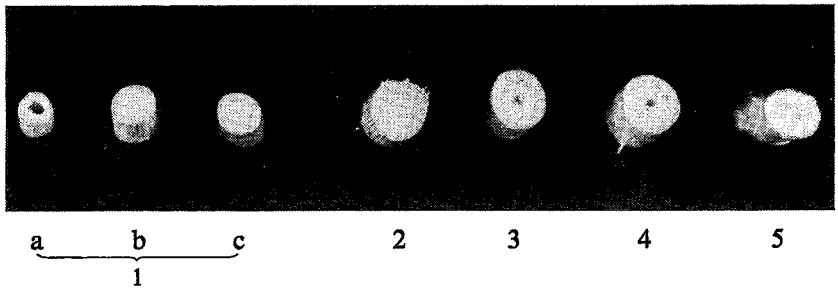

Fig. 1 Sectioned internodes of stem solidity in the winter triticale T-AD-592 (MBX-11-7×T-AD-17-B) F_1×AD-No. 11. 1a. 2.5 cm below ear; 1b. in the middle of the topmost internode; 1c. 2.5 cm above the base of the topmost internode; 2, 3, 4, 5 pieces in the middle of the next internodes from top to bottom.

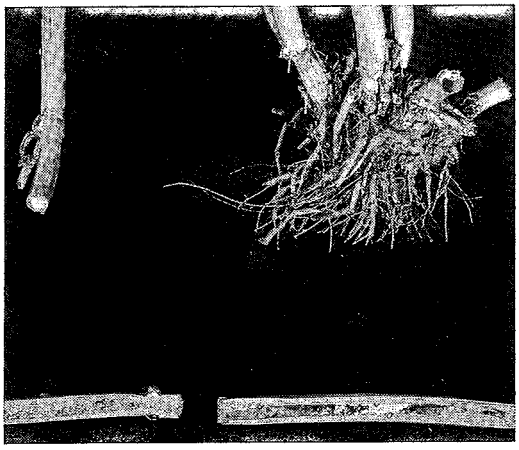

Fig. 2 Damages on a hollow stem of *T. aestivum* by *Cephus pygmaeus* L.

Table 1 shows considerable meiosis stability in the F_2 hybrid with a solid stem of the cross T-AD-592 compared in F_1. The average number of meiotic disturbances in F_2 were 66.2%, while those in F_1 were 96.8% (Tsvetkov 1992).

B. Fourth hybrid generation (F_4)

Table 2 shows that solid stem of the hybrid studied in F_4 is successfully with major agronomical characters, ie, a comparatively short stem, large spike, a very good grain formation and heavy grain. The average grain number of the solid-stemmed hybrid plants varies from 56 to 94 grains and the spike grain weight from 3.2 to 5.4 g, compared to 40 grains and 1.8 g of spike grain weight for Sadovo 1 (winter common wheat).

The breeding value of this solid-stemmed triticale selected from the cross T-AD-592 will be evaluated against *Cephus pygmaeus* L. (Fig. 2).

Table 1. Degree and character of disturbances at the meiosis of PMC in triticale hybrids with a solid stem in F_2 derived from the cross T-AD-592 (MBX-11-7 × T-AD-17-B) × AD-No. 11

Parent and hybrid	Stage of meiosis*	No. of cells tested	No. of cells with disturbances					Total no. of cells with disturbances	Disturbances (%)
			with univalents	with lagging chromosomes	with bridges	with micronuclei	polyads		
♂ AD-No. 11 (Triticale, st.)	M_I	437	201	—	—	—	—	201	46.0
	A_I	467	—	223	3	—	—	226	48.4
	M_{II}	244	106	—	—	—	—	106	43.4
	A_{II}	322	—	160	—	—	—	160	50.0
	T	503	—	—	—	197	3	200	40.0
T-AD-592 (MBX-11-7 ×	M_I	618	388	—	—	—	—	388	62.8
T-AD-17-B) × AD-No. 11	A_I	398	—	265	2	—	—	267	67.1
	M_{II}	635	416	—	—	—	—	416	65.5
	A_{II}	541	—	382	7	—	—	389	71.9
	T	866	—	—	—	565	—	565	65.2

* M_I: First metaphase, A_I: First anaphase, M_{II}: Second metaphase, A_{II}: Second anaphase, T: Telophase.

Table 2. Potentialities of some promising lines of triticale with solid stem in F_4 progenies of T-AD-592 (MBX-11-7×T-AD-17-B)× AD-No. 11

Breeding number	No. of plants tested	Plant height (cm)	No. of grains per spike	Degree of solidness in internodes*						
				First top internode			Lower internodes			
				2.5 cm below ear	Middle	2.5 cm above base	Second	Third	Fourth	Fifth
Sadovo 1 (*T. aestivum*) standard, with hollow-stem	75	102.5	39.9	1	1	1.2	1.1	1.3	1.6	1.8
Triticale ($2n=42$) with solid-stem										
T-AD-592-24	60	90.0	94.0	2	5	5	4	4	4	4
T-AD-592-20	80	91.0	60.0	5	5	5	4	5	5	5

* Solid index: 1=hollow stem; 5=solid stem; from 1.1 to 4.9=medial degrees from hollow to solid stem.

Table 3. Resistance of hexaploid triticale to *Cephus pygmaeus* L. during 1988 in General Toshevo

Strain or cultivar	Origin	No. of stems studied	Damaged stems by *Cephus pygmaeus* L	
			No.	%
Hollom stemmed				
Sadovo 1 (*T. aestivum*)	Bulgaria	287	112	39.0
No. 59 (*S. cereale* L.)	Bulgaria	188	82	43.6
AD-206 (Triticale, $2n=42$)	USSR	385	208	54.0
AD-206-A (Triticale, $2n=42$)	USSR	205	92	44.9
Welsch (Triticale, $2n=42$)	Canada	421	207	49.2
KS-60 (Triticale, $2n=42$)	CSFR	320	141	44.1
Mapache (Triticale, $2n=42$)	Mexico	276	109	39.5
AD-7291 (Triticale, $2n=42$)	Mexico	293	134	45.7
Solid stemmed				
MBX-11-7 (*T. aestivum*)	Bulgaria	376	16	4.3
T-AD-592 (Triticale, $2n=42$)	Bulgaria	268	7	2.6

Table 3 indicates that both Sadovo 1 and all the hollow-stemmed foreign triticale are a high susceptibility to the attack of *Cephus pygmaeus* L. (from 39.0 to 54.0%). Under the same conditions, the new-developed solid-stemmed triticale showed a high resistance to this pest, that is, the damaged stem was only 2.6%.

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Utilization of short-stemmed common wheat, Tom Pouce Blanc for common and durum wheat breeding. I. Analysis in F_1 and F_2

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Summary

New original common and durum types of wheat were found in F_2 population derived from hybridization of the short-stemmed common wheat Tom Pouce Blanc (*Triticum aestivum* ssp *vulgare*) with the tall-stemmed durum wheats No. 13 and No. 1522 (*T. turgidum* ssp *durum*), suggesting successful breeding of short stem (61–80 cm) cultivar with high seed set per the spike (51–80 grains). It was also found that the genetic effect for the short stem of Tom Pouce Blanc is incompletely dominant, and moreover mean plant height of F_1's is about 15% shorter than that of midparents in the crosses involved Tom Pouce Blanc.

Introduction

In connection with development of genetic diversity in wheat breeding, great possibilities are revealed in the interspecific hybridization between *T. aestivum* ssp *vulgare* × *T. turgidum* ssp *durum*. From this view point the short-stemmed common wheat Tom Pouce Blanc (Zeven 1969, Rudenko and Udachin 1969, Gale et al 1981) is particular interest. On its basis, a great diversity in hybrid progenies derived from crossing between common and different durum forms, was released, that is lines differing in stem height and spike productivity (Tsvetkov 1973).

Materials and methods

Six interspecific crosses between *T. aestivum* ssp *vulgare* and *T. turgidum* ssp *durum* were done. The common wheat, Avrora (Russia), Tom Pouce Blanc (Tibet) and the durum wheats, No. 13 (Bulgaria), No. 1522 (Bulgaria) were used as parents. The comparison of the results obtained was done with the interspecific hybrids of Avrora and No. 13 or No. 1522.

Results and discussion

1. Plant height and fertility in F_1

Two common wheat cultivars, Avrora and Tom Pouce Blanc differ from each other in plant height. Avrora is 105.5 cm, while Tom Pouce Blanc is 48.7 cm (Table 1). In the hybrids with the two cultivars of durum, No. 13 and No. 1522, the genotypes of these two common wheats showed a rather different response regarding the plant height. The plant height observed in the F_1 of Avrora with the tall-stemmed durum wheats No. 13 and No. 1522 was

Table 1. Plant height and spike characters in common and durum wheat and their F_1 hybrids

Parents and hybrids	Plant height		Main spike ($\bar{X} \pm S\bar{x}$)			
	$\bar{X} \pm S\bar{x}$ (cm)	Dominance rate (d/a)	Length (cm)	Spikelet no.	Grains no.	Fertility (%)
T. aestivum ssp *vulgare* vs (2n=42)						
Avrora	105.5±0.8	–	10.9±0.0	23.8±0.4	48.0±1.3	75.01±2.8
Tom Pouce Blanc	48.7±0.1	–	11.3±0.7	24.4±1.1	48.8±1.9	61.55±2.8
T. turgidum ssp *durum* (2n=28)						
No. 13	140.5±1.5	–	8.8±0.0	20.8±0.5	54.7±3.1	84.37±2.2
No. 1522	144.9±1.8	–	8.9±0.0	22.1±0.3	50.7±3.8	79.50±2.2
F_1 hybrids (2n=35)						
Avrora×No. 13	139.9±1.6	+0.96	10.4±0.5	24.9±0.3	18.4±1.6	28.57±2.8
Avrora×No. 1522	142.8±1.2	+0.89	10.8±0.3	25.3±0.1	21.4±1.8	33.76±2.3
Tom Pouce Blanc×No. 13	72.3±1.4	−0.54	9.4±0.3	22.4±0.5	34.3±2.9	48.34±1.4
No. 13×Tom Pouce Blanc	72.2±0.7	−0.54	10.2±0.6	23.3±0.6	33.5±2.3	42.44±2.8
Tom Pouce Blanc×No. 1522	78.3±1.7	−0.43	11.1±0.6	23.5±1.8	33.3±2.9	44.81±2.9
No. 1522×Tom Pouce Blanc	71.9±1.1	−0.57	11.4±0.1	24.2±1.2	33.0±2.1	47.37±0.7

a b c d

Fig. 1. Plants of interspecific F_1 hybrids and the parents
a. Tom Pouce Blanc
b. Tom Pouce Blanc × No. 13
c. No. 13 × Tom Pouce Blanc
d. No. 13

complete dominance (dominance degree: +0.96 and +0.89) in the direction of the tall-stemmed parents (No. 13 and No. 1522). On the contrary, the inheritance of the plant height in the crosses of the short-stemmed common wheat Tom Pouce Blanc with the same durum wheats was incompletely dominant (dominance degree: -0.43 and -0.57), but the directions towards the short-stemmed cultivar Tom Pouce Blanc. Essential difference were not found between reciprocal crosses (Fig. 1).

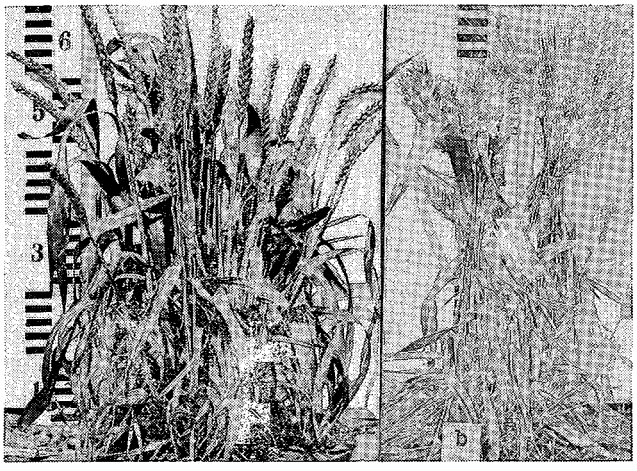
The fertility of the interspecific F_1 hybrids with short-stemmed common wheat Tom Pouce Blanc, varied from 42.44 to 48.34% compared to 61.55 to 84.37% for the parents.

2. Potentialities for selection of forms with a short stem and high productivity in F_2

In F_2 progenies between common and durum wheats there was a very large morphological segregation (groups: ssp *vulgare*, ssp *durum*, intermediate, *compactum*, *spelta* types, etc.). This investigations showed that all F_2 plants with ssp *vulgare* like spike had chromosomes of 36 to 41. On the contrary, those with ssp *durum* like spike had chromosomes of 29 to 34. There is a possibility of common and durum types with varied productivity and plant height to be bred. In this respect, the research on cross combinations to produce plants with a short stem and high productivity is of great importance for the breeding of these two useful grain crops.

