The International Journal for Wheat Genetics and Breeding

WIS

Wheat Information Service

1996 No.83

ISSN 0510-3517

Kihara Memorial

Yokohama Foundation for the Advancement of Life Sciences

Wheat Information Service (WIS), a biannual international journal on wheat genetics and breeding, was founded in 1954. Now this journal is published by *Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences* to aim at exchanging of information among world wheat researchers.

For this purpose, WIS publishes Research articles, Invited reviews, Research information, Proposals, Gene catalogues, Publication lists, and any other information useful for wheat geneticists and breeders. Research articles report the results of original researches after reviewed by the Editorial Board. Research information is short and informal reports without reviewing.

Finance and subscription

Cost for printing of WIS is financed by Kihara Memorial Foundation. Cost for editing and mailing is expected to be supported by voluntary donation from readers (2,000 Japanese Yen per year; ca. US $25). Credit Cards (Visa and MasterCard) are available for donation. For subscription, write to Business Office of WIS.

Manuscript preparation and submission

Double-space all text in English on 216 x 280 mm or 210 x 297 mm (A4 size) bond paper with 30 mm margins. Prepare manuscript carefully referring styles of text, references, figures and tables in this issue. Use new pages for tables and figures. Research articles consist of Title, Author's name(s) and address(es) (e-mail address of corresponding author, if available), Summary (maximum 300 words), Key words (5 words), Introduction, Materials and Methods, Results, Discussion, Acknowledgments (optional), and References, followed by figure captions, Tables and Figures. Results and Discussion may be combined. Research information includes Title, Author's name(s) and address(es), Text, and References, followed by Figures and Tables. Use either underlining or italic type for scientific names of species and gene symbols. Nomenclature of genes and chromosomes should follow the rule in "Catalogue of gene symbols for wheat" (McIntosh et al.; 8th Int. Wheat Genet. Symp., 1993). Very long papers will not be accepted. Limitation of printed pages is five for Research articles and two for Research information.

Original manuscript and the copy are required for submission. Authors will have an opportunity to examine the first proof. After acceptance, submission of the final revision on disk is encouraged. Microsoft Word, WriteNow, Claris Works in Macintosh computer disk are welcome. Authors of Research articles, Research Information, Invited reviews and Proposals will receive 50 reprints free of charge. Mail registration manuscripts to the Business Office of WIS.

WIS welcomes to receive any information on wheat researches, such as meetings, books, jobs, etc. E-mail is now convenient (address of the secretary; tsujimot@yokohama-cu.ac.jp).

Business Office

Wheat Information Service
c/o Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
641-12 Maioka-cho, Totsuka-ku, Yokohama 244, Japan.
Phone: +81-45-825-3487, Fax: +81-45-825-3307, E-mail: tsujimot@yokohama-cu.ac.jp.

Wheat Information Service
Number 83: 1-6 (1996)

I. Articles

Crossability of D-genome chromosome substitution lines of durum wheat (*Triticum turgidum* ssp. *turgidum* conv. *durum*) with *Secale cereale* and *Aegilops squarrosa*

Ibrahim Genç, Hakan Özkan and Tacetttin Yagbasanlar

Department of Field Crops, Faculty of Agriculture, University of Çukurova, 01330 Adana / Turkey

Summary

Durum wheat cultivar Langdon (LDN) and the fourteen disomic D-genome chromosome substitution lines of Langdon where A or B genome chromosomes were replaced with homoeologous D genome chromosomes of Chinese Spring (CS), were used to determine the effect of each substitution on the crossability with rye (*Secale cereale*) and *Aegilops squarrosa*.

Hybridizations carried out between D-genome substitution lines and rye revealed a range from high to low levels of crossability percentage between them. In the present study, it was demonstrated that not only chromosome 5B, 5A and 5D, but also chromosome 3A and 3B were involved in the-crossability of wheat with rye. Also, 3D chromosome may be contributing to the development of embryo.

Also, a wide range in crossability percentage was obtained by crosses of *Ae. squarrosa* x LDN-D genome substitution lines. In this study, it has been clearly shown that chromosome 5D is also responsible for the crossability of wheat with *Ae. squarrosa*. Also, this results suggested that 6D chromosome may be partly responsible for the crossability of wheat with *Aegilops squarrosa*.

Introduction

Since 1960, there has been an increasing interest in using wild relatives of crop plants in breeding programs. Although wild relatives have been exploited most often as sources of disease, insect and nematode resistance, they have also proven to be valuable sources of variation for wider adaptation, resistance to stress, short stature, yield and other traits (Harlan, 1976).

Dominant alleles of crossability genes in wheat, *Kr1 Kr2, Kr3* and *Kr4* located on chromosome 5B, 5A, 5D and 1A, respectively, are known to reduce crossability with *Secale cereale, Hordeum bulbosum, Aegilops squarrosa* and *Zea mays* (Riley and Chapman 1967; Krolow 1970; Snape et al. 1979; Falk and Kasha 1981; Zheng et al. 1992; Koba and Shimada 1993; O'Donoughue and Bennett 1994).

Although some crosses between *Aegilops squarrosa* and common wheat were obtained recently by some workers (Gill and Raupp 1987; Cox et al. 1990), hybridization between wheat and *Aegilops squarrosa* is still difficult. Genetic analysis on the crossability of wheat with *Aegilops squarrosa* would provide useful information not only for practical breeding, but also on the genetics and evolution of wheat (Koba and Shimada 1993).

Krolow (1970) revealed that tetraploid wheat, like the hexaploid wheat, has the *Kr* system which regulates hybrid kernel set in wheat x rye crosses. Halloran (1981) reported that mutation(s) in wheat from high to low crossability with rye took place at least as early as the tetraploid level of wheat evolution. Scoles (1983) found that the genotype used in the cross affected both hybrid endosperm and embryo development, when tetraploid and hexaploid wheats were crossed with different inbred lines of *Secale cereale*.

The objective of this study was to determine if specific chromosome replacement can affect the crossability of durum wheat with *Secale cereale* and *Aegilops squarrosa*.

Materials and methods

A set of 14 disomic substitution lines, in which each of A and B genome chromosome pairs of durum wheat (*Triticum turgidum* ssp. *turgidum* conv. *durum*) cultivar Langdon was replaced by a homoeologous pair from the D-genome of Chinese spring, was kindly provided by Dr. L.R. Joppa, North Dakota State University, Fargo, ND, USA. These disomic substitution lines and Langdon, were used as female parent in crosses with rye, *Secale cereale* L. (a diploid open pollinate Turkish landrace). However, these disomic substitution lines and Langdon were used as male parent in crosses with *Aegilops squarrosa* (collected from Azerbejcan and, obtained from ICARDA, Accession no: 400630). The crosses were made in field conditions in the 1994-95 growing season.

Emasculation and pollination were made in the early morning between 7.00 and 10.00 am, emerging spikes of wheat were selected for emasculation in field conditions. Emasculated spikes were bagged with parchement bags and checked in the next morning. When the stigmas were fully receptive, mature anthers were taken from Langdon and rye just before the bursting of the pollen sacs, and at least one anther was carefully placed on each stigma of Langdon and *Aegilops squarrosa* spikes. The spikes were harvested at maturity. Crossability percentages were estimated as the ratio of the number of kernels set to number of florets pollinated. The hybrid kernels were germinated on wet filter paper in petri dishes at 22°C and numbers of germinating seedlings were scored six days later.

The t-test was adopted to detect the crossability differences between D-genome substitution lines of Langdon and Langdon (control) with rye. Also, this statistical analyses were carried out by using transformed values to angles of the percentages in individual spikes.

Results and discussion

D-genome substitution lines x *Secale cereale* crosses

A wide range in crossability percentage was obtained in different substitution lines and the control "Langdon" as seen in Table 1. Analysis of t-test of all the crosses, except 3D(3A) x rye and 4D(4A) x rye, revealed a highly significant ($p<0.01$) each the D-genome substitution lines in crossability with rye according to control.

Table 1. Crossability of D-genome substitution lines of Langdon (*Triticum trurgidum* ssp. *turgidum* conv. *durum*) with rye (*Secale cereale*)

Disomic substitution lines (female parent)	Rye(male parent)			
	No. of floret pollinated	Number of kernels	Crossability percentage	Germination percentage
LDN-1D(1A)	98	33	33.7*	0.0
LDN-2D(2A)	80	21	26.3*	0.0
LDN-3D(3A)	100	32	32.0	0.0
LDN-4D(4A)	83	26	31.3	0.0
LDN-5D(5A)	70	9	12.9*	0.0
LDN-6D(6A)	118	39	33.1*	0.0
LDN-7D(7A)	102	54	52.9*	0.0
LDN-1D(1B)	83	32	25.9*	0.0
LDN-2D(2B)	102	13	12.7*	0.0
LDN-3D(3B)	72	17	23.6*	5.9
LDN-4D(4B)	116	28	24.1*	0.0
LDN-5D(5B)	106	39	36.8*	0.0
LDN-6D(6B)	110	40	36.4*	0.0
LDN-7D(7B)	116	30	25.9*	0.0
LANGDON (control)	108	34	31.5	0.0

*Significant at 1% level according to control

Mean crossability percentage ranged from 12.7 for the 2D(2B) to 52.9 for the 7D (7A). When the crossability percentages are compared, it was shown that the crossability percentages in five of the disomic substitution, viz, 1D(1A), 6D(6A), 7D(7A), 5D(5B) and 6D(6B) were significantly higher than the control, while other of the disomic substitution lines, except 3D(3A) and 4D(4A) were significantly lower than the control. Especially, 7D(7A) line showed the highest crossability with rye, while 2D(2B) and 5D(5A) lines showed the lowest crossability with rye. Crossability percentages in three of the disomic substitution lines of A genome chromosomes with rye were significantly higher than the control, while those in only two of the disomic substitution lines of B genome chromosome with rye were significantly higher than the control. These results showed

that B genome chromosome substitutions had a more detrimental effect on kernel set than A genome chromosome substitutions. Similar results were obtained by Pienaar and Marais (1986).

As can be seen in Table 1, the 5D(5B) substitution line showed a higher crossability with rye than the 5D(5A) substitution line. It was clearly shown that, as previously reported by Riley and Chapman (1967), gene *Kr1* located on the 5B chromosome was more detrimental to kernel seed set than gene *Kr2* located on the 5A. Zheng et al. (1992) reported that the gene *Kr4* is located on chromosome 1A of wheat. As can be seen in Table 1, the 1D(1A) substitution line showed significantly high crossability with rye, suggesting that 1A chromosome may be partly responsible for the crossability of wheat with rye.

At the same time, Miller et al. (1983) reported that the homoeologous group 3 chromosomes carry genes affecting chromosome pairing and crossability. As can be seen in Table 1, the 3D(3A) substitution line showed normal crossability according to control (Langdon), while 3D(3B) substitution line showed significantly lower than control. In this study, it was also observed that the crossability percentage drastically decreased when 3B was absent. This results indicate that the 3A chromosome has a more detrimental effect on kernel seed set than the 3B chromosome. Also, this data supports Romero and Cuadrado (1992) who reported that crossability level of CS-mono 3B line was lower than CS-mono 3A line. This results showed that 3A chromosome has more important effect on crossability with rye than 3B chromosome.

On the other hand, Tanner and Falk (1981) reported that rye has a single dominant gene for crossability with wheat. The cause of variation in crossability percentage in these crosses, except 3D(3A) x rye, 3D(3B) x rye, 5D(5A) x rye, 5D(5B) x rye and 1D(1A) x rye, could not be explained. Perhaps, the heterozygosity for a factor affecting crossability percentage was present in the *Secale cereale* parent.

The endosperm development in all hybrids, except hybrid kernels produced by 3D (3B) and 6D(6B), was very poor and all of the kernels were shrivelled. However, hybrid kernels produced by 3D(3B) germinated (5.9%), while no hybrid kernels produced by other substitution lines germinated. These data indicate that the 3D chromosome may contribute to the development of embryo. At the same time, Miller et al. (1983) reported that 3D chromosome effected embryo development in Chinese Spring x *Hordeum bulbosum* crosses.

From the results of this study, it was demonstrated that not only chromosome 5B, 5A and 5D, but also chromosome 3A and 3 B were involved in the crossability of wheat with *Secale cereale* . Also, 3D chromosome may be contributing to the development of embryo.

Aegilops squarrosa x D-genome substitution lines

Crossability of D genome substitution lines of Langdon with *Aegilops squarrosa* is presented in Table 2.

As can be seen in Table 2, a wide range in crossability percentage was obtained by crosses of *Aegilops squarrosa* x LDN-D genome substitution lines. When the crossability percentages are compared, it was shown that in 3D(3A), 6D(6A), 3D(3B) and 6D(6B) disomic substitution lines it was higher than other disomic substitution lines. The crossability percentage of these lines ranged from 15.0 % to 46.2 %, while in six substitution lines, viz. 1D(1A), 2D(2A), 1D(1B), 2D(2B), 4D(4B)

and 7D(7B), it ranged from 3.6 % to 9.4 %. The crossability of the control and 5D(5A), 7D(7A) and 5D(5B) lines were zero. This result suggested that 3A, 6A, 3B and 6B chromosomes had a gene/genes that inhibit crosses between *Aegilops squarrosa* and durum wheat. It has been clearly shown that chromosome 5D is also responsible for the crossability of wheat with *Aegilops squarrosa*. At the same time, Koba and Shimada (1993) reported that, like 5A and 5B, 5D chromosome carried genetic factor(s) controlling the crossability with *Aegilops squarrosa*.

Table 2. Crossability of D-genome substitution lines of Langdon (*Triticum turgidurn* ssp. *turgidurn* conv. *durum*) with *Aegilops squarrosa*

Disomic substitution lines (male parent)	*Aegilops squarrosa* (Female parent)			
	No. of floret pollinated	Number of kernels	Crossability percentage	Germination percentage
LDN-1D(1A)	54	3	5.6	0.0
LDN-2D(2A)	54	3	5.6	0.0
LDN-3D(3A)	52	10	19.2	0.0
LDN-4D(4A)*	-	-	-	-
LDN-5D(5A)	50	0	0.0	-
LDN-6D(6A)	52	24	46.2	0.0
LDN-7D(7A)	56	0	0.0	-
LDN-1D(1B)	54	3	5.6	0.0
LDN-2D(2B)	56	2	3.6	0.0
LDN-3D(3B)	80	12	15.0	0.0
LDN-4D(4B)	60	4	6.7	0.0
LDN-5D(5B)	50	0	0.0	-
LDN-6D(6B)	60	15	25.0	6.7
LDN-7D(7B)	64	6	9.4	0.0
LANGDON (control)	54	0	0.0	-

*This line was not crossed with *Aegilops squarrosa*

The endosperm development in all hybrid kernels, except hybrid kernels produced by 6D(6A), 6D(6B) and 2D(2B), was very poor and all kernels were shriveled. The hybrid kernels produced by 6D(6B) germinated (6.7 %), while no hybrid kernels produced by other substitution lines germinated. This results suggested that 6D chromosome may be partly responsible for the embryo development of *Aegilops squarrosa* x durum wheat crosses.

However, we could have had a permissive accession of *Aegilops squarrosa* because most researchers have found it very difficult to cross *Aegilops squarrosa* with wheat when *Aegilops*

squarrosa used as the female (Dr. Joppa, pers. com.). At the same time, if we can find a permissive accessions of *Aegilops squarrosa*, this accession(s) could be used to improve new durum or bread wheat in future.

Also, main reasons for low and high crossability of Langdon D-genome substitution lines with *Aegilops squarrosa* can be the technique used, and climatic conditions during crossing. Similar results were obtained in wheat x *Aegilops* crosses by Özgen (1983).

Acknowledgements

We acknowledge Dr. L.R. Joppa, North Dakota State University, for supplying the seed of Langdon D genome chromosome substitution lines. Also, We thanks Dr. L.R. Joppa and Dr. S.M. Reader (John Innes Centre, Cereals Research Department, UK) for their valuable critical review of the manuscript.

References

Cox TS, Hatchett JH, Gill BS, Raupp WJ and Sears GR (1990) Agronomic performance of hexaploid wheat lines derived from direct crosses between wheat and *Aegilops squarrosa*. Plant Breeding, 105: 271-277.

Falk DE and Kasha KJ (1981) Comparison of the crossability of rye (*Secale cereale*) and *Hordeum bulbosum* on to wheat (*Triticum aestivum*). Can J Genet Cytol 23: 81-88.

Gill BS and Raupp WJ (1987) Direct genetic transfer from *Aegilops squarrosa* L. to hexaploid wheat. Crop Sci 27: 445-450.

Halloran MG (1981) Tetraploid wheat crossability with rye (*Secale cereale*). Genetica 55: 191-194.

Harlan JR (1976) Genetic resources in wild relatives of crops. Crop Sci 16: 329-333.

Koba T and Shimada T (1993) Crossability of common wheat with *Aegilops squarrosa*. Wheat Inf Serv 77:7-12

Krolow KD (1970) Untersuchungen über die Kreuzbarkeitz zwischen Weizen und Roggen. Z. Pflanzenzücht 64: 44-72.

O'Donoughue SL and Bennett MD (1994) Comparative responses of tetraploid wheats pollinated with *Zea mays* L. and *Hordeum bulbosum* L. Theor Appl Genet 87: 673-680.

Özgen M (1983) Hybrid seed set in wheat x *Aegilops* crosses. Wheat Inf Serv 56: 9-11.

Miller TE, Reader SM and Gale MD (1983) The effect of homoeologous group 3 chromosomes on chromosome pairing and crossability in *Triticum aestivum*. Can J Genet Cytol 25: 634-64.

Pienaar RDeV and Marais FG (1986) Effect of D-genome chromosome substitutions on hybrid seed development and viability in *T. turgidum* var. *durum* x *S. cereale* crosses. Plant Breeding 97:112-118.

Ramero C and Cuadrado C (1992) Parental genotype influence on seed-set in different wheat x rye crosses. Cereal Res Comm 20(3-4) :193-199

Riley R and Chapman V (1967) The inheritance in wheat of crossability with rye. Genet. Res., 9: 259-267.

Tanner DG and Falk DE (1981) The interaction of genetically controlled crossability in wheat and rye. Can J Genet Cytol 23: 27-32.

Scoles GJ (1983) The effect of rye genotype on wheat-rye crossability and on the development of F1-seed. Can J Genet Cytol 25: 668-670.

Snape JW, Chapman V, Moss J, Blanchard CE and Miller TE (1979) The crossability of wheat varieties with *Hordeum bulbosum*. Heredity 42: 291-298.

Zheng YL, Luo MC, Yen C, Yang JL (1992) Chromosome location of a new crossability gene in common wheat. Wheat Inf Serv 75: 36-40.

Wheat Information Service
Number 83: 7-14 (1996)

Spontaneous translocations in *Triticum araraticum* Jakubz.

T. Kawahara[1], E.D. Badaeva[2], N.S. Badaev[3] and B.S. Gill[2]

[1]Plant Germ-plasm Institute, Faculty of Agriculture, Kyoto University, Mozume, Muko 617, Japan
[2]Wheat Genetics Resource Center, Department of Plant Pathology, Kansas State University, Throckmorton Hall, Manhattan, KS 88506 5502, USA
[3]Centre of Bioengineering, Russian Academy of Sciences, Vavilov Str. 34/5, Moscow 117334, Russia

Summary

Spontaneous reciprocal translocations were identified in *Triticum araraticum* Jakubz. by crossing experiments. Seventy nine strains had the standard chromosome arrangements without translocation. Twenty one strains were classified into 14 chromosome types based on these translocations but 35 strains remained unidentified. Furthermore, karyotypes were analyzed by C-banding on 17 strains representing all the chromosome types. Of 18 translocations, 12 were between G genome chromosomes, five were between the G and A^t genome and one was between A^t genome chromosomes. Within the G genome, 4G and 6G had higher frequencies of their involvement in translocations than the others. The present study revealed the wide structural variation of chromosomes and the high frequency of breakpoints on the G genome in *T. araraticum*.

Key words: *Triticum araraticum*, reciprocal translocation, translocation breakpoint, C-banding

Introduction

Triticum araraticum Jakubz. is a wild tetraploid wheat belonging to the Timopheevi group with A^tA^tGG genome (2n=4x=28). It grows in Eastern Turkey, Northern Iraq, Western Iran and in Transcaucasus, Armenia, Azerbaijan and Nachichevan. It differs cytogenetically from another wild tetraploid wheat, *T. dicoccoides* Körn. with AABB genome. Hybrids of the two species can be easily obtained but they are completely male sterile due to abnormal meiosis. *T. araraticum* is highly polymorphic in morphological characters, resistance to disease and DNA amounts (Tanaka and Sakamoto 1979, Saito and Ishida 1979, Nishikawa et al. 1979, 1988). Thus, it has a high potential as a gene resource for breeding of cultivated wheats.

Analysis of chromosome pairing at meiosis of intraspecific hybrids, as well as karyotype analysis by C-banding, showed that chromosomal rearrangements played an important role in

the formation of intraspecific diversity of *T. araraticum* (Kawahara and Tanaka 1977, 1983, Badaeva et al. 1990). Badaeva et al. (1994) observed karyotypes of 185 accessions by C-banding and described chromosomal divergence in this species. However, several translocations reported earlier could not be detected by C-banding alone due to an insufficient number of marker bands on the A^t genome chromosomes. To clarify the whole pattern of chromosomal rearrangements we synthesized the data obtained from chromosome pairing and C-banding.

Materials and methods

A total of 135 strains of *T. araraticum*, 47 from Turkey, 67 from Iraq, 4 from Iran and 17 from

Table 1. Chromosome types due to spontaneous translocations in different strains of *Triticum araraticum* Jakubz.

Chromosome type	Strain No. (KU-)[a]
T_1	196-2, 1901, 1902, 1903, 1904, 1905, 1906, 1914, 1923, 1924, 1925, 1926A, 1927, 1928, 1929, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1939, 1960, 1963, 1964, 1965, 1969, 1978A, 8456, 8469, 8478, 8491, 8528A, 8529, 8543, 8551, 8561, 8593, 8597, 8616, 8673, 8697, 8700, 8707, 8709, 8711, 8712, 8718A, 8724, 8731, 8735, 8742, 8761, 8770, 8779, 8797, 8799B, 8802, 8819, 8821B, 8822, 8827, 8831, 8873, 8880, 8882, 8884, 8890, 8907, 8912, 8913, 8924, 8926, 8928, 8933, 8940, 8947, 8948
T_2	196-1
T_3	1907A, 1908A, 1909A, 1909B
T_4	8567, 8572, 8732
T_5	8674
T_6	8714A, 8719
T_7	8824A, 8824B
T_8	8784
T_9	1909C
T_{10}	1911
T_{11}	8460
T_{12}	8715
T_{13}	8725
T_{14}	8866
T_{15}	8713
unidentified	1907B, 1908B, 1938, 1943, 1946, 1950, 1958, 1962, 1966, 1967, 1972A, 1979A, 1980A, 1981A, 1982, 1983, 1985, 1986, 1987, 1988, 1990, 8497, 8500, 8514, 8521, 8544, 8601, 8662, 8668, 8720, 8729, 8733, 8734, 8944, 8945

[a] Strain no. of the Plant Germ-plasm Institute, Kyoto University.

Table 2. Multivalents observed among 15 chromosome types of *T. araraticum*

	T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}
T_2	IV													
T_3	IV	VI												
T_4	IV	2 IV	2 IV											
T_5	IV	NO[a]	VI	VI										
T_6	IV	2 IV	2 IV	VI	2 IV									
T_7	IV	2 IV	VI	VI	NO	VI								
T_8	VI	IV+VI	VIII	VI	VIII	VIII	IV							
T_9	2 IV	IV+VI	NO	2 IV	VIII	IV+VI	VIII	VI						
T_{10}	2 IV	3 IV	3 IV	IV+VI	IV+VI	3 IV	NO	IV+VIII	2 IV+VI					
T_{11}	2 IV	3 IV	IV+VI	VIII	IV+VI	IV+VI	NO	VI	X	2 IV+VI				
T_{12}	IV	3 IV	3 IV	NO	IV+VI	2 IV	NO	X	IV+VIII	NO	NO			
T_{13}	2 IV	3 IV	3 IV	3 IV	3 IV	3 IV	3 IV	2 IV+VI	4 IV	2 IV+VI	4 IV	2 IV+VI		
T_{14}	2 IV	IV+VI	3 IV	IV+VI	IV+VI	IV+VI	3 IV	IV+VIII	2 IV+VI	2 IV+VI	2 IV+VI	2 VI	2 IV+VI	
T_{15}	IV+VI	2 VI	2IV+VI	X	2 VI	VI +VI	IV+VIII	XII	IV+X	NO	VI+VIII	VIII	2 IV+VIII	VIII

a NO indicates not observed.

Armenia were used (for strain No., see Table 1). All the materials were maintained by controlled selfing at the Plant Germplasm Institute, Faculty of Agriculture, Kyoto University. Detailed passport data of the materials are listed in the Catalogue of the Institute (Tanaka 1983). These strains were intercrossed and chromosome pairing patterns of the hybrids were observed at first meiotic metaphase (MI) by the acetic-orcein squash method. Seventeen strains were further analyzed by C-banding; chromosome preparation and C-banding technique were described earlier (Badaeva et al. 1994).

Results and discussion

Reciprocal translocations in *T. araraticum* and their geographical distribution.

Based on the analysis of chromosome pairing at first meiotic metaphase of intraspecific hybrids (detailed data not shown), strains were grouped into 15 chromosome types as listed in Table 1. Seventy nine strains were grouped into T1

type and meiosis was normal with 14 bivalents in hybrids within this type. This was regarded as standard chromosome structure because the majority (58.5%) of the strains examined belonged to this group. Types T_2 to T_7 differ from T_1 by one translocation, T_8 to T_{14} differ from T_1 by two and T_{15} had three translocations relative to T_1 (Table 2). Thirty five strains were tentatively classified as unidentified. They have one or two translocations relative to T_1 but the chromosome type was not determined due to the lack of several cross combinations with other chromosome types.

Table 3 summarizes the geographical distribution of each chromosome type. T_1 is found in all the regions where this species was sampled, while the derived types were mostly restricted in a single locality. Types T_2, T_3, T_9 and T_{10} were found in Armenia. The remaining ten types were found in Iraq. Two types, T_4 and T_8, were not restricted to a single site. 8567 and 8572 of T_4 were found in Sulaymaniyah, Iraq, and the third strain, 8732 was collected in Rowanduz, Iraq. The two strains of T_8, 8714A and 8719, were collected at two sites in Rowanduz, Iraq. Apparently, strains with certain structural rearrangements have a wider geographical distribution as also reported by Badaeva et al. (1994). This further suggests that derived types other than T_4 and T_8 also are found in two or more localities if more strains of *T. araraticum* are examined.

Identification of chromosomes involved in translocations.

Chromosomes involved in each translocation were estimated from the occurrence of multivalents among 15 translocation types. Chromosomes involved in the translocation between T_1 and T_2

Table 3. Geographical distribution of chromosome types in *T. araraticum*

Country /Region	No. of strains	Chromosome type														
		T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}	T_{15}	unidentified
Armenia	17	8	1	4	0	0	0	0	0	1	1	0	0	0	0	0	2
Turkey																	
Hozat	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Silvan	20	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Mardin-Midyat	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Maras-Gaziantep	24	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	18
Iraq																	
Amadiyah	14	11	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0
Rowanduz	22	11	0	0	1	0	2	0	1	0	0	0	1	1	0	1	4
Koi Sanjaq	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sulaymaniyah	25	13	0	0	2	1	0	0	0	0	0	1	0	0	0	0	8
Iran	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Total	135	79	1	4	3	1	2	2	1	1	1	1	1	1	1	1	35

Table 4. Chromosome classification of translocations in *T. araraticum*

Chromosome type	Origin	No. of translocations	Chromosome classification[a]	
			pairing data	pairing and banding data
T_1	Iran, Iraq Turkey, Armenia	0	Standard type	Standard type
T_2	Armenia	1	1-2	1G-5G (1GS:5GL+5GS:1GL)[b]
T_3	Armenia	1	1-3	1G-2G (1GS:2GL+2GS:1GL)
T_4	Iraq	1	4-5a	4G-6Ga (4GS:6GL+6GS:4GL)
T_5	Iraq	1	1-5	1G-4G (1GS:4GL+4GS:1GL)
T_6	Iraq	1	4-6a	6G-7Ga (6GS:7GL+7GS:6GL)
T_7	Iraq	1	3-4	2G-6G (2GS:6GL+6GS:2GL)
T_8	Iraq	2	3-4.4-5b	2G-6G. 4G-6Gb (2GS:6GL+4GS:6GS+2GL:4GL)
T_9	Armenia	2	1-3, 4-5b	1G-2G, 4G-6Gb (1GS:2GL+2GS:1GL, 4GS:6GS+4GL:6GL)
T_{10}	Armenia	2	5-8, 9-10	$2A^t$-4G, A^t_1-3G ($2A^tS$:4GS+$2A^tL$:4GL, -)
T_{11}	Iraq	2	3-4, 5-11	A^t_2-4G, 2G-6G (- , 2GS:6GL+6GS:2GL)
T_{12}	Iraq	2	4-6b, 5-x (x=8 or 9)	3G-4G, 6G-7Gb (3GS:4GS+3GL:4GL, -)
T_{13}	Iraq	2	7-x, 12-13	A^t_3-A^t_4, $5A^t$-3G (- , 3GS:$5A^tL$+$5A^tS$:3GL)
T_{14}	Iraq	2	2-5, 6-7	$5A^t$-7G, 4G-5Ga ($5A^tS$:7GS+$5A^tL$:7GL, 5GL-4GS:4GL)
T_{15}	Iraq	3	2-5, 4-6b.4-x	3G-6G.6G-7Gb, 4G-5Gb (3GS:6GS+3GL:6GL, - , 4GS:5GS+4GL:5GL)

a Correspondence of chromosomes are as follows; 1=1G 2=5G 3=2G, 4=6G, 5=4G, 6=7G, 7=$5A^t$, 8=$2A^t$, 9=x=3G, 10=A^t_1, 11=A^t_2, 12=A^t_3 and 13=A^t_4.

b Structures of the translocation are indicated in parentheses. Dash indicates arm combination could not be detected by banding.

were numbered as 1 and 2. Chromosomes of other translocations were numbered successively based on the presence or absence of common chromosomes involved in translocations as summarized in Table 4. For example, T_2 and T_3 have one translocation relative to T_1, and forms a sexivalent in hybrids between them (Table 2). Thus translocations of these two types share a pair of chromosomes in common. This shared pair of chromosomes was arbitrarily assumed as 1 and the translocation of T_3 assigned as 1 and 3. In some cases, two or more translocations occurred independently on the same chromosome pair. T_4 have 4-5 translocation and T_8 have two translocations, 3-4 and 4-5. If these two types share a common 4-5 translocation, a quadrivalent will be observed at MI in the hybrid $T_4 \times T_8$. However, since a sexivalent was found we concluded that the 4-5 translocation carried by the two types had a different origin.

Karyotypes of 17 strains representing 15 chromosome types were further analyzed by C-banding. Chromosomes were identified according to the genetic nomenclature (Badaeva et al. 1991, Gill et al. 1991). By combining two types of data, pairing and banding, it was possible to identify chromosomes involved in these translocations completely (Table 4). However, only two chromosomes, $2A^t$ and $5A^t$, were identified genetically in the A genome because others lacked marker bands. Then, the remaining four A^t chromosomes were tentatively numbered from A^t_1 to A^t_4.

Pattern of chromosomal rearrangements in *T. araraticum*.

Since the chromosomes involved in spontaneous translocations have all been identified, we can determine the patterns of chromosomal rearrangements in *T. araraticum*. Eighteen different translocations were identified from the chromosome pairing of intraspecific hybrids and C-banding. Therefore these translocations are assumed to represent a random sample of entire structural rearrangements. The 4G chromosome was included in 8 translocations, 6G in 6 followed by 3G (4), 1G, 5G and 7G (3). 2G and $5A^t$ were involved in two different translocations and $2A^t$, A^t_1, A^t_2, A^t_3 and A^t_4 in one translocation, respectively. Differences in the number of breakpoints on each chromosome would reflect structural variability of respective chromosomes. Apparently, chromosomes of the G genome are more frequently included in translocations (29 breakpoints) while the A^t genome chromosomes are included in 7 translocations. The present findings confirm those reported earlier (Badaeva et al. 1994) demonstrating the difference in variability among chromosomes and between the two genomes, A^t and G. Thus the G genome chromosomes are three to four times more variable than the A^t genome chromosomes. This may be caused by the higher amount of heterochromatin which increases the probability of chromosome breaks and consequently the frequencies of chromosomal aberrations as was suggested by Badaeva et al. (1994).