Table 2. Frequency (%) of plants with the indicated plant height and number of grains per spike in the F_2 progenies from the interspecific hybrid between Tom Pouce Blanc (*T. aestivum* ssp *vulgare*) × No. 1522 (*T. turgidum* ssp *durum*)

No. of grains/ spike	Plants tested	Plant height in groups (cm)									
		30–40	41–50	51–60	61–70	71–80	81–90	91–100	101–110	≧111	Total
Common wheat types in F_2 (%)											
≦30		5.01	12.32	11.48	12.73	7.93	5.43	5.01	2.09	3.97	65.97
31–40		—	1.04	1.46	2.09	1.46	2.73	1.25	2.09	2.71	14.83
41–50		—	—	0.83	1.67	2.30	2.50	0.63	0.42	0.83	9.18
51–60		—	—	—	0.83	0.83	0.63	1.04	1.46	1.04	5.83
61–70		—	0.21	—	—	0.83	0.63	0.63	0.42	0.21	2.93
71–80		—	—	—	0.21	0.21	0.21	—	0.21	0.21	1.05
81–90		—	—	—	—	—	—	—	0.21	—	0.21
Total	479	5.01	13.57	13.77	17.53	13.56	12.13	8.56	6.90	8.97	100.00
Durum wheat types in F_2 (%)											
≦30		8.38	14.37	11.98	9.58	4.79	0.60	3.59	1.20	1.80	56.27
31–40		—	—	2.39	2.39	1.20	2.99	5.99	2.39	2.39	19.74
41–50		0.60	1.20	1.80	1.20	0.60	1.20	0.60	1.80	1.80	10.80
51–60		—	—	0.60	—	1.80	1.80	0.60	1.20	2.39	8.39
61–70		—	—	—	1.20	—	—	—	1.20	0.60	3.00
71–80		—	—	—	0.60	—	0.60	0.60	—	—	1.80
81–90		—	—	—	—	—	—	—	—	—	—
Total	167	8.98	15.57	16.77	14.97	8.39	7.19	11.38	7.79	8.98	100.00



a b

Fig. 2. Potentialities of breeding for the spike and the stem in wheat: common (a) and durum (b) types in F_2 hybrids derived from Tom Pouce Blanc and durum wheat.

This investigation suggests that in the interspecific crossing of the short-stemmed common wheat Tom Pouce Blanc with the durum wheat cultivar No. 13 and No. 1522, there are significantly higher possibilities for a selection of short-stemmed forms of common and durum wheat with high productivity (Fig. 2). For example, in F_2 population of the cross Tom Pouce Blanc × No. 1522, the frequency of common wheat type with short (41–90 cm) plant height and many grains in a spike (41–90) are 11.9%, while the percentage in the *durum* wheat type is 12.6 (Table 2). This is also the case in the cross Tom Pouce Blanc × No. 13, where the number of common wheat type with short plant height and many grains per spike was 9.7%, and in durum type 12.5% in the F_2 progeny.

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Chromosome location of a new crossability gene in common wheat

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Summary

By genetic analysis, a new wheat-rye crossability gene, *kr4*, was localized on chromosome 1A of "J-11", a selection line from a common wheat landrace, Sichuan White Wheat complex. The effect of this *kr4* gene was stronger than *kr2* but weaker than *kr1*. The *Kr* alleles were completely dominant. The effect of a *kr* allele, when being hemizygous, seemed to be enhanced by other heterozygous *kr* loci or suppressed by other homozygous *kr* loci.

Introduction

The crossability of common wheat (*Triticum aestivum* L.) with rye (*Secale cereale* L.) has long been known as a quantitative trait (Backhouse 1916; Taylor and Quisenbrry 1935). Lein (1943) showed that this trait was genetically controlled by two recessive genes, *kr1* and *kr2*, and that *kr1* was more effective than *kr2*. Riley and Chapman (1967) concluded that the crossability genes *kr1* and *kr2* were located on the chromosomes 5B and 5A, respectively. Lange and Riley (1973) mapped the *kr1* gene on the long arm of the chromosome 5B by a telo-centric mapping procedure. Using the same strategy, Sitch et al (1985) confirmed the location of *kr1* on 5BL and localized the *kr2* gene on the long arm of the chromosome 5A according to linkage with *Vrn1* (controlling vernalization requirement) and *q* (controlling spike morphology). Krowlow (1970) proposed that the chromosome 5D carried *kr3* gene. Snape et al (1979) showed that the effect of *kr3* was somewhat effective on controlling the crossability between common wheat and *Hordeum bulbosum*. Falk and Kasha (1983) suggested that the chromosome 5D carried no strongly effective gene that controlled the crossability with rye or *H. bulbosum*. Most common wheat cultivars are poorly crossable or non-crossable with rye. Zeven (1987) summarized the crossabilities of 1400 wheat cultivars with rye and found out that only 76 cultivars had a crossability of 40% or higher. A common wheat cultivar "Chinese Spring" is well known for its high crossability with rye. However, Yen et al (1986) and Luo et al (1989) discovered, in Chinese common wheat landraces of Sichuan White Wheat complex, some lines that had much higher crossability with rye than Chinese Spring, and thus proposes that these crossable lines might have a new gene for the crossability with rye.

In this paper, we describe monosomic analysis of J-11, one of these highly crossable lines and confirm the proposal of Yen et al (1986). We also localized this new wheat-rye crossability gene on chromosome 1A.

Materials and methods

The test line J-11 was selected from a Chinese common wheat landrace (*Triticum aestivum* L.), Sichuan White Wheat complex, by Luo et al (1990). The crossability of this line with rye is close to 100%. Two sets of monosomic lines, Abbondanza and Chinese Spring, were used in the monosomic analysis. From each monosomic line, two or three monosomic plants were pollinated with J-11. Three to five monosomic and at least one disomic plants were mitotically selected from each F_1 population. The selected F_1 plants were then pollinated with rye (*Secale ceraele* L. cv. Qinling).

Number of seed-set per spike was counted 20 days after pollination. The crossability of a test line with rye was represented by the average percentage of seed set of all the spikes pollinated of that line. The crossability of each spike was converted to angle and the converted data were then subjected to analysis of variance.

For cytological checking of the chromosome numbers, pollen-mother-cells (PMCs) or root-tip cells were fixed with a 3:1 (95% ethanol-glacial acetic acid) solution and then stained by Feulgen procedure.

Results

Analysis by using Abbondanza monosomic lines

Monosomic analysis of the J-11 line with Abbondanza monosomic lines showed that all the disomic F_1 plants had very low crossability with rye (an average of 2.1%). This results suggested that cultivar Abbondanza carried only the *Kr* alleles on all the corresponding loci. On the other hand, the crossabilities of the monosomic 1A, 5A, and 5B F_1 plants were 53.0%, 36.1% and 56.9%, respectively (Table 1). The analysis of variance for the crossabilities of the F_1 monosomic plants indicated significant differences within the monosomic 1A, 5A, 5B and 5D lines and also between these monosomic F_1 lines and the remaining monosomic F_1 lines (Table 2). No significant difference was observed within the remaining monosomic F_1 lines. The effects of chromosomes 1A, 5A and 5B on the wheat-rye crossability were observed to be significantly greater than any other chromosomes. The effect of chromosome 5B was observed to be greater than chromosome 5A. The effect of chromosome 1A was not significantly lower than either chromosome 5A or 5B. The data also showed that the effect of monosomic 5D F_1 line was greater than that of disomic F_1 line at the 0.10 significant level.

Analysis by using Chinese Spring monosomic lines

Since Chinese Spring carries only the *kr* alleles, all the F_1 lines from the crosses between J-11 and Chinese Spring monosomic lines had good crossabilities with rye as expected (Table 1). However, the analysis of variance showed that significant differences did exist between lines (Table 2). On the other hand, no significant difference was observed within F_1 monosomic 1A, 5A and 5B lines. The wheat-rye crossability of the F_1 monosomic 5D line

was found to be significantly different from those of the F_1 monosomic 1A, 5A and 5B lines at the 0.05, 0.01 and 0.10 significant levels, respectively. These results indicate that chromosomes 1A, 5A and 5B of the J-11 line apparently had greater influence on the crossability with rye than other chromosomes did. The crossabilities of the F_1 monosomic 1A, 5A and 5B lines were obviously lower than those of the other F_1 lines. This result suggests that hemizygous *kr* alleles might be less effective than homozygous *kr* alleles. On this aspect, the effect of chromosome 5A was reduced larger than those of chromosomes 1A and 5B, and chromosome 5B was less effective than chromosome 1A.

Table 1. Seed-set of the monosomics X J-11 F_1 hybrids pollinated with rye

Monosomic or disomic line	Abbondanza monosomic			Chinese Spring monosmoics		
	No. florets pollinated	No. of seed-sets	Seed-set (%)	No. florets pollinated	No. of seed-sets	Seed-set (%)
1A	100	53	53.00**	74	46	62.18***
2A	80	1	1.25	79	61	78.03
3A	80	3	3.75	78	62	80.14
4A	95	6	6.56	59	43	73.95
5A	199	72	36.13***	99	59	60.05***
6A	80	6	7.50	71	56	79.51
7A	80	6	7.25	99	76	76.47
1B	100	5	5.00	96	81	84.94
2B	119	6	5.09	96	75	78.75
3B	120	2	1.67	76	64	84.23
4B	120	7	5.83	75	60	80.74
5B	160	91	56.88***	96	65	67.47**
6B	80	1	1.25	97	72	74.32
7B	80	2	2.50	78	59	75.69
1D	80	4	5.00	117	89	76.19
2D	80	1	1.25	118	95	80.83
3D	80	1	1.25	94	68	72.34
4D	80	5	6.25	158	111	70.40
5D	180	16	8.33*	95	76	79.82
6D	140	8	5.71	116	83	71.96
7D	138	8	5.04	135	114	84.87
F_1 disomic	405	8	2.13	420	354	84.21

*, **, *** represent significance at the 0.10, 0.05 and 0.01 levels respectively.

Table 2. Analyses of variance of the F_1 seed-set after angle conversion

Source	Abbondanza			Chinese Spring		
	DF	MS	F	DF	MS	F
Lines	21	1180.67	14.55***	21	556.07	12.37***
A (1A,5A,5B,5D)	3	1855.90	22.87***	3	153.87	3.50**
B (others)	17	58.91	0.73	17	34.32	0.76
A vs B	1	18224.81	224.62***	1	645.75	14.37***
Within spikes	113	81.14		103	44.94	

, * represent significance at the 0.05 and 0.01 levels respectively.

Discussion

The genes *kr1*, *kr2* and *kr3*, which control wheat-rye crossability have been located on 5BL (Riley and Chapman 1967; Lange and Riley 1973; Sitch et al 1985), 5AL (Riley and Chapman 1967; Sitch et al 1985) and 5D (Krowlow 1970; Snape et al 1979; Sitch et al 1985), respectively. In this study we further confirmed the location of *kr1* on 5B and *kr2* on 5A of the test line J-11 and the effect of *kr1* was stronger than that of *kr2*. The existence of *kr3* gene on chromosome 5D of the line J-11 was confirmed by its very weak effect on the crossability with rye only when this gene was analyzed with Abbondanza monosomic lines.

More importantly, a new gene, *kr4*, which was discovered in the special Chinese landrace, Sichuan White Wheat complex, by Yen et al (1986) was localized on chromosome 1A. Both of our results from monosomic analyses with Chinese Spring and Abbondanza monosomic lines showed that the promoting effect of the *kr4* gene on wheat-rye crossability was stronger than that of *kr2* but weaker that of *kr1*.

Falk and Kasha (1983) reported that the lines that were heterozygous on all the *kr* loci were still able to cross with rye and thus concluded that the suppress of the wheat-rye crossability by the *Kr* genes was incompletely dominant over the *kr* genes. Their conclusion was based on their regression of the crossability (y) values against doses of *Kr1* (x_1) and *Kr2* (x_2), and found $y=75.1-30.7\,x_1-12.6\,x_2$. Based on this regression equation, the wheat-rye crossability of a *Kr1kr1Kr2kr2* genotype would be 31.8%. This does not fit to our data. Our results showed that, when analyzed with Abbondanza monosomic lines, the *Kr1kr1Kr2kr2Kr3kr3Kr4kr4* genotype had a wheat-rye crossability of only 2.1%, which is not statistically different from 0%. Therefore, the *Kr* genes should be completely dominant over the *kr* genes.

Our results showed that, in a hemizygous status, a *kr* gene was more effective in the monosomic plant that were derived from Abbondanza monosomic lines than in those that were derived from Chinese Spring monosomic lines. The Abbondanza monosomic lines

contain only *Kr* alleles and the Chinese Spring monosomic lines have only *kr* alleles. Besides the hemizygous *kr* allele on the monosomic chromosome, the monosomic F_1 plants involving Abbondanza monosomic 1A, 5B, 5A or 5D line would be heterozygous at other *Kr-kr* loci. On the other hand, all the monosomic F_1 plants involving Chinese Spring monosomic lines will have only *kr* alleles. Therefore, it seems that *Krkr* heterozygous loci might have promoting effect on other hemizygous *kr* loci. Alternatively, a recessive *krkr* locus might be able to suppress the effect of a hemizygous *kr* locus.

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Inheritance of resistance to leaf rust (*Puccinia recondita* f. sp. *tritici*) in two durum wheats

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Summary

Inheritance studies were conducted on two leaf rust resistant durum wheats. *Triticum durum* cvs. Malvika and CPAN 6051 were crossed with susceptible durum wheat Malvi Local. The F_2 and F_3 generations were tested against leaf rust races 1, 77 (biotype A) and 108. Single dominant gene was effective against race 108 and two independently inherited dominant genes were effective against each of the races 1 and 77A in cultivar Malvika. Cultivar CPAN 6051 carried single dominant gene against races 1 and 108, whereas two independently inherited dominant genes were operative against race 77A. At least one resistance gene was common in cultivars Malvika and CPAN 6051.

Introduction

Breeding resistant cultivars depends primarily upon the availability of diverse and effective resistance genes. Sources of resistance to leaf rust caused by *Puccinia recondita* f. sp. *tritici* have been identified both from *Triticum aestivum* (Gras 1980, Zitelli et al 1981, Tomerlin et al 1984, Dyck et al 1987) and *Triticum durum* (Leonari 1973, Mishra et al 1989, Casulli et al 1983). Durum wheats have been identified as donors of new leaf rust resistance (*Lr*) genes which are effective against highly virulent races like 77 and 104 prevalent in the Indian sub-continent (Sharma et al 1986). Durum wheats also contribute towards superior quality characteristics (Quick and Crawfod 1983). Identification of *Lr* genes in *Triticum aestivum* is based on allelic tests with near isogenic lines developed in the background of cultivars Thatcher and Prelude (Dyck and Samborski 1970, Samborski and Dyck 1976, Dyck 1977). Such testers with designated genes are not available for durums, therefore, only temporary designations have been given to *Lr* genes identified from *T. durum* (Ataullah 1969, Statler 1972). The present report deals with the inheritance of resistance and allelic relationship between *Lr* genes from two important durum wheats.

Material and methods

The experimental material comprised of two highly resistant durum wheats namely Malvika

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and CPAN 6051, and a susceptible cultivar Malvi Local. The pedigree, seedling reactions against race 1, 77 (biotype A) and 108 and the field scores of these wheats in an epiphytotic of race 77A are given in Table 1. Both resistant wheats were crossed to the susceptible cultivar Malvi Local. The F_2 and F_3 generations obtained from these crosses were tested against leaf rust races 1, 77A and 108 at seedling stage under controlled conditions in a growth house maintained at 20±1°C. Simple χ^2-test was applied to test the goodness of fit of different genetic ratios. Race 1 is avirulent on all the *Lr* genes from *T. aestivum* except *Lr20* and *Lr23* from *T. durum* both on seedlings and adult plants. At seedling stage race 77A is virulent on all the *Lr* genes from *T. aestivum*, but the adult plants carrying genes *Lr12*, *Lr14b*, *Lr23* and *Lr27* + *Lr31* from *Triticum aestivum* are resistant. Race 108 is also virulent on all the *Lr* genes from *T. aestivum* except *Lr3* and *Lr15* at seedling stage. The adult plants carrying *Lr3*, *Lr12*, *Lr13*, *Lr14a*, *Lr14b*, *Lr16*, *Lr17*, *Lr22*, *Lr22b*, *Lr23*, *Lr27* + *Lr31* and *Lr30* are resistant to this race.

The two resistant durums were also intercrossed and the F_2 generation seedlings thus obtained were studied against races 1, 77A and 108 to establish allelic relationship between genes from these two wheats.

The infection types were recorded 14 days after inocultaion of seven day old seedlings according to a modification of the scale given by Stakman et al (1962).

Table 1. Durum cultivars, their pedigree, seedling infection types and field scores against leaf rust races

S. No.	Cultivar	Pedigree	Infection types at seeding stage			Field score
			1	77A	108	
1.	Malvika	(Pi'S'/By^2-Tc)(Z-B/W)4	;1$^-$	;1	;12$^-$	Free
2.	CPAN 6051	Ruff'S'-Fg'S'	;12$^+$	1$^+$	1$^+$2$^-$	Free
3.	Malvi Local	Local selection from Madhya Pradesh, India	33$^+$	33$^+$	33$^+$	80S

Results and discussion

Segregation for seedling reactions in F_2 and F_3 generations and its intercross obtained from the crosses of resistant cultivars with Malvi Local are given in Table 2. The F_2 and F_3 generations obtained from the cross Malvika × Malvi Local segregated in a 15 resistant (R): 1 susceptible (S) ratio and in a 7 homozygous resistant (HR): 8 segregating (Seg): 1 homozygous susceptible (HS) ratio against race 1, respectively. This indicates the presence of two independently inherited dominant genes in Malvika against the race 1. The F_2 and F_3 generations obtained from the cross CPAN 6051 × Malvi Local segregated in an 3R : 1S ratio and in a 1 HR : 2 Seg : 1 HS ratio respectively indicating presence of one dominant

Table 2. Segregation for seedling reaction in F_2 and F_3 generations from the crosses of resistant durums with Malvi Local and their intercrosses against leaf rust races

Cross	Race	No. of F_2 seedlings		Expected ratio	χ^2-value	No. of F_2 plant progenies (F_3 generation)			Expected ratio	χ^2-value
		Resistant	Susceptible			HR	Seg	HS		
Malvika × Malvi Local	1	188	20	15:1	4.02*	25	40	4	7:8:1	1.79
	77A	476	30	15:1	0.89	32	35	3	7:8:1	0.49
	108	62	26	3:1	0.97	20	35	10	1:2:1	3.46
CPAN 6051 × Malvi Local	1	108	36	3:1	0.00	15	27	17	1:2:1	0.56
	77A	161	15	15:1	1.55	26	25	7	7:8:1	3.71
	108	57	21	3:1	0.15	17	23	12	1:2:1	1.65
Malvika × CPAN 6051	1	69	0	—	—	—	—	—	—	—
	77A	350	0	—	—	—	—	—	—	—
	108	311	0	—	—	—	—	—	—	—

* = Significant at 5% level of significance, HR = Homozygous resistant, Seg = Segregating, HS = Homozygous susceptible

gene against race 1. Against race 77A, the F_2 and F_3 generations obtained from the crosses Malvika × Malvi Local and CPAN 6051 × Malvi Local segregated in a 15R : 1S ratio and in a 7 HR : 8 Seg : 1 HS ratio. These observations indicated presence of two independently inherited dominant genes in Malvika against race 77A. The F_2 and F_3 generations from the cross CPAN 6051 × Malvi Local segregated in a 3R : 1 S ratio and 1 HR : 2 Seg : 1 HS ratio, respectively, indicating presence of a dominant gene in CPAN 6051 against race 108.

Susceptible seedlings against races 1, 77A and 108 were not observed in F_2 generation obtained from the cross Malvika × CPAN 6051, indicating that at least one of the genes present in Malvika and CPAN 6051 is allelic or tightly linked.

Inheritance studies and allelic tests revealed the presence of at least two different leaf rust resistance genes from cultivars Malvika and CPAN 6051. Since the near isogenic testers are not available in durum background it is not possible to designate *Lr* genes in any of these two wheats. Saini (1987) has identified *Lr23* from CPAN 6051 using Australian rust cultures. Since CPAN 6051 did not segregate for susceptible seedling against race 1 in its cross with Malvika therefore this cultivar may also have *Lr23*. This gene gives post seedling resistance against races 77A and 108 (Saini et al 1988, Dhindsa et al 1991), therefore, resistance of both these cultivars in epiphytotic of race 77A may be due to *Lr23*. The other gene conferring resistance to races 77A and 108 in seedlings of CPAN 6051 needs to be identified as yet. Although virulence against *Lr23* is now available in the Indian subcontinent (Nayer et al 1988), the other gene(s) from these wheats are still effective and can be used in breeding programmes.

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Genetic variability in grain yield and its component characters and their association under salt stress conditions in tissue culture lines of bread wheat (*Triticum aestivum* L. em. Thell)

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Summary

An experiment was conducted to study genetic variability and associations among different characters under saline and sodic stress conditions in 24 wheat lines developed through tissue culture. The study showed that the means of all the characters declined under both types of stress conditions, the decrease being maximum under sodic conditions. There was reduction in genetic variability, genetic advance and heritability for important character like grain yield per plant. The associations among characters indicated that, under saline conditions, number of ear-bearing tillers per plant, and under sodic conditions, grain weight, number of grains per ear, number of ear-bearing tillers per plant, plant height and number of spikelets per ear were important contributors toward grain yield.

Introduction

The magnitude of heritable variability in any genetic stock has a close bearing on the success of selection programs. Since there is no such information on wheat tissue culture lines under stress conditions, an experiment was conducted under edaphic stress conditions to study genetic variability in grain yield and its component characters and their correlations in bread wheat lines which were developed through tissue culture. Path coefficient analysis was also made to determine the contribution of each character on grain yield under normal, saline and sodic stress conditions.

Materials and methods

The experimental materials consisted of 24 bread wheat lines selected from 137 lines originally obtained in 1989–90 from CIMMYT, Mexico, which were developed through tissue culture technique. The materials were sown with four replications, each in normal soil, sodic soil (pH_2 9.3) and under saline water irrigation conditions (EC_{iw} 20 dSm^{-1}). The experiment was laid out in a split plot design, with three edaphic environments in the four replicated main plots and 24 tissue culture lines in the sub plots. Each line was sown in one row of 80 cm in length and with a row-to-row distance of 23 cm. Randomly taken 5 representative plants from each entry in each replication provided the material for the evaluation of seven characters, viz., plant height, number of ear-bearing tillers per plant,

main ear length, number of grains per ear, number of spikelets per ear, 1000 grain weight and grain yield per plant. Statistical analysis of the split plot design was done according to the method described by Panse and Sukhatme (1967). Genotypic and phenotypic variances, heritability, and genetic advance were estimated according to Burton and de Vane (1953), Johnson et al (1955) and Robinson et al (1949), respectively. Genotypic correlations were computed according to Al-Jibouri et al (1958) and path coefficients following the method suggested by Dewey and Lu (1959).

Results and discussion

There were significant differences among tissue culture lines as well as the edaphic environments for all the seven traits studied under normal, saline and sodic soil conditions. The ANOVA results of grain yield per plant and its component traits are shown in Table 1. There were significant lines × edaphic environment interactions for all the characters. The means of all the characters declined when the lines were grown in saline and sodic soil conditions, the depreciation being maximum under sodic conditions (Table 2). The mean grain yield was 6.63 g/plant under normal soil, decreased to 4.36 g/plant under saline soil, and further to 2.02 g/plant under sodic conditions. The reduction in the means of various characters studied was more under sodic conditions than saline conditions. Similarly, the range of all the characters narrowed down as the stress was imposed.

The genotypic and phenotypic variances decreased under the stress conditions for grain

Table 1. Analysis of variance for grain yield and its component characters in 24 CIMMYT tissue culture lines of wheat grown under three edaphic environments

Source of variation	degree of freedom	Mean sum of squares of various characters						
		Grain yield/ plant (g)	1000 grain weight (g)	Number of grains/ear	Number of ear-bearing tillers/plant	Plant height (cm)	Ear length (cm)	Number of spikelets /ear
Edaphic environments	2	510.35**	1335.70**	5160.40**	88.96**	33589.00**	250.39**	857.91**
Error(b)	6	1.18	6.59	51.02	0.38	60.69	3.31	11.10
Lines	23	1.64**	9.38**	101.94**	0.36**	88.21**	0.81**	3.77**
Edaphic environment × lines	46	2.40**	6.48**	20.31**	0.51**	28.89**	0.52**	3.21**
Error	207	0.18	2.18	8.07	0.10	12.35	0.31	1.83

** significant at the 0.01 level.

Table 2. Means, genotypic and phenotypic variances, genetic advance and heritability in 24 CIMMYT tissue culture lines of wheat under normal, saline and sodic stress environments

Parameter	Environment	Characters						
		Grain yield/plant (g)	1000 grain weight (g)	Number of grains/ear	Number of ear-bearing tillers/plant	Plant height (cm)	Ear length (cm)	Number of spikelets/ear
Mean	Normal	6.63	38.15	40.94	4.18	107.46	10.64	19.70
	Saline	4.36	37.27	38.94	2.85	91.03	9.73	17.71
	Sodic	2.02	31.30	27.29	2.31	70.14	7.50	13.79
Range	Normal	4.42–8.40	36.32–40.15	35.67–46.99	3.30–5.00	102.68–114.60	9.80–11.40	17.55–21.35
	Saline	3.68–5.49	34.51–39.74	33.04–45.03	2.45–3.45	84.90–102.20	9.00–10.40	16.55–19.20
	Sodic	1.41–3.06	27.42–34.00	21.21–41.96	1.70–2.95	66.40–78.50	6.55–8.05	12.70–15.00
Genotypic variance	Normal	1.15	0.40	6.42	0.16	8.91	0.07	0.43
	Saline	0.21	1.21	8.26	0.03	10.71	0.07	0.29
	Sodic	0.13	2.34	15.35	0.07	7.61	0.08	0.13
Phenotypic variance	Normal	1.22	0.73	8.30	0.20	11.03	0.14	0.54
	Saline	0.24	1.56	10.39	0.06	13.16	0.12	0.53
	Sodic	0.16	3.31	17.59	0.09	12.32	0.20	0.48
Genotypic coefficient of variation	Normal	16.17	1.66	6.19	9.57	2.78	2.49	3.33
	Saline	10.51	2.95	7.38	6.08	3.60	2.72	3.04
	Sodic	17.85	4.89	14.36	11.45	3.93	3.77	2.61
Phenotypic coefficient of variation	Normal	16.66	2.24	7.04	10.70	3.09	3.52	3.73
	Saline	11.24	3.35	8.28	8.59	3.99	3.56	4.11
	Sodic	19.80	5.81	15.37	12.99	5.00	5.96	5.02
Heritability	Normal	0.94	0.55	0.77	0.80	0.81	0.50	0.80
	Saline	0.88	0.78	0.79	0.50	1.81	0.58	0.55
	Sodic	0.81	0.71	0.87	0.78	1.62	0.40	0.27
Genetic advance (5%)	Normal	2.14	0.97	4.59	0.75	5.53	0.40	1.20
	Saline	0.87	2.00	5.28	0.30	6.08	0.42	0.81
	Sodic	0.66	2.65	7.54	0.50	4.47	0.38	0.38

yield per plant, effective tiller number per plant and number of spikelets per ear, while it was reverse for the others (Table 2). The genotypic and phenotypic coefficients of variation, which are more appropriate parameters for the comparison, decreased under saline conditions for grain yield per plant, effective tiller numbers per plant and number of spikelets per ear, while the coefficients were nearly the same under sodic soil conditions as compared to normal conditions. Reduction in genetic variability under stress has also been reported by Johnson and Frey (1967) in oats and by Mederski and Jeffers (1973) in soybean. For characters like 1000 grain weight, number of grains per ear, plant height and ear length, the coefficients of variation increased under stress conditions. The reason for such an increase in variability under stress conditions may be attributed to an enhanced primary effect of the stress as has been discussed by Rosielle and Hamblin (1981) under disease stress. Similar trends were also observed for genetic advance. Heritability of grain yield and number of spikelets per ear decreased under both types of stress, while that for number of ear-bearing tillers per plant decreased only under salinity and remained the same under sodic conditions. Most of the characters exhibited high heritabilities owing to the high genotypic variances among the tissue culture lines.