Furthermore, such a high variability of the G genome chromosome has great implications in the evolutionary process of this species. Two second genomes of tetraploid wheats, B and G, are assumed to have originated from some species of the section Sitopsis of genus *Aegilops*, most likely from *Ae. speltoides* (Sarker and Stebbins 1956, Shands and Kimber 1973, Tanaka et al. 1978, Tsunewaki 1989, Dvorák and Zhang 1990). In the initial stage of tetraploid formation, raw amphidiploid AASS would have formed various progenies with a wide range of chromosomal

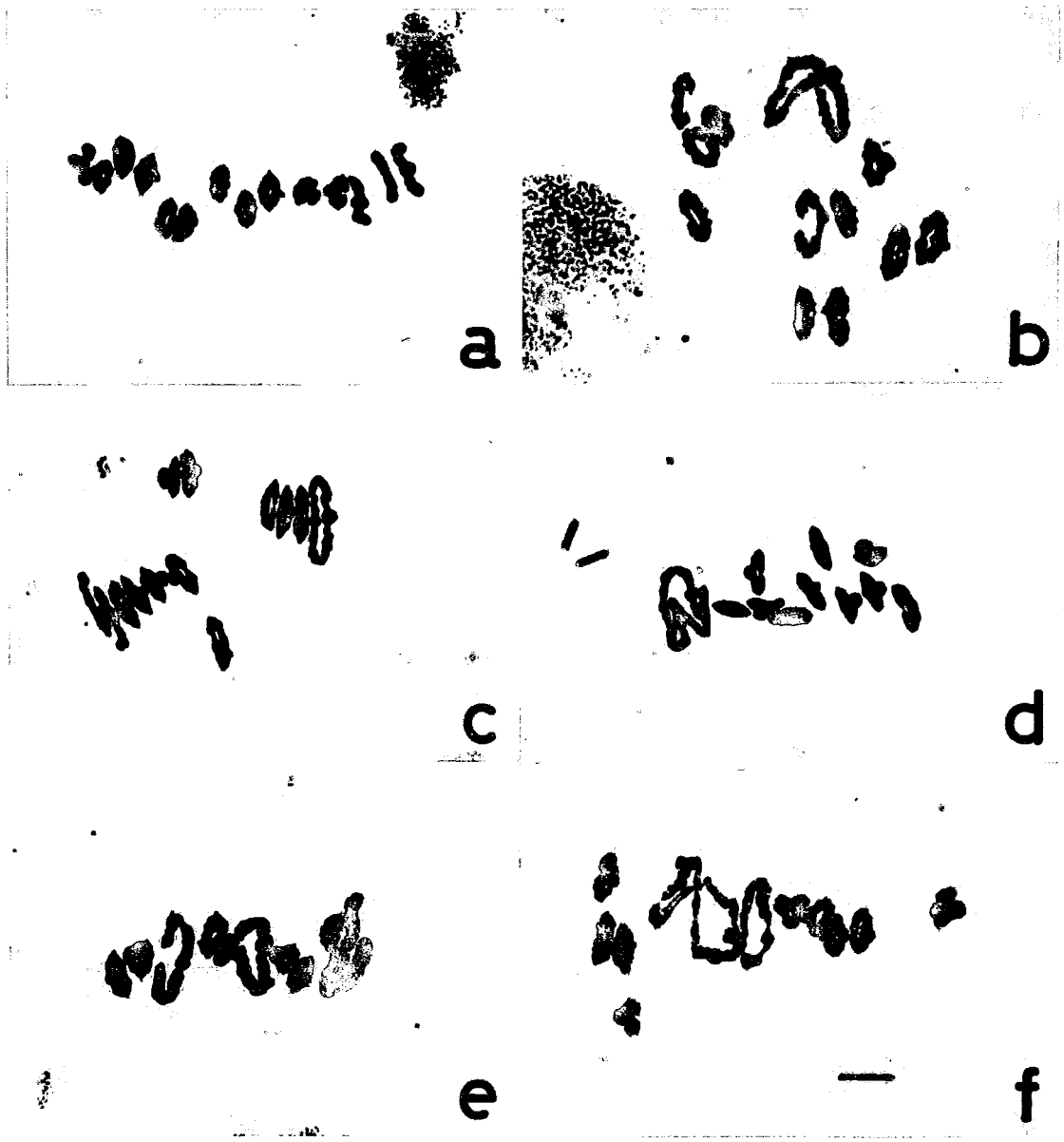

Fig. 1. Chromosome pairing at MI in hybrids among chromosome types in *T. araticum* (bar=10μm), a: 14II in 8731 x 107-1(*T. timopheevi*) (T_1 x T_1), b:11II + 1VI in 8824A x 8719(T_7 x T_6), c: 10II + 2 IV in 8572 x 196-1 (T_4 x T_2), d: 10 II + 1 VIII in 1908A x 8784 (T_3 x T_8), e: 7 II + 2 IV + 1 VI in 8866 x 8725 (T_{14} x T_{13}), f: 9 II + 1 X in 8732 x 8713 (T_4 x T_{15})

rearrangements, in which rearrangements including the S genome chromosomes occurred more frequently. From this wide array of recombinants, better adapted types would be selected. The degree of chromosomal rearrangements was so high in S genome that we could not detect high homoeology between S and G genomes. Stable A genome chromosomes would serve as a genetic buffer in this chromosome repattering stage and we can easily detect high homoeology between A genome of diploid wheat and A^t genome. During this process of chromosome repattering, species specific translocations of $6A^t$-1G-4G (Jiang and Gill 1994) would have been fixed. Thus the G genome chromosomes played a major role in the polyploid formation and adaptation process in *T. araraticum*.

References

Badaeva ED, Boguslavsky RL, Badaev NS and Zelenin AV (1990) Intraspecific chromosomal polymorphism of *Triticum araraticum* (Poaceae) detected by C-banding technique. Pl Syst Evol 169:13-24.

Badaeva ED, Boguslavsky RL, Badaev NS, Kalinina NP and Shkutina FM (1991) General features of chromosome substitutions in *Triticum aestivum* x *T. timopheevi* hybrids. Theor Appl Genet 82: 227-232.

Badaeva ED, Badaev NS, Gill BS and Filatenko AA (1994) Intraspecific karyotype divergence in *Triticum araraticum* (Poaceae). Pl Syst Evol 192: 117-145.

Dvorák J and Zhang HB (1990) Variation in repeated nucleotide sequences sheds light on the phylogeny of the wheat B and G genomes. Proc Nat Acad Sci (USA) 87: 9640-9644.

Gill BS, Friebe B and Endo TR (1991) Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat (*Triticum aestivum*). Genome 34: 830-839.

Jiang J and Gill BS (1994) Different species-specific chromosome translocations in *Triticum timopheevi* and *T. turgidum* support diphyletic origin of polyploid wheats. Chromosome Res 2: 59-64.

Kawahara T and Tanaka M (1977) Six chromosome types in *Triticum araraticum* Jakubz. different with reciprocal translocations. Jpn J Genet 52: 261-267.

Kawahara T and Tanaka M (1983) Chromosomal interchanges and the evolution of the B and G genomes. Proc 6th Int Wheat Genet Symp Kyoto: 977-981.

Nishikawa K, Furura Y, Kudo S and Ujihara K (1979) Differentiation of tetraploid wheat in relation to DNA content of nucleus and α-amylase isozymes. Rep Plant Germ-plasm Inst Kyoto Univ 4:30-38.

Nishikawa K, Furuta Y and Kudo S (1988) Genetic studies of α-amylase isozymes in wheat. VI. Variation and differentiation in tetraploid wheat. Jpn J Genet 63: 425-434.

Saito H and Ishida N (1979) Speciation of wild tetraploid wheats concerning susceptibility to leaf rust. Rep. Plant Germ-plasm Inst Kyoto Univ 4: 18-22.

Sarker P and Stebbins GL (1956) Morphological evidence concerning the origin of the B genome in wheat. Amer J Bot 43: 297-304.

Shands H and Kimber G (1973) Reallocation of the genomes of *Triticum timopheevi*. Proc 4th Int Wheat Genet Symp Missouri: 101-108.

Tanaka M (ed.) (1983) Catalogue of *Aegilops-Triticum* germ-plasm preserved in Kyoto University. Plant Germ-plasm Inst Kyoto Univ Kyoto. pp 1-179.

Tanaka M, Kawahara T and Sano J (1978) The evolution of wild tetraploid wheats. Proc 5th Int Wheat Genet Symp New Delhi:73-80.

Tanaka M and Sakamoto S (1979) Morphological and physiological variations in wild tetraploid wheats collected from the Zagros Mountains. Rep Plant Germ-plasm Inst Kyoto Univ 4: 12-17.

Tsunewaki K (1989) Plasmon diversity among *Triticum* and *Aegilops* species and its implication in wheat evolution. Genome 31: 143-154.

Wheat Information Service
Number 83: 15-18 (1996)

Maintenance of haploid genome of *Agropyron junceum* in wheat

H.C. Sharma

Department of Agronomy, Purdue University, West Lafayette, IN 47907, U.S.A.

Summary

Gametocidal chromosomes have been reported in wide crosses in wheat (*Triticum aestivum*, 2n=AABBDD=42), and asymmetric genome reduction is known to occur in polyploids. Here I report on the maintenance of 7 univalents, like a gametocidal genome, of *Agropyron junceum* (syn. *Thinopyrum bessarabicum*, 2n=JuJu=14) which resisted elimination for several generations of selfing of the backcross-1 (BC_1) of a wheat x *A. junceum* hybrid. The BC_1 plant had 49 chromosomes. The chromosome number in BC_1F_2 varied from 45 to 52. Of the 12 BC_1F_3 seeds analyzed from a 49-chromosome BC_1F_2 plant, 9 had 49 and 3 had 49+t chromosomes. Among the 28 BC_1F_4 seeds studied from a 49-chromosome BC_1F_3 plant, only one plant had 46+2t while the rest all had 47+t - 51 chromosomes. When BC_1F_5 seeds of the bulk harvest from the BC_1F_4 plants having 49+t or 49+2t chromosomes were scored, they had 48-49+2t chromosomes. The occurrence of plants with 49 chromosomes up to several generations of selfing shows that the 7 chromosomes of *A. junceum* have a selective advantage. It is likely that these chromosomes are being transmitted through only female gametes. Even though, the phenomenon of directed movement of the univalents cannot be ruled out, the study provides an example where the whole genome from a diploid alien species is retained in wheat due to preferential transmission like individual gametocidal chromosomes.

Introduction

Gametocidal chromosomes have been reported in wide crosses of wheat (*Triticum aestivum*) with alien species. These chromosomes are preferentially transmitted and maintained from generation to generation. Such chromosomes have been reported in various species of *Aegilops* (Maan 1975, Endo 1982, Endo and Tsunewaki 1975, Miller et al. 1982, Finch et al. 1984, Tsujimoto and Tsunewaki 1984). A chromosome of *Agropyron elongatum* (Kibirige-Sebunya and Knott 1983) and a chromosome segment of *A. distichum* (Marais 1990) have also been reported to be gametocidal.

Asymmetric genome reduction, rather than a random loss of chromosomes, is known to

occur in allopolyploids, in hybrids of polyploids with other species as well as in artificially induced amphiploids (Gottschalk 1971). Ladizinsky and Fainstein (1978) described a case of genome partition in a hybrid of hexaploid oat (2n= 42) x wild tetraploid oat (2n=28) where a backcross plant with 42 chromosomes produced a tiller with 14 chromosomes which showed chromosome pairing of 6-7 bivalents. This meant that most probably a set of homologous genomes had split to give rise to this tiller. Dewey (1980) gave examples in grasses where higher ploidy amphiploids spontaneously stabilized at the octoploid level indicating loss of some genomes and retention of some others. Backcross-2 (BC_2) data for *Agropyron ciliare* (2n=28) x wheat hybrids, and for *A. trachycaulum* (2n=28) x wheat hybrids showed a high proportion of 49-chromosome plants having 7-8 univalents (Sharma and Gill 1983a), indicating splitting of genomes of the *Agropyron* species. The 49-chromosome plants likely arose from the fusion of 28 chromosome (21 wheat+7 *Agropyron*) female gametes and 21 chromosome (wheat) male gametes. When Tomar et al. (1995) backcrossed monosomic 5B of wheat x *A. junceum* (2n=14) F_1 to wheat, the chromosome number among BC_2 plants varied from 38 to 48, and the mean number of univalents in a 48-chromosome plant studied was 7. This chromosome number was attributed to meiotic non-reduction in the hybrid and backcrosses. Likewise, partial amphiploids from wheat x segmental polyploid *Agropyron* species backcrosses have been recovered due to fusion of unreduced gametes of the hybrids with wheat gamete (see Sharma et al. 1987).

Perpetuation of 7 univalent chromosomes, like a gametocidal genome, of *A. junceum* which resisted elimination for several generations of selfing of the BC_1 of a wheat x *A. junceum* hybrid is reported.

Materials and methods

Wheat cv. Chinese Spring (CS) (2n=AABBDD) x *A. junceum* (j) (syn. *Thinopyrum bessarabicum*, 2n=14, JuJu) F_1 hybrids and their BC_1 to CS were described earlier (Sharma and Gill 1983b). Both wheat and *A. junceum* parents had normal chromosome pairing, mean chromosome pairing being 0.28 I+20.86 II, and 7 II, respectively. As expected, the hybrids had 2n = 28. The level of chromosome pairing in the ABDJu F_1 hybrids provided no evidence of homologous or homoeologous pairing: I=26.23, rod II=0.83, ring II=0.04, III=0.01. Among the nine BC_1 plants studied, six had 49, one had 48 and two had 46 chromosomes. Chromosome pairing in a 49-chromosome BC_1 plant (plant no. CS x j x CS-7) was 5-8 I (mean=6.83), 1-4 rod II (mean=2.50), 16-20 ring II (mean=18.33) and 0-1 III (mean=0. 17). Self (BC_1F_2) seeds from this BC_1 plant were followed in the present study. Chromosome counts were made from root-tips of germinated seeds. For chromosome pairing studies, spikes were fixed in 1:3 acetoalcohol and squashed in 1% acetocarmine.

Results and discussion

Of the 92 BC_1F_2 seeds set on selfing the BC_1 plant CS x j x CS-7, 2n = 49, the chromosome number of 14 seeds was studied. One had 45, four had 46, three had 47, two had 48, two had variable (44-48), one had 49, and one had 52 chromosomes. Twelve BC_1F_3 seeds from the 49-chromosome BC_1F_2 plant were analyzed. Of these, nine had 2n=49 and three had 2n=49+t (t= telocentric, classification of broken chromosomes into telo or fragment is arbitrary). Twenty-eight BC_1F_4 seeds from one of these BC_1F_3 plants (plant # CS x j x CS-7self-2self-1, 2n=49) analyzed had a chromosome composition: 1 = 46+2t, 4= 47+t, 3 = 47+2t, 1 = 48, 5 = 48+t, 5 = 48+2t, 3 = 49+t, 2 = 49+2t, 1 = 50, 2 = 50+t and 1 = 51. When ten BC_1F_5 seeds of the bulk harvest from the three BC_1F_4 plants with 49+t chromosomes were scored, five had 48, two had 48+t and the other three had 49+t chromosomes. Similarly, when three BC_1F_5 seeds of the bulk harvest from the two BC_1F_4 plants having 2n = 49+2t were scored, all had 49+2t chromosomes.

From these results, it is evident that the chromosome number in the wheat x *A. junceum* derivatives was maintained throughout several generations of selfing, and that the *Agropyron* chromosomes could not be eliminated. The occurrence of plants with 49 chromosomes up to several generations of selfing shows that the 7 chromosomes of *A. junceum* have a selective advantage in perpetuation through the gametes from generation to generation. Furthermore, there is evidence of chromosome breakage. Genes on gametocidal chromosomes have been found to cause breakage of chromosomes (Feldman and Strauss 1983, Tsujimoto and Noda 1988). Meiotic behavior observed in 4 cells of a 49-chromosome BC_1F_3 plant had an average of 6.50I (range=5-7), 2.75 rod II (range=2-3) and 18.50 ring II (range= 18-19) which remained about the same as in BC_1. It appears, therefore, that the pair construction of *A. junceum* chromosomes has not taken place in spite of repeated selfing. It is, therefore, likely that these chromosomes are being transmitted through only female gametes. The study provides an example where the whole genome from a diploid alien species is retained due to the preferential transmission like individual gametocidal chromosomes. Retention of all *A. junceum* chromosomes solely due to gametocidal effect dictates that these chromosomes must have different non-interacting gametocidal genes. In addition, fertility of the female gametes must be extremely low due to the very low frequency of gametes carrying all the Ju genome chromosomes considering random segregation of univalents. The actual data on fertility were not recorded but casual observations indicated that it was not extremely low. Thus, the phenomenon of directed movement of the seven univalents to one of the cells that forms embryo sac could not be ruled out.

Acknowledgements

This work is a contribution from the Purdue Agricultural Programs, West Lafayette, IN 47907. The research was supported in part by the USAID/PSTC Grant No. 5600-G-00-2032-0, and by Public Varieties of Indiana. Purdue Agric. Exp. Stn. Journal No. 14998.

References

Dewey DR (1980) Some applications and misapplications of induced polyploidy to plant breeding. In: Polyploidy: Biological relevance. Ed: Lewis WH, pp.445-470, Plenum Publishing Co, New York.

Endo TR (1982) Gametocidal chromosomes of three *Aegilops* species in common wheat. Canad J Genet Cytol 24: 201-206.

Endo TR and Tsunewaki K (1975) Sterility of common wheat with *Aegilops triuncialis* cytoplasm. J Hered 66: 13-18.

Feldman M and Strauss I (1983) A genome restructuring gene in *Aegilops longissima*. Proc 6th Int Wheat Genet Symp, Kyoto Japan pp.309-314.

Finch RA, Miller TE and Bennett MD (1984) "Cuckoo" *Aegilops* addition chromosome in wheat ensures its transmission by causing chromosome breaks in meiospores lacking it. Chromosoma 90: 84-88.

Gottschalk W (1971) The phenomenon of "asymmetric genomic reduction". J Indian Bot Soc Golden Jubilii 50A: 308-317.

Kibirige-Sebunya I and Knott DR (1983) Transfer of stem rust resistance to wheat from an *Agropyron* chromosome having gametocidal effect. Canad J Genet Cytol 25:215-221.

Ladizinsky G and Fainstein R (1978) A case of genome partition in polyploid oats. Theor Appl Genet 51: 159-160.

Maan SS (1975) Exclusive preferential transmission of an alien chromosome in common wheat. Crop Sci 15: 287-292.

Marais GF. (1990) Preferential transmission in bread wheat of chromosome segment derived from *Thinopyrum distichum* (Thunb.) Love. Plant Breed 104:152-159.

Miller TE, Hutchinson J and Chapman V (1982) Investigation of a preferentially transmitted *Aegilops sharonensis* chromosome in wheat. Theor Appl Genet 61:27-33.

Sharma HC and Gill BS (1983a) New hybrids between *Agropyron* and wheat. 3. Backcross derivatives, effect of *Agropyron* cytoplasm and production of addition lines. Proc 6th Int Wheat Genet Symp, Kyoto Japan pp. 213-221.

Sharma HC and Gill BS (1983b) New hybrids between *Agropyron* and wheat. 2. Production, morphology and cytogenetic analysis of F1 hybrids and backcross derivatives. Theor Appl Genet 66:111-121.

Sharma HC, Aylward SG and Gill BS (1987) Partial amphiploid from *Triticum aestivum* x *Agropyron scirpeum* cross. Bot Gaz 148: 258-262.

Tomar SMS, Vari AK and Kochumadhavan K (1995) Meiotic studies in an intergeneric hybrid between *Triticum aestivurn* and *Thinopyrum bessarabicum* and their backcross progenies. Indian J Genet Pl Breed 55: 154-159.

Tsujimoto H and Noda K. (1988) Chromosome breakage in wheat induced by the gametocidal gene. Proc 7th Int Wheat Genet Symp , Cambridge UK pp.455-460.

Tsujimoto H and Noda K (1990) Deletion mapping by gametocidal genes in common wheat: position of speltoid suppressor (*Q*) and beta-amylase (*β-Amy-A2*) genes on chromosome 5A. Genome 33: 850-853.

Tsujimoto H and Tsunewaki K (1984) Gametocidal genes in wheat and its relatives. I. Genetic analyses in common wheat of a gametocidal gene derived from *Aegilops speltoides*. Can J Genet Cytol 26: 78-84.

Wheat Information Service
Number 83: 19-27 (1996)

Genetics and interrelationships of grain yield and its related traits in bread wheat under irrigated and rainfed conditions

S.S. Dhanda[1] and G.S. Sethi[2]

[1]Department of Plant Breeding, CCS Haryana Agricultural University, Hisar, India
[2]Department of Plant Breeding and Genetics, H.P. Agricultural University, Palampur (H.P.) India

Summary

Genetic control of yield and its related traits in nine generations (P_1, P_2, F_1, F_2, F_3, B_1, B_2, B_{1s} and B_{2s}) under irrigated and rainfed conditions were investigated in a cross of two contrasting wheat varieties, CPAN 1992 and Kharchia 65. The mean performance of all the characters was considerably lower under rainfed (E_2) conditions than under irrigated (E_1) conditions. Although both the additive and dominance components were involved in the expression of all the traits under both the environments, yet the dominance component, in general, suffered more than the additive component under rainfed conditions. Additive component appeared to be the main source of genetic variance under both environments. Dominance gene effects were also significant and more pronounced in some characters, but these were not stable in controlling the inheritance except grain yield, tillers/plant and days to maturity only under rainfed conditions. Epistasis was observed for all these traits under both the environments. Duplicate types of epistasis, in general, prevailed for all the characters under both the environments. The estimates of heritability and genetic advance were higher under irrigated than under rainfed conditions which may be due to better expression of genotypes under normal conditions. The estimates of heritability, genetic advance and correlation coefficients revealed that tillers/plant and biological yield were important for yield improvement under E_1 and E_2, respectively, whereas the harvest index was important under both kinds of situations.

Introduction

Water supply is restricted in many parts of the world and productivity in these areas can only be increased by the development of crops that are well adapted to dry conditions. Since yield potential has a net effect on yield performance under drought stress, the ideotype must be drought resistant and of a reasonably high yield potential. Development of cultivars for drought resistance thus requires identification of potential drought resistant traits and their transfer to agronomically

acceptable varieties. Blum et al. (1982) have also argued that a knowledge of influence of drought resistant character on yield is not essential. Rather if a particular morphological or physiological character can be identified and shown to improve the drought resistance of the crop, and if the character and yield are separately inherited, incorporation of that character into a high yielding variety should improve the performance of the crop under drought stress.

Thus genetic improvement of wheat requires exploitation of genetic variation for drought resistance and its utilization in breeding programmes. The present investigations involving nine generations (P_1, P_2, F_1, F_2, F_3, B_1, B_2, B_{1s} and B_{2s}) were undertaken to study the gene action, correlations, heritability and genetic advance under irrigated and rainfed conditions.

Materials and methods

The experimental materials were developed from a cross involving two varieties of bread wheat, Kharchia 65 and CPAN 1992. Kharchia 65 is drought resistant and tall in height, whereas CPAN 1992 is drought susceptible, medium in height and well adapted agronomically. The F_1 was backcrssed in 1991-92 to each of the parents (P_1 and P_2) to produce the first backcross generations B_1 ($P_1 \times F_1$) and B_2 ($P_2 \times F_1$). Seeds produced by self pollination of F_1, F_2, B_1 and B_2 generations were used to produce F_2, F_3, B_{1s} and B_{2s} generations, respectively. The final experiment was conducted during 1992-93 with the experimental materials comprising P_1, P_2, F_1, F_2, F_3, B_1, B_2, B_{1s} and B_{2s} generations under irrigated and rainfed conditions. The study was carried out at the experimental farm of the CCS Haryana Agricultural University, Hisar which is situated at 29°1'N latitude and 75°46'E longitude and 215m above msl. In rainfed experiment only presowing irrigation was applied to ensure proper germination, whereas four irrigations were applied to irrigated experiment during growth period. The total rainfall during the growth period was 40 mm which was sufficient to maintain moisture stress conditions under field conditions in this area. The experiment was laid out in compact family block design with three replications. The row length was kept to 2 m, each row included 20 plants spaced 10 cm apart. Rows were spaced 30 cm apart. All measurements were taken on an individual plant basis. The non-segregating generations, i.e., parents and F_1 were grown in single rows, B_1 and B_2 in 2 rows, B_{1s} and B_{2s} in 8 rows, and F_2 and F_3 in 10 rows. Data were collected on five plants from each row for days to heading, number of tillers, days to maturity, biological yield, grains/ear, 100-grain weight, grain yield and harvest index. The statistical analysis for generation means and components of variance was done according to Mather and Jinks (1982). The phenotypic correlations among all the variables were computed from F_2 generation by the method suggested by Sidwell et al. (1976). Heritability in narrow sense (h^2ns) was estimated following Warner (1952). Expected gain from selection (GS) was calculated following Allard (1960), as G.S. = $K\sigma_p h^2ns$, where K is the selection differential in standard units, σ_p is the phenotypic standard deviation (estimated as the square root of the within-plot variance for F_2 population), and h^2ns is defined as above.

Table 1. Mean performance of parents for various characters under irrigated (E_1) and rainfed (E_2) conditions in wheat

Parent	Environment	Character							
		Grain yield/ plant	Tillers/ plant	100 grain weight	Grains/ spike	Days to heading	Days to maturity	Harvest index	Biological yield/plant
CPAN 1992	E_1	14.1±0.60	6.6±0.41	4.4±0.05	50.2±1.78	85.6±0.84	140.1±1.48	47.5±1.20	36.1±0.80
	E_2	3.1±0.29	3.0±0.36	2.9±0.08	23.2±1.22	70.2±0.80	114.5±1.06	21.6±0.85	14.5±0.93
Kharchia 65	E_1	10.1±0.69	7.5±0.52	3.9±0.07	39.2±0.99	92.8±0.89	147.2±0.92	39.1±0.98	21.3±0.99
	E_2	5.7±0.38	6.0±0.40	2.7±0.05	26.7±1.42	79.1±0.81	129.5±1.40	30.6±0.95	18.8±0.70

Results and discussion

Mean performance of parents

Performance of parental means under both irrigated (E_1) and rainfed (E_2) environments are given in Table 1. Considerable variation was observed in the mean values among the parents under E_1 and E_2 for all the characters. The mean values under irrigated conditions were considerably higher than that under moisture stress conditions. CPAN 1992 showed significantly higher mean values than Kharchia 65 for all the characters except tillers/plant under irrigated (E_1) conditions, whereas Kharchia 65 was significantly superior to CPAN 1992 for all the traits under moisture stress (E_2) conditions.

Gene action

The joint scaling tests indicated that both the additive-dominance model and digenic epistatic model were inadequate to explain the nature of the gene action for all the characters in either of the environments (Table 2). This may be due to influence of the higher order interactions and/or linkage among the genes governing the inheritance of these traits, but further testing of data was not feasible due to the limited number of generations. Both additive and dominance gene effects played an important role in determining inheritance of majority of the traits under both environments. The magnitudes of dominance gene effects prevailed over their respective additive gene effects for all the characters under irrigated conditions (E_1), and indicated that the dominance gene action was more important under E_1 for all the characters. But under rainfed conditions (E_2) the dominance gene action was more pronounced only for grain yield/plant, tillers/ plant, days to heading and maturity, and biological yield,

Table 2. Estimates of gene effects for various characters under irrigated (E_1) and moisture stress (E_2) conditions in wheat

Character	Environment	Parameter							
		m	d	h	i	j	l	χ^2 at 6 df	χ^2 at 3 df
Grain yield/ plant	E_1	7.6*±0.6	2.0*±0.1	6.0*±2.0	4.5*±0.6	3.0*±0.9	-0.5±1.6	168.8*	25.9*
	E_2	1.8*±0.6	-0.3±0.2	10.6*±2.1	2.6±0.7	-4.1*±1.0	7.1*±1.6	53.9*	21.6*
Tillers/ plant	E_1	7.4*±0.6	0.1±0.2	-7.9*±2.1	-0.1±0.6	-3.3±1.9	8.4*±1.7	57.5*	8.1*
	E_2	3.2*±0.4	1.4*±0..2	7.1*±2.0	1.1*±0.5	2.7*±1.2	-4.4*±1.7	37.9*	22.9*
100-grain weight	E_1	37.2*±1.1	10.1*±0.2	38.3*±3.3	11.9*±1.1	3.5*±1.3	-21.3±2.4	256.6*	25.5*
	E_2	25.7*±0.5	1.7*±0.2	3.4±1.8	-0.7±0.5	6.4*±1.0	3.7*±1.4	64.8*	8.3*
Grains/ spike	E_1	37.1*±1.0	10.0*±0.2	28.7*±3.3	11.0*±1.1	2.4±1.3	-21.2*±2.4	265.6*	25.5*
	E_2	26.6*±0.4	-1.6*±0.1	-3.4±1.7	-0.7±0.5	-6.4*±0.9	3.6*±1.4	64.8*	8.3*
Days to heading	E_1	91.1*±0.8	3.3*±0.5	-11.3*±3.2	-1.8±0.9	13.2*±2.0	9.6*±2.8	89.2*	38.7*
	E_2	69.4*±0.5	4.9*±0.2	16.4*±2.2	5.7*±0.6	15.7*±1.3	10.0*±1.7	686.4*	228.6*
Days to maturity	E_1	148.0*±0.5	3.4*±0.2	-20.2*±2.3	-4.1*±0.5	7.7*±1.4	21.3*±1.9	248.2*	24.9*
	E_2	115.1*±0.6	6.0*±0.4	20.5*±2.4	6.4*±0.7	9.0*±1.5	-12.2*±1.9	105.4*	13.4*
Harvest index	E_1	44.6*±1.3	4.0*±0.2	-9.2*±5.1	1.2±5.1	2.0±2.2	7.6*±3.6	24.2*	14.0*
	E_2	24.0*±1.0	5.2*±0.3	2.9±3.5	2.5*±1.0	3.6*±1.0	3.9±2.8	90.6*	52.5*
Biological yield/plant	E_1	16.8*±0.8	7.8*±0.2	20.1*±3.1	11.9*±0.8	18.5*±1.8	-6.7*±2.5	721.5*	143.8*
	E_2	13.5*±0.7	1.9*±0.2	26.4*±2.6	3.2*±0.7	19.4*±1.4	-19.3*±2.2	620.9*	295.4*

*Significant at 5% level of probability

while additive for the remaining traits. This implied that selection in later segregating generations would be effective especially under irrigated conditions. These results are also in agreement with those of Tripathi et al. (1983) and Redhu (1988). As the results are based on mean performance and may be influenced by cancellation effects, the information generated through variance approach should also be considered.

Considering the interactions, it was revealed that the majority of the characters were largely influenced by dominance x dominance (l) type of gene effects for all the characters. A greater portion of genetic variability can be attributed to dominant genetic effects under both the environments. The signs of h and l components were screened for all characters where both the components were significant. It was noted that the h and l components possessed opposite signs for majority of the characters irrespective of the environments, thereby suggesting that difficulty would be encountered in selecting for these characters. The complementary type of interaction for grain yield and days to heading under E_2 also indicated the chances of direct selection for these characters. Gene dispersion was also verified by comparing the magnitude of h and d, and the higher estimates of h than d for majority of the characters indicated that the parents were in dispersion phase and there was an accumulation of dominant parental genes in the hybrids.

The results of components of variances, heritability in narrow sense and genetic advance are shown in Table 3. All the components of variances were significant under both the environments. In addition, the magnitude of variances was, in general, higher under E_1 than under E_2. The lower magnitude of variation under E_2 may be due to suppressed expression of genotypes under stress conditions (Ludlow and Muchow 1990). Degree of dominance indicated that additive gene effects appeared to be the important factor contributing to the genetic control of majority of the characters under both the environments. This does not agrees with the results obtained on the basis of generation mean analysis which may due to cancellation of positive and negative gene effects responsible for dominance at most of the loci. The relative magnitude of degree dominance under E_1 and E_2 revealed that, in general, expression of dominance component suffered more than the additive component under stressed soil. This also agrees with the results obtained from gene effects (Table 2). The estimates of various effects are valid under the assumptions: (i) diploid segregation, (ii) homozygous parents, (iii) absence of multiple alleles, (iv) absence of linkage and (v) no genotype-environment interaction. The first two assumptions are fairly met in wheat population. Multiple alleles arise as a result of mutation. If the individual chosen to be the parents do not exhibit multiple allelism, there is a very remote possibility that multiple alleles will bias the estimates. In addition, there is no available report on multiple alleles in the literature for the characters under study. The remaining assumptions could not be tested. The failure of any assumption may cause bias in estimates. The estimates of effects are expected to be biased due to linkage in the presence of epistasis (Kempthorne 1957).

Heritability estimates were high to moderately high for all the characters except grain yield and tillers/plant under E_1, under E_2, moderately high estimates of heritability were observed for days to heading, moderate for harvest index and biological yield/plant, and low for the remaining traits. The values of expected genetic advance show possible gain from selection as per cent increase in the F_3 over the F_2 mean when most desirable 5% (K=2.06) of the F_2 plants are selected.

Table 3. Estimates of components of variances for various characters under irrigated (E_1) and rainfed (E_2) conditions in wheat

Compo-nent	Environ-ment	Character							
		Grain yield/pl.	Tillers/ plant	100 grains weight	Grains/ spike	Days to heading	Days to maturity	Harvest index	Biological yield/plant
Additive (D)	E_1	10.58*±2.54	3.96*±0.18	0.14*±0.06	122.60*±15.40	68.00*±3.30	134.50*±14.51	100.20*±14.51	39.84*±7.32
	E_2	1.32*±0.90	1.66*±0.17	0.04*±0.02	27.38*±3.28	46.02*±2.96	37.20*±13.42	22.80*±8.42	19.74*±6.07
Dominance (H)	E_1	7.52*±3.68	3.84*±0.61	0.10*±0.03	130.12*±16.81	33.36*±5.21	53.40*±6.16	60.32*±14.52	38.48*±3.99
	E_2	2.16*±0.16	4.24*±1.83	0.00±0.00	10.17*±4.74	30.64*±4.05	44.16*±4.78	16.12*±3.96	10.58*±4.22
Environ-ment(E)	E_1	7.24*±0.08	2.48*±0.13	0.04*±0.02	33.13*±4.11	13.48*±0.92	22.72*±1.58	21.47*±2.84	9.48*±0.81
	E_2	2.18*±0.18	1.95*±0.09	0.06*±0.01	22.65*±6.12	9.88*±1.53	24.36*±3.81	11.07*±4.35	8.02*±2.41
Degree of dominance (H/D)	E_1	0.84	0.98	0.85	1.03	0.70	0.63	0.78	0.98
	E_2	1.27	1.59	0.00	0.63	0.81	1.09	0.73	0.73
Heritability (h^2ns)	E_1	36.71	36.53	51.85	48.28	60.91	65.08	57.81	51.06
	E_2	19.52	21.61	33.33	35.09	56.75	34.44	47.50	48.06
Genet.adv. (% of mean)	E_1	28.42	34.35	9.34	21.88	10.76	13.62	27.17	26.18
	E_2	21.88	17.11	6.00	18.13	10.48	4.30	21.69	23.36

*Significant at 5% level of probability

The combined estimates of heritability and genetic advance indicated the scope of selection for biological yield, harvest index, grains/spike and tillers/plant under both the environments. Although, 100-grain weight, days to heading and days to maturity had moderate to high heritability values under both the environments, yet the poor variation in F_2 limited their scope of selection. As majority of these characters are interrelated, therefore, the correlations among the characters should also be considered in the process of selection.

Correlations among characters

In order to identify the suitable plant traits for selection under irrigated and rainfed conditions, the correlation coefficients among various characters were worked out in F_2 generation (Table 4). Grain yield/plant was positively associated with tillers/ plant, harvest index and biological yield under both environments. In addition, plants with higher number of grains/spike were also higher yielders (r=0.17*) under E_1, whereas the plants with high 100-grain weight and early heading type had high yields under E_2. Although direct selection for grain yield could be practised on the basis of correlations especially under rainfed conditions, yet its low heritability, involvement of high magnitude of non-additive variations within and between environments could limit the progress through selection (Blum 1988, Acevedo et al. 1991). Therefore, the selection for the characters having high heritability and relatively simply inherited could be more fruitful than the grain yield alone.

Among yield components, plants having high tillers/plant under E_1 also had high grain yield (r=0.24*), 100-grain weight (r=0.27*), grains/spike (r=0.16*) and harvest index (r=0.22*). Similarly, the plants having high 100-grain weight under E_2 were also high in yield (r=0.19*), harvest index (r=0.18*) and biological yield (r=0.34**). The positive association of 100-grain weight with biological yield under rainfed conditions may be due to the better ability of biological yield to support the kernel growth by stem reserve mobilization under moisture stress conditions (Aggarwal and Sinha 1987, Blum 1989, Bansal and Sinha 1991). However, this trait has considerable heritability, but the limited variation in the progenies may restrict its exploitation through selection in this material. Grains/spike was relatively unimportant character because of its negative correlation with 100-grain weight (-0.23*) under E_1 and, with tillers/plant (-0.17*) under E_2.

Days to heading and days to maturity had, in general, poor correlations under both the environments which may be attributed either to high sampling errors or limited variations in the progenies (Table 3). Biological yield and harvest index appeared to be more important traits under E_2 than under E_1 because of their associations with each other as well as with other variables in terms of magnitude and number. Tanner and Sinclair (1983), Blum et al. (1983) and Turner and Nicholas (1988) have also suggested that the grain yield was strongly dependent on biological yield under water-limited environments.

Thus, the correlation studies indicated that tillers/plant under E_1 and biological yield under E_2 were the important traits for improving the grain yield. Harvest index was appeared to be an important character under both the environments. Gene action studies indicated that these characters were predominantly governed by additive genetic variance with the involvement of

Table 4. Phenotypic correlations among yield and its components under irrigated (E_1) and moisture stress (E_2) conditions

Character	Environ-ment	Tillers/ plant	100-grain wight	Grains/ spike	Days to heading	Days to maturity	Harvest index	Biological yield/plant
Grain yield/plant	E_1	0.24**	0.06	0.17*	-0.15	-0.07	0.27**	0.16**
	E_2	0.25**	0.19*	-0.07	-0.20*	-0.14	0.25**	0.23**
Tillers/plant	E_1		0.27**	0.16*	-0.08	-0.12	0.22**	0.14
	E_2		0.07	-0.17*	-0.10	-0.14	0.23**	0.30**
100-grain weight	E_1			-0.23**	-0.16	-0.10	0.16*	0.05
	E_2			-0.15	0.14	0.12	0.18*	0.34**
Grains/spike	E_1				0.13	0.01	0.19*	0.18*
	E_2				0.08	0.10	0.15	-0.12
Days to heading	E_1					0.31	-0.08	-0.10
	E_2						-0.12	-0.21**
Days to maturity	E_1						-0.28	-0.10
	E_2						-0.05	0.01
Harvest index	E_1							0.13
	E_2							0.16*

* and ** Significant at 5% and 1% level of probability, respectively

dominance and epistatic effects. Therefore, selection would be effective if dominance and epistatic effects are reduced after a few generations of selfing and/or intermating in early segregating generations (Singh et al., 1986). This would not only reassemble the adaptive genes in the population but also increase the population mean and retain greater variability for selection over a longer span of time.

Acknowledgements

The financial assistance given to the first author in the form of Senior Research Fellowship by the Council of Scientific and Industrial Research, New Delhi, towards his Ph.D. thesis is duly acknowledged.

References

Acevedo E, Craufurd PQ, Austin RB and Paraze-Marco (1991) Traits associated with high yield in barley in low rainfed environments. J Agric Sci Cambridge 116: 23-26.

Aggawal PK and Sinha SK (1987) Performance of wheat and triticale varieties in variable soil water management. Field Crop Res 17: 45-53.

Allard RW (1960) Principles of plant breeding. John Wiley & Sons Inc, New York.

Bansal KC, and Sinha SK (1991) Assessment of drought resistance in 2 accessions of *Triticum aestivum* and related species I. Total dry matter and grain yield stability. Euphytica 56: 7-14.

Blum A (1988) Plant breeding of stress environments. CRC Press USA.

Blum A (1989) Breeding methods for drought resistance. In: Plant under stress. Ed. Jones HG, Flowers TJ and Jones MB, Cambridge Univ Press: 197-216.

Blum A, Mayer J and Golzan G (1982) Infrared thermal sensing of plant canopies as a screening technique for dehydration avoidance in wheat. Field Crop Res 5: 137-146.

Blum A, Mayer J and Golzan G (1983) Association between plant production and some morphological components of drought resistance. Plant Cell Environ 6: 219-225.

Kempthorne O (1957) An introduction to genetic statistics. John Wiley & Sons Inc, New York.

Ludlow MM and Muchow RC (1990) A critical evaluation of traits for improving crop yields in water limited environments. Adv Agron 42: 107-153.

Mather K and Jinks JL (1982) Biometrical genetics. Chapman and Hall, London.

Redhu AS (1988) Genetic analysis and selection criteria under salinity in bread wheat. PhD thesis submitted to CCS HAU Hisar, Haryana India (unpubl).

Sidwell RJ, Smith EL and McNew RW (1976) Inheritance and interrelationships of grain yield and selected yield related traits in a hard winter wheat cross. Crop Sci 16: 650-654.

Singh IS, Bhullar GS and Gill KS (1986) Genetic control of grain yield and its related traits in bread wheat. Theor Appl Genet 72: 536-540.

Tanner CB and Sinclair TN (1983) Limitation to efficient water use in crop production. Am Soc Agron,Madison Wisconsin: 1-17.

Tripathi ID, Chandra S and Singh M (1983) Inheritance studies of metric traits in three barley populations under normal and saline-alkali soils. Theor Appl Genet 66: 15-21.

Turner NC and Nicholas NE (1988) Drought resistance of wheat for light textured soil in a mediterranean climate. In: Drought tolerance in winter cereals. Ed. Srivasta JP, Porceddu E, Acevedo E and Varma S, John Wiley & Sons, New York: 203-216.

Warner JN (1952) A method of estimating heritability. Agron J 44: 427-430.

Wheat Information Service
Number 83: 28-30 (1996)

II. Research Information

Screening of spontaneous major translocations in Israeli populations of *Triticum dicoccoides* Körn.

T. Kawahara[1] and E. Nevo[2]

[1]Plant Germ-plasm Institute, Faculty of Agriculture, Kyoto University, Mozume, Muko 617, Japan
[2]Institute of Evolution, University of Haifa, Mt. Carmel, Haifa 31905, Israel

Triticum dicoccoides Körn. is a wild tetraploid species with AABB genome. It is the ancestral species of cultivated Emmer wheats and the progenitor of all hexaploid common wheats. Several studies have shown that spontaneous translocations are common in this species. Kawahara (1987) reported 8 translocations among 46 *dicoccoides* strains from Iran, Iraq, Turkey, Syria and Israel, which have been preserved at the Plant Germ-plasm Institute, Faculty of Agriculture, Kyoto University. Thus, overall frequency of translocations is 0.174 in these samples. Recently, Joppa et al. (1995) studied translocations in 17 populations, 16 from Israel and one from Turkey, and reported a high overall frequency of 0.70. In the present paper, our results on the screening of major translocations in Israeli populations are reported to obtain different estimation of translocation frequency in natural populations.

Total of 127 genotypes representing 10 populations (10 to 16 each) and two genotypes from Mt. Gilboa were examined for presence or absence of translocations. Each genotype was established from the original seed sample by controlled selfing for two or three generations. They were then crossed with tetraploid testers with the standard chromosome structure or hexaploid Chinese Spring that also has the standard AABB genome structure together with the DD genome (Kawahara 1988). Chromosome pairing at meiosis in F_1 hybrids were observed by ordinary squash method stained by aceto-orcein. In most of the hybrids, 33 cells or more were examined but 19 to 21 cells were available in four hybrids.

Of 129 hybrids examined, 70 formed no quadrivalent. 34 hybrids formed quadrivalents at a low frequency, 0.03 to 0.09 per cell, one had a frequency of 0.16 and 23 showed high frequencies from 0.64 to 1.03 (Table 1). Since we found a gap in the frequency of quadrivalents, we determined that a genotype is homozygous for a 'major' translocation when a hybrid with testers forms a quadrivalent at a frequency higher than 0.50. Thus, each of 23 genotypes was regarded to have one spontaneous translocation relative to the standard. The remaining one hybrid formed a quadrivalent and a sexivalent (IV+VI) or a quadrivalent and a quinquevalent (IV+V) per cell. Multivalent frequencies of this hybrid were 0.11 III + 0.84 IV + 0.21V + 0.79VI. This was regarded to be heterozygous for three translocations. In conclusion, one genotype had three translocations in homozygous condition, 23 had one translocation and the remaining 105 had standard

Table 1. Frequency of quadrivalents in the hybrids of *T. dicoccoides* with testers

Location	Genotype															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Qazrin (A)	0.00	0.00	0.00	0.00	0.00	0.09	0.03	0.03	0.00	0.00	0.00	0.00	0.06	0.00	0.03	-[a]
Yehudiyya (B)	0.00	0.00	0.00	0.94	0.00	0.03	0.00	0.06	0.00	0.03	-	-	-	-	-	-
Rosh Pinna (C)	0.00	0.00	0.00	0.94	0.70	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	-	-
Sanhedriyya (E)	0.00	0.16	0.84[b]	0.09	0.06	0.09	0.05	0.06	0.03	0.09	-	-	-	-	-	-
Bet Meir (F)	0.00	1.03[c]	0.09	0.00	0.00	0.00	0.77	0.64	0.03	0.00	-	-	-	-	-	-
Mt. Hermon (G)	0.00	0.00	0.97	0.88	0.85	0.00	0.00	0.03	0.94	1.03[d]	1.00	0.97	-	-	-	-
Tabigha (H)	0.82[e]	0.91	0.00	0.00	0.03	0.00	0.97	0.00	0.00	0.95	0.00	0.03	0.06	0.03	0.00	0.00
Bat Shelomo (I)	0.09	0.91	0.00	0.00	0.03	0.00	0.09	0.03	0.00	0.00	1.00	0.03	0.00	0.97	0.06	-
Taiyiba (J)	0.03	0.00	0.00	0.00	0.00	0.00	0.85	0.00	0.00	0.82	-	-	-	-	-	-
Kokhav Hashahar(K)	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.03	0.00	0.00	0.00	0.00	-
Mt. Gilboa (L)	0.00	0.09	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a - indicates no data.
b 0.11 III + 0.84 IV + 0.21 V + 0.79 VI. This genotype has three translocations.
c One cell had two quadrivalents.
d One cell had no quadrivalent but tow had two quadrivalents.
e 0.09 III + 0.82 IV + 0.03VI.

Table 2. Frequency of major translocations in Israeli populations of *T. dicoccoides*

Location	No. geneotypes observed	No. of translocations	Translocation frequency
Qazrin	15	0	0.000
Yehudiyya	10	1	0.100
Rosh Pinna	14	2	0.143
Sanhedriyya	10	3	0.300
Bet Meir	10	3	0.300
Mt. Hermon	12	7	0.583
Tabigha	16	4	0.250
Bat Shelomo	15	3	0.200
Taiyiba	10	2	0.200
Kokhav Hashahar	15	1	0.067
Mt. Gilboa	2	0	0.000
Total	129	26	0.202

chromosome arrangements.

Frequency of translocations in each population is summarized in Table 2. The frequency varied greatly among populations from 0.00 in Qazrin to 0.583 in Mt. Hermon. Overall major translocation frequency in Israel was 0.202. This value agrees quite well to that reported by Kawahara (1987) but is much lower than the value of 0.70 obtained by Joppa et al. (1995), where the threshold for translocation was 0.04. In order to clarify the cause of this difference, data of seven common populations of the two reports are compared as shown in Table 3. Joppa et al. (1995) considered that quadrivalent frequencies greater than 0.04 represent translocation heterozygotes. According to our present criteria (more than 0.50), translocation

frequency became lower in all the populations and became 0.00 in two population, Qazrin and Yehudiya. Overall frequency in seven populations listed in Table 3 is 0.260 in the materials studied by Joppa et al. (1995) and 0.187 in our samples. The two values did not differ greatly and thus are considered to represent frequency of 'major' translocation in natural populations of *T. dicoccooides*.

Another factor which affects overall frequency is that the two reports observed different populations in some cases. Some of the populations studied by Joppa et al. (1995) are homogeneous for one or more translocations. For example, all 10 genotypes from Beit Oren had two translocations with very high frequency of quadrivalents, from 0.95 to 1.00. But we could not find populations that are homozygous for one or more translocations. Such a population would increase overall frequency even when it is homogeneous. We conclude that there are two major causes for the difference in estimation of overall translocation frequency of *T. dicoccoides* in Israel. One is the difference in the sampling of population and the other is the criterion of presence of translocation. In the present report, we regarded that a genotype is homozygous for a 'major' translocation when hybrids with testers formed a quadrivalent at a frequency more than 0.50. Therefore, 'minor' translocation with very short interchanged segment is not counted here. Apparently, the frequency of quadrivalents will be very low in hybrids heterozygous for minor translocation. More extensive and detailed studies are needed to determine the frequency of translocation in natural populations.

Table 3. Comparison of translocation frequency between Joppa et al. (1995) and the present report

Location	Joppa et al. 1995[a]			Present report		
	No. genotypes observed	No. genotypes with TR[b]	TR frequency (Original value)	No. genotypes observed	No. of TR	TR frequency (>0.04[c])
Qazrin	9	0	0.000(0.444)	15	0	0.000(0.133)
Yehudiyya	12	0	0.000(0.667)	10	1	0.100(0.200)
Rosh Pinna	11	3	0.273(0.455)	14	2	0.143(0.143)
Bet Meir	11	3	0.273(0.273)	10	3	0.300(0.400)
Mt. Hermon	11	8	0.727(0.818)	12	7	0.583(0.583)
Bat Shelomo	11	5	0.455(1.000)	15	3	0.200(0.400)
Kokhav Hashahar	12	1	0.083(0.417)	15	1	0.067(0.067)
Total	77	20	0.260	91	17	0.187(0.264)

a From Joppa et al. (1995) Table 1.

b TR: Translocation. Frequency of quadrivalents higher than 0.50 was regarded to be genotype with translocation as in the present study.

c Same criteion as Joppa et al. (1995).

Reference

Kawahara T (1987) Identification of reciprocal translocation chromosome types in the emmer wheats. III. Six chromosome types in *Triticum dicoccoides*. Jpn J Genet 62: 197-204.

Kawahara T (1988) Confirmation of primitive chromosome structure in the hexaploid wheats. Theor Appl Genet 75: 717-719.

Joppa LR, Nevo E and Beiles E (1995) Chromosome translocations in wild populations of tetraploid wheat in Israel and Turkey. Theor Appl Genet 91: 713-719.

Wheat Information Service
Number 83: 31-32 (1996)

Research Information

Verification of the identity of the Chinese Spring ditelosomic stocks Dt7DS and Dt7DL.[1]

B.R. Friebe*, E.N. Jellen and B.S. Gill

Wheat Genetics Resource Center and Department of Plant Pathology, Throckmorton Hall, Manhattan, Kansas 66506- 5502, U.S.A.

The 'Chinese Spring' (CS) aneuploid series produced by Dr. E.R. Sears (1954) is an invaluable tool for allocating genes and markers to specific chromosomes and chromosome arms. The identity of most of these lines has been verified by chromosome banding analysis. This process exposed a discrepancy in the ditelosomic stocks Dt7DS and Dt7DL.

All lines designated as either Dt7DS or Dt7DL obtained from different institutions (University of Columbia, Missouri, USA; University of Riverside, California, USA; Kyoto University, Japan; Plant Breeding Institute, Cambridge, UK, and Technical University of Munich, Germany) were identified as Dt7DS. The 7DS arm is homoeologous to 7AS and 7BS arms,

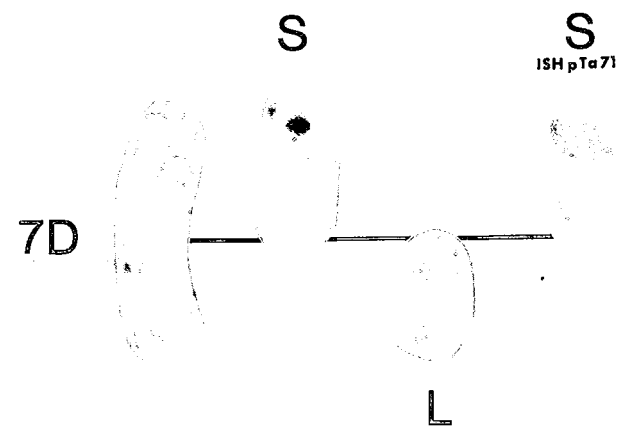

Fig. 1. C-banding and *in situ* hybridization patterns using the NOR rDNA probe pTa71 of chromosome 7D and its derived telosomes, from left to right: C-banding pattern of 7D (with the physically longer arm at top), telosome 7DS, telosome 7DL (from the dDt7D stock) and pTa71 ISH pattern of the telosome 7DS. All ditelosomic 7D stocks presently available had telosomes with C-banding and pTa71 ISH patterns identical to 7DL.

*Corresponding author, E-mail: friebe @ ksu.ksu.edu

[1]Contribution no. 97-42-J from the Kansas Agricultural Experimental Station, Kansas State University, Manhattan, Kansas, U.S.A.

although it is the physically longer arm (Werner et al. 1991). 7DS has two diagnostic C-bands at a telomeric and a subtelomeric location (Fig. 1, upper arm in complete chromosome 7D and telosome shown second from left) (Gill et al. 1991). In addition, this arm also has an *in situ* hybridization (ISH) site with the NOR rDNA probe pTa71, which contains the 18S, 5.8S, and 26S rRNA genes (Fig. 1, telosome on the right) (Mukai et al. 1991). The C-banding pattern of the 7DL arm homoeologous to 7AL and 7BL, which is the physically shorter arm, is different in having one proximal, one interstitial, and one telomeric C-band (lower arm in complete chromosome 7D and telosome shown third from left) and also lacks the pTa71 ISH site.

Sears and Sears (1978) sampled 2.000 gametes, but failed to recover the Dt7DL. The stock labeled Dt7DL was originally isolated by Kerber in 'Canthach' wheat (see Sears and Sears, 1978) and the 7DS telosome was transfered to Chinese Spring (Sears, unpublished data). However, all the CS ditelosomic stocks analyzed by C banding and ISH analyses had the genetically short arm of chromosome 7D in the form of a pair of telosomes.

Evidently, the 7DS telosomes are present in the CS double ditelosomic stock dDt7D, but information on the production of this line is not available. We are now attempting to isolate the Dt7DL line from the dDt7D stock.

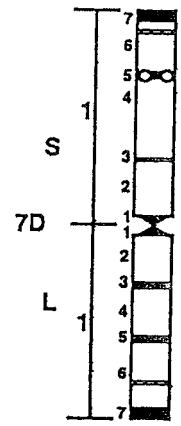

Fig. 2. Idiogram of chromosome 7D Landmark C-bands are shown in black, inconsistently observed minor bands are hatched and the pTa71 ISH site is shown as open circles and coincides with C-band 7DS1.5.

References

Gill BS, Friebe B, Endo TR (1991) Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat (*Triticum aestivum*). Genome 34: 830-839.

Mukai Y, Endo TR, Gill BS (1991) Physical mapping of the 18S.26S rRNA multigene family in common wheat: Identification of a new locus. Chromosoma 100: 71-78.

Sears ER (1954) The aneuploids of common wheat. Res. Bull. Missouri Agric. Exp. Stn. 572.

Sears ER and Sears, LMS (1978) The telocentric chromosomes of common wheat. Proc 5th Int Wheat Genet Symp, New Delhi pp 389-407.

Werner JE, Endo TR and Gill BS (1992) Towards a cytogenetically based physical map of the wheat genome. Proc Nat Acad Sci USA 89:11307-11311.

Wheat Information Service
Number 83: 33-34 (1996)

Research Information

Adult plant resistance genes with potential for durability to *Puccinia recondita* in wheat

R.N. Sawhney, J.B. Sharma and D.N. Sharma

Genetics Division, Indian Agricultural Research Institute, New Delhi-110012, India

Adult plant resistance (APR) is conferred by genes that are ineffective in seedlings but become operative during stages of adult plant growth. They are implicated in durability of resistance. This communication deals with diverse APR genes/sources and their potential to impart durability.

Among the described genes for adult plant resistance, *Lr34* has already been established to confer durable resistance (Sawhney, 1992; Sawhney et al. 1995a). In an expanded series of resistance genes, *Lr35* deriving resistance from RL5347-*Triticum speltoides/Triticum monococum* (Sawhney et al. 1994) and Lr37 deriving resistance from *Triticum ventricosum* have been identified to be effective in adult plants. *Lr35* resistance being operative only in adult plants and non-specific is likely to be durable but its durability can only be confirmed after this gene is introduced in commercial cultivar and grown extensively (Sawhney et al. 1994).

Thatcher near-isogenic lines carrying *Lr14b, Lr14ab, Lr30* showing seedling susceptibility to pathotypes exhibit resistance to the same pathotypes in adult plants (Sawhney et al. 1992). These lines also show APR against the highly virulent and newly evolved pathotype 77-5 and may confer durability.

In the variety Arjun seedling tests of SSD lines in F_7 of the cross Arjun x Kalyansona tested at higher temperature of 28 °C classified lines into (a) those that possess *Lr13* and therefore show resistance, (b) those that lack this gene and were susceptible. F_2 and F_3 of the cross of the line lacking *Lr13* with Agra Local (susceptible) gave segregates resistant at adult plant and therefore, established the presence of an APR gene which also possibly accounts for durability of resistance in Arjun.

Resistance responses on the Fed*4/Kavkaz and F_1 of the cross Federation x Kavkaz to pathotypes virulent on both Federation and Kavkaz was attributed to the possible complementation of adult plant resistance genes derived from Federation and Kavkaz (Sawhney et al. 1993). Resolution of this hypothesis was achieved by genetical data establishing that the leaf rust resistance in the stock is controlled by interaction of complementary adult plant genes. Additional interaction resistance to leaf rust in the class of 1BL/1RS (wheat-rye translocation) wheats is likely to achieve durability for resistance to all the three rusts combined with high yields and environmental stability (Sawhney 1995).

Inheritance studies in certain wheats drawn from each of the groups carrying different APR sources (Sawhney et al. 1992) suggested the operation of 1-3 genes to the control of resistance. Allelism tests have been conducted which established the presence of *Lr34* in wheats, Kundan (DL153-2), BW11, UP301, HD2189, HD2160.

Study of ninety Australian wheats recognized that for adult plant resistance, seven wheats in four groups existed. Each group was postulated to be of diverse APR source (Sawhney et al. 1995b).

Acknowledgements

Thanks to Dr. R.A. McIntosh, University of Sydney, Australia for certain seed materials used in the study and to the Council of Scientific and Industrial Research for award of research grant to R.N. Sawhney.

References

Sawhney RN (1992) The role of *Lr34* in imparting durable resistance to wheat leaf rust through gene interaction. Euphytica 61: 9-12.

Sawhney RN (1995) Genetics of wheat-rust interaction. Plant Breeding Reviews 13:293-343.

Sawhney RN, Sharma JB, and Sharma DN (1992) Genetic diversity for adult plant resistance to leaf rust (*Puccinia recondita*) in near isogenic lines and in Indian wheats. Plant Breeding 100: 248-254.

Sawhney RN, Sharma JB and Sharma DN (1993) Adult plant interactive genes for durable resistance to leaf rust with increased yield potential in wheat (abst. 220). Proc 8th Int Wheat Genet Symp, Beijing China: 120.

Sawhney RN, Sharma JB and Sharma DN (1994) Non-specific adult plant resistance to leaf rust with potential for durability. Cereal Rusts and Powdery Mildews Bull. 22 (part 2): 9-13.

Sawhney RN, Sharma JB and Sharma DN (1995a) Identification of adult plant resistance and its role for durable resistance to leaf rust in Indian wheats. In: Genetic Research and Education: Current Trends and the Next 50 years. Ed: Sharma B et al. Indian Soc. Genet. Pl. Breeding 1:356-362.

Sawhney RN, Sharma JB, Sharma DN and Nagarajan S (1995b) Adult plant resistance sources for breeding durably leaf rust resistant wheats. Cereal Rusts and Powdery Mildews Bull. 23 (In press).

Wheat Information Service
Number 83: 35-46 (1996)

III. Compendium

A compendium of reciprocal translocations in wheat: 2nd Edition

R. Schlegel

Institute of Wheat and Sunflower Research, BG-9520 General Toshevo/Dobrich, Bulgaria

Summary

Wheat varieties and wheat species are frequently differentiated by reciprocal translocations of inhomologous chromosomes. Therefore, for several studies the knowledge about interchanges is required. A list was compiled summarizing available data on the presence and number of translocations, on configurations observed and their frequencies of occurrence and on involved chromosomes from 466 wheat combinations. The modified chromosomes are usually identified after common chromosome studies, intercrossing and meiotic analysis in F_1 hybrids. Among the wheat accessions listed 19.7% show a non-translocated karyotype, while the remaining show multivalent configurations of types 1^4 (51.3%), 2^4 (20.4%), 3^4 (3.4%), 4^4 (0.6%), 1^6 (1.7%), 1^8 (0.4%), 1^4+1^6 (1.7%) and 2^4+1^6 (1.6%). The chromosomes 1A, 7B and 2D are most frequently associated with translocations. Between the genomes the B genome exhibits the most interchanges (A=12.3%, B=61.4%, D=26.3%). However, no close correlations were evident between individual chromosome length (μm), 4C DNA content per chromosome (pg) and the frequency of chromosome involved in translocations (r=<0.4**).

Introduction

Wheat varieties are often differentiated by structural changes of the genome such as reciprocal translocations, deletions, inversions, duplications or heterochromatin polymorphisms. The translocations are mostly identified after crossing analysis and karyological studies. Critical F_1 hybrids show multivalent interchange configurations with different frequencies per pollen mother cell. Meanwhile, there are quite a number of cultivars in wheat characterized by the presence of reciprocal translocations and/or their absence. For monosomic analysis, chromosome identification, identity proof of a variety and for several other reasons the knowledge on interchanges is required. Therefore, a second compilation was prepared summarizing available data on the presence and number of translocations, on configurations and chromosomes involved in the interchanges as well as on the origin of the material.

The nomenclature for types of translocated chromosomes follows recommendation of Koebner and Miller (13). The origin of release of the variety/strain is included in the inventory. The pairs of critical varieties were alphabetically arranged, according to the number of translocations found in the material. Although in some combinations several types of interchanges were found possibly

introduced by different genotypes / karyotypes of the populations, they all were considered but separated by a comma. Hybrids with more than one interchange in a given hybrid are characterized by the types of association connected with a plus sign(+). 1^4 designates one quadrivalent present in the hybrid, 1^6=one hexavalent, 1^8=one octovalent, 2^4=two quadrivalents, 1^4+1^6=one quadrivalent plus one hexavalent, etc. The chromosomes 4A and 4B are considered after the new nomenclature of wheat chromosomes.

(left to right: cv/acc, origin, chromosomes involved, % of expression in parenthesis and reference)

Triticum araraticum
to *T. araraticum* W3111
1^4
T. aestivum cv. Apollo NDL - 58

Triticum turgicum
to *T. turgidum*
1^4
T. turgidum var. *durum* cv. Nodak
1BS.2BS(1BL.2BL) 58

Triticum searsii
to *T. searsii*
1^4
T. searsii ISL $1S^sS.4S^sS(1S^sL.4S^lL)$ 68

Triticum dicoccoides
to *T. dicoccoides* HTRI 7483
1^4
T. aestivum cv. Poros DDR 7B/2D 58

2^4
T. aestivum cv. Alcedo DDR
3BS.6BS(3BL.6BL)+?/? 58

Triticum aestivum* ssp. *spelta
to *T. spelta* acc. 415 IRN
2^4
T. spelta var. *saharense* IRN - 55

to *T. spelta* acc. 417a IRN
2^4
Chinese Spring CHN - 55
Taiching 29 JPN - 55
T. spelta var. album IRN - 55
T. spelta acc. 415 IRN - 55

Triticum aestivum* ssp. *tibetanum
to *T. aestivum* ssp. *tibetanum* **CHN**
no translocation
Chinese Spring CHN - 56

***Triticum turgidocereale* (6x triticale)**
to Chinese Spring CHN
no translocation
Beagle MEX 64
Bronco 90 MEX - 64
Currency MEX - 64

1^4
Armadillo MEX 4B/6B (72) 64
Beaver MEX 4B/6B (70) 64
Camel MEX 4B/6B (73) 64
Rosner CAN 4B/6B (70) 64

to Armadillo MEX
1^4
Thatcher USA 4B.6B
(4BS.6BL) (75) 64

Triticum aestivum* to *Triticum aestivum
to Alcedo DDR
no translocation
Rinaldo DDR - 57

1^4
Atlas 66 USA - 57
Asosan JPN - 57
Axminster AUS - 57
Besoztaya USR - 57
Carola GDR - 57
Chinofuz USA - 50
Emika ??? - 57
Halle Stamm DDR - 57
Hope USA - 57
Jukseng KOR - 50
Jukseng 3 KOR - 50
Kenya Civet KEN - 57
M 30 HUN - 57
Mara ITA - 57
Mario ??? - 57

Maris Mardler	GBR	-	57
Maris Hobbit	GBR	-	57
Maris Nimrod	GBR	-	57
Miras	DDR	-	57
Plainsman V	USA	-	57
Regina	ITA	-	57
Strubes Dickkopf	GER	-	57
Swjosda I	USR	-	57
Taras	DDR	-	57

2^4

Fakir	GDR	-	57
Flandres Desprez	FRA	-	57
Hachiman Komugi	JPN	-	50
Hadmersleben 4001/84	DDR	-	57
Mikuni	JPN	-	50
Poros	DDR	7B/2D;?/?	40, 57
Roazon	FRA	-	57
VPM 1	FRA	-	57
Weihenstephan M1	FRG	-	57

$1^4 + 1^6$

Fujimi	JPN	-	50

3^4

Cappelle Desprez	FRA	-	57

to Alonso Pena 113 ESP

1^4

Alonso Pena 114	ESP	3DL/4DS	7
Alonso Pena 115	ESP	-	7
Alonso Pena 117	ESP	-	7
Alonso Pena 119	ESP	-	7
Alonso Pena 121	ESP	4BL / ?	7
Alonso Pena 122	ESP	-	7

2^4

Alonso Pena 116	ESP	-	7
Alonso Pena 118	ESP	4BL / ?;?/?	7

$1^4 + 1^6$

Alonso Pena 120	ESP	-	7

to Alonso Pena 114[4] ESP

1^4

Alonso Pena 118	ESP	3DL/4DS	7

2^4

Alonso Pena 122	ESP	-	7

3^4

Alonso Pena 120	ESP	1AL/?;1BL/6BS;2BL/?	7
Alonso Pena 121	ESP	1AL/?;6BL/?;3DL/4DS	7

4^4

Alonso Pena 115	ESP	1AL/?;3BL/?;6BL/?; 3DL/?	7
Alonso Pena 116	ESP	1AL/?;4BL/?;1BS/?; 3DL/?	7
Alonso Pena 117	ESP	1AL/?;4BS/?;2BL/?; 3DL/4DS	7

$2^4 + 1^6$

Alonso Pena 119	ESP	-	7

to Alonso Pena 119 ESP

1^4

Alonso Pena 116	ESP	-	7
Alonso Pena 120	ESP	-	7
Alonso Pena 122	ESP	4D/6D	7

2^4

Alonso Pena 118	ESP	-	7

$1^4 + 1^8$

Alonso Pena 117	ESP	-	7

to Amigo[1] USA

1^4

Glennson 81[2]	MEX	6BL/?	52

2^4

S149	USA	6BL/?;7BS/?	52

to April Bearded GBR

2^4

Kavkaz	USS	-	54

to Beijing Red 1 CHN

1^4

Feng Kang 13	CHN	4B/1D	48

to Bersee FRA

2^4

Persus[2]	GER	-	54

to Bezostaja 1 USS

2^4

Cappelle Desprez	FRA	5B/7B;3B/3D	24
Grana	POL	3B/3D;7B/2D	24,25

to Cabezorro ESP

1^4

Cabezorro 2	ESP	-	35

2^4

Florence Aurore	TUN	-	35

3^4

Canaleja	ESP	-	35
Candeal de Teruel	ESP	-	35

1^6

Candeal de Castilla	ESP	-	35
Caspino 4	ESP	-	35
San Bruno	ITA	-	35

2^4, 1^6

Roma	ITA	-	35

to Cabezerro 2 ESP

3^4

Candeal de Teruel	ESP	-	35

$1^4 + 1^6$

Mentana	ITA	-	35
San Bruno	ITA	-	35

$2^4 + 1^6$

Canaleja	ESP	-	35

2^4, 1^6

Caspino 4	ESP	-	35
Florence Aurore	TUN	-	35
Mara	ITA	-	35

1^8

Roma	ITA	-	35
Yaktana	MEX	-	35

to Canaleja ESP

2^4

Roma	ITA	-	35

3^4

Candeal de Castilla	ESP	-	35
Florence Aurore	TUN	-	35
Mara	ITA	-	35
San Bruno	ITA	-	35