The association among the characters of bread wheat grown on normal soils was modified under salinity and sodicity stresses. It was evident from Table 3 that grain yield per plant was significantly correlated with 1000 grain weight, number of grains per ear, number of ear-bearing tillers per plant, plant height and number of spikelets per ear only under sodic conditions, while it had significant, positive correlation with tiller number under normal as well as stress conditions. Grain yield was only significantly correlated with number of ear-bearing tillers per plant and ear length under salinity conditions. It appeared quite apparent that number of ear-bearing tillers per plant was one of the most significant component characters under normal and stress conditions. Under sodic conditions most of the characters were correlated with grain yield, except for ear length. A significant correlation was observed between 1000 grain weight and number of grains per ear only under normal soil conditions, and number of grains per ear was highly correlated with plant height and ear length under sodic conditions. Number of tillers per plant was negatively correlated with plant height under normal conditions, as tillering ability was higher for semi-dwarf types than for tall types, while under sodic condition it was positively correlated to plant height, because both tiller number and plant height decreased under sodic stress. Ear length was positively correlated to number of spikelets per ear under normal and saline conditions while uncorrelated under sodic conditions.

To get an idea of relative contribution of the yield components on grain yield under normal and stress conditions, path coefficient analysis was conducted. Table 4 gives the direct and indirect effects on grain yield per plant under normal and stress conditions. A high direct effect was observed for 1000 grain weight under saline and sodic conditions, while that had a high indirect effect via number of grains per ear, under normal conditions. Number of grains per ear had a high direct effect under normal conditions but it was counter

Table 3. Genotypic correlations among grain yield and component characters in 24 CIMMYT tissue culture lines of wheat under normal, saline and sodic stress environments

Character	Environment	Characters					
		1000 grain weight (g)	Number of grains/ear	Number of ear-bearing tillers/plant	Plant height (cm)	Ear length (cm)	Number of spikelets/ear
Grain yield per plant	Normal	0.07	0.17	0.80**	−0.22	0.34	0.10
	Saline	0.19	0.36	0.50*	0.11	0.42*	0.12
	Sodic	0.40*	0.68**	0.50*	0.53*	0.34	0.68**
1000 Grain weight	Normal		0.63**	−0.34	−0.04	0.05	0.25
	Saline		0.07	−0.23	0.25	0.27	0.31
	Sodic		−0.15	0.22	−0.35	−0.11	−0.45
Number of grains/ear	Normal			−0.50*	−0.14	−0.01	0.46*
	Saline			−0.19	0.41*	0.15	0.35
	Sodic			−0.03	0.84**	0.70**	1.31
Number of ear-bearing tillers/plant	Normal				−0.43*	0.20	−0.27
	Saline				0.04	0.38	0.27
	Sodic				0.48*	−0.22	−0.36
Plant height (cm)	Normal					0.10	0.40
	Saline					0.53**	0.50*
	Sodic					0.91**	1.01
Ear length (cm)	Normal						0.55**
	Saline						0.61**
	Sodic						0.37

*, ** Significant at the 0.05 and 0.01 level, respectively.

Table 4. Path coefficient analysis of direct and indirect effects of component characters on grain yield in 24 CIMMYT tissue culture lines of wheat under normal, saline and sodic stress environments

Character	Environment	Characters					
		1000 grain weight (g)	Number of grains/ear	Number of ear-bearing tillers/plant	Plant height (cm)	Ear length (cm)	Number of spikelets/ear
1000 grain weight	Normal	*−0.125*	0.965	−0.583	−0.036	0.012	−0.162
	Saline	*0.451*	0.050	−0.172	−0.059	0.103	−0.183
	Sodic	*0.629*	−0.057	0.033	−0.157	0.032	−0.076
Number of grains/ear	Normal	−0.078	*1.536*	−0.858	−0.031	−0.003	−0.294
	Saline	0.031	*0.719*	−0.145	−0.097	0.057	−0.203
	Sodic	−0.095	*0.373*	−0.004	0.376	−0.198	0.224
Number of ear-bearing tillers/plant	Normal	0.043	−0.770	*1.711*	−0.411	0.054	0.175
	Saline	−0.102	−0.138	*0.755*	−0.010	0.147	−0.155
	Sodic	0.133	−0.010	*0.154*	0.216	0.063	−0.061
Plant height (cm)	Normal	0.005	−0.211	−0.737	*0.953*	0.027	−0.256
	Saline	0.111	0.293	0.031	*−0.239*	0.205	−0.290
	Sodic	−0.221	0.314	0.074	*0.448*	−0.256	0.173
Ear length (cm)	Normal	−0.006	−0.071	0.348	0.098	*0.266*	−0.352
	Saline	0.120	0.106	0.287	−0.217	*0.385*	−0.356
	Sodic	−0.072	0.262	−0.034	0.406	*−0.283*	0.063
Number of spikelets/ear	Normal	−0.032	0.710	−0.469	0.384	0.147	*−0.637*
	Saline	0.142	0.250	0.200	−0.119	0.235	*−0.584*
	Sodic	−0.281	0.490	−0.055	0.454	−0.104	*0.171*

Diagonal values (in italic) are the direct effects and the others are the indirect effects via respective characters on grain yield.

balanced by high negative, indirect effects via number of ear-bearing tillers per plant, as a result there was no significant genotypic correlation with grain yield. The situation was nearly the same under saline conditions. However, under sodic conditions there were high direct effects as well as indirect effects through plant height and number of spikelets per ear. Number of effective tillers per plant had high direct effects under normal conditions, with some negative indirect effects via grain number per ear and plant height, resulting in a high genotypic correlation with grain yield. Under salinity, tiller number had high direct effects, while under sodic conditions it had comparatively low direct effects and more indirect effects via plant height and 1000 grain weight. Plant height had high direct effects under normal conditions, though its effect was canceled by high negative indirect effects via number of ear-bearing tillers per plant. Under sodic conditions, there were equal contributions of direct effect of plant height and indirect effects via number of grains per ear. Ear length had a positive direct effect and indirect effect via number of ear-bearing tillers per plant under salinity, while number of spikelets per ear had high indirect effects via number of grains per ear and plant height under sodic stress. To conclude, under normal conditions number of ear-bearing tillers per plant contributed to grain yield per plant, while under salinity conditions, that and ear length contributed directly, and indirectly through number of ear-bearing tillers per plant. Under sodicity, 1000 grain weight contributed directly to grain yield per plant; grain number per ear directly and indirectly via plant height; number of ear-bearing tillers per plant directly and indirectly via plant height and grain weight; plant height directly and indirectly via number of grains per ear; and number of spikelets per ear directly and indirectly via plant height. However, grain weight, number of grains per ear, plant height and number of spikelets per ear were the most important characters under sodic stress. Thus, number of ear-bearing tillers per plant under salinity stress and grain weight, number of grains per ear, tiller number, plant height and number of spikelets per ear under sodic stress were the important characters which require breeders' attention for achieving increases in grain yield under such edaphic conditions.

Bread wheat lines produced through tissue culture techniques thus showed considerable variability in grain yield and its component characters under normal as well as stress conditions, indicating that they can be a good source of variability under salt stress. The information on genotypic correlations and path coefficients does provide criteria to help plant breeders in deciding the appropriate selection strategy under saline and sodic stress conditions for such materials.

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Phosphorus utilization by induced high temperature tolerant wheat

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Introduction

During last two decades, the productivity of wheat crop has been doubled. This increase was mostly due to the introduction of high yielding varieties, increase in fertilizer consumption and increase in irrigation facility. The high cost of fertilizers is still limiting the farmers to apply balanced doses of fertilizers to exploit the full potentials of different wheat varieties. The availability of native nutrients from the soils depend upon temperature and moisture. The high yielding semi-dwarf wheat varieties generally complete their grand growth periods when the temperature of soil is low. Contrarily, the high temperature tolerant wheat mutants suitable for early sown after the cessation of monsoon rains are exposed to high temperature coupled with adequate soil moisture during early growth stages (Behl et al 1986). High temperature coupled with moisture could mobilize higher native P and thus resulting in reduction of phosphatic fertilizer application. The present study was undertaken on the utilization of applied P by radiation induced mutants of wheat (WH 147, C 306).

Materials and methods

Surface soil for the present study was collected from Research Area of Soil Science Department. The field was classified as "Typic Ustochrept". The physico-chemical properties of the soil were: pH (1 : 2) 7.3, EC (1 : 2) 0.19 dSm^{-1}, sandy loam in texture, organic C 0.43%, available P 11 mg kg^{-1}. Earthen pots of 25 cm diameter lined with polyethylene were filled with 4 kg air dried, crushed (2 mm) soil. Basal dose of N (40 mg kg^{-1}), P (30 mg kg^{-1}), K (25 mg kg^{-1}), Zn (5 mg kg^{-1}), Fe (5 mg kg^{-1}), Mn (5 mg kg^{-1}) and Cu (2.5 mg kg^{-1}) were applied in each pot. Phosphorus was tagged with ^{32}P @0.25 mCi g^{-1} P. All these nutrients were applied through their analytical grade salts and mixed thoroughly with soil before filling the pots.

Ten seed of wheat varieties, WH 147, C 306 and their mutants were sown in each pot. Four plants in each pot were maintained after complete germination. Demineralized water was applied for irrigating the pots as and when required. All the pots were placed after randomization keeping three repeats for each treatment. The crop was harvested 40 days after sowing. Plant samples were washed, dried (65±2°C), weighed and ground in a stainless steel grinder. Plant samples were digested in H_2SO_4 and $HClO_4$ in the ratio of 5 : 1.

Phosphorus in the plant digests was estimated by phosphomolybdovanadate yellow color method of Koenig and Johnson (1942). Radio-essay of plant digests was done on 1209. Recbeta scintillation counter using PPO-POPOP as scintilattors. Fertilizer P in plant and fertilizer use efficiency was calculated as suggested by Mackenzie and Dean (1948). The data was subjected to statistical test of significance using single factor completely randomized design.

Results and discussion

The dry matter yield of both the mutants was significantly ($p<0.05$) less as compared to the varieties (Table 1). The dry matter yield of C 306 was also higher as compared to WH 147. Phosphorus concentration of WH 147 mutant was significantly ($p<0.05$) higher to WH 147 but it was significantly less in C 306 mutant as compared to variety C 306. Total P uptake by mutant and variety of WH 147 was statistically at par, but it was significantly ($p<0.05$) less in mutant than variety of C 306. The less P uptake by the mutant of C 306 was primarily due to low yield and P content. The mutant of WH 147 absorbed about 5% less fertilizer P, indicating thereby that the utilization of native P by mutant of WH 147 was higher as compared to variety WH 147. Whereas, incase of mutant and variety of C 306, there was very little difference in the utilization of native and added phosphorus. These observations lend support to the earlier findings of Behl and Malhotra (1991) that grain F content of WH 147M was significantly higher than that of WH 147. The fertilizer use efficiency by both the varieties was significantly ($p<0.05$) higher as compared to their mutants.

From these results, it can be concluded that the mutants of wheat varieties can utilize native soil F and thus reduce the fertilization cost of phosphatic fertilizers. However, these results are to be tested in field experiments.

Table 1. Dry matter yield (DMY), P content, P uptake and fertilizer P utilization by wheat mutants and their mother cultivars

Variety/ Mutant	DMY g/pot	P content %	P uptake μg/pot	Fertilizer P		
				in plant %	Uptake μg/pot	Efficiency %
WH 147	1.22	0.62	7.53	36.77	2.77	2.31
WH 147M	1.11	0.71	7.84	31.35	2.45	2.04
C 306	1.99	0.66	13.15	26.84	3.52	2.94
C 306M	1.63	0.58	9.52	27.29	2.60	2.16
LSD ($p<0.05$)	0.19	0.05	1.68	NS	0.45	0.37

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First report on occurrence of *Aegilops ventricosa* Tausch in Greece

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Introduction

Aegilops ventricosa Tausch, an allotetraploid species with a DM^V (Kihara, 1954) or a DUn genomic constitution (Kimber and Sears 1983) was never found in Greece in past explorations. According to distribution maps produced by Eig (1929), Zhukovski (1928), Harlan and Zohary (1966) and Chapman (1985), the species has a medium-sized geographical distribution in West Mediterranean (Fig. 1), whose East limits are fixed by some scattered collection places in SW Italy and Libya.