2^4, 1^6

Caspino 4	ESP	-	35
Mentana	ITA	-	35
Yaktana	MEX	-	35

3^4, $1^4 + 1^6$

Candeal de Teruel	ESP	-	35

to Candeal de Castilla ESP

1^4

Florence Aurore	TUN	-	35
Mara	ITA	-	35
Mentana	ITA	-	35
Yaktana	MEX	-	35

2^4

Caspino 4	ESP	-	35
San Bruno	ITA	-	35

$1^4 + 1^6$

Candeal de Teruel	ESP	-	35

2^4, 1^6

Roma	ITA	-	35

to Candeal de Teruel ESP

no translocation

Mara	ITA	-	35

$1^4 + 1^6$

Caspino 4	ESP	-	35

1^4, 1^6

Florence Aurore	TUN	-	35

$2^4 + 1^6$

Roma	ITA	-	35
Yaktana	MEX	-	35

to Cappelle Desprez FRA

2^4

Sava	YUG	3B/3D;5B/7B	24
Starke	SWE	2B/2D;5B/7B	15

3^4

Grana	POL	3B/3D;5B/7B;7B/2D	24

$1^4 + 1^6$

Poros	DDR	3B/3D+5B/7B/2D	21

to Carola DDR

no translocation

N 66	ISL	-	50
N 69	ISL	-	50

1^4

Bangor Nies 12290	IND	-	50
Haya Komugi	JPN	-	50
Shirodarumasai 1	JPN	-	50
Shirasaya 1	JPN	-	50
Whitel 8156	TUR	-	50

to Caspinno 4 ESP

1^4

San Bruno	ITA	-	35

2^4

Florence Aurore	TUN	-	35
Mara	ITA	-	35
Mentana	ITA	-	35
Roma	ITA	-	35

to Chinese Spring CHN
no translocation

Amor	OST	-	54
Atlas 66	USA	-	30
Avon	USA	-	54
Banatka Kresowa	POL	-	54
Beijing Red 1	CHN	-	48
Bezostaya 1	USS	-	18
Blumenweizen	GER	-	54
Bocquian	FRA	-	30
Bretonischer Bartweizen	FRA	-	54
Calatrava	ESP	-	37
Carola	DDR	-	3
Cato	NDL	-	30
Cheyenne	USA	-	29
Chikago American Landwheat	USA	-	54
Cluj 11/54	ROM	-	54
Cote d'Or	FRA	-	54
Criewener 27	GER	-	54
Diamant 2	SWE	-	18
Dippes Dickkopf 9	GER	-	54
Dunav	YUG	-	30
El Gaucho	ARG	-	54
Eshima	JPN	-	66
Fakir	DDR	-	50
Fakon	DDR	-	50
Favorit	ROM	-	18
Friedrichswerther Granne	GER	-	54
G 38 290	GRC	-	7
Glennson 81[2)]	MEX	-	18
Goya	FRA	-	54
Griechischer 15	GRC	-	54
Had. 7400/85	DDR	-	31
Hebros	BGR	-	30
He-Zuo 2	CHN	-	54
Hohenthurm 8181/70	DDR	-	30
Hohenthurm 8836/64	DDR	-	30
Hohenthurm 12106/57	DDR	-	30
Iljitschjewka	USS	-	30
Inia 660.19	MEX	-	21
J1	AUS	-	37
Japanischer Weisser	JPN	-	54
Justin	USA	-	30
Kent	CAN	-	54
Kenya Settler	KEN	-	54
Kharkov Min. 211	USA	-	54
Kranich	FRG	-	30
Loosdorfer	OST	-	30
Loosdorfer Bartweizen	OST	-	54
Luna	POL	-	18
M30	HUN	-	46, 57
Mara	ITA	-	18
Maris Settler	GBR	-	30
Milturum 553	USS	-	18
Novosadska Rana 1	YUG	-	18
Novostepnjachka	USS	-	18
NP 875	IND	-	30
NS 76-56	YUG	-	30
Opal	FRG	-	18
P 67-256	DNK	-	30
Priboi	USS	-	18
Ruso	FIN	-	54
Saladin	DDR	-	21
Saline	USA	-	54
Sanolika	IND	-	30
Saratovskaya 29	USS	-	18, 30
Sava	YUG	-	18
South Africa 43	KEN	-	54
Suwon	KOR	-	54
Suwon 92	KOR	-	50
Tirgu Frumos	ROM	-	30
Torre	POR	-	54
Tumult	NDL	-	54
Turcicum 57	USS	-	54
Turpin 7	SAF	-	30
Ungarischer Begrannter	HUN	-	54
Uralskaya 52	USS	-	54

1^4 (to Chinese Spring)

AF59 223	BEL	-	(4)30
Ai-bian		-	20
Aida	FRA	-	(5)30
Alcedo	DDR	3BS.6BS(3BL.6BL)	32, 57
Alonso Pena 119	ESP	-	7
April Bearded	GBR	-	27
Aradi	ESP	-	35
Aragon 3	ESP	-	35
Ardent	FRA	-	(7)30
Ariana 8	ALG	-	12, 35
Ariana 66	TUN	-	(7)30
Aster	FRA	-	(13)30
Atlas 66	USA	2AL/2DL	43, 44
Atys	FRA	-	(13)30
Aureo 23	ESP	-	35
Bersee	FRA	5B/7B	17, 18
Bezostaya 1	USS	-	(3)30
Blaukorn[5)]	FRG	-	23
Boulmiche	FRA	5BS/7BS	37
C-591-2	IND	-	54
Cabezorro	ESP	-	35, 37

Calatrava	ESP	-	35
Candeal de Castilla	ESP	-	35
Candeal de Teruel	ESP	-	37
Capset	FRA	-	(16)30
Capnord	FRA	-	(3)30
Caribo	FRG	5B/7B	5
Carlotta Strampelli	ITA	-	54
Cascon	FRA	-	35
Caspino 4	ESP	-	35, 37
Cierzo	ESP	5BS/7BS	37
Delphin	DDR	-	(26)30
Dimas	???	-	35
Domus	FRG	-	(10)30
Erythrospermum	USS	-	(3)30
Eshimashiriki	JPN	4B/6B(4BS.6BL)	63
Favorit	ROM	-	(4)30
Feng Kang 13	CHN	4B/1D	48
Flambar	ESP	6BL/?	37
Florence Aurore	TUN	-	35
Frondoso	BRA	-	(6)67
Gabo	AUS	-	54
Gaines	USA	-	21
Galba	FRG	-	(13)30
Gaudenz	FRG	-	(3)30
Grana	POL	7B/2D	18, 24
Had. 36159/69	DDR	-	(3)30
Had. 1673/80	DDR	-	31
Had. 4001/84	DDR	5BS.7BS	31
Hembrilla de Jaca	ESP		35
Hinal	SCH	-	(13)30
Hohenthurm 7731/71	DDR	-	(10)30
Hohenthurm 27391/68	DDR	-	(14)30
Holdfast	GBR	3B/3D	18, 27
Igachikugo Oregon	JPN	3A/7A(3AS.7AL)	63
Indian	USA	3B/7B	33
Iva	POL	-	(10)30
J1	AUS	-	35
Janus	FRG	-	(13)30
Jubilar	FRG	5BS.7BS(5BL.7BL)	61
Jukseng	KOR	-	54
Kinki 2	JPN	4BS.6BL	66
Klaven	NDL	-	(16)30
Koga II	FRG	3B/3D	18
Lembkes Obotriten	GER	-	54
Line 84001/1-33	CHN	5BS.7BS(5BL.7BL)	41
Lundi	ZIM	-	(3)30
Magdalena	ESP	-	35, 37
Manitoba	CHL	-	51
Mara	ITA	-	35
Maris Ensign	GBR	7B/2D	16
Maris Hobit 'sib'	GBR	5B/7B	18
Maris Nimrod	GBR	-	(4)30
Marne	FRA	-	4
Matador	NDL	-	37
Mayo 64	MEX	-	(16)30
Mej-Go-Jij-Pi	CHN	-	54
Mentana	ITA	-	35, 37
Michigan Amber	USA	-	(3)30
Michigan Bronce	USA	-	54
Mironovskaya 808	USS	-	21
Mironovskaya Jublenja	USS		(7)30
MM 7	???	-	35
Moisson	FRA	-	4
Norin19,20,23,25,34,36,37,45,51,52,56,65,72,73,80	JPN	4BS.6BL	(25)66
Norteno 67	MEX	-	(10)30
Oroel	ESP	5BS/7BS	37
Oroten 60	CHL	-	(3)30
P 67-253	DNK	-	(3)30
Pane 247	ESP	2A?/4BL	12, 42
Piamontes	ARG	-	(16)30
Pin-Juj 50	CHN	-	54
Pluto	DDR	-	(50)30
Poros	DDR	7B/2D	(80)21, 30
Poso	USA	5BS/7BL	26, 33
Punjab 519	IND	-	54
Rannaya 12	USS	1B/2D	18
Rieti	ITA	-	35
Roazon	FRA	5B/7B	4
Robert	FRG	-	(13)30
Rusalka	BGR	-	(3)30
S 1556	AUS	5A/?	11
S 2303	NZL	4B/1B	2
Saikai 102	JPN	4BS.6BL	(35)66
Saitama 27	JPN	3A/7A(3AS.7AL)	63
San Bruno	ITA	-	35
Saria	ESP	-	35, 37
Shinriki	JPN	4BS.6BL	(26)66
Shirodaruma	JPN	4B/6B(4BS.6BL)	63
Siete Cerros	MEX	-	37
Sin Tizon 35	ESP	-	35
Sinvolocha	ARG	1B/6B	47
Sonora	MEX	3A/7B	2
Starke 2	SWE	-	(28)30
Sur (V256)	IND	-	27
Synthetic hexaploid	SWE	6B/7D	16
Talento	ESP	5BS/7BS	37
Thatcher	USA	4B/6B	33
Tobari 66	MEX	-	(10)30
Traquejos	ESP	-	35
V 12	CHN	-	27
V 13	CHN	-	27
Veka	FIN	-	(3)30
Viking	DNK	5BS.7BS(5BL.7BL)	39
Viking-hairy neck[3]	DNK	5BS.7BS(5BL.7BL)	39
Vilmorin 27	FRA	5B/7B	17, 34

VPM	FRA	5B/7B	4
Wachtel	FRG	1D/6D	28
Weibull	SWE	-	(16)30
Widgeon	GBR	-	(95)54
Xelaju	MEX	-	(7)30
Yaktana	MEX	-	35
Yangmai 3	CHN	1BL/4AL (1BS.L2.2-4AL1.4)	62
Yuusyouki	JPN	4B/6B(4BS.6BL)	63
Zipa 68	COL	-	(3)30

2^4 (to Chinese Spring)

Alonso Pena 113	ESP	6AL/6BL;3BS/5BS	7
Alonso Pena 114[4]	ESP	1AL/?;3DL/4DS	7, 8
Amigo[1]	USA	6A/6B;7A/7B	51
Canaleja	ESP	4BL/3DL;5BS/7BS	36, 37
Candeal de Teruel	ESP	-	35
Cappelle Desprez	FRA	3B/3D;5BL/7BL	27
Cappelle Desprez	FRA	5B/7B;2B/2D	15
Diamant 2	SWE	6B/1D;6D/7D	9
Dwarf A	GBR	-	54
Elysee	FRA	-	(54)30
Eshimashiriki	JPN	4BS.6BL;3B/7B	66
Had. 4116/84	DDR	-	31
Heima	FRA	-	(13)30
Hembrilla de Jaca	ESP	3BL/?;?/?	37
Hybride du Joncquois	FRA	3B/3D;5B/7B	17
Mironovskaya 808	USS	3A/3B;1B/2D	18
Probus	SCH	5B/7B;?/?	18
Roma	ITA	-	35
S 615	AUS	4B/6B;2B/3B	27
Saitama 27	JPN	1A/?B;3A/7A (3AS.7AS)	65
San Bruno	ITA	2BL/?;?/?	37
Sansa	ESP	5AL/?;?/?	37
Saratovskaya 29	USS	5A/1D;3B/6B	10
Saratovskaya 210	USS	6A/3D;6A/7D	10
Starke	SWE	7AL/7DS;2B/2D**	15, 19
Toroma	ESP	5BL/?;?/?	37
W 1007/53	FRG	3A,2B;?/?	38
Xiaoyan 6	CHN	1A,6A,3B,2D,4D	49
Zlatka	CSK	5A/6D;3D/5D	14

3^4 (to Chinese Spring)

Mutant T-13	USS	3A/3B;1B/3D;6B/7D	45
Norrona	USS	4B/4D;1B/1D;2B/6D	45
Solo	FRG	2A/4D;7A/7D;5B/7B	1
Starke	SWE	7A/7D;2B/2D;3B/3D	18

1^6 (to Chinese Spring)

Azteka	MEX	-	21
Eligulate	USS	4B/6A/7B	2
Sudeten Winterweizen	GER	-	(11)54

1^4, 0 (to Chinese Spring)

Dacia	ROM	-	(3)30,54

1^4, 2^4 (to Chinese Spring)

Cabezorro 2	ESP	-	35

to Chou-Fung CHN

1^4

Concorde	FRA	-	54

to Cote d'Or FRA

no translocation

Povon 76	GER	-	54
Solaris	CSK	-	54
Zemon	BEL	-	54

to Fakon DDR

no translocation

Gaang-Uk 5	CHN	-	54
N 67	ISL	-	50
Rena	CSK	-	50

1^4

Konosu 25	JPN	-	50
Shirodarumasai 1	JPN	-	50

2^4

Kavkaz[2]	USS	-	54
BT 2223	TUN	-	50

to Florence Aurore TUN

1^4

Mentana	ITA	-	35
San Bruno	ITA	-	35

2^4

Mara	ITA	-	35
Roma	ITA	-	35
Yaktana	MEX	-	35

to Friedrichswerther Granne GER

1^4

Lawrence	AUS	-	54

to Giza 150 EGY

2^4

Widgeom	GBR	-	54

to Grana POL

1^4

Sava	YUG	7B/2D	24, 25

to Kavkaz [2] **USS**

2^4

Widgeon	GBR	-	54

to Lerma Rojo **MEX**

1^4

Czao Se-Zu-Mej	CHN	-	50
Polukarlikovkaya 49	USS	-	50
Saitama 125	JPN	-	50
Shirodarumasai	JPN	-	50

2^4

Rjukson	KOR	-	50

to M30 **USA**

1^4

Poros	DDR	7B/2D	46

to Manitoba **CHL**

no translocation

Maris Huntsman	GBR	-	54

to Mara **ITA**

1^4

Mentana	ITA	-	35
Poros	DDR	7B/2D	21

2^4

Roma	ITA	-	35
San Bruno	ITA	-	35
Yaktana	MEX	-	35

to Maris Huntsman **GER**

1^4

Svalofs Rubin	SWE	-	54

to Mentana **ITA**

1^4

Yaktana	MEX	-	35

1^6

San Bruno	ITA	-	35

2^4, 1^6

Roma	ITA		35

to Mutant 146-155 **USS**

1^4

Thatcher	USA	-	53

to Napo **COL**

no translocation

Maris Huntsman	GBR	-	54

1^4

Widgeon	GBR	-	54

to Orlandi **ITA**

no translocation

TRI 12083	JPN	-	50

1^4

Chinofuz	USA	-	54
Hanagasa Komugi	JPN	-	50
Kokeshi Komugi	JPN	-	50
Rjourjuk 4	KOR	-	50
Rjukson	KOR	-	50
Shirasaya 1	JPN	-	50
TRI 5270	CHN	-	50
TRI 11905, landrace	POL	-	50
Yammang You Mang 685	CHN	-	50

2^4

Bangor NIES	IND	-	50
Haya Komugi	JPN	-	50
Maniton	YUG	-	50
Shirodarumasai 1	JPN	-	50

to Poros **DDR**

1^4

Atlas 66	USA	7B/2D	21
Inia	MEX	7B/2D	21
N 501 JSWR	CSK	7B2D	50
Saladin	DDR	7B/2D	21

2^4

Gains	USA	7B/2D;?/?	21
Mironovskaya 808	USS	7B/2D;?/?	21
Saitama	JPN	7B/2D+?/?	50
TRI 12083	JPN	7B/2D+?/?	50

1^6

Azteka	MEX	7B/2D/?	21

to Roma **ITA**

2^4

Yaktana	ESP	-	35

2^4, 1^6

San Bruno	ITA	-	35

to San Bruno **ITA**

2^4

Yaktana	MEX	-	35

**2B is a duplication deficiency chromosome carrying a duplicated part of chromosome 2D
[1] variety shows also a 1AL.1RS wheat-rye translocation
[2] variety shows also a 1BL.1RS wheat-rye translocation
[3] variety shows also a 4BS.4BL-5RL wheat-rye translocation
[4] variety shows also a ?/2R wheat-rye translocation
[5] variety shows also a 5R(4A) wheat-rye translocation

Acknowledgements

The author acknowledges support for this catalogue by A. C. Baier(Brasil), T. R. Endo (Japan), N. Jouve (Spain), W. Lange (Netherlands), V. Schubert, E. Schumann, W. D. Bluthner, W. Junghans, F. J. Zeller (Germany).

References

1 Baier AS, Zeller FJ and Fischbeck G (1974) Identification of three chromosomal interchanges in common wheat, *Triticum aestivum* L. Can J Genet Cytol 16: 349-354.
2 Baker EP and McIntosh RA (1966) Chromosome translocations identified in varieties of common wheat. Can J Genet Cytol 8: 592- 599.
3 Bannier E (1976) MonosomenanalytischeUntersuchungen über das zytologische und genetische Verhalten von Kreuzungsnachkommenschaften ausgewahlter Sorten des Weizens (*Triticum aestivum* L). PhD thesis, Akademie Landwirtschaftswiss Berlin DDR P.146.
4 Bourgeois SF, Dosba G and Dounaire G (1978) Analyse et identification des translocation reciproques presented chez le geniteur VPM et les varietes 'Marne','Moisson' et 'Roazon'. Ann Amelior Planted 28: 411-429.
5 Chae KC, Zeller FJ and Fischbeck G (1979) Chromosomal location of genes for quantitative characters using monosomic lines of the wheat cultivar 'Caribo". Z Pflanzenzüchtg 83: 114-120.
6 Coucoli H and Skorda EA (1970) Metaphase I studies of the F1 from crosses between Chinese Spring monosomics and Greek cultivar. Caryologia 23: 135-142.
7 Fominaya A and Jouve N (1985) C-banding at meiosis as a means of analyzing cytogenetic structure in wheat. Can J Genet Cytol 27: 689-696.
8 Fominaya A and Jouve N (1986) Analysis of interference in a double interchange heterozygote of wheat (*Triticum aestivum* L.). Heredity 56: 1-6.
9 Gaidalenok RF (1973) Study of meiosis in F1-hybrid from crosses between monosomics of Chinese Spring and a wheat variety showing disturbed chromosome pairing. russ. Tsitogenet Isled Aneuploidov Mayagk Pschenitsy: 94-106.
10 Gaidalenok RF and Maistrenko OT (1973) Study of metaphase I of meiosis in F1-hybrids from crosses between monosomics of Chinese Spring and several varieties showing undisturbed chromosome pairing. Tsitogenet Isled Aneuploidov Mayagk Pschenitsy: 77-94.
11 Hair BJ (1968) Analysis of a compactoid wheat. Proc 3rd Int Wheat Genet Symp, Canberra: 324-326.
12 Jouve N, Ferrer E and Fernandez JA (1984) Development of aneuploids. EWAC Newsletter Cambridge: 31
13 Koebner RMD and Miller TE (1986) A note on the nomenclature for translocated chromosomes in the *Triticeae*. Cer Res Comm 14: 315-316.
14 Kosner J and Bares I (1979) Determinations of desynaptic disorders and detection of translocations in the 'Zlatka' cultivar of wheat. Genet i Slecht 15: 105-118.
15 Lange W, Linde-Laursen I, Larsen J, Ljundberg A and Ellerstrom S (1987) Cytogenetic analysis of structural rearrangements in three varieties of common wheat, *Triticum aestivum*. Theor Appl Genet 73: 635-645.
16 Larsen J (1973) Diallel analysis of interchanges between five spring wheat varieties. EWAC Newsletter Cambridge: 81.

17 Law CN (1971) Co-operative projects. EWAC Newsletter Cambridge: 45-46.
18 Law CN (1984) Monosomic series being developed or maintained in Europe. EWAC Newsletter Cambridge: 38-39.
19 Linde-Laursen I and Larsen J (1974) The use of double-monotelodisomic to identify translocation in *Triticum aestivum*. Hereditas 78: 245-250.
20 Liu BH (1987) Isolation of a spontaneous chromosome translocation in common wheat. Plant Breed 98: 266-267.
21 Mettin D and Klein U (1974) Meiotic pairing behaviour and interchanges in intervarietal hybrids of common wheat. EWAC Newsletter Cambridge: 30-34.
22 Mettin D, Meyer H and Bannier E (1969) Wheat aneuploidy within Europe. EWAC Newsletter Cambridge: 31-35.
23 Mettin D, Schlegel R and Lehmann CO (1988) Instability of blue grain colour in common wheat, *T. aestivum* L. Genome 30 (Suppl 1): 267.
24 Miazga D and Petrovic S (1986) Translocations in the Polish wheat variety Grana. EWAC Newsletter Cambridge: 45-47.
25 Miazga D and Petrovic S (1987) Chromosome translocations in wheat (*Triticum aestivum* L.) of the cv Grana. Genetica Polonica 28: 11-15.
26 Quinn CJ and Driscoll CJ (1970) Analysis of the 'Poso' wheat translocation. Chromosoma 31: 285-290.
27 Rilley R, Coucoli H and Chapman V (1967) Chromosomal interchanges and the phylogeny of wheat. Heredity 22: 233-248.
28 Röbellen G (1968) Desynapsis als Fehlerquelle bei der Aufstellung von Monosomen-Sortimenten des Weizens. Z Pflanzenzüchtg 60: 1-18.
29 Sasaki M, Morris R, Schmidt JW and Gill BS (1963) Metaphase I studies on F_1 monosomics from crosses between the Chinese Spring and Cheyenne common wheat varieties. Can J Genet Cytol 5: 318-325.
30 Schlegel G (1976) Cytogenetische Untersuchungen zur partiellen Hybrid-Desynapsis an Bastarden des Saatweizens (*Triticum aesticum* ssp *vulgare*). PhD Thesis, Martin-Luther-Universität Halle Wittenberg: p 105.
31 Schlegel R and Thiele M (1989) Cytogenetic investigation of eyespot resistant wheat strains. Res Rep: unpublished data.
32 Schubert V (1989) Untersuchungen an *Triticum aestivum* x *Aegilops markgrafii* Kreuzungen und die Nutzung hochrepetitiver DNA-Sequenzen in der squash dot Technik. PhD thesis, Martin-Luther-Universität Halle-Wittenberg: p 79.
33 Sears ER (1953) Nullisomic analysis in common wheat. Amer Nat 87: 245-252.
34 The TT and Baker EP (1970) Homoeologous relationships between *Agropyron intermedium* chromosomes and wheat. Wheat Inf Serv 31: 29-31.
35 Vega C and Lacadena JR (1982) Cytogenetic structure of common wheat cultivars from or introduced into Spain. Theor Appl Genet 61: 129-133.
36 Vega C and Lacadena JR (1983) Identification of two chromosomal interchanges in cv. Canaleja of common wheat, *Triticum aestivum* L. Euphytica 32: 485-491.
37 Vega C, Fominaya A and Ferrer E (1987) Influence of chromosome structure on the degree of meiotic pairing on intercultivar wheat hybrids (*Tritivum aestivum* L.). Heredity 58: 357-364.
38 Zeller FJ (1973) 1B/1R wheat-rye chromosome substitutions and translocations. Proc 4th Int Wheat Genet Symp, Columbia USA: 209-222.
39 Schlegel R, Werner T and Hülgenhof E (1991) Confirmation of a 4BL/5R wheat-rye chromosome translocation in the wheat cultivar 'Viking' showing high copper efficiency. Plant Breed 107: 226-234.
40 Schubert V (1989) pers comm.
41 Xu J, Zhong SB, Jiang JD and Ya JX (1988) Identification of a new reciprocal translocation of chromosome 5B/7B in a Chinese common wheat using C-banding technique. Jiangs J Agric Sci 4: 78-81.
42 Ferrer E, Gonzalez JM and Jouve N (1984) The meiotic pairing of nine wheat chromosomes. Theor Appl Genet 69: 193-198.
43 Primard SJ, Morris R and Papa CM (1989) Heterozygous translocation study of 'Atlas 66'. Ann Wheat Newslett 35: 170.
44 Primard SJ, Morris R and Papa CM (1991) Cytogenetic studies on a heterozygous reciprocal translocation in the wheat (*Triticum aestivum*) cultivar Atlas 66. Genome 34: 313-316.

45 Prillinn O, Enno T, Peusha H, Tohver M and Timfejeva L (1991) Analysis of MI of meiosis in monosomic hybrids. Ann Wheat Newslett 37: 57-59.
46 Khan MF (1993) Monosomenanalytische Untersuchung von Mehltauresistenz-, Ertrags-, und Proteinmerkmalen an der *Triticum aestivum* L.-Herkunft 'M30' . PhD thesis Martin-Luther- Universität Halle-Wittenberg: p 86.
47 Suarez EE (1992) pers comm, tissue culture induced.
48 Rongjin S, Yulan Z and Xiaodong Y (1990) Research on a chromosome translocation 4B-1D of *Triticum aestivum*. Biotechnology in Plants, Columbia USA: 228-234.
49 Li WL, Li ZS and Mu SM (1990) Cytological study of chromosme structural changes in common wheat variety Xiaoyan 6. Acta Genet Sinica 17: 430-437.
50 Schlegel R and Börner A (1992) unpublished data.
51 Hollenhurst MM and Joppa LR (1983) Chromosomal location of genes for resistance to greenbug in 'Largo' and 'Amigo' wheat. Crop Sci 23: 91-93.
52 Bittel DC, Fominaya A, Jouve N and Gustafson JP (1992) Dosage response of rye genes in a wheat background. I. Selection of lines with multiple copies of 1RS. Plant Breed 108: 283-289.
53 Prillinn O, Enno T, Peuscha H and Tohver M (1992) Transfer of leaf rust resistance from *Triticum timopheevi* and *T. militinae* into common wheat. Ann Wheat Newslett 38: 102.
54 Schlegel R and Voigtländer A (1992) unpublished data.
55 Lange W (1992) pers comm.
56 Chen PD, Huang L and Liu DJ (1991) Analysis of the genomic constitution of Xizang wheat (*Triticum aestivum* ssp. *tibetanum* Shao) using doubleditelosomics of *Triticum aestivum* Chinese Spring.Acta Genetica Sinica 18:39-43.
57 Schubert V (1992) pers comm.
58 Schumann E (1992) pers comm.
59 Schulz-Schaeffer J and Friebe B (1992) Karyological characterization of a partial amphiploid, *Triticum turgidum* L. var. *durum* x *Agropyron intermedium* (Host) PB. Euphytica 62: 83-88.
60 Fominaya A, Olmedo A and Jouve N (1986) Morphological, cytological and isozyme divergence in wheat lines derived from wheat x rye hybrids. Z Pflanzenzüchtg 96: 207-217.
61 Kazman ME (1992) Eine neue Methode zur Substitution von D-Chromosomen in das A- und B-Genom des hexaploiden triticale. PhD thesis Universität Göttingen: 1-63.
62 Zong SB and Yao JX (1993) Cytogenetic studies on a reciprocal chromosome translocation between 1B and 4A in common wheat. Proc 8th Int Wheat Genet Symp, Beijing China: 279-281.
63 Nakata N, Ali AM, Tomita M and Yasumuro Y (1993) Translocated chromosomes detected in Japanese common wheat varieties. Proc 8th Int Wheat GenetSymp, Beijing China: 273-286.
64 Taketa S, Nakazaki M and Yamagata H (1993) Interchange between the wheat chromosomes of hexaploid triticale. Proc 8th Int Wheat GenetSymp, Beijing China 287-292.
65 Ali AM, Nakata N and Yasumuro Y (1994) Identification of translocated chromosomes in a Japanese common wheat variety Saitama 27. Wheat Inf Serv 79: 37-41.
66 Ali AM, Nakata N, Tomita M and Yasumuro Y (1994) Identification and breeding significance of translocated chromosomes in a Japanese variety Eshimashinriki. Breed Sci 44: 391-396.
67 Berzonsky WA (1993) Detection of quadrivalents in Brazilian wheat 'Frondoso'. Wheat Inf Serv 77: 19-22.
68 Friebe B, Tulenn NA and Gill BS (1995) Standard karyotype of *Triticum searsii* and its relationship with other S-genome species and common wheat . Theor Appl Genet 91 248-254.

Nationality Code

AFG	Afghanistan
AGL	Angola
ALB	Albania
ALG	Algeria
ARG	Argentina
AUS	Australia
AZR	Azores
BEL	Belgium
BDG	Bangladesh
BGR	Bulgaria
BOL	Bolivia
BRA	Brazil
CAN	Canada
CHL	Chile
CHN	China
CNR	Canary Islands
COL	Columbia
CSK	Czechoslovakia <1990
CYP	Cyprus
DDR	German Dem Rep, 1949-1990
DNK	Denmark
ECU	Ecuador
EGY	Egypt
EIR	Ireland
ESP	Spain
EST	Estonia
ETH	Ethiopia
FIN	Finland
FRA	France
FRG	Fed Rep Germany, 1949- 1990
GBR	Great Britain
GER	Germany <1949 and >1990
GRC	Greece
GTM	Guatemala
HUN	Hungary
IDN	India
IRN	Iran
IRQ	Iraq
ISL	Israel
ITA	Italy
JOR	Jordan
JPN	Japan
KEN	Kenya
KOR	Korea
LBN	Lebanon
LBY	Libya
LSO	Lesotho
MAR	Morocco
MDG	Madagascar
MEX	Mexico
NER	Niger
NGA	Nigeria
NDL	Netherlands
NOR	Norway
NPL	Nepal
NZL	New Zealand
OST	Austria
PAK	Pakistan
PER	Peru
PHI	Philippines
POL	Poland
POR	Portugal
PRY	Paraguay
ROM	Rumania
SAF	South Africa
SAU	Saudi Arabia
SCH	Switzerland
SDN	Sudan
SWE	Sweden
SYR	Syria
TAN	Tanzania
TCD	Chad
TUN	Tunisía
TUR	Turkey
TWN	Taiwan
URU	Uruguay
USA	USA
USS	USSR<1991
VEN	Venezuela
YEM	Yemen
YUG	Yugoslavia<1991
ZAI	Zaire
ZIM	Zimbabwe

Wheat Information Service
Number 83: 47-105 (1996)

IV. Gene symbol

Catalogue of gene symbols for wheat: 1996 Supplement

R.A. McIntosh[1], G.E. Hart[2], K.M. Devos[3] and M.D. Gale[3]

[1]Plant Breeding Institute, The University of Sydney, 107 Cobbitty Rd., Cobbitty, N.S.W., Australia, 2570
[2]Department of Soil & Crop Sciences, Texas A&M University, College Station, Texas, USA, 77843
[3]John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk, NR4 7UH, UK

The most recent edition of the Catalogue (9441) appears in the Proceedings of the 8th International Wheat Genetics Symposium held in Beijing, China, 1993, pp. 1333-1500. Revised Guidelines for Nomenclature of Biochemical/Molecular Loci (including QTLs) in Wheat and Related Species were included with the 1994 Supplement. Further proposals were included in the 1995 Supplement.

This Supplement has been offered to the editors of Annual Wheat Newsletter and Wheat Information Service for inclusion in the respective journals.

As the Catalogue evolves, the co-ordinators do not always make appropriate changes to past entries. Researchers and readers are encouraged to advise updatings and errors to make the Catalogue more useful to others.

Additions and revisions to symbols list:

β–Atp	β-ATPase
Cab	Chlorophyl a/b binding protein
Chs	Chalcone synthase
CM16	Chloroform/methanol-soluble protein
Cyp	Cyclophilin
Dor	Dormancy associated
Esi	cDNAs corresponding to 'early-salt-induced' mRNAs
Gsp	Grain softness related protein
Hsp	Heat shock protein
Kb	Reaction to *Tilletia indica*
Pk	Protein kinase
PsbO	Photosystems II protein
Sbe	Starch branching enzyme
SuPm	Suppressor of powdery mildew resistance
SuLr	Suppressor of leaf rust resistance
tsn	Insensitivity to tan spot toxin
Tha	Thaumatin
VAtpA	Vacuolar ATPase subunit A
VAtpB	Vacuolar ATPase subunit B
Vdac	Voltage-dependent anion channels
Wsip	Water-stress-induced protein
Wsm	Reaction to wheat streak mosaic virus

Additions to Laboratory Designators list

abl Forster, J.W.
Institute of Biological Sciences,
Sir George Stapleton Building,
University of Wales,
Aberystwyth,
Dyfed SY23 3DD, UK

cr Robinson, C.
Dept. of Biological Sciences,
University of Warwick,
Coventry, CV4 7AR, UK

fba (cv Courtot clones)
Leroy, P.
Station d'Amélioration des
Plantes de Clermont-Ferrand,
INRA, Domaine de Crouelle,
F-63039 Clermont-Ferrand Cedex,
France

ggo Jakobsen, K.S.
Division of General Genetics
University of Oslo
Pb. 1031 Blinders
N-0316
NORWAY

pkg Gausing, K.
Department of Molecular Biology,
Aarhus University,
C.F. Møllers Allé, Bldg. 130,
DK. 8000 Århus,
Denmark

ttu (cDNAs corresponding to stress-responsive proteins and 'known-function' genes)
Nguyen, H.
Department of Plant and Soil Science,
Texas Tech University,
Box 42122,
Lubbock, TX 79409-2122, USA

cmwg (Barley cDNAs)
Graner, A. (see mwg)

csc Chandler, P.M.
Division of Plant Industry
CSIRO, Black Mountain
GPO Box 1600
Canberra, ACT2601
Australia

csu Coe, E.

fbb (cv Chinese Spring clones)
Leroy, P. (see fba)

fdp DuPont, F. M.
USDA-ARS,
Western Regional Research Center,
800 Buchanan Street,
Albany, CA94710,
USA

labc (Barley cDNAs)
Shewry, P.
IACR-Long Ashton Research Station,
Long Ashton,
Bristol, BS18 9AF, UK

rz (Rice cDNA clones)
Sorrells, M.E. (see bcd)

tav Breiman, A.
Tel Aviv University,
University Campus,
Ramat Aviv,
Israel

ubp Spagnoletti, P.
Dip. Biologia, Difesa e Biotecnologie,
Agro-Forestali,
Universita della Basilicata,
85, Via N. Sauro,
I-85100 Potenza, Italy

ucd Dvorák, J.
University of California,
Dept. of Agronomy and
Range Science,
Davis,
California CA95616, USA

whe Anderson, O.
USDA,
ARS - WRRC,
800 Buchanan Street,
Albany CA94710, USA

zens Schuch, W.
Zeneca Plant Science
Jeolatts Hill Research Station
Bracknell
Berkshire RG12 6BY
UK

utv D'Ovidio, R.
Università della Tuscia,
Dipartimento di Agrobiologia
e Agrochimica,
Via S. Camillo de Lellis,
01100 Viterbo, Italy

wsu Walker-Simmons, M.K.
Wheat Genetics, Quality and
Disease Research Unit,
209 Johnson Hall,
Washington State University,
Pullman WA 99164-6420, USA

Organisation of the Catalogue

ma: Reference to mapping information involving agronomic and morphological traits and molecular markers under gene entries will be restricted to values of less than 10 cM. Values higher than this would be of less use in genetics and plant breeding and, in any case, should be available from the genetic linkage section of the Catalogue or from genetic maps.

DNA Markers:

Three revisions have been made in the organization of the DNA Markers section in this supplement, as follows:

1. Markers in homoeologous chromosome groups 4, 5 and 7 (with the exception of those in *T. monococcum* chromosome $4A^m$; see #2 below) are listed in groups composed of loci located in homoeologous segments. The groups include the six classical homoeologous arm groups, namely, 4S (4AL:4BS:4DS), 4L (4AS:4BL:4DL), 5S (5AS:5BS:5DS), 5L (5AL:5BL:5DL), 7S (7AS:7BS:7DS) and 7L (7AL:7BL:7DL), and five new groups, 4AL:4BL:4DL, 5AL:4BL:4DL, 4AL:5BL:5DL, 7BS:5BL:7DS, and 7AS:4AL:7DS. Evidence is not available regarding the correct group location for a few of the markers listed in groups 4S, 4L, and 7S; a double asterisk (**) after the locus reference identifies these markers.