The species has arisen from the hybrid between *Ae. squarrosa* and *Ae. uniaristata*:

Ae. squarrosa	×	*Ae. uniaristata*
2n = 2x = 14		2n = 2x = 14
D genome		Un genome

Ae. ventricosa
2n = 4x = 28
DUn genome

However, there is an enormous gap between the distributions of its two putative diploid parents (Fig. 1), for which satisfactory account has yet to be given.

Ae. uniaristata occupies areas with average conditions of water supply in West Greece, west coast of Yugoslavia and Albania, in contrast to *Ae. squarrosa* which grows in dwarf shrub steppes of the fertile crescent, with eastern-most distribution limits reaching China (Tanaka and Tsujimoto 1991). In addition, the distribution area of *Ae. ventricosa*, being larger than that of *Ae. uniaristata* but smaller than that of *Ae. squarrosa*, does not overlap with either of its progenitors.

Collecting expedition: Preliminary characterization

In a gramineae collecting expedition in Central Makedonia, Greece, jointly organized by the Greek Gene Bank, and the Agricultural University of Athens (Collecting team: Athanasios Zamanis, Nikolaos Stavropoulos and Stelios Samaras from the Greek Gene Bank, and Panagiotis Efthymiadis from the Agricultural University of Athens), a small population of *Aegilops ventricosa* was found in a location some 7 km west of Veria, capital of the prefecture of Imathia, at the outskirts of village Georgiani, near the old road to Kozani (Fig. 2). The collection site is located in the SE slopes of Vermion mountain, at an

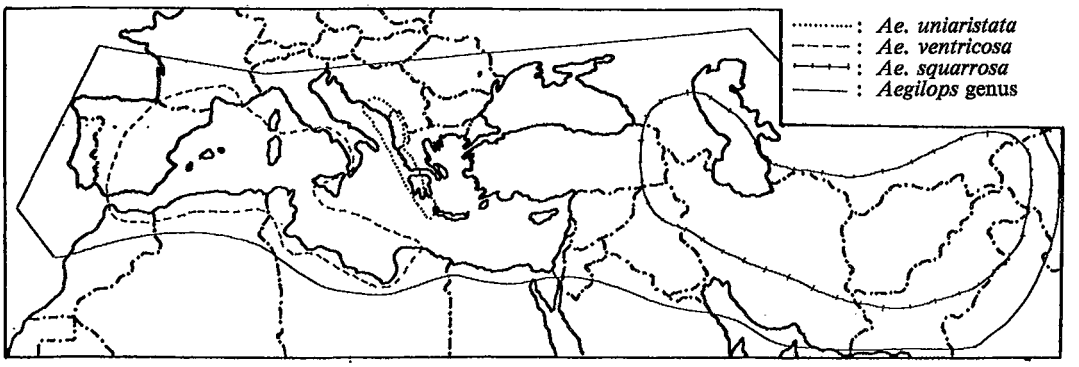

Fig. 1. Geographic distribution of *Ae. ventricosa* Tausch and its putative parents *Ae. uniaristata* and *Ae. squarrosa*. The area of *Ae. uniaristata* has been expanded downwards along the western Greek coasts on the basis of our recent explorations.

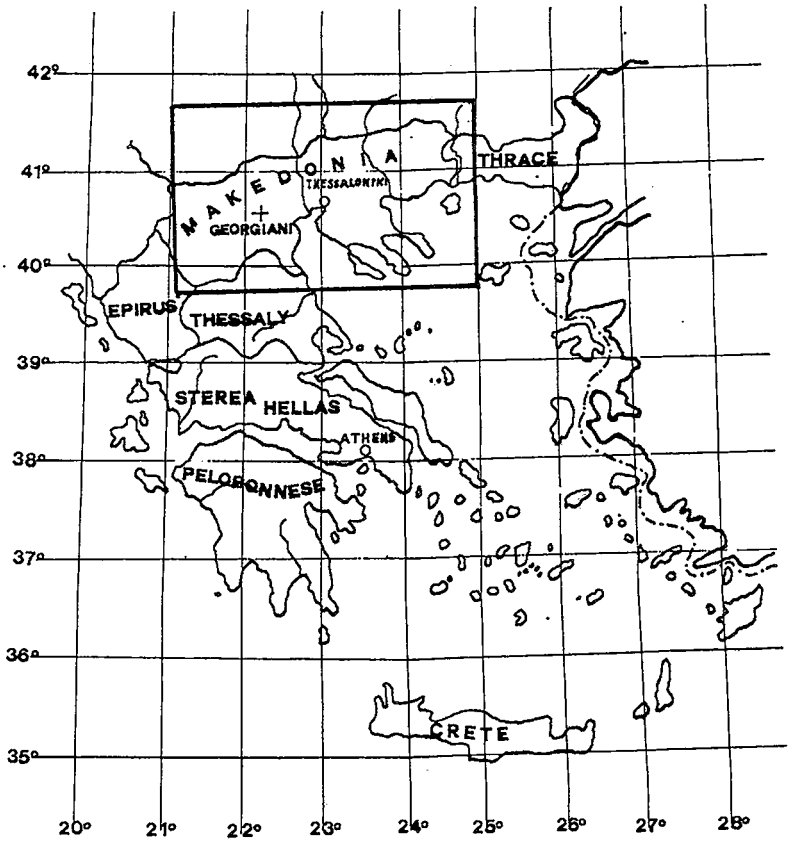

Fig. 2a. Map of Greece. The explored region is delimited by the bold rectangular. Collection site (Georgiani village) of *Ae. ventricosa* is marked with a +.

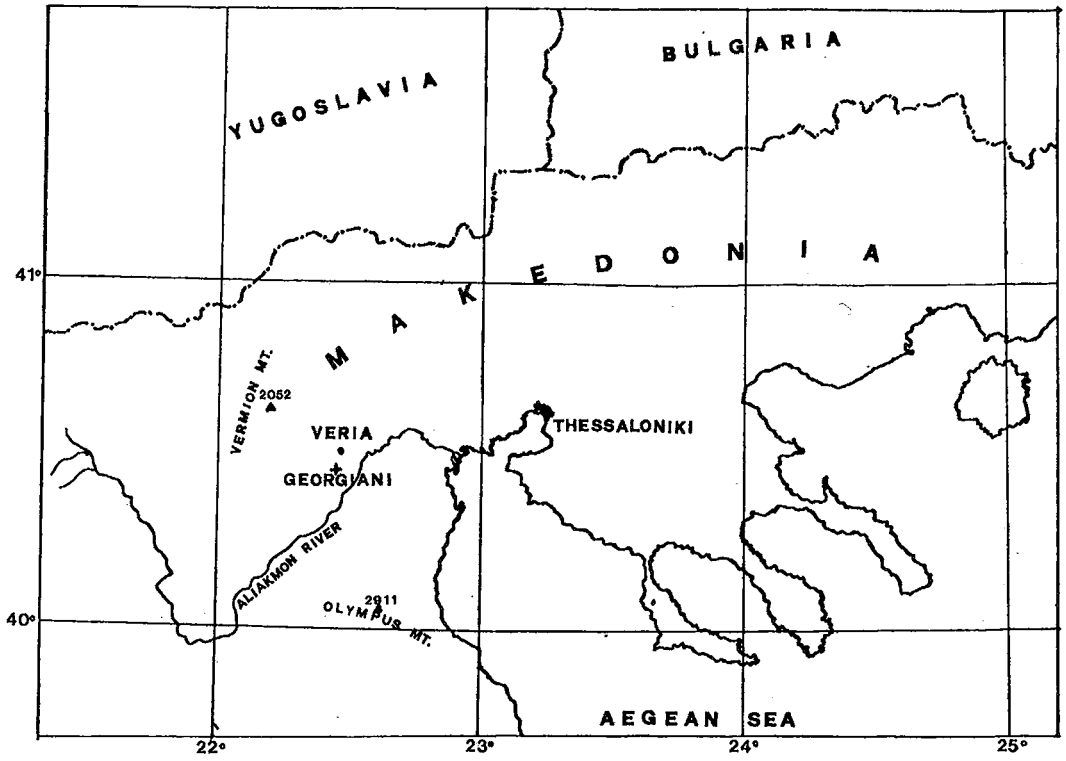

Fig. 2b. Enlarged map of the explored area. Collection site of *Ae. venticosa* is marked with a +.

altitude of 450–470 m above sea level, and is a disturbed denuded oak forest with deciduous Mediterranean forest species and "maquis". The species was grown sympatrically with *Ae. triunicialis* L., *Ae. ovata* L., *Ae. biuncialis* Vis, *Ae. triaristata* Willd (UM), *Ae. triaristata* Willd (UM), *Ae. triaristata* Willd (UMUn), *Ae. comosa* Sibth & Sm and *Ae. caudata* L. The flora of the site included also a large population of *Triticum boeoticum* never reported to exist in that region.

The collected seed was sown for multiplication, characterization and preliminary evaluation in the experimental fields of the Greek Gene Bank, in Thessaloniki, in the autumn of 1991, along with some other *Ae. ventricosa* accessions kindly provided by Dr. J. C. Graddock, used as controls. The plants showed all typical *Ae. ventricosa* characteristics. Natural habitat, plant habit and spike morphology are shown in Fig. 3.

Discussion-conclusions

The discovery of an *Ae. ventricosa* population in Makedonia, northern Greece, distant from the distribution area of the polyploid species and in the gap between its parent species (analysers) distributions, gives room for assumptions regarding the occurrence of this

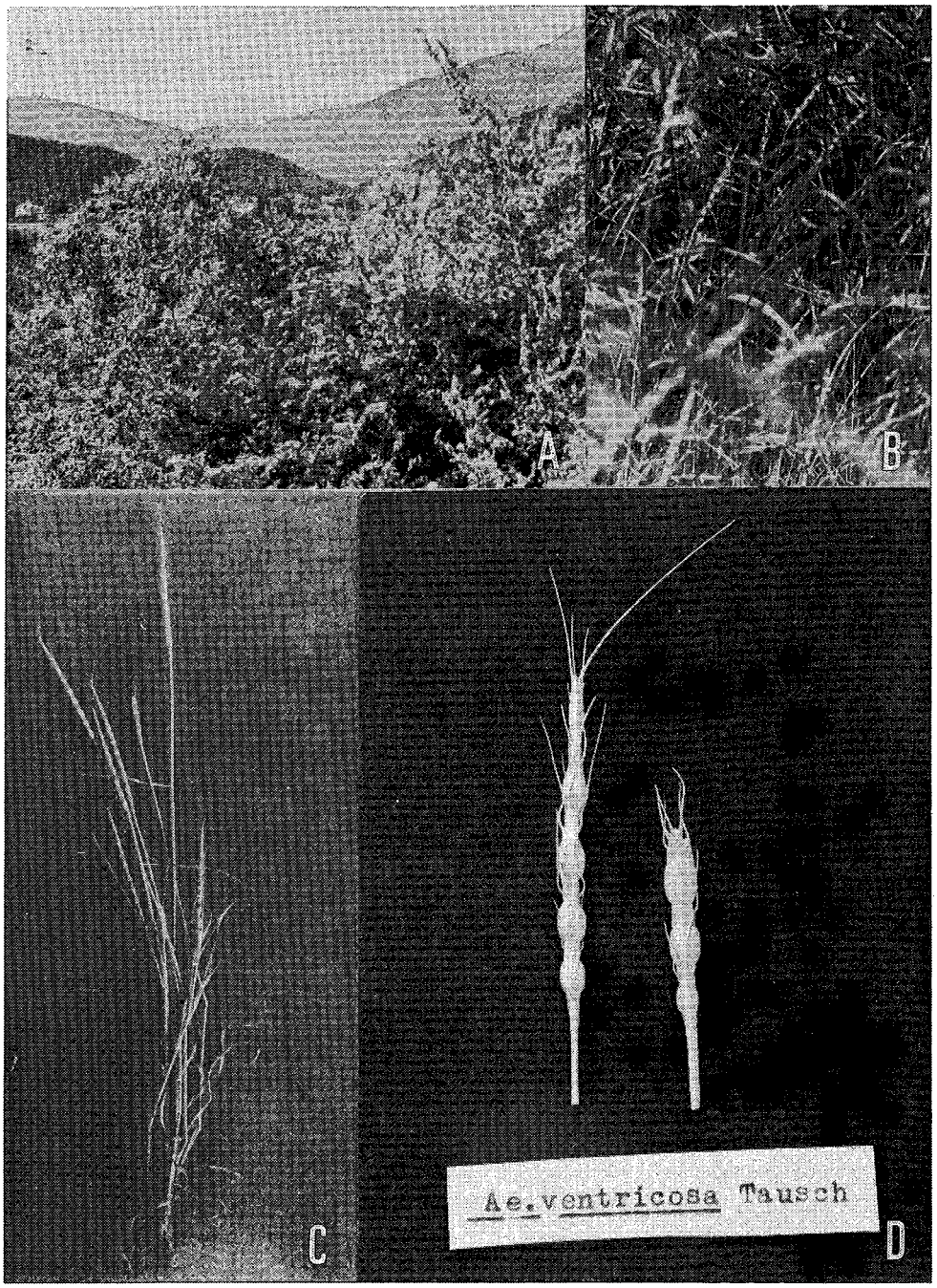

Fig. 3. Natural habitat of collection site (A and B), and plant and spike morphology (C and D) of *Ae. ventricosa* collected in Greece

population and the evolution of the species.

According to Eig (1929), the genus has been developed in the Upper Tertiary, when Balcan peninsula, Asia Minor, Crete and Cyprus were united in one continent called "Aegeide", and South Europe and Africa were united by land bridges. *Aegilops ventricosa* was probably developed somewhere along the axis from North Greece to Middle East and migrated through the existing land bridges to Africa. The parent species gradually moved widely apart to areas bestly suited for their growth because of changes in the climate of the region.

However, Kihara (1954) proposed an alternative theory, according to which polyploid species were distributed rather recently from the center of their origin to the Mediterranean coasts and islands through migration of man.

On the basis of the above theories, the possible explanations for the incidence of the discovered *Ae. ventricosa* population in North Greece are:

1. *Recent migration:* The collection site is in the transport axis from Italy to North Greece to Asia minor. Passive accidental transport from South Italy is possible. Passive transport by migrating birds from south Italy or northern Africa is a questionable alternative.
2. *Early migration:* Mediterranean had seen big population migrations and trade transactions at least some thousand years BC. and Greece was among the most active places in this respect. North Greece was the bridge between western Europe and Asia minor from early times. The collection site lies on the transport axis from Rome to Constantinoupolis (Istanbul) constructed by the Romans for trade or military purposes, the famous "Egnatia Way". An early accidental transfer of *Ae. ventricosa* by man in that area is an alternative hypothesis.
3. *Ancient remnant:* A very slim possibility for the population to be a relic from the Upper Tertiary distribution of the then created polyploid has also to be considered.

In conclusion, further comparative morphological, cytological and biochemical studies are needed to elucidate things. Seeds of the species are available on request for such studies. However, it must be emphasized that Greece has not been adequately explored in the past. Recent short multicrop explorations by Gene Bank scientists discovered many cereal species never before reported to exist in Greece i. e., *Hordeum agriocrithon*, and *Aegilops speltoides* var. *aucheri*.

Therefore species oriented systematic explorations might prove both theoretically and practically rewarding and are scheduled for the near future.

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Storage effect on seedling characters of monosomics in wheat

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Summary

The study of the storage effect on the gene products (controlled by individual chromosomes) stored in the embryo and endosperm which are responsible for the initial development of plant parts in monosomic and disomic lines of wheat variety Pb. C591 has revealed the facts listed below.

1. Coleoptile length is promoted by at least nine chromosomes (1B, 2B, 3A, 4A, 5A, 6A, 6B, 7A, and 7D), while chromosome 7B was found to inhibit the coleoptile length. It is observed that chromosomes 1B, 4A and 5A carry genes for major effect to promote the trait.
2. Chromosomes 1B, 4A, 5A and 6A carry genes for seedling height promoter, while chromosome 7B inhibits the seedling height.
3. Root length is affected by at least ten chromosomes, 1A, 1B, 4A, 4B, 4D, 5A, 5D, 6D, 7A and 7D respectively.

Introduction

The development of initial plant parts like coleoptile, root and shoot are as important as the other traits related directly to wheat yield. These traits are extremely important for initial development and proper stand of the plant. It is therefore very necessary to study the effect of genetic factors on the development of coleoptile, roots and shoots in hexaploid wheat. These developmental stages are greatly influenced by the stored material present in the embryo and endosperm which are under the control of genetic factors. The environmental conditions like temperature and moisture also affect these processes to some extent. It was therefore thought necessary to study the storage effect on these developmental processes in monosomic lines of variety Pb. C591.

Materials and methods

To study the effect of storage on individual chromosomes of variety Pb. C591, all the monosomic lines except monosomic 5B were used. The monosomic plants were identified cytologically at first meiotic metaphase continuously for four years. The seeds were harvested from all the cytologically identified monosomic and disomic plants separately and were stored every year at 12 ± 1°C inside the refrigerator. From each of the monosomic and disomic line, 200 seeds were germinated in separate petridishes (four petridishes in each

case) at 25±1°C. After 8 or 9 days of imbibition, data were recorded on coleoptile length, seedling height and root length.

Results and discussion

The statistical analysis of the data had revealed that the mean values of two and three years old seeds were significantly lower than those of the freshly harvested seeds. It was therefore thought proper to consider percentages in reduction over the disomic lines to suggest the involvement of the chromosome(s).

Coleoptile length

The one year old seeds of all the monosomic lines were affected at almost same degree. Storage effect became more conspicuous in two years old seeds (Table 1). In monosomic line 5A, the coleoptile length was found only 47% compared to the fresh seeds. In other monosomic lines for chromosomes 1B, 2B, 3A, 4A and 7D, the reduction was over 35%. Monosomic line 7B showed only 10% reduction which was much lower than disomic line (25%). The reduction in coleoptile length in the seeds stored for three years was more than 50% in the monosomic lines for chromosomes 1B, 4A, 5A, 6A, 6B, 7A and 7D. The disomic line showed 29% reduction. Interestingly enough, monosomic line 7B again showed less reduction (20%) compared to disomic line.

These observations suggest that the factors for coleoptile length promoter are located on at least nine chromosomes, 1B, 2B, 3A, 4A, 5A, 6A, 6B, 7A and 7D in variety Pb. C591. The involvement of chromosomes 1B, 2B, 3A, 6A, 6B, 7A, and 7D in this character was demonstrated by Gale and Spencer (1974). Allan and Vogel (1964) observed the involvement of at least eleven chromosomes for the development of normal coleoptile length. Logically the progress in improving the length of coleoptile will be slow, because of the involvement of so many chromosomes. Besides these chromosomes which possess genes for length promotion, chromosome 7B was found to carry a gene or gene complex which inhibits the length of coleoptile (hemizygous ineffective). It leaves an opportunity to modify the effect of the gene or gene complex located on chromosome 7B through mutation, recombination or both and increase the length of coleoptile.

Seedling height

Freshly harvested monosomic and disomic seeds did not show much differences in their seedling height (Table 2). Monosomic line 7A showed 20% reduction while the reduction in disomic line was 6% in one year old seeds. The reduction in seedling height became more apparent in the seeds stored for two years. Monosomic lines 1B, 5A and 5D showed reduction in the seedling height to the tune of 59%, 53%, and 50%, respectively, while disomic line showed only 35% reduction. In the monosomic line 6D and 7B, the reduction were 18% and 16%, respectively. The reduction in seedling height was much more in three years old seeds. Monosomic line for chromosomes 1B, 4A, 5A, and 6A showed more than 63% reduction, while it was 53% in disomic line. The maximum reduction of 70% was

observed in monosomic line 4A. Based on these observations it is presumed that chromosomes 1B, 4A, 5A and 6A carry genes for promoting the seedling height in an Indian tall variety Pb. C591. Chromosome 4A has been reported to carry dwarfing genes *Rht1* (Gale and Marshall 1976) and *Rht3* (Gale et al 1975). Similarly chromosome 5A has been reported to carry dwarfing gene *Rht12* (Sutka and Kovacs 1987). It is therefore likely that variety Pb. C591 may be carrying alleles of the dwarfing genes *Rht1*, *Rht3* and *Rht12*. Since many chromosomes are common in promoting coleoptile length and seedling height, it will appear as if these traits are positively correlated.

The reduction in seedling height in the monosomic line 7B was much lower than disomic line, suggesting that the chromosome 7B may be carrying gene or gene complex which inhibits the seedling height. Chromosome 7B has been reported to carry Rht 9 by Law and Worland (1985).

Table 1. Storage effect on coleoptile length in monosomic and disomic lines of wheat.

Monosomic line	Fresh seed Mean (cm)	Two years seed			Three years seed		
		Mean (cm)	%Reduction	"t"value	Mean (cm)	%Reduction	"t"value
1A	4.4±0.2	3.1±0.3	30	3.7	3.0±0.5	42	3.4
1B	4.2±0.2	2.7±0.3	35	4.7	2.0±0.1	55	6.3
1D	4.6±0.2	3.5±0.1	25	4.8	2.6±0.3	44	6.2
2A	4.0±0.2	3.2±0.3	20	2.1	3.0±0.2	25	3.1
2B	4.3±0.2	2.7±0.4	37	3.5	2.3±0.3	46	5.3
2D	4.4±0.3	3.6±0.4	18	1.9	3.4±0.3	22	3.2
3A	4.7±0.2	3.0±0.3	36	4.4	2.8±0.3	41	6.0
3B	4.1±0.1	3.3±0.6	20	1.6	3.1±0.3	24	3.4
3D	4.5±0.2	3.1±0.3	30	4.2	2.9±0.4	35	4.7
4A	4.5±0.2	2.9±0.2	36	6.3	2.0±0.3	56	8.7
4B	4.9±0.1	3.3±0.3	33	6.1	3.1±0.3	37	7.7
4D	4.8±0.1	3.3±0.3	31	5.4	3.1±0.5	36	4.2
5A	4.9±0.2	2.3±0.3	53	6.7	2.0±0.4	59	9.6
5D	4.4±0.2	3.2±0.3	26	3.6	2.8±0.3	37	4.7
6A	5.0±0.1	3.6±0.3	28	5.6	2.4±0.4	52	7.1
6B	4.6±0.2	3.4±0.4	26	3.1	2.3±0.4	50	6.0
6D	4.6±0.2	3.7±0.4	20	2.4	2.6±0.2	44	7.7
7A	5.3±0.2	3.7±0.4	30	4.9	2.6±0.4	50	7.2
7B	4.3±0.3	3.9±0.4	10	0.9	3.4±0.4	20	1.6
7D	5.2±0.2	3.3±0.2	37	7.8	2.5±0.2	51	10.8
Disomic	5.2±0.2	3.9±0.2	25	4.4	3.7±0.2	29	5.0

Root length

Like seedling height and coleoptile length, root length was also affected severely by storing the seeds (Table 3). The effect in fresh and one year old seeds was not much. In two years stored seeds, the disomic line showed 24% reduction. The monosomic line 5D showed highest reduction (64%) followed by monosomic lines 1B (62%), 7D (60%) and 1A (58%). The reduction in three years old seeds was much more than two years old seeds. The disomic line itself showed about 47% of reduction in root length. The reduction in root length in monosomic lines 1A, 1B, 4A, 4B, 4D, 5A, 5D, 6D, 7A and 7D was more than 60%. Monosomic line 5A showed reduction of 79%. Joshi et al (1970) also pointed out the effect of chromosome 5A on faster root growth.

Table 2. Storage effect on seedling height in monosomic and disomic lines of wheat.

Monosomic line	Fresh seed Mean (cm)	Two years old seed			Three years seed		
		Mean (cm)	%Redction	"t"value	Mean (cm)	%Reduction	"t"value
1A	11.0±0.6	6.1±0.7	45	5.5	5.1±0.5	54	6.3
1B	11.3±0.7	4.6±0.5	59	7.5	3.8±0.8	66	6.9
1D	12.0±0.5	6.7±0.5	44	7.8	6.0±0.5	50	8.0
2A	12.0±0.6	8.9±0.6	26	3.9	7.2±0.4	40	6.9
2B	12.1±0.7	6.4±0.6	47	5.9	6.0±0.8	50	5.5
2D	11.9±0.7	8.9±0.8	25	2.9	7.7±0.9	35	3.9
3A	12.7±0.7	8.1±0.9	36	4.2	5.8±0.8	54	6.8
3B	12.2±0.5	8.1±0.9	34	4.2	7.7±0.6	37	5.9
3D	11.5±0.8	7.5±1.0	35	3.3	7.0±0.8	39	3.9
4A	13.4±0.6	9.0±0.9	33	4.6	4.0±0.7	70	9.6
4B	13.0±0.3	9.8±0.9	25	3.4	6.2±0.5	52	11.3
4D	14.6±0.5	10.4±0.6	29	5.2	6.9±0.6	53	9.3
5A	13.2±0.7	6.2±0.8	53	6.5	4.5±0.6	66	8.7
5D	12.7±0.6	6.4±0.8	50	6.8	5.5±0.6	57	8.5
6A	13.5±0.5	9.5±0.9	30	4.5	5.0±0.9	63	8.6
6B	12.2±0.7	10.0±0.7	23	2.1	6.1±0.8	50	5.3
6D	12.7±0.2	10.4±0.8	18	3.2	6.5±0.5	49	12.5
7A	14.1±0.2	8.5±0.6	40	9.4	6.5±0.8	54	9.8
7B	11.3±0.8	9.5±0.9	16	1.6	7.9±0.8	30	2.9
7D	13.7±0.3	8.2±0.3	40	12.4	6.4±0.8	53	9.5
Disomic	15.8±0.5	10.3±0.6	35	6.9	7.9±0.7	53	9.5

Table 3. Storage effect on root length in monosomic and disomic lines of wheat.