2. Markers in *T. monococcum* $4A^m$ are listed separately (under $4A^mS$, $4A^mL$, or $4A^m$), due to the several rearrangements that distinguish 4A and $4A^m$.

3. Superscripts appended to locus references designate the species in which loci were analyzed, as follows,

'1' *T. aestivum,*
'2' *T. turgidum,*
'3' *T. monococcum,*
'4' *T. tauschii,* and
'5' Species hybrid,

with the exception that the superscript is omitted for markers studied only in *T. aestivum*..

Group 1S

Revise:

Xpsr13(Gli-1-1)-1A,B,D; delete 9441 as reference for the synonym and insert '1130,1129'.

Xcsc19(Adh)-1A,B,D; in the synonym column, insert *'Xadh3'-1D'* in place of *'Xadh3'*.

Xhhu(Pdk1)-1A,B,D; change the reference for the synonym to '138'.

XLhcb1-1A,B,D; change the probe entry to 'Primers for exon of wheat gene *Lhcb1*1*'.

Xmsu488(Lec)-1A,B,D; delete 9441 as a reference for the synonym and insert '1130,1129'.

Xpsr82(Em)-1A,B,D; place the reference for the locus in square brackets and change the reference for the synonym to '269'.

Xpsr121-1A,B,D; delete (but do not delete *'Xpsr121(Glb3)-1A,B,D'*).

Xpsr121(Glb3)-1A,B,D; change the reference for the locus to '140' and place it in square brackets, change the synonym column to '[*Xpsr121-1A,B,D* (140), *XGlb3-1A,B,D* (342)]', and add the following comment: 'The clones PSR121 and pLW2.1 (*Xwia484(Glb3)-7A,B,D*) detect the same loci (96125).'

Xpsr361(Pgk1)-1A,B,D; change the reference for the synonym to '138'.

Xwia482(Glb)-1A,B,D; change the reference for the synonym to '342' and add the following comment: 'The clones PSR121 and pLW2.1 (*Xwia484(Glb3)-1A,B,D*; *7A,B,D*) detect the same loci (96125).'

Add:

XChs3-1A (9668)[1,3,5].	CHS3 (9671).	(2A).
XGlu3-1A (9668)[1,3,5].	pTdUCD1 (9658).	
XTri-1A (9668)[1,3,5].	Tri25-11 (9688).	
Xabc156-1A,B,D (9666).	ABC156 (96110).	
Xabc249-1A (96119)[3].	ABC249 (96110).	
Xabg500-1A (9668)[5].	ABG500 (96110).	
Xbcd98-1A.1 (9666)[1],(9668)[1,5].	BCD98 (96124).	(7B,D).
Xbcd98-1A.2 (9666).	BCD98 (96124).	(5A, 7B).
Xbcd249-1A (9668)[5], *1B,D* (9685)[1].	BCD249 (96124).	
Xbcd340-1B (9666).	BCD340 (96124).	(6B).
Xbcd446-1A (9668)[5].	BCD446 (96124).	
Xbcd1072-1A (9666)[1],(9668)[5], *1D* (9666)[4].	BCD1072 (96124).	
Xbcd1124-1A (9668)[5], *1B* (9666)[1].	BCD1124 (96124).	
Xbcd1434-1A (9668)[3,5], *1D* (9615)[1].	BCD1434 (96124).	
Xbcd1796-1A (9668)[5], *1B* (9666)[1].	BCD1796 (96124).	
Xcdo99-1D (9666)[4].	CDO99 (96124).	
Xcdo388-1B (9666)[1], *1D* (9666)[4].	CDO388 (96124).	(2B, 4A, 5A, 6A).
Xcdo426-1A (9666).	CDO426 (96124).	
Xcdo442-1A,B,D (9685).	CDO442 (96124).	

Xcdo580-1A (9668)[1,3,5],(9666)[1]. CDO580 (96124).
Xcdo658-1A (9668)[3,5]. CDO658 (96124).
Xcdo1173-1A (9668)[3,5], *1B* (9666)[1]. CDO1173 (96124).
Xcdo1188-1A (9668)[3,5]. CDO1188 (96124).
Xcdo1340-1B (9666). CDO1340 (96124).
XChs-1A [96119][3]. [*XChs3-1A* (96119)]. pcCHS11 (96120).
Xcmwg645-1A.1 (9668)[3,5].
[*Xmwg645-1A.1* (9668)]. cMWG645 (96109). (1AL,BL, 5A).
Xcsih69-1A [9666][5]. [*csIH69-1A* (9666)]. csIH69 (541). (1DS,L, 2D).
Xcsih69-1D.1 [541][4]. [*csIH69* (541)]. csIH69 (541). (1A, 1DL, 2D).
XksuD14-1A.1 (9666)[1],(9668)[3], *1B* (96117,9666)[1],
1D (309,9666)[4], 1D.1,.2 (9666)[1].
pTtksuD14 (309)
XksuE18-1A (9668)[1,5],(9666)[1], *1B* (96117,9666)[1], *1D* (309,9666)[4].
pTtksuE18 (309). (6B, 7A,B).
XksuE19-1B (96117,9666)[1], *1D* (309,9666)[4]. pTtksuE19 (309).
XksuF43-1B.1,.2 (9666). pTtksuF43 (309). (2D, 4D,
5D, 6D).
XksuG9-1A (9666)[1], *1B* (96117)[1], *1D* (309,9666)[4].
pTtksuG9 (309). (1D).
XksuH9-1B (96117)[1], *1D* [309,9666][4].
[*XksuH9(D)-1D* (309)]. pTtksuH9. (1AL, 2A,D,
4A, 5A, 7A).
XksuM148-1B (96117). pTtksuM148 (309).(1D).
Xlabc882(Gli-1)-1A [9668][1,3,5],[9666][1], *1B,D* [9666][1].
[*XGli1-1A* (9668,9666)]. pcP387 (9670).
Xlabc882(Gli-3)-1A [9668][1,3,5],[9666][1], *1B* [9666][1].
[*XGli3-1A* (9668,9666)]. pcP387 (9670).
Xmwg60-1A (9668)[1,5]. MWG60 (96109).
Mapping of the same $1A^m$ locus with MWG60 and MWG2048 was reported in 96119.
Xmwg67-1A (9666). MWG67 (96109). (6A).
Xmwg68-1A (9668)[5], *1B* (9666)[1]. MWG68 (96109).
Xmwg835-1A.1,.2 (96119)[3]. MWG835 (96109). (2A, 5A).
Mapping of the same $1A^m$, $2A^m$, and $5A^m$ loci with MWG835 and MWG920 was reported in 96119.
Xmwg837-1B.1,D (9666). MWG837 (96109). (1BL).
Xmwg920-1A.1,.2 (96119)[3]. MWG920 (96109). (2A, 5A).
Mapping of the same $1A^m$, $2A^m$, and $5A^m$ loci with MWG920 and MWG835 was reported in 96119.
Xmwg938-1B,D (9666). MWG938 (96109). (7A).
Xmwg2021-1A.1 (9668)[3,5], *1A.2* (9668)[1]. MWG2021 (96109). (2A, 3A).
Xmwg2048-1A (96119)[3]. MWG2048 (96109).
Mapping of the same $1A^m$ locus with MWG60 and MWG2048 was reported in 96119.
Xmwg2083-1A (9668)[5]. MWG2083 (96109).
Xpsr149-1D (9666)[4]. PSR149 (429). (6A,B,D).
Xpsr540-1A (96119)[3]. PSR540 (9547). (2A,B,D, 7B).
Xpsr549-1A.2 (9547). PSR549 (182). (1AL, 2B, 3A).
Xpsr963-1A (9547), *1B* (9669). PSR963. (5A).
Xpsr1327-1D (9547). PSR1327. (1AL, 4A, 5D).
Xrz166-1B (9666). RZ166 (96111).
Xrz244-1A (9666). RZ244 (96111).
Xutv1(Glu-1-1)-1A [9691]. UTV1F/UTV1R.
Xutv2(Glu-1-1)-1B [9691]. UTV2F/UTV2R.
Xutv3(Glu-1-1)-1D [9691]. UTV3F/UTV3R.

Xutv4(Glu-1-2)-1A,B,D [9691]. UTV4F/UTV4R.
Xubp19-1A.1,B.1,D.1 (9547). pTdubp19.
Xubp19-1D.2 (9547). pTdubp19.
Xubp22-1B.2 (9547). pTdubp22. (1BL, 3B).
Xwg789-1A (9668)[5], *1D* (9666)[4]. WG789 (96124).
Xwg811-1A (9668)[5], *1B* (9666)[1], *1D* (9666)[4]. WG811 (96124).
Mapping of the same 1A locus with WG789 and WG811 was reported in 9668.
Xwhs179-1B,D.1 (9666). WHS179 (96124).
Xwhs179-1D.2 (9666). WHS179 (96124).

Group 1L
Revise:
XEsi47; change symbols for loci to *'Xucd110(Esi47)'*, add '(96119)[3].' as a reference for the 1A locus, and add *'XEsi47'* as a synonym for each locus.
Xglk558-1D; add '(2B,D).' in the last column.
Xpsr549-1A; change symbol for locus to *'Xpsr549-1A.1'* and replace last column entry with '(1AS, 2B, 3A).'.
Xpsr946-1D; add (186) as reference, and in the last column, add '3A' and replace 7A with '7AS,AL'.
Xtam2-1A,B,D and *Xtam7-1A,B.D*; add '(9666)[1]' as reference.
Xpsr462(Pgk)-1A,B,D; add the following comment: 'Mapping of the same $1A^m$ locus with clones P7 and BCD738 was reported in 9668.

Delete previous corresponding entries and substitute:
Xglk136-1B (594,9666). pTag136 (594).
Xglk163-1D (594)[1],(9666)[4]. pTag163 (594).
Xglk710-1A (594)[1],(9668)[3]. pTag710 (594).
XksuD49-1B (96117)[1], *1D* (309)[1,4],(9666)[1]. pTtksuD49 (309).
The arm location of *XksuD49-1D* in *T. tauschii* was not reported in 309.
Xwye838(Adpg2)-1A,B,D (9546,9547). pAGP-L101(9655) [pSh2.25].

Add:
ATPase-1D (9666). cNP5 (9692).
XGlb1-1A (9668)[3]. Subclone of λHv29(9683).
Xabc151-1D (9666)[4] . ABC151 (96110).
Xabc152-1A.1,.2 (9668)[3,5]. ABC152 (96110). (7A).
Xabc160-1A (9668)[5]. ABC160 (96110).
Xabc257-1A (96119)[3]. ABC257 (96110).
Xabc261-1A (9668)[3]. ABC261 (96110).
Xabg55-1A.1,.2 (96119)[3]. ABG55 (96110). (3A, 4A, 5A).
Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG55 and ABG387 was reported in 96119.
Xabg373-1A,B (9666)[1], *1D* (9666)[4]. ABG373 (96110).
Xabg387-1A.1,.2 (96119)[3]. ABG387 (96110). (3A, 4A, 5A).
Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG387 and ABG55 was reported in 96119.
Xabg452-1A (9666)[1],(9668)[1,3,5]. ABG452 (96110).
Xabg464-1A (9668)[3]. ABG464 (96110).
Xbcd12-1A (9668)[1,3,5], *1B* (9666)[1]. BCD12 (96124).
Xbcd22-1A (9668)[5]. BCD22 (96124). (3D).
Xbcd200-1A (9668)[5], *1B* (9666)[1]. BCD200 (96124).
Xbcd207-1A (9668)[5]. BCD207 (96124).
Xbcd249-1A (9668)[3]. BCD249 (96124).
Xbcd265-1A (9666)[1],(9668)[5]. BCD265 (96124). (4D, 5A).

Xbcd304-1A (9668)[5], *1B* (9666)[1].	BCD304 (96124).
Xbcd338-1B (9666).	BCD338 (96124).
Xbcd386-1A (9668)[5], *1B* (9666)[1].	BCD386 (96124).
Xbcd441-1B (9666).	BCD441 (96124).
Xbcd442-1A (9668)[3,5], *1B* (9666)[1].	BCD442 (96124).
Xbcd454-1A (9666)[5].	BCD454 (96124).
Xbcd508-1A (96119)[3], *1B,D* (9666)[1].	BCD508 (24,96124). (5A,B).
Xbcd592-1A (9668)[5].	BCD592 (96124).
Xbcd738-1A (9668)[5].	BCD738 (96124).

Mapping of the same locus with clones BCD738 and P7 [*(Xpsr462(Pgk)-1A*] was reported in 9668.

Xbcd762-1A (9668)[5], *1B* (9666)[1].	BCD762 (96124).
Xbcd808-1A.1 (9666)[1],(9668)[1,3,5],*1A.2* (9666)[1].	BCD808 (96124). (4A).
Xbcd921-1A (9668)[5].	BCD921 (96124).
Xbcd1150-1B.1 (9666).	BCD1150 (96124).
Xbcd1150-1B.2 (9666).	BCD1150 (96124).
Xbcd1261-1A (96119)[3], *1B,D* (9666)[1].	BCD1261 (24,96124).
Xbcd1407-1A (9666).	BCD1407 (96124). (6B).
Xbcd1449-1B (9666).	BCD1449 (96124).
Xbcd1514-1B (9666).	BCD1514 (96124).
Xbcd1562-1B (9666).	BCD1562 (96124).
Xbcd1889-1A (9666).	BCD1889 (96124).
Xbcd1930-1A (9666)[1],(9668)[5], *1D* (9668)[1].	BCD1930 (96124).
Xbg522-1D (9666)[4].	BG522 (96110).
Xbg542-1D (9666)[4].	BG542 (96110)
Xbg958-1D (9666)[4].	BG958 (96110).
Xcdo89-1D (9666).	CDO89 (96124).
Xcdo92-1B (9666).	CDO92 (96124).
Xcdo98-1A,B (9666).	CDO98 (96124).
Xcdo105-1A (9668)[1,5].	CDO105 (96124). (3B).
Xcdo278-1B (9666).	CDO278 (96124).
Xcdo312-1A (9666)[1], (9668)[5], *1D* (9666)[1].	CDO312 (96124).
Xcdo346-1B (9666).	CDO346 (96124). (5D).
Xcdo393-1A (9666)[1],(9668)[3].	CDO393 (96124).
Xcdo473-1A (9666).	CDO473 (96124).
Xcdo572-1A (9668)[3,5].	CDO572 (96124).
Xcdo637-1B (9666).	CDO637 (96124).
Xcdo1160-1A (9666).	CDO1160 (96124).
Xcdo1189-1B (9666).	CDO1189 (96124). (5A,B,D).
Xcdo1396-1A (9668)[5].	CDO1396 (96124).
Xcdo1420-1D (9666).	CDO1420 (96124).
Xcmwg645-1A.2 (9668)[5], *1B* (9666)[1]. [*Xmwg645* (9668,9666)].	cMWG645 (96109). (1AS, 5A).
Xcmwg676-1A (9668)[1,3,5]. [*Xmwg676-1A* (9668)].	cMWG676 (96109).
Xcmwg693-1D (9666).	cMWG693 (96109).
Xcmwg701-1A (9668)[5],(96119)[3], *1D* (9666)[1]. [*Xmwg701-1A* (9668,96119)].	cMWG701 (96109). 5A.

Mapping of the same 1A and 5A loci with cMWG701 and pKG1490 [*Xpkg1490(Cab2)-1A* and *Xpkg1490(Cab2)-5A*] was reported in 9668 and 96119.

Xcmwg706-1A (9666)[1],(9668)[3,5].
[*Xmwg706-1A* (9666,9668)]. cMWG706 (96109).

Xcmwg733-1A [9668][3,5],(9666)[1],*1B,D* (9666)[1].
[*Xmwg733-1A* (9668,96119)]. cMWG733 (96109).

Xcmwg758-1A (9668)[1,3,5],*1B* (9666)[1].
[*Xmwg758-1A* (9668,9666)]. cMWG758 (96109).

Xcsa117-1D [9666][4]. [*XcsA117-1D* (9666)]. csA117 (541).

Xcsih52-1D [9666][4]. [*XcsIH52-1D* (9666)]. csIH52 (541).

Xcsih69-1D.2 [541][4]. [*XcsIH69* (541)]. csIH69 (541). (1A, 1DS, 2D).

Xcsl24-1D [9666][4]. [*XcsL24-1D* (9666)]. csL24 (541).

Xcsl26-1D [9666][4]. [*XcsL26-1D* (9666)]. csL26 (541).

Xggo1(Em)-1A [9673][3].[*XEm-1A* (9673)]. pB19.1 (9681).

XksuE3-1A (9666). pTtksuE3 (309). (2A,D, 3A, 4A, 6A, 7A,D).

XksuE8-1A (9668)[1,5], *1B* (96117)[1], *1D* (309,9666)[4].
pTtksuE8 (309).

XksuE11-1A.1,.2,1B.1,.2 (9666)[1], *1D* (9666)[1,4].
pTtksuE11 (309).

A *T. aestivum* 1BL *XksuE11* locus was also reported in 96117.

XksuG2-1B (96117)[1], *D* (309,9666)[4],(9666)[1]. pTtksuG2 (309).

XksuG30-1A (96119)[3]. pTtksuG30 (309). (2D, 4A, 6A,B).

XksuG34-1A (9668)[1,3,5], *1B* (9666)[1], *1D* (309,9666)[4].
pTtksuG34 (309). (7A,B).

XksuG55-1D.1,.2 [309][4],(9666)[4].
[*XksuG55(D),(E)-1D* (309)]. pTtksuG55 (309). (7A, 4D).

XksuH9-1A (9666). pTtksuH9 (309). (1BS, 2A,D, 4A, 5A, 7A).

XksuH14-1A (9666). pTtksuH14 (309). (6B).

XksuI27-1B,D.1,D.2 (9666)[1], *1D* (9666)[4]. pTtksuI27 (309).

XksuM114-1B (96117)[1], *D* (9666)[4]. pTtksuM114 (309).

Xmsu433(Lec)-1A [9668][1,3,5].
[*XLec-1A* (9668)]. pNVR20 (9632).

Xmwg10-1A (96119)[3]. MWG10 (96109).

Xmwg69-1B (9666). MWG69 (96109). (3B).

Xmwg504-1A (9668)[3,5]. MWG504 (96109).

Xmwg632-1A (9666). MWG632 (96109).

Xmwg710-1A [9668][1,3]. MWG710 (96109). (7A, 4A, 7D)

Xmwg837-1B.2 (9666). MWG837 (96109).

Xmwg912-1A (9666),(9668), *1B* (9666). MWG912 (96109).

Xmwg947-1A (96119)[3]. MWG947 (96109).

Xmwg984-1A (9668)[3,5]. MWG984 (96109).

Xmwg2028-1A (96119)[3]. MWG2028 (96109).

Xpkg1490(Cab2)-1A [9668][5],[96119][3].
[*XCab2-1A* (9668)]. pKG1490 (9690). (5A).

Mapping of the same 1A and 5A loci with pKG1490 and MWG701 was reported in 9668 and 96119.

Xpsr95(Em)-1A,B,D (9547). PSR95.

Xpsr375-1A (96119)[3]. PSR375 (9547). (4A,B,D, 5B,D).

Xpsr544-1A,B,D (9547). PSR544.

Xpsr648-1B (9547). PSR648. (4A, 7A,D).

Xpsr1201-1A (9547). PSR1201 [a39 (159)].
(5A,4D, 5B).
Xpsr1327-1A (9547). PSR1327 (9541). (1DS, 4A, 5D).
Xtav1931(β-Atp)-1A,B,D (9547) TAV1931 (9659).
Xtav1960(Dac2)-1A,B,D (9550). Tavdac2 (9663).
Xubp22-1B.1 (9547). pTdubp22. (1BS, 3B).
Xwg180-1A (9668)[5]. WG180 (96124). (7BS,L).
Xwg222-1D (9666)[4]. WG222 (96124).
Xwg241-1A (9668)[3], *1A,D* (9666)[1], *1D* (9666)[4]. WG241 (96124).
Xwg605-1A (9666)[1],(9668)[5], *1B* (9666)[1]. WG605.
Xwg983-1A (9668)[1,5]. WG983 (96124).
Xwhe1(Glu-1)-1A [9666][1],[9668][1,3,5].
[*XGlu1-1A* (9666)]. pwhe1(Dy10) [pDY10A] (9689).
Xwsu6(Dor2)-1A [9668][3,5].
[*XDor2-1A* (9666), *XEm-1A* (9673)].
pMA1959 (9674).
Xzens1(Adpg4)-1A [9668][3], *1D* [541][4].
[*XAga7-1A* (9666), *XAga7* (541)].
WE:aga7 (774).

Group 1
Note:
Xglk136, *Xglk163*, *Xglk710* and *XksuD49* moved to 1L.
XksuD16-1D; add '(5D).' in the last column.

Add:
Xcdo127-1B (9666). CDO127 (96124). (3A).
Xcdo618-1B (9666). CDO618 (96124).
Xcdo675-1D (9666). CDO675 (96124).
Xcsiha117-1D [541][4]. [*XcsIHA117* (541)]. csIHA117 (541).
Xcsl140-1D [541][4]. [*XcsL140* (541)]. csL140 (541).
XksuM112-1B (96117)[1], *1D* (309)[4]. pTtksuM112 (309).
XksuM113-1D (9666)[4]. pTtksuM113 (309).
XksuM148-1D (309)[4]. pTtksuM148 (309).
(1B).
Xmwg77-1B (9669). MWG77 (96109). (5A).
Xpsr386-1A [9669]. [*Xpsr386.1* (9669)]. PSR386. (3B, 5A, 7A).
Xpsr2019(Aba8)-1A,B [9669].
[*XABA8* (9669)]. ABA8 (323). (2A,B,D).
Xwg232-1A [9669]. [*Xwg232.4* (9669)] WG232 (96124). (4A, 5A, 7A).
Xwg908-1A [9669]. [*Xwg908.1* (9669)]. WG908 (96124). (5AL,B).

Group 2S
Revise:
Xpsr108-2A,B,D and *Xpsr137-2A,B,D*; add (9547) as reference.
Xpsr549-2B; replace last column with '(1AS, 1AL, 3A)'.
Xpsr649-2A,D; add '(3D).' in last column.
Xpsr946-2D; add '3A' and replace 7A with '7AS,BL' in the last column.
Xpsr899-2B; add '(6B).' in the last column.

Delete previous corresponding entries and substitute:
Xglk578-2B [594](96126).
[Xglk578b (594)]. pTag578.

XksuD18-2A (9652)[1], *2D.1,.2* [309][1,4].
[*XksuD18(A)-2D* (309),
XksuD18-2D(1) (9441);
XksuD18(B)-2D (309),
XksuD18-2D(2) (9441)]. pTtksuD18. (4D).
The arm locations of the *T. tauschii XksuD18* loci were not reported in 309.
XksuF19-2A,B (96126), *2D* (309,96126). pTtksuF19. (6B,D).
Xpsr109(RbcS)-2A,B,D.1,.2,.3 [952,186].
[*Xpsr109-2A,B,D(1),(2),(3)* (952,186)].
PSR109.
Xtam18-2B (179,9652). TAM18 (179).

Add:
Xabg378-2A (96119)[3]. ABG378 (96110). (7A).
Xabg459 (96119)[3]. ABG459 (96110).
Xbcd18-2B,D (9652). BCD18 (96124).
Xbcd102-2D (9652). BCD102 (96124). (6B).
Xbcd152-2A,B (9652). BCD152 (96124).
Xbcd161-2A (9652). BCD161 (96124).
Xbcd260-2B,D (9652). BCD260 (96124).
Xbcd262-2D (9652). BCD262 (96124).
Xbcd348-2A.1,.2 (9652), *2B,D* (96126). BCD348 (96124).
Xbcd348-2A.2 (9652). BCD348 (96124).
Xbcd611-2D (9652). BCD611 (96124).
Xbcd718-2A,D (9652). BCD718 (96124).
Xbcd855-2A (9652), *2B,D* (96126). BCD855 (96124).
Xbcd1184-2A,B (9652). BCD1184 (96124).
Xbcd1688-2A (9652). BCD1688 (96124).
Xbcd1709-2B (9652). BCD1709 (96124).
Xbcd1970-2A,D (9652). BCD1970 (96124).
Xcdo57-2A (9652). CDO57 (96124). (5A,D, 7A,B,D).
Xcdo64-2A,B,D (96126). CDO64.
Xcdo370-2B (9652). CDO370 (96124).
Xcdo405-2A,B,D (9652). CDO405 (96124).
Xcdo447-2A (9652). CDO447 (96124).
Xcdo456-2A.1,A.2,D (9652). CDO456 (96124).
Xcdo783-2A,B,D (96126). CDO783.
Xcdo1090-2A (9652). CDO1090 (96124). (5A).
Xcdo1281-2A (9652). CDO1281 (96124).
Xcdo1376-2A (9652). CDO1376 (96124).
Xcdo1379-2D (9652). CDO1379 (96124).
Xcdo1479-2D (9652). CDO1479 (96124).
XChs-2A.1 [96119][3]. [*XChs1-2A.1* (96119)]. pcCHS11 (96120). (1A, 2AL).
Xcmwg682-2A,D (9652). cMWG682 (96109).
Xcsih74-2D [541][4]. [*XcsIH74* (541)]. csIH74 (541).
Xfba4-2B (9652). FBA004. (4A).
Xfba29-2B (9652). FBA029.
Xfba38-2D (9652). FBA038.
Xfba65-2D (9652). FBA065. (4A, 6A, 7A).
Xfba70-2A.1,.2 (9652). FBA070.
Xfba82-2A (9652). FBA082.
Xfba83-2D (9652). FBA083.
Xfba88-2D (9652). FBA088.
Xfba106-2A,B (9652). FBA106.

Xfba178-2A (9652).		FBA178.	
Xfba198-2A (9652).		FBA198.	
Xfba272-2A,B,D (9652).		FBA272.	
Xfba280-2A,B (9652).		FBA280.	
Xfba300-2A (9652).		FBA300.	
Xfba341-2D.1 (9652).		FBA341.	
Xfba349-2D (9652).		FBA349.	
Xfba374-2A,B (9652).		FBA374.	
Xfba400-2D (9652).		FBA400.	
Xfbb40-2B (9652).		FBB040.	(6A).
Xfbb47-2B (9652).		FBB047.	
Xfbb61-2A (9652).		FBB061.	
Xfbb62-2B [9652],(9641).	[*Xfbb62-2B.1* (9652)].	FBB062.	
Xfbb72-2A (9652).		FBB072.	
Xfbb121-2B (9652).		FBB121.	(4B, 5B, 7A).
Xfbb274-2B,D (9652).		FBB274.	(3B).
Xfbb279-2D (9652).		FBB279.	
Xfbb289-2A (9652).		FBB289.	
Xfbb329-2A (9652).		FBB329.	
Xfbb347-2B (9652).		FBB347.	
Xfbb359-2A [9652],(9641).	[*Xfba359-2A* (9652)].	FBB359.	(6B).
XksuC2-2A (96119)[3].		pTtksuC2 (309).	(5A, 4B,D).
XksuF11-2B (9652).		pTtksuF11 (309).	(2AL,BL).
XksuH9-2A (96119)[3].		pTtksuH9 (309).	(1A,B,D, 2DL, 4A, 5A, 7A).
Xmwg858-2A (96119)[3].		MWG858 (96109).	
Xmwg950-2B (9652).		MWG950 (96109).	
Xpsr332-2A (96119)[3].		PSR332 (9547).	(4A,B,D).
Xpsr335-2B (9547).		PSR335.	(5D).
Xpsr551-2B (9547).		PSR551.	(6B).
Xpsr920-2A,B,D (9547).		PSR920 (9541).	(4A,B,D).
Xrz69-2B (9652).		RZ69.	
Xrz395-2A (9652).		RZ395.	(5A,D).
Xrz444-2B (9652).		RZ444.	(2DL).
Xtam72-2B (9652).		TAM72 (179).	(3B, 4A, 5B).
Xwsu1(Dor6)-2A,B,D [9652].	[*Xbs128-2A,B,D* (9652)].	pBS128 (9653).	

Group 2L

Revise:

Xpsr102-2A,B,D; add the following comment: 'Mapping of the same $2A^m$ locus with PSR102, ABC451 and CDO588 was reported in 96119.'

Xpsr540; add '(1A).' in the last column.

Xpsr471; change the locus symbol from '*Xpsr471(Gadp)*' to '*Xpsr471(Gapd)*'.

Delete previous corresponding entries and substitute:

XksuD22-2A,B (9652)[1], *2D* (309)[1,4]. pTtksuD22 (309).

The arm location of *XksuD22-2D* in *T. tauschii* was not reported in 309.

XksuF41-2A,B (9547)[1], *2D* (9547)[1],(309)[1,4]. pTtksuF41 (309).

The arm location of *XksuF41-2D* in *T. tauschii* was not reported in 309.

XksuG5-2A (9652)[1], *2B* (96126)[1], *2D* (309)[1,4],(96126)[1].
pTtksuG5 (309).
The arm location of *XksuG5-2D* in *T. tauschii* was not reported in 309.
Xtam8-2D (179,9652). TAM18 (179).

Add:
XChs-2A.2,.3 [96119][3].
[*XChs1-2A.2,.3* (96119)].
pcCHS11 (96120). (1A, 2AS).
XGer-2A (9673)[3]. pWJHGermin (9675).
(4A).
Xabc153-2A (96119)[3]. ABC153 (96110).
Xabc451-2A (96119)[3]. ABC451 (96110).
Mapping of the same $2A^m$ locus with ABC451, CDO588 and PSR102 was reported in 96119.
Xabg496-2A (96119)[3]. ABG496 (96110).
Xbcd111-2D (9652). BCD111 (96124).
Xbcd120-2D (9652). BCD120 (96124).
Xbcd135-2B (9652), *2D* (9615). BCD135 (96124)
Xbcd266-2D (9615). BCD266 (96124).
Xbcd292-2A (9652), *2D* (9615). BCD292 (96124).
Xbcd307-2B (9652). BCD307 (96124). (5B).
Xbcd410-2A,D (9652). BCD410 (96124).
Xbcd445-2B (9652). BCD445 (96124).
Xbcd453-2A (96119)[3], *2B* (9669). BCD453 (24,96124).
Xbcd543-2A (9652). BCD543 (96124).
Xbcd1095-2A,B (9652). BCD1095 (96124).
Xbcd1119-2B (9652). BCD1119 (96124).
Xbcd1231-2A.1,A.2 (9615), *2B* (9652), *2D* (9615).
[*Xbcd1231-2A(1),(2)* (9615)].
BCD1231 (96124).
Xbcd1779-2B (9652). BCD1779 (96124).
Xbg123-2A (96119)[3]. BG123 (96110).
Xcdo36-2B,D (9652). CDO36 (96124).
Xcdo388-2B (9652). CDO388 (96124). (1B,D, 4A, 5A, 6A).
Xcdo588-2B (96119)[3]. CDO588 (24).
Mapping of the same $2A^m$ locus with CDO588, ABC451 and PSR102 was reported in 96119.
Xcdo678-2A,B (9652). CDO678 (96124).
Xcdo684-2B (9652). CDO684 (96124).
Xcdo1008-2D (9652). CDO1008 (96124).
Xcdo1410-2A (9652). CDO1410 (96124).
Xcmwg649-2A (96119)[3].[*Xmwg649-2A* (96119)]. cMWG649 (96109).
Xcmwg660-2B (9652). cMWG660 (96109).
Xcmwg720-2A (96119)[3].[*Xmwg720-2A* (96119)]. cMWG720 (96109).
Xcr872(Psb0)-2A,B,D (9547). p33K-2 (9660).
Xcsih93-2D [541][4]. [*XcsIH93-2* (541)]. csIH93-2 (541).
Xfba8-2A (9652). FBA008. (3B, 4B, 6A, 7D).
Xfba61-2B,D (9652). FBA061.
Xfba62-2B [9652],(9641), *2D* (9652).
[*Xfba62-2B.2* (9652)]. FBA062.
Xfba64-2D (9652). FBA064.

Xfba74-2D (9652).	FBA074.	
Xfba102-2D (9652).	FBA102.	
Xfba111-2D (9652).	FBA111.	(6A,B).
Xfba116-2B,D (9652).	FBA116.	
Xfba199-2B (9652).	FBA199.	
Xfba209-2D.1 (9652).	FBA209.	(5D).
Xfba209-2D.2 (9652).	FBA209.	(5D).
Xfba276-2A [9652],(9641), *2B* (9652). [*Xfbb276-2A* (9652)].	FBA276.	
Xfba310-2B (9652).	FBA310.	(3B,D).
Xfba311-2D (9652).	FBA311.	(3B, 7AS, 7BL).
Xfba314-2A,D (9652).	FBA314.	
Xfba341-2D.2 (9652).	FBA341.	
Xfba345-2B (9652).	FBA345.	(6B).
Xfba359-2B (9652).	FBA359.	(4A, 6B).
Xfba385-2A,B (9652).	FBA385.	
Xfbb9-2D (9652).	FBB009.	(7A).
Xfbb32-2D (9652).	FBB032.	
Xfbb68-2D (9652).	FBB068.	
Xfbb72-2D (9652).	FBB072.	
Xfbb99-2D (9652).	FBB099.	
Xfbb113-2B (9652).	FBB113.	
Xfbb122-2D (9652).	FBB122.	
Xfbb251-2D (9652).	FBB251.	(4D).
Xfbb284-2A,B,D (9652).	FBB284.	
Xfbb335-2B (9652).	FBB335.	
Xfbb377-2D (9652).	FBB377.	(6B).
Xglk558-2B,D (9652).	pTag558 (594).	(1D).
XksuD8-2A,B (96126).	pTtksuD8 (309).	(2D).
XksuD23-2A.1,.2 (96119)[3], *2B* (9652)[1].	pTtksuD23 (309).	(2D).
XksuE3-2A (96119)[3].	pTtksuE3 (309).	(1A, 2D, 3A, 4A, 6A, 7A,D).
XksuE16-2A (9652)[1], *2B* (96126)[1], *2D* (309)[4],(96126)[1].	pTtksuE16 (309).	
The arm location of *XksuE16-2D* in *T. tauschii* was not reported in 309.		
XksuF1-2A (96119)[3].	pTtksuF1 (309).	(5A).
XksuF2-2A (96126)[1], *2D.1,.2,.3,.4* [309][4], *2D* (96126)[1]. [*XksuF2(A)-2D, XksuF2(B)-2D, XksuF2(D)-2D, XksuF2(E)-2D* (309)].	pTtksuF2 (309).	(7D).
The arm locations of the *XksuF2-2D* loci in *T. tauschii* were not reported in 309.		
XksuF11-2A (9652), *2B* (96126).	pTtksuF11 (309).	(2BS).
XksuF15-2A,B (96126)[1], *2D* (309)[4],(9615)[1].	pTtksuF15 (309).	
The arm location of *XksuF15-2D* in *T. tauschii* was not reported in 309.		
XksuF43-2D (96126).	pTtksuF43 (309).	(1B, 4D, 5D, 6D).
XksuG30-2D (309)[4],(96126)[1].	pTtksuG30 (309).	(1A, 4A, 6A,B).
The arm location of *XksuG30-2D* in *T. tauschii* was not reported in 309.		
XksuH9-2D.1,.2,.3 [309][4],(9652)[1]. [*XksuH9(A),(B),(C)-2D* (309)].	pTtksuH9 (309).	(1A,B,D, 2AS, 4A, 5A, 7A).
The arm location of *XksuH9-2D* in *T. tauschii* was not reported in 309.		

XksuH16-2A (9547)[1], *2D* (309)[4],(96126)[1]. pTtksuH16 (309).
The arm location of *XksuH16-2D* in *T. tauschii* was not reported in 309.
XksuI24-2A,B (96126)[1], *2D.1,.2* [309][4], *2D* (96126)[1].
[*XksuI24(A),(B)-2D* (309)].
pTtksuI24 (309).
The arm location of *XksuI24-2D* in *T. tauschii* was not reported in 309.
Xmwg41-2A (96119)[3]. MWG41 (96109). (3A).
Xmwg503-2A (96119)[3]. MWG503 (96109).
Xmwg546-2B (9652). MWG546 (96109).
Xmwg835-2A (96119)[3]. MWG835 (96109). (1A, 5A).
Xmwg920-2A (96119)[3]. MWG920 (96109). (1A, 5A).
Mapping of the same $1A^m$, $2A^m$ and $5A^m$ loci with MWG920 and MWG835 was reported in 96119.
Xmwg949-2A (96119)[3]. MWG949 (96109).
Xmwg2021-2A (96119)[3]. MWG2021 (96109). (1A, 3A).
Xmwg2025-2B (9652). MWG2025. (4B).
Xpsp3-2B (9547). PSP3F/PSP3R.
Xpsr1923-2B (9547). PSR1923. (3B, 7B).
Xrz444-2D (9652). RZ444. (2BS).
Xwg184-2D (9615). WG184 (96124). (4D).
Xwg645-2A,D (96126). WG645.
Xwg996-2B (9652). WG996 (96124).
Xwsu2(Pk)-2B [9652]. [*XKABAG-2B* (9652)]. pKABAg1 (9654).
Xwye1922(Sbe)-2A,B,D (9547). pWBE6 (9661).

Group 2

Note: *Xglk578-2B*, *XksuF19-2D* and *Xtam18-2B* moved to 2S and *XksuF41-2D*, *XksuG5-2D* and *Xtam8-2D* moved to 2L.

Delete: *XksuD18(A)-2,4D.*

Revise:
Xglk546-2B; add '(7B).' in the last column.
XksuD8-2D; add superscripts '[1,3]' to reference.
Xpsr2019(Aba8)-2A,B,D; add '(1A,B).' in last column.
Xtam2-2A,B,B; add '(7B).' in the last column.

Add:
Xbg1485(Ger)-2A (96119)[3]. BG1485 (96110). (4A).
Xcsiha114-2D [541][4].
[*XcsIHA114-2* (541)]. csIHA114-2 (541).
Xcsih69-2D [541][4]. [*XcsIH69* (541)]. csIH69 (541).
Xcsih89-2D [541][4]. [*XcsIH89* (541)]. csIH89 (541).
Xcsih97-2D [541][4]. [*XcsIH97e* (541)]. csIH97 (541). (3D, 5D).
Xfbb4-2B (9652). FBB004.
Xfbb21-2B (9652). FBB021.
Xfbb75-2B (9652). FBB075.
Xfbb212-2A (9652). FBB212.
Xfbb226-2A [9652],(9641), *2B* (9652)
[*Xfba226-2A* (9652)]. FBA226. (4D, 7B).
Xfbb353-2A (9652). FBB353. (3A).
XksuD23-2D (309)[4]. pTtksuD23 (309). (2A,B).
XksuE3-2D (96119)[3]. pTtksuE3 (309). (1A, 2A, 3A, 4A, 6A, 7A,D).

XksuF36-2D [309][4]. [*XksuF36(A)-2D* (309)]. pTtksuF36 (309) (6D).
XksuG49-2D.1,.2,.3,.4 [309][4].
[*XksuG49(A),(B),(C),(D)-2D* (309)].
pTtksuG49 (309).
XksuG57-2D [309][4]. [*XksuG57(C)-2D* (309)]. pTtksuG57 (309). (5D).
XksuM1-2D [309][4]. [*XksuM1(A)-2D* (309)]. pTtksuM1 (309). (4D).
XksuM149-2D [309][4]. [*XksuM149(A)-2D* (309)]. pTtksuM149 (309).
(4D).
Xmwg844-2A (96119)[3]. MWG844 (96109). (4A).
Xmwg2033-2A (96119)[3]. MWG2033 (96109). (4A).
Xpsr1870(Aba12)-2B [9669].
[*XABA12* (9669)]. ABA12 (323).
Xpsr575-2A [9669]. [*Xpsr575.1* (9669)]. PSR575. (5A,D).

Group 3S
Revise: *Xpsr547-3B*; add (9547) as reference.

Delete previous corresponding entries and substitute:
XksuD19-3A (96129)[1], *3D* (309)[1,4]. pTtksuD19.
The arm location of *XksuD19-3D* in *T. tauschii* was not reported in 309.
Xglk683-3A (9655), *3B* (594,96129). pTag683 (594).
Xglk724-3A (96129), *3B* (594,96129), *3D* (96129).
pTag683 (594). (5A, 6A,B,D).

Add:
Xabc171-3A (96119)[3]. ABC171 (96110).
Xabg390-3A (96119)[3]. ABG390 (96110). (4A).
Xabg395-3A (96119)[3]. ABG395 (96110).
Xabg460-3A (9655). ABG460 (96110). (4A).
Mapping of the same $3A^m$ and $4A^m$ loci with ABG460 and MWG584 was reported in 96119.
Xabg471-3A,B (9655). ABG471 (96110).
Xbcd15-3A (9655). BCD15 (96124). (4D).
Xbcd706-3A (9655). BCD706 (96124).
Xbcd907-3B,D (9655). BCD907 (96124).
Xbcd1428-3A (9655). BCD1428 (96124).
Xbcd1532-3A,D (9655). BCD1532 (96124).
Xbcd1802-3D (9655). BCD1802 (96124).
Xbcd1823-3A (9655). BCD1823 (96124).
Xcdo395-3A (9655). CDO395 (96124).
Xcdo407-3D (9655). CDO407 (96124).
Xcdo460-3A,B (9655). CDO460 (96124).
Xcdo549-3D (9655). CDO549 (96124).
Xcdo638-3A (9655). CDO638 (96124).
Xcdo1164-3A,B (9655). CDO1164 (96124).
Xcdo1345-3A (9655). CDO1345 (96124).
Xcdo1435-3A,D (9655). CDO1435 (96124).
Xcmwg691-3A (96119)[3].[*Xmwg691-3A* (96119)]. cMWG691 (96109).
Xfba91-3A,B,D (9655). FBA091.
Xfba127-3A (9655). FBA127. (5B, 7A).
Xfba190-3B,D (9655). FBA190. (5A).
Xfba241-3D (9655). FBA241.
Xfba311-3B (9655). FBA311. (2D, 7AS, 7BL).
Xfba366-3A (9655). FBA366.

Xfbb24-3B (9655). FBB024.
Xfbb142-3B (9655). FBB142.
Xfbb147-3B.1 [9655]. [*Xfbb147-3B* (9655)]. FBB147. (3BL,DL, 6A).
Xfbb166-3B (9655). FBB166. (6A).
Xfbb185-3B (9655). FBB186.
Xfbb315-3B (9655). FBB315.
Xfbb370-3A,D (9655). FBB370.
XksuA6-3A (9655)[1], *3D* (309)[4],(9655)[1]. pTtksuA6 (309).
The arm location of *XksuA6-3D* in *T. tauschii* was not reported in 309.
XksuE2-3A,B,D (96129). pTtksuE2. (3BL,3D, 4B).
XksuF34-3D [309][4],(96129)[1].
[*XksuF34(A)-3D* (309)]. pTtksuF34 (309).
The arm location of *XksuF34-3D* in *T. tauschii* was not reported in 309.
XksuG13-3A,B,D (96129). pTtksuG13.
XksuG53-3A (96129), *3B* (9655), *3D* (9547). pTtksuG53 (309).
XksuI32-3A (96129)[1], *3D.1,.2* [309][4],(96129)[1].
[*XksuI32(A),(B)-3D* (309)].
pTtksuI32 (309).
The arm location of *XksuI32-3D* in *T. tauschii* was not reported in 309.
Xmwg14-3A (9655). MWG14 (96109).
Xmwg22-3A,D (9655). MWG22 (96109).
Xmwg584-3A (96119)[3]. MWG584 (96109). (4A).
Mapping of the same $3A^m$ and $4A^m$ loci with ABG460 and MWG584 was reported in 96119.
Xmwg813-3A (96119)[3]. MWG813 (96109). (4A, 6A).
Xmwg2021-3A (96119)[3]. MWG2021 (96109). (1A, 2A).
Xpsr926-3A,B,D (96129). PSR926.
Xpsr946-3A (96119)[3]. PSR946 (9547). (1D, 2D, 5D, 7AS,AL,DS,DL).
Xtam47-3B (9555). TAM47 (179). (3A,D).
Xttu1934(Hsp16.9b)-3A (9673)[3]. pTaHSP16.9b (9677). (5A).
Xttu1935(Hsp17.3)-3A,B,D (9547). pTaHSP17.3 (9662).

Group 3L
Revise:
XEsi48; change symbols for loci to *'Xucd111(Esi48)'*, add '(96119)[3].' as a reference for the 3A locus, and add *'XEsi48-3A'* as synonym for each locus.
Xpsr549-3A; replace last column with '(1AS, 1AL, 2B).'.
Xtam47-3A,D; add '(3BL).' in the last column.

Delete previous corresponding entries and substitute:
Xbcd115-3A (9655),*3D* [9589].
[*Xcn1BCD115-3D* (9589)]. BCD115 (96124).
Xbcd451-3A (9655),*3D* [9589].
[*Xcn1BCD451-3D* (9589)]. BCD451 (96124).
Xcdo482-3A (9655),*3D* [9589].
[*Xn1cCDO482-3D* (9589)]. CDO482 (96124).
XksuH2-3A (9655)[1], *3B* (96129)[1], *3D* (309)[1,4],(96129)[1].
pTtksuH2 (309).
The arm location of *XksuH2-3D* in *T. tauschii* was not reported in 309.
XksuG48-3B (96129)[1], *3D* [309][4],(9547)[1].
[*XksuG48(B)-3D* (309)]. pTtksuG48 (309). (6A,B,D).
The arm location of *XksuG48-3D* in *T. tauschii* was not reported in 309.

Add:

ATPase-3A,3B.1,B.2 (9655).	cNP5.	
Clone 'cNP5' was obtained from Nam Chua (9641).		
Xabc166-3A (96119)[3].	ABC166 (96110).	
Xabc176-3D (9655).	ABC176 (96110).	
Xabc172-3A.1 (9655).	ABC172 (96110).	
Xabc172-3A.2 (9655).	ABC172 (96110).	
Xabc174-3B,D (9655).	ABC174 (96110).	
Xabc176-3D (9655).	ABC176 (96110).	
Xabg4-3A (96119)[3].	ABG4 (961010).	
Xabg55-3A (96119)[3].	ABG55 (96110).	(1A, 4A, 5A).
Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG55 and ABG387 was reported in 96119.		
Xabg377-3A (96119)[3].	ABG377 (96110).	
Xabg387-3A (96119)[3].	ABG387 (96110).	(1A, 4A, 5A).
Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG387 and ABG55 was reported in 96119.		
Xbcd22-3D (9655).	BCD22 (96124).	(1A).
Xbcd115-3A (9655).	BCD115 (96124).	
Xbcd131-3B,B,D (9547).	BCD131 (96124).	
Xbcd134-3D (9655).	BCD134 (96124).	
Xbcd141-3B (9655).	BCD141 (96124).	
Xbcd147-3B (9655).	BCD147 (96124).	
Xbcd288-3D (9655).	BCD288 (96124).	
Xbcd361-3D (9655).	BCD361 (96124).	
Xbcd366-3A (9655).	BCD366 (96124).	
Xbcd372-3A,D (9655).	BCD372 (96124).	
Xbcd451-3A (9655).	BCD451 (96124).	
Xbcd515-3D (9655).	BCD515 (96124).	
Xbcd809-3B (9655).	BCD809 (96124).	
Xbcd828-3A (9655).	BCD828 (96124).	
Xbcd1380-3B.1,.2 (9655).	BCD1380 (96124).	
Xbcd1418-3B (9655).	BCD1418 (96124).	
Xbcd1555-3B,D (9655).	BCD1555 (96124).	
Xbcd1773-3A (9655).	BCD1773 (96124).	
Xbcd2044-3A (9655).	BCD2044 (96124).	
Xbg131-3B (9655).	BG131.	
Xcdo54-3A (9655).	CDO54 (96124).	
Xcdo105-3B (9655).	CDO105 (96124).	(1A).
Xcdo118-3A (9655).	CDO118 (96124).	
Xcdo127-3A.1,.2 (96119)[3].	CDO127 (24).	(1B).
Xcdo189-3A (96119)[3].	CDO189 (24).	(4A,B,D).
Xcdo281-3A (9655).	CDO281 (96124).	
Xcdo328-3B (9655).	CDO328 (96124).	
Xcdo482-3A (9655).	CDO482 (96124).	
Xcdo583-3B (9655).	CDO583 (96124).	
Xcdo718-3B (9655).	CDO718 (96124).	
Xcdo1174-3A (9655).	CDO1174 (96124).	
Xcdo1406-3D (9655).	CDO1406 (96124).	
Xcsiha258-3D [541][1,4].		
[*XcsIHA258-1* (542)].	csIHA258-1 (541).	
Xfba8-3B (9655).	FBA008.	(2A, 4B, 6A, 7D).

Xfba27-3D (9655).	FBA027.	
Xfba133-3B (9655).	FBA133.	
Xfba167-3B (9655).	FBA167.	
Xfba171-3B (9655).	FBA171.	
Xfba175-3A (9655).	FBA175.	
Xfba213-3B (9655).	FBA213.	
Xfba214-3B (9655).	FBA214.	
Xfba217-3B (9655).	FBA217.	
Xfba220-3B (9655).	FBA220.	
Xfba235-3B (9655).	FBA235.	
Xfba242-3B (9655).	FBA242.	
Xfba310-3B,D (9655).	FBA310.	(2B).
Xfba360-3B (9655).	FBA360.	
Xfba389-3D (9655).	FBA389.	
Xfbb23-3D (9655).	FBB023.	
Xfbb117-3B,D.1,D.2 (9655).	FBB117.	
Xfbb147-3B.1 [9655], *3D* (9655). [*Xfbb147-3B* (9655)].	FBB147.	(3BS, 6A).
Xfbb156-3B (9655).	FBB156.	(5D, 7A).
Xfbb168-3B (9655).	FBB168.	
Xfbb177-3B (9655).	FBB177.	
Xfbb237-3A,D (9655).	FBB237.	(5B).
Xfbb269-3D (9655).	FBB269.	
Xfbb271-3A (9655).	FBB271.	
Xfbb274-3B (9655).	FBB274.	(2B,D).
Xfbb277-3A (9655).	FBB277.	(5B).
Xfbb283-3B (9655).	FBB283.	(6A).
Xfbb293-3A.1,A.2,B (9655).	FBB293.	
Xfbb316-3B,D (9655).	FBB316.	
Xfbb332-3A (9655).	FBB332.	
Xfbb348-3B (9655).	FBB348.	
Xfbb353-3A (9655).	FBB353.	(2A).
Xfbb378-3B (9655).	FBB378.	
Xglk609-3A (96129).	pTag609	
Xglk718-3A,B,D (96129).	pTag718.	
XksuE3-3A (96119)[3].	pTtksuE3 (309).	(1A, 2A,D, 4A, 6A, 7A,D).
XksuD19-3D (9655).	pTtksuD19 (309).	
XksuE14-3D (9655).	pTtksuE14 (309).	(6A,B,D).
XksuG59-3A (96119)[3], *3D* (309)[4],(9655)[1].	pTtksuG59 (309).	
The arm location of *XksuG59-3D* in *T. tauschii* was not reported in 309.		
XksuG62-3A,B (96129)[1], *3D* [309][4],(96129)[1].	pTtksuG62 (309).	
The arm location of *XksuG62-3D* in *T. tauschii* was not reported in 309.		
XksuE2-3B (96119).	pTtksuE2 (309).	3AS,BS,DS, 3D, 4B).
XksuH7-3A (96129), *3B* (9655).	pTtksuH7 (309).	(3D).
XksuH15-3A,B (96129)[1], *3D* (309)[4],(9655)[1].	pTtksuH15 (309).	
The arm location of *XksuH15-3D* in *T. tauschii* was not reported in 309.		
Xmwg11-3A,B (9655).	MWG11 (96109).	
Xmwg12-3A (9655).	MWG12 (96109).	
Xmwg30-3A (9655).	MWG30 (96109).	
Xmwg41-3A (96119)[3].	MWG41 (96109).	(2A).
Xmwg69-3B (9655).	MWG69 (96109).	(1B).
Xmwg571-3A (96119)[3].	MWG571 (96109).	

Xmwg802-3A (9655).		MWG802 (96109).	
Xmwg818-3B (9655).		MWG818 (96109).	
Xmwg961-3A (9655).		MWG961 (96109).	
Xpsr388-3D (9676).		PSR388 (186).	(2A,B,D).
Xpsr649-3D (9547).		PSR649 (186).	(2A,D).
Xpsr1923-3B (9547).		PSR1923.	(2B, 7B).
Xrgc250-3A,B,D (9547).		RGC250.	
Xtav1933(Vdac3)-3A,B,D (9547).		Tavdac3 (9663).	
Xubp20-3A,B,D (9547).		pTdubp20.	
Xubp22-3B (9547).		pTdubp22.	(1BS,1BL).
Xwg110-3A,B,D (9547).		WG110 (96124).	(4B).
Xwg177-3A (9655).		WG177 (96124).	
Xwsu4(Dor4)-3A [9673][3].	[*XDor4-3A* (9673)].	pMA1949 (9674).	

Group 3

Note:

Xglk724-3D and *XksuI32-3D* moved to 3S and *Xglk718-3A,B* and *XksuH2* moved to 3L.

Revise:

Xglk546-3B; add '(7B)' in the last column.

XksuD7-3D; add '(7A,D).' in the last column.

Delete previous corresponding entries and substitute:

XksuG36-3B (96129)[1], *3D* (309)[4],(9589,96129)[1]. pTtksuG36 (309).

The arm location of *XksuG36-3D* in *T. tauschii* was not reported in 309.

Add:

Xbcd1145-3A (9655).		BCD1145 (96124).	
Xcsiha159-3D.1,.2,.3 [541][4].	[*XcsIHA159a,b,c* (541)].	csIHA159 (541).	(5D).
Xcsih72-3D [541][4].	[*XcsIH72* (541)].	csIHA72 (541).	
Xcsih97-3D [541][4].	[*XcsIH97d* (541)].	csIH97 (541).	(2D, 5D).
Xfba330-3D (9655).		FBA330.	
Xfbb324-3D (9655).		FBB324.	
XksuE2-3D (309)[4].		pTtksuE2 (309).	(3AS,BS,L, DS, 4B).
XksuH7-3D (309)[4].		pTtksuH7 (309).	(3AL,BL).
Xmwg688-3D (9655).		MWG688 (96109).	
Xpsr386-3B [9669].	[*Xpsr386.3* (9669)].	PSR386.	(1A, 5A, 7A).

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

Note:

Xabc310, Xcdo484,Xpsr115, Xpsr580, Xpsr1206 and *Xpsr1316* moved to 4AL:5BL:5DL.

Xak466(Nra1), Xbcd93, Xcdo780, Xpsr119, Xpsr160(Plc), Xpsr392, Xpsr470(Wx), Xpsr573, Xpsr604, Xpsr833(Per), Xumc190(Sus) and *Xwye835(Wx)* moved to 7AS:4AL:7DS.

Revise:

Xrsq808(Glob)-4A,B,D; change the reference for the synonym to '718'.

Xpsr332-4A,B,D; add '(2A).' in the last column.

Xpsr1327-4A; replace last column with '(1AL, 1DS, 5D)'.

Delete previous corresponding entry and substitute:
Xwg622-4A (9541), *4B* (9541,96112), *4D* (96112). WG622.

Add:

XGer-4A (9673)[3].	pWJHGermin (9675).	
Xbcd8-4A (9657).	BCD8 (96124).	
Xbcd265-4D (9657).	BCD265 (96124).	(1A, 5A).
Xbcd327-4D (9657).	BCD327 (96124).	(4A).
Xbcd402-4A (9657).	BCD402 (96124).	(5A,4B,D).
Xbcd749-4B (9657).	BCD749 (96124).	
Xbcd808-4A (96112).	BCD808.	(1A).
Xbcd1250-4B (9657).	BCD1250 (96124).	
Xbcd2026-4B (9657).	BCD2026 (96124).	
Xbg1485(Ger)-4A,B,D (9541).	Germin (5961).	(3B).
Xcdo669-4A (9541)[1], *4B* (9672,96128)[5], *4D* (9657)[1].	CDO669 (96124).	
Xcdo795-4B (9657).	CDO795 (96124).	
Xcdo1128-4B (9657).	CDO1128 (96124).	(6B).
Xcdo1338-4A (96112).	CDO1338.	(5A).
Xcdo1400-4A (96112).	CDO1400.	
Xcsc6(Dhn6)-4B,D [9672,96128][5]. [*XDhn6-4B,D* (9672,96128)].	pTZ19R-dhn6 (9673).	(4A).
Xcsu25-4B (9657).	UMC317.	
Xfba4-4A (9657).**	FBA004.	(2B).
Xfba8-4B (9657).	FBA008.	(2A, 3B, 6A, 7D).
Xfba65-4A (9657).**	FBA065.	(2D, 6A, 7A).
Xfba78-4B (9657).	FBA078.	
Xfba147-4A,B (9657).	FBA147.	
Xfbb13-4D (9657).	FBB013.	
Xfbb22-4B (9657).	FBB022.	
Xfbb121-4B (9657).	FBB121.	(2B, 5B, 7A).
XksuE3-4A (9657).**	pTtksuE3.	(1A, 2A,D, 3A, 6A, 7A,D).
XksuG12-4A (9657).	pTtksuG12.	(7A).
Xmwg634-4D (9657).	MWG634.	
Xpsr155-4A,B,D (9541).	PSR155.	
Xpsr541-4D (96112).	PSR541.	
Xpsr921-4A,B,D (9541).	PSR921.	
Xpsr922-4A,B,D (9541).	PSR922.	
Xwg184-4D (96112).	WG184	
Xwg212-4B (96112).	WG212.	(4D).
Xwg622-4A (9541)[1], *4B,D* (9672,96128)[5].	WG622 (24).	
Xwg875-4A,B,D (96112).	WG875.	

4A^{m}S

Xabg55-4A (96119)[3].	ABG55 (96110).	(1A^m, 3A^m, 5A^m).

Mapping of the same 1A^m, 3A^m, 4A^m, and 5A^m loci with ABG55 and ABG387 was reported in 96119.

Xabg387-4A (96119)[3].	ABG387 (96110).	(1A^m, 3A^m, 5A^m).

Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG55 and ABG387 was reported in 96119.

Xabg460-4A.1 (96119)[3].	ABG460 (96110).	(3A[m], 4A[m]L).

Mapping of the same $3A^m$ and $4A^m$ loci with ABG460 and MWG584 was reported in 96119.

Xbcd327-4A (9541,96119)[3],	BCD327 (24).	(4BS).
Xbg1485(Ger)-4A (96119)[3].	BG1485 (24).	(2A[m]).
Xcdo669-4A (9541,96119)[3].	CDO669.	(4AL,BS,DS).
Xcsc6(Dhn6)-4A [9673][3].		
[*XDhn6-4A* (9673)].	pTZ19R-dhn6 (9673).	
		(4BS,DS).
Xmwg584-4A.1 (96119)[3].	MWG584 (96109).	(3A[m], 4A[m]L).

Mapping of the same $3A^m$ and $4A^m$ loci with MWG584 and ABG460 was reported in 96119.

Xmwg635-4A (9541,96119)[3].	MWG635 (96109).	(2A[m]).
Xmwg844-4A (96119)[3].	MWG844 (96109).	(2A[m]).
Xmwg2033-4A (9541,96119)[3].	MWG2033 (96109).	(2A[m]).
Xpsr153-4A (9541,96119)[3].	PSR153.	(4AL,BS,DS).
Xpsr921-4A (9541,96119)[3].	PSR921.	(4AL,BS,DS).
Xpsr922-4A (9541,96119)[3].	PSR922.	(4AL,BS,DS).
Xwg622-4A (9541,96119)[3].	WG622 (24).	(4AL,BS,DS).
Xwg876-4A (96119)[3].	WG876 (24).	

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

Note:

Xbg1485(Ger) and *Xpsr921* moved to 4AL:4BS:4DS.

Xß-Amy-1, *Xbcd1302*, *Xcdo1312*, *Xpsr164*, *Xpsr484(Cat)*, *Xpsr567*, *Xpsr1201* and *Xwg114* moved to 5AL:4BL:4DL.

Xpsr1051 moved to 4AL:4BL:4DL.

Revise:

Xpsr920-4A,B,D; add '(2A,B,D)' in last column.

Xpsr164; add'(1B, 7A).' in the last column.

Delete previous corresponding entry and substitute:

Xucd102(Esi3)-4B,D [9583].		
[*XEsi3-4B,D* (9583)].	pESI3 (9584).	(4AS[m]).

Add:

Xabg484-4A (9547), *B* (9657).	ABG484.	
Xbcd110-4A,B,D (96112).	BCD110.	
Xbcd734-4A,B (96112).	BCD734.	
Xbcd1006-4A (96112)[1], *4B,D* (9672)[5],(96112)[1].	BCD1006.	
Xbcd1051-4B (9657).	BCD1051 (96124).	
Xbcd1092-4A,B,D (96112).	BCD1092.	
Xbcd1117-4D (9657).	BCD117 (96124).	
Xbcd1265-4B (9657).	BCD1265 (96124).	
Xbcd1652-4A (9657,96112), *4B* (96112).	BCD1652 (96124).	
Xbcd1738-4A (9657).	BCD1738 (96124).	
Xcdo38-4A,B,D (96112).	CDO38.	
Xcdo189-4A,B,D (96112).	CDO189.	(3A).
Xcdo488-4A (96112).	CDO488.	
Xcdo541-4A,B,D (96112).	CDO541.	
Xcdo938-4B (9657).	CDO938 (96124).	
Xcdo959-4A (9657).	CDO959 (96124).	(5B).

Xcdo1333-4B,D (96112).	CDO1333.	(5A).
Xcdo1337-4A,B (96112).	CDO1337.	
Xcdo1387-4A (9657)[1], *4B* (9672,96128)[5], *4D* (9672)[5],(96112)[1].	CDO1387.	
Xcdo1395-4B (96112).	CDO1395.	(7A).
Xcdo1401-4B (9657).	CDO1401 (96124).	
Xfba40-4A (9657).	FBA040.	
Xfba41-4B (9657).**	FBA041.	
Xfba78-4A (9657).	FBA078.	
Xfba320-4A (9657).	FBA320.	
Xfbb1-4A (9657).	FBB001.	
Xfbb58-4B (9657).**	FBB058.	
Xfbb227-4A (9657).	FBB227.	
Xfbb332-4A (9657).	FBB332.	
Xfbb336-4D (9657).	FBB336.	
XksuF8-4A,B,D (9541).	pTtksuF8.	
Xmwg2180-4B,D (9672,96128).	MWG2180.	(4A).
Xpsb37-4A,B,D (9541).	PSB37.	
Xpsr648-4A 9541).**	PSR648.	(1B, 7A,D).
Xrz251-4B (9657).	RZ251.	
Xrz574-4A (9657).	RZ574.	
Xrz672-4B (9657).	RZ672.	
Xwg110-4B (9541).	WG110.	(3A).
Xwg181-4A,B,D (96112).	WG181.	
Xwg212-4D (96112).	WG212.	(4B).

$4A^mL$

Xabc310-4A (9541,96119)[3].	ABC310 (96110).	(4AL, 5BL, $7A^m$, 7B).
Xabg390-4A (9541,96119)[3].	ABG390 (96110).	($3A^m$).
Xabg460-4A.2 (96119)[3].	ABG460 (96110).	($3A^m$, $4A^m$S).
Mapping of the same $3A^m$ and $4A^m$ loci with ABG460 and MWG584 was reported in 96119.		
Xabg463-4A (9541,96119)[3].	ABG463 (96110).	
Xabg484-4A (9541,96119)[3].	ABG484 (96110).	(4AS,BL).
Xbcd734-4A (96119)[3].	BCD734 (24).	(4AS,BL).
Mapping of the same $4A^m$ locus with BCD734 and BCD1092 was reported in 96119.		
Xbcd1006-4A (96119)[3].	BCD1006 (24).	(4AS,BL,DL).
Xbcd1092-4A (96119)[3].	BCD1092 (24).	
Mapping of the same $4A^m$ locus with BCD1092 and BCD734 was reported in 96119.		
Xbcd1262-4A (96119)[3].	BCD1262 (24).	(4BL,DL).
Xbcd1652-4A (96119)[3].	BCD1652 (24).	(4AS,BL).
Xcdo484-4A (96119)[3].	CDO484 (24).	(4AL, 5BL, 5DL).
Xcdo541-4A (96119)[3].	CDO541 (24).	(4AS,BL,DL).
Xcdo1387-4A (96119)[3].	CDO1387 (24).	(4AS,BL,DL).
Xcmwg677-4A (96119)[3].[*Xmwg677-3A* (96119)].	cMWG677 (24).	
XksuG10-4A (9541,96119)[3].	pTtksuG10 (309).	(4AL,BL,DL).
XksuG30-4A (96119)[3].	pTtksuG30 (309).	($1A^m$, 2D, $6A^m$, 6B).
XksuH9-4A (96119)[3].	pTtksuH9 (309).	(1A,B,D, $2A^m$, 2D, $5A^m$, $7A^m$, 7A).
Xmwg584-4A.2 (96119)[3].	MWG584 (96109).	($3A^m$,$4A^m$S).
Mapping of the same $3A^m$ and $4A^m$ loci with MWG584 and ABG460 was reported in 96119.		
Xmwg813-4A (96119)[3].	MWG813 (96109).	($3A^m$, $6A^m$).

Xmwg851-4A (9541,96119)[3]. MWG851 (96109).
Xmwg948-4A (9541,96119)[3]. MWG948 (96109). (4AS).
Xmwg2180-4A (9541,96119)[3]. MWG2180 (96109). (4AS,BL,DL).
Xpsr115-4A (9541,96119)[3]. PSR115. (4AL,BL,DL).
Xpsr375-4A (9541,96119)[3]. PSR375. (1A[m], 4BL,DL, 5BL,DL).

Xpsr567-4A (9541,96119)[3]. PSR567. (5AL, 4BL,DL).
Xpsr914-4A (9541,96119)[3]. PSR914. (4AS,BL,DL).
Xpsr920-4A (9541,96119)[3]. PSR920. (4AS,BL,DL).
Xpsr1051-4A (9541,96119)[3]. PSR1051. (4AL,BL,DL).
Xpsr1316-4A (9541,96119)[3]. PSR1316 [L3-17 (1131)]. (4AL, 5BL).

Xttu1936(Hsp26.6a)-4A (9673)[3]. pTaHSP26.6a (9678).
Xucd102(Esi3)-4A (9673)[3]. pESI3 (9584). (4BL,DL).
Xwg464-4A (9541,96119)[3]. WG464 (24). (4AS).

4AL:4BL:4DL

Xbcd1262-4B (9657,96112), *4D* (96112). BCD1262 (96124).
Xpsr1051-4A,B,D (9541). PSR1051.
XksuG10-4A (96112)[1], *4B* (9657,96112)[1], *4D* (309)[4],(96112)[1]. pTtksuG10 (309).
The arm location of *XksuG10-4D* in *T. tauschii* was not reported in 309.
Xmwg2025-4B (9657). MWG2025. (2B).

5AL:4BL:4DL

Delete previous corresponding entry and substitute:
Xwg114-5A [24][1],(9541)[3], *4B,D* [24](9541)(96112)[1].
[XcnlWG114-5A,4B,D (9441)].
WG114 (24).

Add:
Xß-Amy-A1,B1,D1 [951].
[A1:PSR1-5A (951), *Xß-Amy-B1* (682);
B1:PSR1-4A (941), *Xß-Amy-A1* (682);
D1:PSR1-4D (951)]. pcßC51 (524). (2A,B,D).
Xabc305-5A (96119)[3], *4B,D* (9672,96128)[5]. ABC305 (96110). (7A).
Xabc397-5A (96119)[3]. ABC397 (96110).
Xabg366-5A (9657). ABG366.
Xabg394-5A (96119)[3]. ABG394 (96110).
Xabg498-5A (96119)[3]. ABG498 (96110).
Xabg601-4B.1,.2,D.1,.2 (9672,96128)[5]. ABG601.
Xbcd15-4D (9657). BCD15 (96124). (3A).
Xbcd402-5A (9541)[3], *4B* (9657)[1], *4B,D* (9672,96128)[5].
BCD402 (96124). (4A).
A 4AL *Xbcd402* locus was reported in 9657.
Xbcd1302-5A (9541)[3],*4B* [24][1],(9672,96128)[5], *4D* [24][1].
[XcnlBCD1302-5A,4B,D (9441)].
BCD1302 (24).
Xbcd1431-4D.1, D.2 (9657). BCD1431 (96124).
Xcdo20-5A,4B (9657). CDO20 (96124)
Xcdo949-4D (9657). CDO949 (96124).
Xcdo1081-4D (9657). CDO1081 (96124).