Monosomic line	Fresh seed Mean (cm)	Two years old seed			Three years seed		
		Mean (cm)	%Reduction	"t" value	Mean (cm)	%Reduction	"t" value
1A	9.0±0.2	3.8±0.2	58	18.2	2.9±0.1	68	18.9
1B	8.3±0.5	3.1±0.3	62	8.9	2.0±0.2	76	10.0
1D	7.5±0.2	3.5±0.3	54	11.5	3.5±0.2	54	15.1
2A	7.7±0.3	5.7±0.3	26	4.4	4.6±0.2	40	7.7
2B	7.1±0.6	4.0±0.2	44	4.5	3.2±0.3	55	4.9
2D	7.7±0.4	5.6±0.2	27	4.9	4.5±0.2	41	7.5
3A	7.4±0.4	5.4±0.3	27	4.6	3.9±0.2	47	7.7
3B	7.5±0.7	5.4±0.4	28	2.7	4.0±0.3	47	4.4
3D	7.8±0.3	5.1±0.3	35	5.7	3.4±0.3	47	9.0
4A	8.3±0.4	4.8±0.3	42	7.5	1.8±0.2	78	13.8
4B	8.5±0.2	6.0±0.3	30	7.2	2.6±0.2	67	17.7
4D	7.8±0.3	6.0±0.3	23	4.5	2.9±0.2	63	11.9
5A	9.0±0.3	5.2±0.5	42	7.1	2.0±0.3	79	15.9
5D	8.1±0.4	2.9±0.3	64	11.0	2.5±0.2	69	12.2
6A	8.3±0.5	5.3±0.3	36	5.2	3.4±0.3	59	7.7
6B	7.1±0.4	6.0±0.4	16	2.0	3.5±0.4	51	5.8
6D	8.5±0.2	5.0±0.4	41	8.5	2.3±0.2	73	20.0
7A	9.4±0.4	5.5±0.3	42	10.1	3.8±0.3	60	14.8
7B	9.0±0.7	5.8±0.4	36	4.7	4.3±0.5	52	6.0
7D	7.2±0.3	2.8±0.2	60	10.6	2.9±0.3	61	9.0
Disomic	9.2±0.3	7.0±0.3	24	5.3	4.9±0.3	47	10.8

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Variability for seed ageing and storability in wheat

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Introduction

The pace as well as process of ageing in stored seeds largely depends on chemical composition of seeds (Mayer and Poljokoff-Mayber 1982), storage temperature, humidity and gaseous exchange (Roos and Manalo 1970). Ageing causes stress on seeds which leads to impaired germination and loss of seedling vigour (Purkar et al 1980). Genotypic variation for seed ageing among wheat genotypes exist (Madan et al 1989). Screening of wheat genotypes for seed ageing under real storage and artificially accelerated ageing conditions would provide guide lines to ensure appropriate storage of germplasm, specific genotypes and commercial seed lots. An experiment was, therefore, conducted to know the effect of various storage conditions on genetically diverse wheat lines.

Materials and methods

Six diverse cultivars, ie, HD 2009, S 308, WH 147, WH 416, WH 283 and C 306 were stored in gunny bags (G), fertilizer bags (F) and polyethylene bags (P, 700 g) kept under ambient conditions for three years (Table 1). The average temperature and relative humidity under ambient storage condition varied from season to season and also within a day (morning-evening hours). The moisture content (%) of all the varieties at the harvest and the beginning of storage experiment was ranging from 14–15 percent and 8.50–8.75 per cent, respectively. Seed samples from each bag were drawn at 3 months interval. One hundred seeds replicated four times were germinated using rolled paper towel and kept in controlled temperature conditions at 20±2°C and relative humidity 100 per cent (approx.). The per cent germination was recorded after 7 days as per ISTA rules (Anonymous 1985).

Simultaneously, to monitor the effects of artificial stress caused by abiotic factors, seeds of all the six varieties were exposed to accelerated ageing (AA) for 72 hours at 40±2°C and 100 per cent relative humidity (approx.) at the beginning of storage experiment. Germination tests in this experiment were also performed as mentioned above. The data were subjected to analysis of variance and treatment means were compared. Angular transformation was used to make the data linear.

Results and discussion

Analysis of variance revealed significant differences among genotypes, periods and bags. This corroborates the earlier observations of Odiemah (1986) and Madan et al (1989). Based

on average germination (%) it appears that S 308, in general, could be stored safely for relatively longer period without much loss of seed germinability. Considerable reduction in germination figured after 12 months storage among varieties, C 306, WH 283, WH 416 and WH 147 particularly in G and F conditions. The loss in germination continued in subsequent observations too (for brevity data is presented upto 21 months storage; Table 2). Loss in germination was highest in C 306 followed by WH 147 and WH 283 after 21 months. Similarly, such a loss was shown by HD 2009 after 15 months of storage and S 308 maintained above 80% germination even after 21 months except in gunny bags. On overall basis loss in germination was significantly lower in polyethylene bags than gunny and fertilizer bags. Loss of seed germinability was maximum and quick in all the varieties having high germ oil percent, eg, C 306, WH 147 and WH 283 (Mayer and Poljakoff-Mayber 1982). Degree of unsaturation of fatty acids might also be implicative in loss of germinability in such cases (Mayer and Poljokoff-Mayber 1982). The rapid deterioration in gunny bags could be due to cumulative effects of high humidity and high temperature which increases fungal attack, membrane damage and respiration as compared to other options (Mayeux et al 1970, Roos and Manalo 1971).

Reduction in germination in accelerated ageing test also varied from variety to variety. Similar observations were recorded by Madan et al 1989. Following the accelerated ageing treatment, the pattern of reduction in germination in all the six varieties was similar to that of ambient storage conditions in polyethylene bags for 21 months.

Thus three important conclusions emanate from this study. Variation for storability exist among wheat genotypes. AA test can be used for the prognosis of variety specific storability. Polyethylene bag is more suitable in each case and cost effective method of storing seeds in ambient conditions as it minimizes reduction in germination effectively against the syndrome of abiotic factors causing ageing stress.

Table 1. Seasonwise temperature (°C) and relative humidity (%) under ambient conditions

Season	Months	Temperature (°C)		Relative humidity (%)	
		Mean $\bar{X}$	Range (Min.~Max.)	Mean $\bar{Y}$	Range (Min.~Max.)
Summer	April, May, June	34	(29~39)	45	(40~50)
Rainy	July, August, September	30	(25~35)	78	(68~88)
Autumn	October, November	25	(21~29)	64	(53~75)
Winter	December, January	18	(16~20)	58	(50~66)
Spring	February, March	22	(20~24)	61	(47~75)

$\bar{X}$ denotes seasonwise mean temperature averaged over 3 years.

$\bar{Y}$ denotes seasonwise mean relative humidity averaged over 3 years.

Table 2. Effect of abiotic stress on seed germination

Variety (a)	Accelerated ageing at 40°C for 72hr	Germination (%) fresh seed	Periods (months) (c) / Containers (b)												Overall mean over		
			12			15			18			21					
			G	F	P	G	F	P	G	F	P	G	F	P	G	F	P
HD 2009	78	89	85	88	90	76	80	87	69	78	82	58	62	78	74	79	86
S 308	84	94	86	89	90	83	82	90	80	83	89	72	80	87	82	84	89
WH 147	71	95	80	78	83	69	70	78	58	58	60	42	58	58	65	68	72
WH 416	72	91	78	78	86	63	73	86	62	70	76	62	64	71	70	73	81
WH 283	68	88	79	79	80	65	63	80	62	70	73	46	64	65	65	71	75
C 306	66	87	74	73	81	68	65	80	48	78	79	26	58	57	58	69	75
Overall mean	73	91	80	81	85	71	72	84	63	78	77	51	64	69	69	74	80

CD (P = 0.05): a = 0.62, b = 0.44, c = 0.57, ab = 1.07, ac = 1.39, bc = 0.98, abc = 2.40, G = Gunny bag, F = Fertilizer bag, P = Polyethylene bag

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Genetic Stocks

List of indigenous *Aegilops comosa* accessions maintained in the Greek Gene Bank

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Record#	COLLNO	ACCNO	GEN	SP	COLLINST	MO	YR	CTY	PROVSTATE	LOCATION	LATI	LONG	ALTI	C	S	LOCALNAME	NP	P	T	F
1	GR133/82	770	AEGI	COMO	GRCGGB	08	82	GRC	PHTIOTIS	MELITEA			450	1	1		60		2	
2	GR061/82	698	AEGI	COMO	GRCGGB	07	82	GRC	TRIKALA	KASTANEA			180	1	1				2	
3	GR080/82	697	AEGI	COMO	GRCGGB	07	82	GRC	TRIKALA	KAKOPLEVRI			800	1	1		40		2	
4	GR128/82	765	AEGI	COMO	GRCGGB	08	82	GRC	KARDITSA	NERAIDA			820	1	1			Y	2	
5	GR056/82	693	AEGI	COMO	GRCGGB	07	82	GRC	TRIKALA	OXINIA			560	1	1		30	Y	2	
6	GR063/82	700	AEGI	COMO	GRCGGB	07	82	GRC	TRIKALA	AMARANTA			905	1	1		50	Y	2	
7	GR062/82	699	AEGI	COMO	GRCGGB	07	82	GRC	TRIKALA	KASTANEA			580	1	1		30	Y	2	
8	GR175/82	812	AEGI	COMO	GRCGGB	08	82	GRC	LARISSA	MESOHORI			210	1	1		80		2	
9	GR019/83	1722	AEGI	COMO	GRCGGB	06	83	GRC	LIMNOS ISL.	PLAKA			30	1	1		100	Y	2	
10	GR084/83	1787	AEGI	COMO	GRCGGB	06	83	GRC	HIOS ISL.	VRONDADES			590	1	1		50	Y	2	
11	GR030/84	3722	AEGI	COMO	GRCGGB	07	84	GRC	TRIKALA	ZARKOS			100	1	1				2	
12	GR052/84	3744	AEGI	COMO	GRCGGB	07	84	GRC	GREVENA	KIPOURIO			560	1	1				2	
13	GR041/84	3733	AEGI	COMO	GRCGGB	07	84	GRC	TRIKALA	AHLADEA			360	1	1				2	
14	GR019/84	3711	AEGI	COMO	GRCGGB	07	84	GRC	LARISSA	AGIOCAMPOS			30	1	1				2	
15	GR013/84	3705	AEGI	COMO	GRCGGB	07	84	GRC	LARISSA	SKITI			140	1	1				2	
16	GR150/84	3842	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	AN.KORINTHOS			100	1	1				2	
17	GR289/84	3981	AEGI	COMO	GRCGGB	08	84	GRC	MESSINIA	TSUKALEIKA				1	1				2	
18	GR275/84	3967	AEGI	COMO	GRCGGB	08	84	GRC	MESSINIA	PROSSILIO				1	1				2	
19	GR285/84	3977	AEGI	COMO	GRCGGB	08	84	GRC	MESSINIA	LAMBENA			60	1	1				2	
20	GR152/84	3844	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	AKROKORIN-THO			450	1	1				2	
21	GR132/84	3824	AEGI	COMO	GRCGGB	07	84	GRC	HALKIDIKI	KALLITHEA			10	1	1				2	
22	GR278/84	3970	AEGI	COMO	GRCGGB	08	84	GRC	MESSINI	SOTIRIANKA				1	1				2	
23	GR298/84	3988	AEGI	COMO	GRCGGB	08	84	GRC	LAKONIA	TRIPI				1	1				2	
24	GR281/84	3973	AEGI	COMO	GRCGGB	08	84	GRC	MESSINIA	LAMBENA			60	1	1				2	
25	GR130/84	3822	AEGI	COMO	GRCGGB	07	84	GRC	HALKIDIKI	KRINI			220	1	1				2	
26	GR310/84	4002	AEGI	COMO	GRCGGB	08	84	GRC	LAKONIA	DAFNI				1	1				2	
27	GR315/84	4007	AEGI	COMO	GRCGGB	08	84	GRC	LAKONIA	PETRINA				1	1				2	
28	GR155/84	3847	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	SOLOMOS				1	1				2	
29	GR118/84	3810	AEGI	COMO	GRCGGB	07	84	GRC	THESSALONIKI	KARDIA			150	1	1				2	
30	GR270/84	3962	AEGI	COMO	GRCGGB	08	84	GRC	MESSINIA	MESSINI				1	1				2	
31	GR303/84	3995	AEGI	COMO	GRCGGB	08	84	GRC	LAKONIA	VAFIO				1	1	SACCOTRUFI			2	
32	GR300/84	3992	AEGI	COMO	GRCGGB	08	84	GRC	LAKONIA	AMYKLES				1	1	SACCOTRUFI			2	