Xcdo1312-5A (9541)[3], *4B,D* (9657)[24][1].			
	[*Xcn1CDO1312-5A,4B,D* (9441)].		
		CDO1312 (96124).	(1B).
Xcdo1528-5A,4B (9657).		CDO1528 (96124).	
Xcmwg708-5A (96119)[3].	[*Xmwg708-5A* (96119)].	cMWG708 (96109).	
Xfba177-4B,D (9657).		FBA177.	
Xfbb67-4B (9657).		FBB067.	(7AS, 7BL).
Xfbb178-4B,D (9657).		FBB178.	
Xfbb182-4B (9657).		FBB182.	
Xfbb226-4D (9657).		FBB226.	(2A,B, 7B).
Xfbb249-5A (9657).		FBB249.	
Xfbb255-4B (9657).		FBB255.	
Xfbb330-5A (9657).		FBB330.	
XksuC2-5A (9541)[3], *4B* (96112)[1], *4D* (309)[1,4],(96112)[1].			
		pTtksuC2.	(2A).
The arm location of *XksuC2-5D* in *T. tauschii* was not reported in 309.			
XksuE2-4B (9657).		pTtksuE2.	(3A,B,D).
XksuH11-5A (96119)[3], *4B,D* (9672,96128)[5].		pTtksuH11 (309).	(6D).
Xmtd862(CM16)-4B,D (9541).		pTd78 (9664).	
Xmwg2112-5A (9541)[3], *4B,D* (9672,96128)[5].		MWG2112.	
Xpsb43-4B,D (9541).		PSB43.	
Xpsr39(Fbr)-4B,D (9672,96128)[5].		PSR39.	
Xpsr164-5A,4B,D (585,1189).		PSR164.	
Xpsr375-4B,D (9541,9672,96128).		PSR375 (9547).	(1A, 4A, 5B,D).
Xpsr484(Cat)-5A,4B,D [1179].			
	[*XCat-5A,4B,D* (1179)].	pCat2.1c (83).	
Xpsr567-5A,4B,D (1179).		PSR567.	(7B, 5B,D).
Xpsr1201-5A,4D (1179).		PSR1201 [a39 (159)].	
			(1A, 5B).
Xwg199-5A (9541)[3], *4B,D* (9672,96128)[5].		WG199.	

Group 4

Note: *XksuC2* moved to 5AL:4BL:4DL.

Revise:

XksuF43-4D.1,.2; change last column entry to '(1B, 2D, 5D, 6D).'.

Add:

Xcsiha114-4D.1 [541][4].			
	[*XcsIHA114-1a* (541)].	csIHA114-1 (541).	
Xcsiha114-4D.2 [541][4].			
	[*XcsIHA114-1b* (541)].	csIHA114-1 (541).	
Xfba43-4A (9657).		FBA043.	
Xfba211-4A (9657).		FBA211.	
Xfba359-4A (9657).		FBA359.	(2B, 6B).
Xfbb176-4A (9657).		FBB176.	
Xfbb251-4D (9657).		FBB251.	(2D).
XksuD18-4D (309)[4].	[*XksuD18(A)-4D* (309)].	pTtksuD18	(2A,D).
XksuE6-4D (309)[4].		pTtksuE6.	
XksuE9-4D (309)[4].		pTtksuE9.	
XksuG55-4D [309][4].	[*XksuG55(A)-4D* (309)].	pTtksuG55.	(1D, 7A).
XksuH5-4D (309)[4].		pTtksuH5.	
XksuM1-4D [309][4].	[*XksuM1(A)-4D* (309)].	pTtksuM1.	(2D).
XksuM74-4D (309)[4].		pTtksuM74.	

XksuM83-4D (309)[4].		pTtksuM83.	
XksuM149-4D [309][4].	[*XksuM149-4D* (309)].	pTtksuM149.	(2D).
Xmwg58-4A (9669).		MWG58.	
Xmwg634-4A,B [9669].	[*Xmwg634.2* (9669)].	MWG634.	
Xwg232-4A [9669].	[*Xwg232.7* (9669)].	WG232.	(1A, 5A, 7A).

4A^m

Xcdo388-4A (96119)[3].		CDO388 (24).	(1B,D, 2B 5A^m, 6A).
XksuH8-4A (96119)[3].		pTtksuH18 (309).	(5A^m, 7AS^m, 7AL,BS,DL).

Group 5S

Revise:

Xpsr946-5D; add '3A' and replace '7A' with '7AS,AL' in the last column.

Xwaxc1(Ac11.1)-5A,B,D; change the reference for the synonym to '184'.

Add:

Xabg497 (96119)[3].		ABG497 (96110).	
Xabg705-5A (96119)[3], *5B* (9657)[1].		ABG705 (96110).	
Xbcd873-5B (9657).		BCD873 (96124).	
Xbcd1871-5A,B (9657), *5D* (9615).		BCD1871 (96124).	
Xcdo677-5A (96119)[3].		CDO677 (24).	
Xcdo749-5A,B (9657).		CDO749 (96124).	
Xcdo959-5B (9657).		CDO959 (96124).	(4A).
Xcdo1338-5A (96119)[3].		CDO1338 (24).	(4A).
Xfba232-5B (9657).		FBA232.	
Xfba342-5B (9657).		FBA342.	
Xfba367-5B (9657).		FBA367.	(6A).
Xfba393-5B,D (9657).		FBA393.	
Xfbb121-5B.1 (9657).		FBB121.	(2B, 4B, 7A).
Xfbb276-5B (9657).		FBB276.	
Xfbb277-5B (9657).		FBB277.	(3A).
XksuG44-5A,B (9547)[1], *5D* (309)[4],(9547)[1].		pTtksuG44.	(6D).

The arm location of *XksuG44-5D* in *T. tauschii* was not reported in 309.

XksuH8-5A (96119)[3].		pTtkwuH8 (309).	(4A, 7AS,L, BS,DL)
Xmwg835-5A (96119)[3].		MWG835 (96109).	(1A, 2A).

Mapping of the same 1A^m, 2A^m and 5A^m loci with MWG835 and MWG920 was reported in 96119.

Xmwg838-5A (96119)[3].		MWG838 (96109).	(6A).
Xmwg920-5A (96119)[3].		MWG920 (96109).	(1A, 2A).

Mapping of the same 1A^m, 2A^m and 5A^m loci with MWG920 and MWG835 was reported in 96119.

Xpsr1327-5D (9547).		PSR1327.	(1AL, 1DS, 4A).
Xwg341-5A (96119)[3].		WG341 (24).	(6B, 7A,B,D).
Xwg541-5A (9541,96119)[3].		WG541 (24).	
Xwsu(Dor5)-5A [9673][3].	[*XDor5-5A* (9673)].	pMA1951 (9674).	

Group 5L

Note:

Xbcd87 and *Xpsr567* moved to 7BS:5BL:5DL.

ß-Amy-A1,B1,D1, *Xbcd1302*, *Xcdo1312*, *Xpsr164*, *Xpsr484(Cat)*, *Xpsr1201* and *Xwg114* moved to 5AL:4BL:4DL.
Xcdo484, *Xpsr115*, *Xpsr580*, *Xpsr1206* and *Xpsr1316* moved to 4AL:5BL:5DL.

Revise:
XEsi28; change symbols for loci to *'Xucd107(Esi28)'* and add *'XEsi28'* as a synonym for each locus.
XEsi32; change symbols for loci to *'Xucd108(Esi32)'* and add *'XEsi32'* as a snyonym for each locus.
Xrsq805(Embp)-5A,B,D; delete 9441 as reference for the synonym and insert '180,1179'.
Xsfr1; revised and moved to 6L.

Delete previous corresponding entries and substitute:

Xcdo504-5A (9542), *5B* (9657).	CDO504 (96124).
Xksu24-5A.1.,2;B.1,.2;D.1,.2 [453].	
[*Xksu24-5A(1),(2);B(1),(2);D(1),(2)*].	pHv24.
Xpsr120-5A.1,.2,.3;B.1,.2,.3;D.1,.2,.3 [585,1179].	
[*Xpsr120-5A(1),(2),(3);B(1),(2),(3);D(1),(2),(3)* (1179)].	PSR120.
Xpsr1201-5B (1179).	PSR1201 [a39 (150)]. (1A, 5A,4D).
Xpsr2021(Aba2)-5A (9542),*5B* [9669].	
[*XABA2* (9669)].	ABA2 (323).
Xucd103(Esi4)-5A [9583][1],(96119)[3], *5B* [9583][1].	
[*XEsi4-5A,B* (9583)].	ESI4 (9584).
Xucd104(Esi14)-5A [9583][1],(96119)[3], *5B,D* [9583][1].	
[*XEsi14-5A,B,D* (9583)].	ESI14 (9584).
Xzens819(Adpg1)-5A,B,D [1179].	
[*XAdpg1-5A,B,D*].	WL:aga1 (774).

Add:

XAga6-5A (96119)[3].	blp1 (96123).
Xabc164-5B (9657).	ABC164.
Xabc310-5B (9657).	ABC310. (4A, 7A,B).
Xabc706-5A (96119)[3].	ABC706 (96110).
Xabg55-5A (96119)[3].	ABG55 (96110). (1A, 3A, 4A).
Xabg387-5A (96119)[3].	ABG387 (96110). (1A, 3A, 4A).
Mapping of the same $1A^m$, $3A^m$, $4A^m$, and $5A^m$ loci with ABG387 and ABG55 was reported in 96119.	
Xabg391-5A (9657).	ABG391.
Xabg473-5B (9657).	ABG473. (6B).
Xbcd9-5A (96119)[3], *B* (9657)[1].	BCD9 (24).
Xbcd157-5A,B (9657).	BCD157 (96124).
Xbcd183-5A (9657).	BCD183 (96124).
Xbcd204-5A (96119)[3].	BCD204 (24).
Xbcd265-5A (96119)[3].	BCD265 (24). (1A, 4D).
Xbcd183-5A (9657).	BCD183 (96124).
Xbcd298-5A (96119)[3].	BCD298 (24).
Xbcd351-5A (9541,96119)[3].	BCD351 (24).
Xbcd450-5B,D (9657).	BCD450 (96124).
Xbcd508-5A (9541,96119)[3], *5B* (9657)[1].	BCD508 (24,96124). (1A,B,D).

Xbcd876-5A (9685).	BCD876.	
Xbcd926-5A (9657).	BCD926 (96124).	
Xbcd981-5A (9657).	BCD981 (96124).	
Xbcd1030-5B (9657).	BCD1030 (96124).	
Xbcd1088-5A (9657).	BCD1088 (96124).	
Xbcd1103-5D (9657).	BCD1103 (96124).	
Xbcd1140-5B (9657).	BCD1140 (96124).	
Xbcd1235-5A.1, A.2 (9657).	BCD1235 (96124).	
Xbcd1355-5A (9657).	BCD1355 (96124).	
Xbcd1874-5D (9657).	BCD1874 (96124).	
Xbcd1949-5A (9657).	BCD1949 (96124).	
Xcdo57-5A,D (9657).	CDO57 (96124).	(2A, 7A,B,D).
Xcdo346-5D (9657).	CDO346 (96124).	(1B).
Xcdo348-5A (96119)[3], *B* (9657)[1].	CDO348 (24,96124).	
Xcdo388-5A (96119)[3].	CDO388 (24).	(1B,D, 2B 4A, 6A).
Xcdo412-5A,B,D (9657).	CDO412 (96124).	
Xcdo457-5A (9657).	CDO457 (96124).	
Xcdo465-5A (96119)[3].	CDO465 (24).	
Xcdo584-5B (9657).	CDO584 (96124).	
Xcdo785-5A (9657).	CDO785 (96124).	
Xcdo786-5A (9685).	CDO786.	
Xcdo1049-5A (96119)[3].	CDO1049 (24).	
Xcdo1090-5A (9657).	CDO1090 (96124).	(2A).
Xcdo1168-5A (9541,96119)[3].	CDO1168 (24).	
Xcdo1189-5A,B,D (9522).	CDO1189.	(1B).
Xcdo1192-5B (9657).	CDO1192 (96124).	
Xcdo1326-5A,B (9657).	CDO1326 (96124).	
Xcdo1333-5A (9541,96119)[3].	CDO1333 (24).	(4B,D).
Xcdo1508-5D (9657).	CDO1508 (96124).	
Xcmwg701-5A.1,.2 (96119)[3].	cMWG701 (96109).	(1A).

Mapping of the same 1A and 5A loci with cMWG701 and pKG1490 [*Xpkg1490(Cab2)-1A*, *Xpkg1490(Cab2)-5A.1* and *Xpkg1490(Cab2)-5A.2*] was reported in 9668 and 96119.

Xcmwg770-5D (9657).	cMWG770.	
Xcsc2(Dhn2)-5A.1, A.2 [9673][3]. [*XDhn2-5A.1,.2* (9673)].	pTZ19R-B9 (161).	(6A).
Xfba68-5A (9657).	FBA068.	
Xfba127-5B (9657).	FBA127.	(3A, 7A).
Xfba166-5A,B (9657).	FBA166.	
Xfba190-5A (9657).	FBA190.	(3B,D).
Xfba209-5D (9657).	FBA209.	(2D).
Xfba332-5B (9657).	FBA332.	
Xfba348-5B (9657).	FBA348.	
Xfba351-5A,B (9657).	FBA351.	
Xfba364-5D (9657).	FBA364.	
Xfbb2-5A (9657).	FBB002.	
Xfbb26-5D (9657).	FBB026.	
Xfbb100-5D (9657).	FBB100.	
Xfbb121-5B.2 (9657).	FBB121.	(2B, 4B, 7A).
Xfbb156-5D (9657).	FBB156.	(3B, 7A).
Xfbb199-5A (9657).	FBB199.	
Xfbb209-5A (9657).	FBB209.	(6A).

Xfbb213-5D.1,.2 (9657).	FBB213.	
Xfbb237-5B (9657).	FBB237.	(3A,D).
Xfbb255-5A (9657).	FBB255.	
Xfbb322-5B (9657).	FBB322.	
Xfbb323-5B (9657).	FBB323.	
Xfbb328-5B (9657).	FBB328.	
XksuA1-5B (9657).	pTtksuA1.	(7D).
XksuD30-5D (9657).	pTtksuD30.	
XksuF1-5A (96119)[3].	pTtksuF1 (309).	(2A).
XksuG14-5A (96119)[3].	pTtksuG14 (309).	
XksuH1-5A (9685).	pTtksuH1.	(5D).
XksuH9-5A (9541,96119)[3].	pTtksuH9 (309).	(1A,B,D, 2A,D, 4A, 7A).
Xmwg52-5B (9657).	MWG52.	
Xmwg77-5A (96119)[3].	MWG77 (96109).	
Xmwg522-5A (9657).	MWG522.	
Xmwg561-5B,D (9657).	MWG561.	
Xmwg624-5A (9657).	MWG624.	
Xmwg820-5A (96119)[3].	MWG820 (96109).	(6A).
Xmwg900-5D (9657).	MWG900.	
Xmwg914-5B (9657).	MWG914.	
Xmwg922-5D (9657).	MWG922.	
Xpkg1490(Cab2)-5A.1,.2 [96119][3]. [*XCab1-5A.1,.2* (96119)].	pKG1490 (9690).	(1A).

Mapping of the same 1A and 5A loci with pKG1490 and cMWG701 was reported in 9668 and 96119.

Xpsr128-5A,B,D (949,9547).	PSR128	
Xpsr152-5A (96119)[3].	PSR152 (9547).	(7A,B,D).
Xpsr335-5D (9667).	PSR335.	(2B).
Xpsr575-5A [9669],*5D* (9667). [*Xpsr575.2* (9669)].	PSR575.	(2A).
Xpsr963-5A (9547).	PSR963.	(1A,B).
Xpsr1201-5B (1179,9547).	PSR1201 [a39(159)].	(1A, 4D,5A).
Xrz395-5A,D (9657).	RZ395.	(2A).
Xtam72-5B (9657).	TAM72 (179).	(2B, 3B, 4A).
Xtav1961(Vdac1)-5A,B,D (9550).	Tavdac1 (9663).	
Xttu1934(Hsp16.9b)-5A (9673)[3].	pTaHSP16.9b (9677).	(3A).
Xttu1937(Wsip16)-5A.1,.2 [9673][3]. [*XDhn2.1,.2* (9583)].	pTaWSP16 (9682).	(6A).
Xucd107(Esi28)-5A [9673][3],(96119)[3]. [*Esi28-5A* (9583)].	ESI28 (9584).	
Xucd108(Esi32)-5A (96119)[3].	ESI32 (9584).	
Xwg530-5A (96119)[3].	WG530 (24).	
Xwg583-5B (9657).	WG583 (96124).	
Xwg889-5A (9541,96119)[3], *5B* (9657)[1].	WG889 (24,96124).	
Xwg908-5A (9541,96119)[3].	WG908 (24).	(1A, 5B).
Xwg909-5B (9657).	WG909 (96124).	(7B).
Xwg1026-5A (9685).	WG1026.	

4AL:5BL:5DL
Delete previous corresponding entry and substitute:
Xcdo484-4A,5B,D [24](9541).
[*XcnlCDO484-4A,5B,D* (9441)].
CDO484.

Add:

Xabc310-4A (9541).	ABC310.	(5B, 7A,B).
Xbcd1421-5D (9657).	BCD1421 (96124).	(6B).
Xbcd1670-4A,5D (9657).	BCD1670 (96124).	
Xglk621-5D (594)[9667].		
[*XpTAG621-5D* (9667)].	pTag621 (594).	
Xmwg549-4A (9657).	MWG549.	(6D).
Xpsr375-5B,D [9669]. [*Xpsr375.2* (9669)].	PSR375.	(1A, 4A,B,D).
Xpsr1206-4A,5B (1179,9541).	PSR1206.	
Xpsr1316-4A,5B (1179,9541).	PSR1316 [L3-17 (1131)].	

7BS:5BL:5DL
Add:
Xbcd87-7B,5B,D [24](9657).
[*XcnlBCD87-7B,5B,D* (9441)].
BCD87.

Xbcd197-5D (9657).	BCD197 (96124).	
Xcdo506-5D (9657).	CDO506 (96124).	
Xfba11-5D (9657).	FBA011.	
Xpsr567-7B,5B,D (1179).	PSR567.	(5A,4B,D).

Group 5
Note: *Xglk621* moved to 4AL:5BL:5DL.

Revise:
Xglk278-5A,B; delete '(6B).' from the last column.
Xglk546-5A; add '(7B).' in the last column.
Xglk724-5A; add '3A,B,D' in the last column.
XksuF43-5D.1,.2; change last column entry to '(1B, 2D, 4D, 6D).'.
Xrgc12-5B; change synonym to [XEif-5B].

Add:

Xcmwg645-5A (96119)[3].		
[*Xmwg645-5A* (96119)].	cMWG645 (96109).	(1A,B).
Xcsiha159-5D [541][4]. [*XcsIHA159d* (541)].	csIHA159 (541).	(3D).
Xcsih97-5D.1 [541][4]. [*XcsIH97b* (541)].	csIH97 (541).	(2D, 3D).
Xcsih97-5D.2 [541][4]. [*XcsIH97c* (541)].	csIH97 (541).	(2D, 3D).
Xfba114-5D (9657).	FBA114.	
Xfba131-5A (9657).	FBA131.	
Xfba137-5D (9657).	FBA137.	
Xfba352-5A (9657).	FBA352.	
Xfbb238-5D (9657).	FBB238.	(7A).
XksuA3-5D (309)[4].	pTtksuA3.	
XksuD16-5D (309)[4].	pTtksuD16.	(1D).
XksuG7-5D.1,.2 [309][4].		
[*XksuG7(A),(B)-5D* (309)].		
	pTtksuG7.	(7A,B,D).

XksuG57-5D.1,.2,.3 [309][4].
[*XksuG57(A),(B),(D)-5D* (309)].
pTtksuG57. (2D).

XksuH1-5D (309)[4]. pTtksuH1. (5A).
XksuI26-5D (309)[4]. pTtksuI26.
XksuM9S-5D (309)[4]. pTtksuM9S. (6D).
Xpsr386-5A [9669]. [*Xpsr386.4* (9669)]. PSR386. (1A, 3B, 7A).
Xrab16-5A [9669]. [*XRAB16* (9669)]. RAB16 (9687).
Xtam40-5A (96119)[3]. TAM40 (179).
Xwg232-5A.1,B [9669] [*Xwg232.3* (9669)]. WG232. (1A, 4A, 7A).
Xwg232-5A.2 [9669]. [*Xwg232.5* (9669)]. WG232. (1A, 4A, 7A).
Xwg908-5B [9669]. [*Xwg908.2* (9669)]. WG908. (1A, 5AL).

Group 6S

Delete previous corresponding entries and substitute:

XksuG48-6A,B (9596)[2], *6D* (309)[4],(96114)[1].
[*XksuG48(A)-6D* (309)]. pTtksuG48. (3D).

The arm location of *XksuG48-6D* in *T. tauschii* was not reported in 309.

XksuH4-6A,B [96114][1],(96113)[1], *6D* (309)[4],[96114][1],(9589)[1].
pTtksuH4.

The arm.location of *XksuH4-6D* in T. *tauschii* was not reported in 309.
Two *XksuH4* loci in 6A, 6B and 6D were reported in 96114.

Xpsr899-6A (186,274), *6B* (96113), *6D* (186,274).
PSR899 (2B).

Add:

Xabc173-6D (96113). ABC173.
Xabg466-6A (96119)[3], *6D* (96113)[1]. ABG466 (96110).
Xabg458-6A (96119)[3]. ABG458 (96110).
Xbcd21-6A,B (9685). BCD21.
Xbcd340-6B (9685). BCD340.
Xbcd342-6A (96113), *6B* (9685), *6D* (9589). BCD342.
Xbcd1383-6B (96113). BCD1383.
Xbcd1398-6D (96113). BCD1398.
Xbcd1821-6A,D (96113). BCD1821.
Xbcd1882-6B (9522). BCD1882.
Xcdo270-6A,D (96113). CDO270.
Xcdo476-6A,B (96113). CDO476.
Xcdo524-6B (96113). CDO524.
Xcdo534-6D (96113). CDO534. (6B, 7A).
Xcdo1128-6B (9685). CDO1128. (4B).
Xcdo1315-6A (96113). CDO1315.
Xcmwg652-6A (96113). cMWG652.
Xfba1-6D (96113). FBA001.
Xfba65-6A (96113). FBA065. (2D, 4A, 7A).
Xfba67-6B (96113). FBA067.
Xfba85-6A,D (96113). FBA085.
Xfba148-6A (96113). FBA148.
Xfba152-6A,B (96113). FBA152.
Xfba187-6D (96113). FBA187.
Xfba234-6A (96113) FBA234. (7A).
Xfba307-6A,D (96113). FBA307.
Xfba328-6B (96113). FBA328.
Xfba336-6D (96113). FBA336.
Xfba344-6B (96113). FBA344.
Xfba345-6B (96113). FBA345. (2B).

Xfba357-6B (96113).	FBA357.	
Xfba359-6B (96113).	FBA359.	(2B, 4A).
Xfba399-6B (96113).	FBA399.	
Xfbb16-6B (96113).	FBB016.	
Xfbb145-6A (96113).	FBB145.	(7A).
Xfbb147-6A (96113).	FBB147.	(3BS,BL,DL).
Xfbb166-6A (96113).	FBB166.	(3B).
Xfbb194-6A (96113).	FBB194.	
Xfbb209-6A (96113).	FBB209.	(5A).
Xfbb222-6D (96113).	FBB222.	
Xfbb231-6D.1 (96113).	FBB231.	(6DL).
Xfbb319-6D (96113).	FBB319.	
Xfbb354-6D (96113).	FBB354.	
Xglk479-6B (96113).	pTAG479 (594).	
XksuE3-6A (96119)[3].	pTtksuE3 (309).	(1A, 2A,D, 3A, 4A, 7A,D).
XksuF43-6D [309][4],(96114)[1]. [*XksuF43(A)-6D* (309)].	pTtksuF43.	(1D, 2D, 4D, 5D).
The arm location of *XksuF43-6D* in *T. tauschii* was not reported in 309.		
XksuG8-6B [96114][1],(9596)[2], *6D* (309)[4],(96114)[1],(9589)[1]. [*XksuG8a-6B* (96114)].	pTtksuG8.	(6A).
The arm location of *XksuG8-6D* in *T. tauschii* was not reported in 309.		
XksuG48-6A,D (96113).	pTtksuG48.	
XksuG58-6A,B (96114)[1], *6D* (309)[4],(96114)[1].	pTtksuG58.	
The arm location of *XksuG58-6D* in *T. tauschii* was not reported in 309.		
XksuH14-6B (96113).	pTtksuH14.	(1A).
XksuI28-6B (96114,9685)[1], *6D* (309)[4],(96114)[1].	pTtksuI28.	
The arm location of *XksuI28-6D* in *T. tauschii* was not reported in 309.		
XksuM90-6B (96114).	pTtksuM90.	
Xmwg67-6A (96113).	MWG67.	(1A).
Xmwg549-6D (96113).	MWG549.	(4A).
Xmwg820-6A (96119)[3].	MWG820 (96109).	(5A).
Xmwg916-6D (96113).	MWG916.	
Xpsr301-6A,B,D (429).	PSR301.	
Xpsr484(Cat)-6A,B,D (429).	pCat2.1c (9656).	(5A,4B,D).
Xpsr551-6B (429).	PSR551.	(2B).
Xpsr563-6A (429).	PSR563.	(4D, 7A,D).
Xpsr967-6A (429).	PSR967.	(1A,B, 4B, 5A).
Xpsp3200-6D (429).	PSP3200F/PSP3200R.	
Xrgc69-6A,B,D (429).	RGC69.	(7A,B,D).
Xrz995-6B (96113).	RZ995.	
Xtav1929(Cyp)-6A.1,B.1,D.1 (429).	TAV1929 (9659).	

Group 6L

Revise:

XEsi-18; change symbols for loci to '*Xucd106(Esi18)*', add '(96119)[3]' as a reference for the 6A loci, and add '*XEsi18*' as a synonym for each locus.

XksuE18-6B; add '(1A,B,D, 7A,B).' in the last column.

Xtam21-6A,B,D; add '[*Xtam30-6A,B,D* (96114,96116)].' as synonym.

Delete previous corresponding entry and substitute:

Xwg933-6A (179,96114), *6D* (96114).	WG933.	(6B).

Add:

Xabc154-6A (96119)[3].	ABC154 (96110).	
Xabc163-6A (96119)[3].	ABC163 (96110).	
Xabc175-6D (96113).	ABC175.	
Xabg388-6A (96119)[3].	ABG388 (96110).	
Xabg473-6B (96113).	ABG473.	(5B).
Xabg652-6A (96119)[3].	ABG652 (96110).	
Xabl26-6A,B,D [429]. [*Xucw26-6A,B,D* (429)].	LMC26.	
Xbcd340-6B (9685).	BCD340.	(1B).
Xbcd357-6D (96113).	BCD357.	(6B).
Xbcd506-6A (96113).	BCD506.	
Xbcd758-6A (96113).	BCD758.	
Xbcd1407-6B (96113).	BCD1407.	(1A).
Xbcd1510-6A,D (96113).	BCD1510.	
Xcdo204-6A (96113).	CDO204.	
Xcdo341-6B (96113).	CDO341.	
Xcdo388-6A (96113).	CDO388.	(1B,D, 2B, 4A, 5A)
Xcdo507-6B (96113).	CDO507.	
Xcdo772-6A (96113).	CDO772.	
Xcdo836-6A,D (96113).	CDO836.	
Xcdo1428-6A (96113).	CDO1428.	
Xcmwg669-6D (96113).	cMWG669.	
Xcmwg684-6A (96119)[3].[*Xmwg684-6A* (96119)].	cMWG684 (96109).	
Xfba8-6A (96113).	FBA008.	(2A, 3B, 4B, 7D).
Xfba20-6A (96113).	FBA020.	
Xfba42-6B (96113).	FBA042.	(7A,B).
Xfba81-6D (96113).	FBA081.	
Xfba111-6A,B (96113).	FBA111.	(2D).
Xfba251-6B (96113).	FBA251.	
Xfba367-6A (96113).	FBA367.	(5B).
Xfba381-6D (96113).	FBA381.	
Xfbb40-6A (96113).	FBB040.	(2B).
Xfbb57-6B (96113).	FBB057.	
Xfbb59-6B.1,.2, D (96113).	FBB059.	
Xfbb70-6A,B,D (96113).	FBB070.	
Xfbb82-6A,B (96113).	FBB082.	
Xfbb130-6B (96113).	FBB130.	
Xfbb164-6B (96113).	FBB164.	
Xfbb169-6B,D (96113).	FBB169.	
Xfbb170-6A (96113).	FBB170.	
Xfbb191-6A (96113).	FBB191.	
Xfbb221-6A (96113).	FBB221.	
Xfbb231-6D.2 (96113).	FBB231.	(6DS).
Xfbb327-6B (96113).	FBB327.	
Xfbb359-6B (96113).	FBB359.	(2A).
Xfbb364-6B (96113).	FBB364.	
Xfbb377-6B (96113).	FBB377.	(2D).
Xfdp3(VAtpB2)-6A [9673][3]. [*XVAtp-B2* (9673)].	pHTB2 (9679).	
XksuD12-6A,B,D (96114).	pTtksuD12.	
XksuD17-6A,B,D (96114).	pTtksuD17.	
XksuD27-6A (96113), *6B* (96114), *6D* (96113).	pTtksuD27.	
XksuE14-6A (96114)[1],(9596)[2], *6B* (96114)[1], *6D* [309][4],(96114)[1]. [*XksuE14(B)-6D* (309)].	pTtksuE14.	(3D).

Two *XksuE14* loci in 6A, 6B, and 6D were reported in 96114. The arm location of *XksuE14-6D* in T. *tauschii* was not reported in 309.

XksuF24-6B (96114).	pTtksuF24.	(6D, 7D).
XksuF37-6A (96114).	pTtksuF37.	
XksuG30-6A (96119)[3], *6B* (96113)[1].	pTtksuG30 (309).	(1A, 4A, 2D).
XksuM11-6A,B (96114)[1], *6D* (309)[4],(96114)[1].	pTtksuM11.	
The arm location of *XksuM11* in *T. tauschii* was not reported in 309.		
XksuM75-6B (96114)[1], *6D* (309)[4],(96114)[1].	pTtksuM75.	
The arm location of *XksuM75* in *T. tauschii* was not reported in 309.		
Xmwg74-6B (96113).	MWG74.	
Xmwg573-6A (96113).	MWG573.	
Xmwg813-6A (96119)[3].	MWG813 (96109).	(3A, 6A).
Xmwg798-6A (96119)[3].	MWG798 (96109).	
Xmwg838-6A (96119)[3].	MWG838 (96109).	(5A).
Xmwg934-6A,B (96113).	MWG934.	
Xmwg2053-6A,B,D (96113).	MWG2053.	
Xnpi253-6A,B,D (429).	Npi253.	(7A,B,D).
Xpsr2(α-Amy-1)-6A,B,D (429).	501 (566).	
Xpsr88-6A,B,D (429).	PSR88.	
Xpsr134-6A,B,D (96114).	PSR134.	
Xpsr966-6A,B,D (429).	PSR966.	
Xrgc74-6A,B,D (429).	RGC74.	(4A, 5A,B,D).
Xsfr1-6B (9552).	J13/1/J13/2.	
Xtav1929(Cyp)-6A.2 (429).	TAV1929 (9659).	
Xttu1937(Wsip16)-6A [9673][3]. [*XDhn3-6A* (9673)].	pTaWSP16 (9682)	(5A).
Xwg223-4A,B,D (96114).	WG223.	
Xwg286-4A,B,D (96114).	WG286.	
Xwg341-6B.1,.2 [96114]. [*Xwg341a,b* (96114)].	WG341.	(5A, 7A,B,D).

Group 6

Note:

XksuH4 moved to 6S and *Xwg933* moved to 6L.

XksuM9S-6D; add '(5D).' in the last column.

Revise:

XksuD1-6D; add superscripts '1,4' to reference and add '6B' in the last column.

XksuG8-6A; add '6D' in the last column

XksuF24-6D; add '6B' in the last column.

Xglk546-6B; add '(7B)' in the last column.

Xglk724-6A,B,D; add '3A,B,D' in the last column.

Xpsr653-6A; delete.

Add:

Xabg20-6A (96119)[3], *6D* (96113)[1].	ABG20 (96110).	
Xbcd102-6B (9685).	BCD102.	(2D).
Xbcd221-6B (9685).	BCD221.	
Xbcd357-6B (9685).	BCD357.	
Xbcd1299-6B (96113).	BCD1299.	
Xbcd1319-6B (9685), *6D* (96113).	BCD1319.	
Xbcd1426-6B (9522).	BCD1426.	
Xbcd1495-6B (9522).	BCD1495.	
Xbcd1716-6B (9685), *6D* (96113).	BCD1716.	

Xbcd1860-6A (96113), *6B* (9685).		BCD1860.
Xbcd2014-6B (9685).		BCD2014.
Xcdo29-6A (96113), *6B* (9522).		CDO29.
Xcdo534-6B (9685).		CDO534. (6D, 7A).
Xcdo1091-6B (9685).		CDO1091.
Xcdo1158-6B (9685).		CDO1158.
Xcdo1380-6B (9685).		CDO1380.
Xcdo1421-6B (9522).		CDO1421. (5D).
Xcsih90-6D [541][4].	[*XcsIH90* (541)].	csIH90 (541).
Xcsih114-6D [541][4].	[*XcsIH114-1c* (541)].	csIH114-1 (541).
Xfba397-6A (96113).		FBA397.
Xfbb95-6A (96113).		FBB095.
Xfbb192-6A (96113).		FBB192.
Xfbb215-6A (96113).		FBB215.
Xfbb283-6A (96113).		FBB283. (3B).
Xksu1-32-4 [309][4].	[*Xksu1-32-4(B)-6D* (309)].	
		pTtksu1-32-4.
XksuD1-6B (9685).		pTtksuD1. (6D).
XksuF19-6D (309)[4].		pTtksuE19. (2A,B,D).
XksuF36-6D [309][4].	[*XksuF36(B)-6D* (309)].	pTtksuF36. (2D).
XksuF37-6D (309)[4].		pTtksuF37.
XksuG51-6D (309)[4],(96114)[1].		pTtksuG51 (309).
XksuH11-6D (309)[4].		pTtksuH11. (5A, 4B,D).
XksuM5-6D (309)[4].		pTtksuM5.
XksuM151-6D (309)[4].		pTtksuM151.
Xtam6-6A (9596)[2].		TAM6 (6B).
Xwg933-6B (9685).		WG933. (6A,D).

Group 7S

Note:

Xbcd87 and *Xpsr567* moved to 7BS:5BL:5DL.

Xak466(Nra1), *Xbcd93*, *Xcdo780*, *Xpsr119*, *Xpsr160(Plc)*, *Xpsr392* and *Xpsr470(Wx)* moved to 7AS:4AL:7DS.

Revise:

Xpsr152-7A,B,D; add '(5A).' in the last column.

Xpsr540-7B; add '(1A).' in the last column.

Xpsr563-7A,D; change reference to '139'.

Delete previous corresponding entries and substitute:

XksuA1-7D (309)[1,4].	pTtksuA1.
The arm location of *XksuA1-7D* in *T. tauschii* was not reported in 309.	
Xpsr490(Ss1)-7A.1,B,D.1 [342,139].	
[*XSs1-7A,B,D* (342), *Ss1* (643)].	
	pST8 (643). (7A,4A).