Record#	COLLNO	ACCNO	GEN	SP	COLLINST	MO	YR	CTY	PROVSTATE	LOCATION	LATI	LONG	ALTI	C	S	LOCALNAME	NP	P	T	F
33	GR267/84	3959	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	PALEO ITILO				1	1				2	
34	GR212/84	3904	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	LOUTRAKI				1	1				2	
35	GR161/84	3853	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	ANC.MYKINA			110	1	1				2	
36	GR241/84	3933	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	GYTHIO				1	1				2	
37	GR186/84	3878	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	LIGURIO			370	1	1				2	
38	GR262/84	3954	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	PIVRIHOS				1	1				2	
39	GR264/84	3956	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	NEO ITILO				1	1				2	
40	GR165/84	3857	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	NAFPLIO				1	1				2	
41	GR224/84	3916	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	IREON				1	1				2	
42	GR259/84	3951	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	HIMARA				1	1				2	
43	GR223/84	3915	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	PERAHORA				1	1				2	
44	GR237/84	3929	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	SPARTI				1	1				2	
45	GR201/84	3893	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	SOFIKO			430	1	1				2	
46	GR253/84	3945	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	KOKALA				1	1				2	
47	GR230/84	3922	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	SOULINARI			180	1	1				2	
48	GR248/84	3940	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	MEZAPOS				1	1				2	
49	GR251/84	3943	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	ALIKA				1	1				2	
50	GR193/84	3885	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	DIMANA				1	1				2	
51	GR252/84	3944	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	LAGIA				1	1				2	
52	GR174/84	3866	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	TOLO				1	1				2	
53	GR194/83	3886	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	N.EPIDAVROS				1	1				2	
54	GR247/84	3939	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	KOKALA				1	1				2	
55	GR244/84	3936	AEGI	COMO	GRCGGB	07	84	GRC	LAKONIA	KOKALA				1	1				2	
56	GR184/84	3876	AEGI	COMO	GRCGGB	07	84	GRC	ARGOLIS	LIGURIO			370	1	1				2	
57	GR202/84	3894	AEGI	COMO	GRCGGB	07	84	GRC	KORINTHIA	ALMIRI				1	1				2	
58	GR007/85	4556	AEGI	COMO	GRCGGB	06	85	GRC	PAROS ISL	VONTAKOS	3701N	2508N	20	1	1		70		2	
59	GR145/85	4695	AEGI	COMO	GRCGGB	06	85	GRC	EVIA	AMARINTHOS	3823N	2355E	5	1	1				2	
60	GR230/85	4783	AEGI	COMO	GRCGGB	07	85	GRC	AETOLOAKARN.	PALEROS	3841N	2053E	1	1	1				2	
61	GR257/85	4810	AEGI	COMO	GRCGGB	07	85	GRC	EVRYRANIA	FRAGISTA	3857N	2235E	600	1	1				2	
62	GR202/85	4754	AEGI	COMO	GRCGGB	07	85	GRC	FOKIDA	GALAXIDI	3821N	2219E	1	1	1		200		2	
63	GR247/85	4800	AEGI	COMO	GRCGGB	07	85	GRC	AETOLOAKARN.	AG.NIKOLAOS	3849N	2228E	760	1	1		100	Y	2	
64	GR220/85	4773	AEGI	COMO	GRCGGB	07	85	GRC	AETOLOAKARN.	VLIZIANA	3829N	2105E	370	1	1			Y	2	
65	GR131/85	4681	AEGI	COMO	GRCGGB	06	85	GRC	EVIA	KOTSIKIA	3858N	2325E	300	1	1			Y	2	
66	GR116/85	4665	AEGI	COMO	GRCGGB	06	85	GRC	EVIA	LIHADA	3850N	2251E	2	1	1		150		2	
67	GR108/85	4657	AEGI	COMO	GRCGGB	06	85	GRC	EVIA	EDIPSOS	3852N	2304E	40	1	1		50		2	
68	GR312/85	4867	AEGI	COMO	GRCGGB	07	85	GRC	KOZANI	NEAPOLI			600	1	1				2	
69	GR245/85	4798	AEGI	COMO	GRCGGB	07	85	GRC	AETOLOAKARN.	A.HRISOVITSA	3834N	2240E	650	1	1		150	Y	2	
70	GR135/85	4685	AEGI	COMO	GRCGGB	06	85	GRC	EVIA	STROPHILIA	3849N	2328E	150	1	1		150		2	
71	GR055/88	6104	AEGI	COMO	GGB/USDA	07	88	GRC	ARKADIA	KERASSITSA	3727N	2224E	440	1	1		50		2	
72	GR050/88	6099	AEGI	COMO	GGB/USDA	07	88	GRC	LAKONIA	MEZAPOS	3632N	2224E	140	1	1		50		2	
73	GR048/88	6097	AEGI	COMO	GGB/USDA	07	88	GRC	LAKONIA	DEMONIA	3640N	2253E	120	1	1		50		2	
74	GR046/88	6095	AEGI	COMO	GGB/USDA	07	88	GRC	LAKONIA	AG.APOSTOLI	3633N	2301E	165	1	1		50		2	

Record#	COLLNO	ACCNO	GEN	SP	COLLINST	MO	YR	CTY	PROVSTATE	LOCATION	LATI	LONG	ALTI	C	S	LOCALNAME	NP	P	T	F
75	GR039/88	6088	AEGI	COMO	GGB/USDA	07	88	GRC	ARKADIA	MARIO	3700N	2250E	430	1	1		50		2	
76	GR032/88	6081	AEGI	COMO	GGB/USDA	07	88	GRC	ARGOLIDA	AG.ANDREAS	3718N	2249E	20	1	1		50		2	
77	GR036/88	6085	AEGI	COMO	GGB/USDA	07	88	GRC	ARKADIA	PELETA	3703N	2253E	660	1	1		50		2	
78	GR030/88	6079	AEGI	COMO	GGB/USDA	07	88	GRC	ARGOLIDA	KIVERI	3732N	2243E	55	1	1		50		2	
79	GR012/88	6061	AEGI	COMO	GGB/USDA	07	88	GRC	KORINTHIA	TRAHIA	3733N	2309E	250	1	1		50		2	
80	GR021/88	6070	AEGI	COMO	GGB/USDA	07	88	GRC	ARGOLIDA	THERMISIA	3724N	2318E	25	1	1		50		2	
81	GR019/88	6068	AEGI	COMO	GGB/USDA	07	88	GRC	KORINTHIA	SARONIDA	3727N	2329E	20	1	1		50		2	
82	GR134/88	6183	AEGI	COMO	GRCGGB	07	88	GRC	THESPROTIA	FILIATES			120	1	1		50		2	
83	GR132/88	6181	AEGI	COMO	GRCGGB	07	88	GRC	THESPROTIA	PETROVITSA			340	1	1		50		2	
84	GR143/88	6192	AEGI	COMO	GRCGGB	07	88	GRC	ETOLOAKARNAN	PALAIROS			50	1	1		50		2	
85	GR139/88	6188	AEGI	COMO	GRCGGB	07	88	GRC	THESPROTIA	PERDIKKA			140	1	1		30		2	

Dictionary of terms and abbreviations. ACCNO: Accession number, COLLNO: Collector's number, COLLINST: Collecting Institute, recorded by its acronym as defined in the IBPGR'S relevant Catalog, MO: Month of collection, YR: Year of collection, CTY: country, recorded by its acronym to UN'S relevant catalog, PROVSTATE: Province or state of a country where the collection was made, LOCATION: The most proximal village or city to the collection site, LATI: Geographic latitude, LONG: Geographic longitude, ALTI: Altitude in meters, C: Collection source (1 wild, 2 farmland etc. according to IBPGR'S General Collection Form), S: Status of sample (1 wild, 2 weedy, 3 breeders line etc. according to IBPGR'S General Collection Form), NP: Number of plants sampled, P: If photographs of the populations were taken (Y(es) or N(o)), T: Type of Sample (1 vegetative, 2 seed, 3 both).

Information

1. VIII International Wheat Genetics Symposium

(July 20–25, 1993 in Beijing, China)

The scientific program: I. Evolutionary and genome relationships of Triticeae, II. Cytogenetics, transfer of alien genetic materials, and genetic resources, III. Molecular genetics and biotechnology, IV. General genetic analysis, gene mapping and marker systems, V. Genetics of resistance to pathogens and pests, VI. Genetics of tolerance to environmental stresses, VII, Genetical approaches to breeding and the application of new breeding technologies.

Presentation of papers: All special lectures and invited papers will be presented orally or as posters. Each participant may present only one paper except when further papers are in collaboration with other registered participants.

Abstract: All participants are requested to send an abstract of their paper by November 30, 1992 to Prof. Shouyi Chen. The abstract must be typed in English. Following the receipt of abstract, contributions will be allocated to the appropriate session by the Program Committee. Contributors will be informed by January 15, 1993 whether their papers are presented in oral form or as poster demonstration. All papers will have equal consideration in the Symposium proceedings.

Manuscript: The manuscripts must be in English and prepared according to the "Notice to the Authors" enclosed with the second announcement. The deadline for receiving of manuscript is January 15, 1993 and they should be sent to Prof. Shouyi Chen.

The second announcement is now available from secretary-general of the symposium:

Prof: Shouyi Chen, Secretary-General 8th IWGS
Institute of Genetics, Chinese Academy of Sciences
Beijing 100101, China
FAX: 861-491-4896

2. Seventeenth International Congress of Genetics

(August 15–21, 1993 in Birmingham, United Kingdom)

The next International congress of Genetics, a major event in the genetics calendar, is sub-titled "Genetics and the Understanding of Life". It will be concerned with the central role of genetics in illuminating contemporary biology, as well as with the contributions that genetics can make to industry, medicine, agriculture and social sciences. A feature of the Congress will be a two-standed programme: a "Professional" programme covering as many as possible of the exciting new developments in genetics, particularly in the exploitation of molecular techniques, which have taken place since the last congress in Toronto in 1988; and a "Public awareness" programme in which important scientific, ethical and social issues will be discussed with members of the non-scientific community. The programme will attract participants from developing and developed countries alike, from East and West, and from

South and North.

Contact the followings for further information and registration particulars which will be sent to you in November 1992.

Professor D. A. Smith
Research Support & Industrial Liaison, the University of Birmingham, Edgbaston, Birmingham B15 2TT. UK.

3. XV International Botanical Congress, Tokyo

(August 28 – September 3, 1993 at Congress Center of Pacifico, Yokohama, Japan)

Last dates for:

Advance payment of registration fee	April 10, 1993
Submission of abstracts	April 10, 1993
Stating preference for excursions	November 30, 1992
Notice of society meeting	November 30, 1992
Booking congress excursions	June 30, 1993

Congress date:

August 22, 1993 13:00	Registration open
August 23–27, 1993	Nomenclature session
August 28, 1993 15:00	Opening ceremonies
August 29 - September 3, 1993	Scientific program
September 3, 1993 14:00	Closing ceremonies

Second circular is now available from:

K. Iwatsuki, Secretary XV IBC,
Botanical Gardens, University of Tokyo,
3–7-1 Hakusan, Bunkyo-ku, Tokyo 112, Japan.
Telephone: (81) 3–3814–2625, FAX: (81) 3–3814–0139

Third circular will be distributed only to those who will have submitted preregistration form until then. Those who have not made preregistration are recommended to let us know your intention in earlier occasion.

4. IV International Workshop on Rice Molecular Biology

An international workshop will be held on rice molecular biology at Yokohama, Japan, on September 4–5, 1993, in cooparation by Department of Agriculture, Forestory and Fishery of Japan, and IRRI.

The detailed informations will be obtained from:

Dr. Korehiro Nakagahra
Division of Genetic Resources
National Institute of Agricultural Resources
Kannondai, Tsukuba-shi, Ibaragi, Japan
Phone (81) 298–38–7431

5. Book

Nuclear and Organellar Genomes in Wheat Species

Edited by T. Sasakuma and T. Kinoshita.

Published by Kihara Memorial Foundation.

The 333-page book is edited on the basis of the proceedings of Dr. H. Kihara memorial International Symposium on Cytoplasmic Engineering in Wheat (ISCEW) held at Sapporo in July, 1991. It containes 35 research articles in five sections, namely; 1) Historical backgrounds of cytoplasmic genetics in wheat species, 2) Nuclear genomes, 3) Organellar genomes and genes, 4) Nuclear-cytoplasmic interactions, and 5) New approaches of wheat breeding.

The contents covers ideas and informations from molecular approaches for genome analysis to classical genetics of alien gene transfer from the view points of evolution as well as wheat breeding.

The book can be purchased for ¥3000 (about US$20) by order to;

Kihara Memorial Foundation
Mutsukawa 3-122-20, Minami-ku, Yokohama, Japan
FAX (81) 45-715-0022

6. T. Tsuchiya Achievement Award

Colorado State University (USA) and the family of late Dr. Takumi Tsuchiya announced to found T. Tsuchiya Achievement Award.

Dr. Takumi Tsuchiya, a plant cytogeneticist, had passed away on May 1st, 1992, at Fort Collins, Colorado, USA. He had contributed to cereal genetics and cytogenetics with his excellent technology and ideas on chromosomes, especially on the establishment of barley trisomic series, as well as on karyotyping and aneuploid analysis.

The award will be given each year to the outstanding graduate student studying plant genetics or related area. If you have an interest in assisting us in the development of this endowed award in memory of Dr. Takumi Tsuchiya, send your contribution to the Colorado State University Foundation, c/o T. Tsuchiya Achievement Award, Colorado State University, Fort Collins, CO 80523 USA.

V. Editorial Remarks

The present issue containes one review and 12 research articles in addition to genetic stock informations. The describers will enjoy the successive coverages of research topics by distinguished researchers. You may recomend the subjects or writers for the reviews.

Editorial Board would appreciate to obtain increasing informations of genetic stock, including the list of cloned DNA libraries, and RFLP linkage map. Also, any informations on meeting, publications, or notice regarding wheat researches will be welcome to be printed in WIS issues.

The back numbers of WIS are aveirable for mailing costs. Some of issues are limitted in their numbers, and some of them (Nos. 4, 5, 8, 9, and 10) will be the photo-copied ones. If you would like to obtain all issues, the mailing cost by ship will be ¥1500. (Send *additional* ¥2000 for exchange expense in case of check).

The next issue of WIS (No. 76) will be published in March 1993. Send the contributing articles, informations, records and/or opinions to the editorial office before Feburuary 15, 1993. Facsimile is convenient for business correspondence; country code of Japan 81, and FAX number is 45-715-0022.

Please notify us if you want to be newly listed or withdrawn from the mailing list.

Erratum

In the review article by Dr. K. Nishikawa in the issue No.74, an erratum was included in Fig. 1. For the illustration of monotelo disomic AS, the figure on the telocentric chromosome should be 1 instead of 2. Please correct this mistakes in the issue.

Explanation of the picture on the cover

Natural habitat of *Ae. ventricosa* found in Greece. See the article by A. Zamanis et al in the present issue for details.

WIS No. 75

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