Add:

Xabc152-7A (96119)[3].	ABC152 (96110). (1A).
Xabc158-7A (9657).	ABC158.
Xabc455-7A (96119)[3].	ABC455 (96110).
Xabc465-7A (96119)[3].	ABC465 (96110).
Xbcd98-7B,D (96118).	BCD98. (1A).
Xbcd310-7B (9657).	BCD310 (96124).
Xbcd349-7A,B,D (96118).	BCD349.
Xbcd385-7A,B,D (96118).	BCD385.

Xbcd1066-7A (9657).		BCD1066 (96124).	
Xbcd1338-7A,B,D (96118).		BCD1338.	
Xcdo17-7A (9657).		CDO17 (96124).	
Xcdo57-7A,B,D (96118).		CDO57.	(2A, 5A,D).
Xcdo91-7D (96118).		CDO91.	
Xcdo534-7A (96118).		CDO534.	(6B,D).
Xcdo595-7A (9657).		CDO595 (96124).	
Xcdo676-7A,B,D (96118).		CDO676	
Xcdo1189-7B (9685).		CDO1189.	
Xcdo1395-7A (96118).		CDO1395.	(4B).
Xfba32-7B (9657).		FBA032.	
Xfba42-7A,B (9657).		FBA042.	(6B).
Xfba248-7A (9657).		FBA248.	
Xfba340-7A (9657).		FBA340.	
Xfba346-7A (9657).**		FBA346.	
Xfba363-7A (9657).		FBA363.	
Xfba371-7B (9657).		FBA371.	
Xfba377-7D (9657).		FBA377.	
Xfbb150-7B (9657).		FBB150.	
Xfbb195-7B (9657).		FBB195.	
Xfbb226-7B (9657).		FBB226.	(2A,B, 4D).
Xfbb264-7A (9657).		FBB264.	
Xfbb343-7A (9657).		FBB343.	
Xglk61-7A [96118].	[TAG61-7A (96118)].	pTag61 (594).	(7DL).
Xglk184-7A,D [96118].	[TAG184-7A,D (96118)].	pTag184 (594).	
Xglk301-7A [96118].	[TAG301-7A (96118)].	pTag301 (594).	
Xglk536-7A,B [96118]	[TAG536-7A,B (96118)].	pTag536 (594).	
Xglk651-7A [96118].	[TAG651-7A (96118)].	pTag651 (594).	
Xglk658-7A,B,D [96118].	[TAG658-7A,B,D (96118)]	pTag658 (594).	
XksuD15-7A (96118)[1], *7B* (9547)[1], *7D* (309)[4],(96118)[1].		pTtksuD15.	
The arm location of *XksuD15-7D* in *T. tauschii* was not reported in 309.			
XksuH8-7A (96119)[3], *7B* (96118).		pTtksuH8 (309).	(4A, 5A, 7AL,DL).
Xpsr946-7D.2 (9547).		PSR946.	(1D, 2D, 3A, 5D, 7AS,AL,DL).
Xpsr1921-7A,B,D (9547).		PSR1921.	
Xrz2-7D (9657).**		RZ2.	
Xrz4-7B (96118).		RZ4.	
Xwg180-7B.1 [96118].	[*Xwg180a* (96118)].	WG180.	(1A, 7BL).
Xwg522-7A,B,D (96118).		WG522.	
Xwg669-7A,B,D (96118).		WG669.	
Xwg909-7B (96118).		WG909.	(5B).

7AS:4AL:7DS

Add:

Xabg378-7A (96119)[3].		ABG378 (96110).	
Xabg704-7A (96119)[3].		ABG704 (96110).	
Xak466(Nra1)-7A,4A,7D [410,9441].	[*XNra-4B* (140), *XNra-7A,4A,7D* (9441)].	bNRp10 (142).	(6A,B,D).
Xbcd93-7A,4A,7D [24].	[*XcnlBCD93-7A,4A,7D* (9441)].	BCD93.	

Xbcd129-7D [9657],(9641).
[*Xbcd129-4A* (9657). BCD129.
Xbcd130-7A (96118), *4A* (9657), *7D* (96118). BCD130.
Xbcd588-7D [9657],(9641).
[*Xbcd588-4A* (9657)]. BCD588.
Xbcd907-7A (9657). BCD907. (3B,D).
Xbcd1438-7D (9657). BCD1438.
Xbcd1872-7D (9657). BCD1872.
Xbcd1975-7D [9657],(9641).
[*Xbcd1975-4A* (1957)]. BCD1975.
Xcdo475-7A (96118), *4A* (9657), *7D* (96118). CDO475.
Xcdo545-4A,7A (9657). CDO545.
Xcdo665-4A (9657). CDO665.
Xcdo780-7A [24](96118), *4A* [24], *7D* [24](96118).
[*Xcn1CDO780-7A,4A,7D* (9441)].
CDO780.
Xcdo1400-7A,D (96118). CDO1400.
Xcmwg710-7A (96119)[3], *4A,7D* (9657)[1].
[*Xmwg710-7A* (9657,96119)].
cMWG710 (96109). (1A).
Xfba8-7D (9657). FBA008. (2A, 3B, 4B, 6A).
Xfba17-7A (9657). FBA017.
Xfba65-7A (9657). FBA065. (2D, 4A, 6A).
Xfba72-7A (9657). FBA072.
Xfba93-7A (9657). FBA093.
Xfba109-7A (9657). FBA109.
Xfba127-7A (9657). FBA127. (3A, 5B).
Xfba231-7D (9657) FBA231.
Xfba243-7D [9657],(9641).
[*Xfba243-4A* (9657)]. FBA243.
Xfba253-7D [9657],(9641).
[*Xfba253-4A* (9657)]. FBA253.
Xfba282-4A (9657). FBA282.
Xfba311-7A (9657). FBA311. (2D, 3B, 7BL).
Xfba321-7A (9657). FBA321.
Xfbb9-7A (9657). FBB009. (2D).
Xfbb67-7A (9657). FBB067. (4B, 7BL).
Xfbb114-4A (9657). FBB114.
Xfbb121-7A (9657). FBB121. (2B, 4B, 5B).
Xfbb154-4A (9657). FBB154.
Xfbb156-7A (9657). FBB156. (3B, 5D).
Xfbb186-7A (9657). FBB186.
Xfbb278-7A (9657). FBB278.
XksuD9-7A.1 (96118), *4A,7D.1* (9541).
[*XksuD9-7A* (96118), *XksuD9-7D* (9541)].
pTtksuD9. (7AL,BL,DL).
XksuF48-7D (96118). pTtksuF48.
Xmwg530-7A (96119)[3]. MWG530 (96109).
Xmwg2018-7A (96119)[3]. MWG2018 (96109).
Xpsr119-7A,4A,7D [140].
[*Xpsr119-4B* (130,140)]. PSR119.

Xpsr160(Plc)-7A,4A,7D [140].
[*Xpsr160-4B* (140),
Xpsr160-7A,4A,7D (9441)].
PSR160.
Xpsr392-7A,4A,7D (9543). PSR392.
Xpsr470(Wx)-7A,4A,7D [140].
[*XWx-4B* (140),
XWx-7A,4A,7D (9441)]. pcwx27 (871).
Xpsr490(Ss1)-7A.2,4A [9669].
[*Xpsr490-7A.3*,
Xpsr490-4A.2 (9669)] pST8 (643). (7A,B,D).
Xpsr573-4A (9541). PSR573.
Xpsr604-7A,4A,7D (181,9541). PSR604.
Xpsr648-7A (96119)[3]. PSR648 (9547). (1B, 4A, 7DL).
Xpsr946-7A.1,.2 (96119)[3].
[*Xpsr946-7A.2,.3* (96119)].
PSR946 (9547). (1D, 2D, 3A,
5D, 7AL,DS,DL).
Xpsr833(Per)-7A,4A,7D [181].
[*XPer-7A,4A,7D* (181)]. BP1 (847). (3A,B,D).
Xumc190(Sus)-7A,4A,7D (9543).
[*Xumc190-7A,B,D* (9543)].
UMC190. (2B,D).
Xwg834-7A,D (96118). WG834.
Xwye835(Wx)-4A (9543). pCSS22 (9555).

Group 7L

Revise:

XEsi2-7A,1,.2; change symbols for the 7AS and 7AL loci to *'Xucd110(Esi2)-7A.1'* and *'Xucd110(Esi2)-7A.2'*, respectively, add '(96119)[3].' as a reference for the 7AL locus, and enter '[*XEsi2-7A.1* (9583)].' in the synonym column for the 7AS locus and '[*XEsi2-7A.2* (9583)].' in the synonym column for the 7AL locus.

Xpsr121(Glb3)-7A,B,D; change the reference for the locus to '140', place '[*Xpsr121-7A,B,D* (140), *XGlb3-7A,B,D* (181,344)].' in the synonym column and add the following comment: 'The clones PSR121 and pLW2.1 (*Xwia484(Glb3)-1A,B,D,7A,B,D*) detect the same loci (96125).'

Xpsr340-7A,B,D; change the reference to '139'.

Xpsr946-7A; delete '7A' from the synonym column and add '3A' and '7AS' in the last column.

Xwia484(Glb3)-7A,B,D; place '[*XGlb3-7A,B,D* (181,344)].' in the synonym column and add the following comment: 'The clones pLW2.1 and PSR121 detect the same loci (96125).'.

Add:

Xabc305-7A (96119)[3]. ABC305 (96110). (5A,B,D).
Xabc310-7A (96119)[3], *7B* (9657). ABC310 (96110). (4A, 5B).
Xabc455-7B (9657). ABC455.
Xabg461-7A (96119)[3]. ABG461 (96110).
Xbcd178-7B (9657). BCD178.
Xcdo53-7A,B,D (96118). CDO53.
Xcdo347-7A (9657). CDO347.
Xcdo414-7B (9657). CDO414.
Xcdo551-7A,B (96118). CDO551.

Xcdo673-7A,B,D (96118).		CDO673.	
Xcdo686-7B (9657).		CDO686.	
Xcdo690-7A (96119)[3].		CDO690 (24).	
Xcdo775-7A,B,D (96118).		CDO775.	
Xcdo920-7A (96118).		CDO920.	
Xcdo962-7A (9657).		CDO962.	
Xcdo1199-7A,B,D (96118).		CDO1199.	
Xcsih81-7A,B (96118)[1], *7D* [541][4],(96118)[1].			
	[*XcsIH81-1* (541)].	csIH81-1 (541).	
The arm location of *Xcsih81-7D* in *T. tauschii* was not reported in 541.			
Xfba21-7B (9657).		FBA021.	
Xfba69-7A,D (9657).		FBA069.	
Xfba97-7A (9657).		FBA097.	
Xfba134-7A (9657).		FBA134.	
Xfba204-7A,D (9657).		FBA204.	
Xfba234-7A (9657).		FBA234.	(6A).
Xfba259-7B (9657).		FBA259.	
Xfba264-7D (9657).		FBA264.	
Xfba301-7B (9657).		FBA301.	
Xfba305-7B (9657).		FBA305.	
Xfba311-7B (9657).		FBA311.	(2D, 3B, 7AS).
Xfba337-7A (9657).		FBA337.	
Xfba350-7A (9657).		FBA350.	
Xfba354-7A,B (9657).		FBA354.	
Xfba382-7A (9657).		FBA382.	
Xfbb18-7A (9657).		FBB018.	
Xfbb67-7B (9657).		FBB067.	(4B, 7AS).
Xfbb79-7D (9657).		FBB079.	
Xfbb112-7D (9657).		FBB112.	
Xfbb145-7A (9657).		FBB145.	(6A).
Xfbb175-7B (9657).		FBB175.	
Xfbb179-7B (9657).		FBB179.	
Xfbb189-7B,D (9657).		FBB189.	
Xfbb193-7A,B (9657).		FBB193.	
Xfbb218-7A (9657).		FBB218.	
Xfbb238-7A (9657).		FBB238.	(5D).
Xfbb258-7B (9657).		FBB258.	
Xfbb325-7D (9657).		FBB325.	
Xfbb352-7B (9657).		FBB352.	
Xfdp1(VAtpA)-7A [9673][3].			
	[*XVAtp-A-7A* (9673)]	pHTA (9680).	
Xfdp2(VAtpB1)-7A [9673][3].			
	[*XVAtp-B1-7A* (9673)]	pHTB1 (9679).	
Xglk35-7A,B,D [96118].			
	[TAG35-7A,B,D (96118)].	pTag35 (594).	
Xglk61-7B [96118].	[TAG61-7B (96118)].	pTag61 (594).	(7AS).
Xglk439-7A,B,D [96118].			
	[TAG439-7A,B,D (96118)].		
		pTag439 (594).	
Xglk478-7B,D [96118].	[TAG478-7B,D (96118)].	pTag478 (594).	
Xglk546-7A,B [96118].			
	[TAG546-7A,B (96118)].	pTag546 (594).	(2B, 3B, 5A, 6B).
Xglk549-7B [96118].	[TAG549-7B (96118)].	pTag549 (594).	

Xglk598-7A,B,D [96118].			
	[TAG598-7A,B,D (96118)].		
		pTag598 (594).	
Xglk642-7A [96118].	[TAG642-7A (96118)].	pTag642 (594).	
Xglk686-7A [96118].	[TAG686-7A (96118)].	pTag686 (594).	
Xglk702-7D [96118].	[TAG702-7D (96118)].	pTag702 (594).	
Xglk750-7A,B,D [96118].			
	[TAG750-7A,B,D (96118)].		
		pTag750 (594).	
XksuA5-7A (96118).		pTtksuA5.	
XksuB7-7B,D (96118).		pTtksuB7.	
XksuD2-7A,B,D (96118).		pTtksuD2.	
XksuD6-7A,D (96118).		pTtksuD6.	
XksuD7-7A (96118).		pTtksuD7.	(3D, 7D).
XksuD9-7A.2 (96119)[3], *7B,7D.2* (96118)[1].			
	[*XksuD9-7A* (96119), *XksuD9-7D* (96118)].		
		pTtksuD9 (309).	(7AS,4AL,7DS).
XksuD39-7A,B,D (96118).		pTtksuD39.	
XksuE3-7A (96118), *7D* (9657).		pTtksuE3.	(1A, 2A,D, 3A, 4A, 6A).
XksuE18-7A (96119)[3], *7B* (9657).		pTtksuE18 (309).	(1A,B,D, 6B).
XksuG7-7A,B,D (96118).		pTtksuG7.	
XksuG12-7A (96118).		pTtksuG12.	(4A).
XksuG34-7A,B (96118).		pTtksuG34.	(1A,B,D).
XksuG39-7A,B (96118)[1], *7D* (309)[4],(96118)[1].		pTtksuG39.	
The arm location of *XksuG39-7D* in *T. tauschii* was not reported in 309.			
XksuH8-7A,D (96118).		pTtksuH8.	(4A, 5A, 7AS,BS).
XksuH9-7A (9657),(96119)[3].		pTtksuH9 (309).	(1A,B,D, 2A,D, 4A, 5A).
Xmwg825-7A (96119)[3].		MWG825 (96109).	
Xmwg938-7A (9657).		MWG938.	(1B,D).
Xmwg975-7D (9657).		MWG975.	
Xmwg2031-7A (96119)[3].		MWG2031 (96109).	
Xmwg2062-7A (96119)[3].		MWG2062 (96109).	
Xpsr121-7A,B,D (96116).		PSR121.	
Xpsr303-7A (9547), *7B,D* (96118).		PSR303.	
Xpsr514-7D (96118).		PSR514.	
Xpsr548-7D (96118).		PSR548.	
Xpsr560-7D (96118).		PSR560.	
Xpsr648-7D (9547).		PSR648.	(1B, 4A, 7AS).
Xpsr680-7A,B,D (9547).		PSR680.	
Xpsr743-7A,B (96118).		PSR743.	
Xpsr1923-7B (9547).		PSR1923.	(2B, 3B).
Xpsr1954(Tha)-7A,B,D (9547).		pBD12b (9665).	
Xrz476-7B (9657).		RZ476.	
Xrz508-7B (9657).		RZ508.	
Xrz682-7A (9657).		RZ682.	
Xtam50-7B (9657).		TAM50 (179).	(2A,B,D).
Xubp2-7A,B,D (9547).		pTdubp2.	
Xubp9-7A,B,D (9547).		pTdubp9.	
Xwg180-7B.2 [96118]. [*Xwg180b* (96118)].		WG180.	(1A, 7BS).
Xwg341-7A,B,D (96118).		WG341.	(5A, 6B).
Xwg380-7A,B,D (96118).		WG380.	

Xwg420-7A (96119)[3], *7D* (9657)[1]. WG420 (24).
Xwg466-7A,B,D (96118). WG466.
Xwg514-7B (9657). WG514.
Xwg686-7A.1,.2,7B.1,.2,7D.2 [96118].
[*Xwg686-7Aa,7Ab,7Ba,7Bb,7Db* (96118)]. WG686.
Xwg719-7A,B,D (96118). WG719.
Xwye1958(Adpg3)-7A,B,D (9547). pAGP-S2 (9555).

Group 7
Note: *Xglk651-7A* moved to 7S.

Revise:
XksuF2-7D.1,.2,.3,.4,.5; add '(2A,D).' in the last column.
XksuF24-7D(2); change locus designation to add '*XksuF24-7D*' and add '(6B).' in the last column.

Add:

XGsp-5D (541)[4].		pGsp (541).	
Xbcd707-7D (9657).		BCD707.	
Xcsih60-7D [541][4].	[*XcsIH60-1* (541)].	csIH60-1 (541).	
XksuD7-7D (309)[4].		pTtksuD7.	(3D, 7A).
XksuG55-7A (96119)[3].		pTtksuG55 (309).	
Xpsr94-7B (9669).		PSR94.	
Xpsr386-7A [9669].	[*Xpsr386.2* (9669)].	PSR386.	(1A, 3B, 5A).
Xpsr558-7A (9669).		PSR558.	
Xpsr927-7B [9669].	[*Xpsr927.1* (9669)].	PSR927.	
Xwg232-7A.1 (9669).		WG232.	(1A, 4A, 5A).
Xwg232-7A.2 [9669].	[*Xwg232.6* (9669)].	WG232.	(1A, 4A, 5A).

Glume Colour

Rg2: Add the following comment:

Kovel (9603) described a brown or smokey-grey glume phenotype in *T. aestivum* var caesium K-28535. This phenotype was also present in accession K-40579 and botanical varieties cinereum, columbina and albiglaucum. Close linkage to *Gli-D1* was shown and the gene designated *Brg* was assumed to be an allele of *Rg2* present in *T. tauschii* and synthetic hexaploid wheats.

i: ANK-23 = Novosibirskaya 67*10/K28535 (9603).

Height

Reduced height.

In *Rht* section, after *Rht12*, replace note with:

'**ma:** *Rht12* is located distally on 5AL cosegregating with *B* and highly linked to *β–Amy-A1* (9531).'

Herbicide Response

3. Chlortoluron insensitivity

Add below the *Su1* section:

'**ma**: Linkage was shown between *Xpsr312 - Su1 - Xpsr477(Pgk2)* with genetic distances of 5.3 cM and 6.8 cM respectively (96108).'

Meiotic Characters

3. Inhibitor of pairing homoeologous

Ph1^{I}. **al:** *Aegilops speltoides* (859, 9612).

Proteins

2. Enzymes
II. Alcohol dehydrogenase

Include at bottom:
'**ma:** *Adh-D1* [*Adh1,Adh2*] was mapped on 4DS 4cM distal to *Xpsr163-4D* and closely proximal to *Xcsiha114-4D.1* [*XcsIHA114-1a*'](541).'

V. β-Amylase

Add at bottom of *β–Amy-1* section:
'Sixty *T. tauschii* lines revealed two *β–Amy-D^{t}1* alleles (9692).'

VI. Endopeptidase

Ep-D1c. **v:** Wheats with *Lr19* (9626) (null allele).

VII. Esterase

Add at bottom of *Est-5* section:
'Sixty *T. tauschii* lines revealed six *Est-D^{t}5* alleles (9692).'

IX. Glutamic oxaloacetic transaminase

Add at bottom:
'Got-D2 [*Got-2*] was mapped 2 cM distal to *Xpsr154-6D* on 6DL (541).'

3. Endosperm storage proteins
Insert: 'This information for the Endosperm Storage Protein section was prepared by W. John Rogers (Facultad de Agronomia, Universidad Nacional del Centro de la Provincia de Buenos Aires, Azul, Argentina) for the 1995 supplement but just missed the press. Comments or suggestions for this section of the 1997 supplement should be addressed to John.'

- In the preamble for I. Glutenins:

In the first paragraph, correct misspelling of 'disulfide', and in the second paragraph, replace 'The *Glu* loci' with 'The *Glu-1* loci'.

Delete the first sentence of the final paragraph, which will now start 'The subunit ....'

- In the notes following the *Glu-A1* list, replace the final sentence with 'A number of alleles in *T. turgidum* var. *dicoccoides* populations, 12 at *Glu-A1-1* and 3 at *Glu-A1-2*, were described in 579. In a further study using different germplasm of this species (9693), 15 alleles at *Glu-A1* were observed, including 12 not previously found; the 15 alleles included up to 14 alleles at *Glu-A1-1* (with up to 10 not previously observed), and 5 alleles at *Glu-A1-2* (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.'

- In the notes following the *Glu-B1* list, replace the final sentence with 'Eight alleles at *Glu-B1-1* and 10 alleles at *Glu-B1-2* in *T. turgidum* var. *dicoccoides* populations were described in 579. In a further study using different germplasm of this species (9693), 19 alleles at *Glu-B1* were observed, including 15 not previously observed; the 19 alleles included 11 alleles at *Glu-B1-1* and 14 alleles (including the null allele) at *Glu-B1-2*, although, as the authors pointed out, it was not conclusively clear how many of these alleles were distinct from each other, or from others previously observed.'

- To the *Glu-D1* list, add:

'***Glu-D1t*** (9694).	43+44 (9694).	**i:**	*T. tauschii* accession TA2450/2*.
Glu-D1u [9695].	2+10' (9695).	**v:**	Coker 68-15.
Glu-D1v [545].	2.1+10.1 (545).	**dv:**	*T. tauschii.*
Glu-D1w [545].	2+T_1+T_2 (545).	**dv:**	*T. tauschii.*
Glu-D1x [545].	2+T_2 (545).	**dv:**	*T. tauschii.*
Glu-D1y [545].	3+T_2 (545).	**dv:**	*T. tauschii.*
Glu-D1z [545].	3+10 (545).	**dv:**	*T. tauschii.*
Glu-D1aa [545].	3+10.3 (545).	**dv:**	*T. tauschii.*
Glu-D1ab [545].	4.1+10 (545).	**dv:**	*T. tauschii.*
Glu-D1ac [545].	4+10 (545).	**dv:**	*T. tauschii.*
Glu-D1ad [545].	5.1+10.2 (545).	**dv:**	*T. tauschii.*
Glu-D1ae [9692].	2.1+T_1+T_2 (9692).	**dv:**	*T. tauschii.*
Glu-D1af [9692].	3+T_1+T_2 (9692).	**dv:**	*T. tauschii.*
Glu-D1ag [9692].	1.5+T_1+T_2 (9692).	**dv:**	*T. tauschii.*
Glu-D1ah [9692].	1.5+10 (9692).	**dv:**	*T. tauschii.*
Glu-D1ai [9692].	2.1+10.5 (9692).	**dv:**	*T. tauschii.*
Glu-D1aj [9692].	1.5+12 (9692).	**dv:**	*T. tauschii.*
Glu-D1ak [9692].	3+10.5 (9692).	**dv:**	*T. tauschii.*'

- To the *Glu-B1-1* list, add:

'***Glu-B1-1ab*** (966).	6*.	**v:**	Dawbull.'

- To the *Glu-D1-1* list, add:

'***Glu-D1-1j*** [9694].	43 (9694).	**i:**	*T. tauschii* accession TA2450/2*.
Glu-D1-1k (545).	4.1 (545).	**dv:**	*T. tauschii.*
Glu-D1-1j (545).	5.1 (545).	**dv:**	*T. tauschii.*
Glu-D1-1l (9692).	1.5 (9692).	**dv:**	*T. tauschii.*'

- To the *Glu-D1-2* list, add:

'***Glu-D1-2i*** [9694].	44 (9694).	**i:**	*T. tauschii* accession TA2450/2*.
Glu-D1-2j [9695].	10' (9695).	**v:**	Coker 68-15.
Glu-D1-2k (545).	T_1 (545).	**dv:**	*T. tauschii.*
Glu-D1-2l (545).	T_2 (545).	**dv:**	*T. tauschii.*
Glu-D1-2m (545).	10.1 (545).	**dv:**	*T. tauschii.*
Glu-D1-2n (545).	10.2 (545).	**dv:**	*T. tauschii.*
Glu-D1-2o (545).	10.3 (545).	**dv:**	*T. tauschii.*
Glu-D1-2p (9692).	10.5 (9692).	**dv:**	*T. tauschii.*'

- In the alien section following the *Glu-D1-2* list, insert the following new allelic list following *Glu-V1*:

'***Glu-V1a*** (9696).	71 (9696).	**al:**	*D. villosum.*
Glu-V1b (9696).	72 (9696).	**al:**	*D. villosum.*
Glu-V1c (9696).	73 (9696).	**al:**	*D. villosum.*
Glu-V1d (9696).	74 (9696).	**al:**	*D. villosum.*
Glu-V1e (9696).	75 (9696).	**al:**	*D. villosum.*
Glu-V1f (9696).	76 (9696).	**al:**	*D. villosum.*
Glu-V1g (9696).	77 (9696).	**al:**	*D. villosum.*
Glu-V1h (9696).	78 (9696).	**al:**	*D. villosum.*
Glu-V1i (9696).	79 (9696).	**al:**	*D. villosum.*
Glu-V1j (9696).	80 (9696).	**al:**	*D. villosum.*
Glu-V1k (9696).	null (9696).	**al:**	*D. villosum.*
Glu-V1l (9696).	81+82 (9696).	**al:**	*D. villosum.*
Glu-V1m (9696).	83+84 (9696).	**al:**	*D. villosum.*
Glu-V1n (9696).	85+86 (9696).	**al:**	*D. villosum.*'

- Following this, give the following preamble and two new lists:

'Alleles and subunits at *Glu-V1* : The following is analogous to the *Glu-1-1* and *Glu-1-2* lists given earlier to identify x-type and y-type subunits in wheat. It has been assumed in the following that where an allele at *Glu-V1* produces only a single subunit, it is an x-type subunit and so encoded by *Glu-V1-1* rather than by *Glu-V1-2*; the electrophoretic mobilities of the subunits are all greater, though some only marginally so, than subunit 7 encoded by *Glu-B1-1a* (an x-type subunit), and extend beyond the mobility of subunit 12 encoded by *Glu-D1-2a* (a y-type subunit) (9696); therefore, it is quite possible that any one of the subunits designated as encoded by *Glu-V1-1* is, in fact, encoded by *Glu-V1-2*. The designation given here is intended to be the most practically useful until the identity of the genes encoding the alleles is directly established.

Glu-V1-1.

Glu-V1-1a [9696].	71 (9696).	**al:**	*D. villosum.*
Glu-V1-1b [9696].	72 (9696).	**al:**	*D. villosum.*
Glu-V1-1c [9696].	73 (9696).	**al:**	*D. villosum.*
Glu-V1-1d [9696].	74 (9696).	**al:**	*D. villosum.*
Glu-V1-1e [9696].	75 (9696).	**al:**	*D. villosum.*
Glu-V1-1f [9696].	76 (9696).	**al:**	*D. villosum.*
Glu-V1-1g [9696].	77 (9696).	**al:**	*D. villosum.*
Glu-V1-1h [9696].	78 (9696).	**al:**	*D. villosum.*
Glu-V1-1i [9696].	79 (9696).	**al:**	*D. villosum.*
Glu-V1-1j [9696].	80 (9696).	**al:**	*D. villosum.*
Glu-V1-1k [9696].	null (9696).	**al:**	*D. villosum.*
Glu-V1-1l [9696].	81 (9696).	**al:**	*D. villosum.*
Glu-V1-1m [9696].	83 (9696).	**al:**	*D. villosum.*
Glu-V1-1n [9696].	85 (9696).	**al:**	*D. villosum.*

Glu-V1-2.

Glu-V1-2a [9696].	null (9696).	**al:**	*D. villosum.*
Glu-V1-2b [9696].	82 (9696).	**al:**	*D. villosum.*
Glu-V1-2c [9696].	84 (9696).	**al:**	*D. villosum.*
Glu-V1-2d [9696].	86 (9696).	**al:**	*D. villosum.*'

- After the final allelic entry for the *Glu-1* part, i.e. after the allele *Glu-H^{t}1* found in CS/*E. trachycaulum*, add this paragraph:

'A Chinese variety of *T. aestivum* named Xiaoyanmai 7 carries a subunit with electrophoretic mobility in 10% SDS-PAGE well beyond that of subunits so far observed in *T. aestivum*. It may derive from *Agropyron elongatum*, which was used in the breeding programme that led to the variety (9697). It has not been given a subunit number or allelic designation, because its genetic control has not been elucidated.'

- In the preamble for *Glu-3*, replace the final sentence with 'In *T. aestivum*, only *Glu-B3* has been shown to recombine with the gliadin genes (1.7 +/- 0.8) (971, 973). However, in *T. durum*, recombination has been observed for both *Glu-A3* and *Glu-B3* with their respective *Gli-1* loci: the map distance between *Glu-A3* and *Gli-A1* has been estimated as 1.3 +/- 0.4 cM (9698), and that between *Glu-B3* and *Gli-B1* as 2.0 +/- 0.8 in 813 and as 2.0 +/- 0.4 in 9698. It appears that *Glu-B3* is proximal to *Gli-B1*, and there is some evidence, albeit only tentative as the authors acknowledge, that *Glu-A3* is proximal to *Gli-A1* (M).

Whereas hitherto it has been widely thought that all the LMW subunits of glutenin were encoded by genes located on the chromosomes of homoeologous group 1, it has now been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of the C subunits must be controlled by loci elsewhere in the genome (9699).'

Add at bottom *Glu-1* section:
'The *Glu-1* loci may be recognised by the DNA probe pTag1290 (1069) and probe pwhe1(Dy10) (9689). Individual *Glu-1-1* loci on 1A,1B and 1D and the *Glu-1-2* loci may be recognised by specific primers (9691).'

Add at bottom of *Glu-3* section:
'The *Glu-3* loci may be recognised with pTag544 (49) and pTdUCD1 (9658) and by specific microsatellite primers (9540)'.

- In the preamble for II. Gliadins:

Replace the short section beginning 'the *Glu-3* set (973).' and ending with 'of group 1 chromosomes is not known' with 'the *Glu-3* set (973); information on map distance and gene order in relation to *Glu-3* and the centromere is given in the preamble for the *Glu-3* loci.'

After the final paragraph, add the following paragraph:

'NB: The catalogue reproduced here only refers to alleles in *T. aestivum*; there is, however, an enormous amount of variation in the gliadins in the close relatives of wheat; see, for example, 96100 for studies in *T. monococcum* (more than 80 gliadin electrophoretic patterns observed in 109 accessions), 96101 for studies in *T. boeoticum* (more than 50 electrophoretic patterns in 60 accessions), and 96102 for studies in *T. durum* (19 electrophoretic patterns, referring only to variation in the omega-gliadins, in 243 accessions).'

- To the *Gli-B1* list, add:

'***Gli-B1q*** (reserved by WJR)
Gli-B1r (96103). **v:** Chinook'

- To the *Gli-B2* list, add:

'***Gli-B2w*** (96103). **v:** Pembina'

- After the final entry in the gliadin section, i.e. *Gli-V3* found in Creso/*D. villosum*, add the following preambles and new lists:

'A locus designated *Gli-A4* controlling omega-gliadins has been mapped at 10 cM proximal to *Gli-A1* on the short arm of chromosome 1A (96104). It has yet to be established whether this is one of a series of orthologous loci.

Gli-A4 (96104). 1AS (96104). **v:** Perzivan biotype 2.

A locus designated *Gli-5* controlling omega-gliadins has been mapped to the short arms of chromosomes 1A and 1B, distal to *Gli-1* (96105). The map distance between *Gli-B5* and *Gli-B1* was estimated as 1.4 cM (recombination value of 1.4 +/- 0.4%), although there was significant variation in recombination values over crosses, ranging from 0 % to 5.9 % over the six crosses analysed, which the authors considered demonstrated genotypic influence on the frequency of recombination. An estimate for the map distance between *Gli-A5* and *Gli-A1* was not reported, although evidence was provided that the linkage is of a similar order of magnitude to the *Gli-B5* - *Gli-B1* distance. Although no orthologous locus was reported for chromosome 1D, the authors cited studies (96106,96107) reporting a recombination distance of 1 % between two gliadin loci on chromosome 1D, which they considered may have been due to the presence of a locus on 1D orthologous to *Gli-B5*.

Gli-A5 (96105). 1AS (96105). **v:** Salmone.

Gli-B5 (96105). 1BS (96105). **v:** Salmone.'

Add at bottom of the *Gli* section:
'The *Gli-1* loci may be recognised by pcP387 (9670), pTag1436 (49) and by specific microsatellite primers (9540).'

5. Other proteins

V. Waxy proteins Previously listed (1993) under Waxy endosperm

Wx-A1.

Wx-A1b.		**v:**	Shirodaruma (9639); Sturdy (9639).
		tv:	8 emmer accessions (9638).
Wx-A1c	(9639).	**v:**	QT105 (9639); WB6 (9639).
Wx-A1d	(9638).	**tv:**	*T. dicoccoides* KU 8937B (9638).
Wx-A1e	(9638).	**tv:**	*T. durum* KU 3655 and KU 3659 (9638).

Wx-B1.

Wx-B1b.		**v:**	Gabo (9639); Satanta (9639).
Wx-B1c	(9639).	**v:**	Cikataba (9639), Junbuk 12 (9639).
Wx-B1d	(9638).	**tv:**	*T. durum* KU 4213D and KU 4224C (9638).

Wx-D1.

Wx-D1a.		**v:**	delete "all wheats".
Wx-D1b	(9639). Null allele.	**v:**	Bai Huo (9639).
Wx-D1c	(9639).		

Response to Photoperiod

Add comment:
'Gene *Ppd-H2* mapped on chromosome 2HS of barley may be a member of the *Ppd* series of orthologous loci (9506).'

Restorers for cytoplasmic male sterility

Add note below *Rf* entry:

'RFLP markers *Xcdo442-1B* and *Xbcd249-1B* were found to be associated with *Rf3* on 1BS. Novel *Rf* genes were also identified on 5AL linked to *Xcdo786-5A* and *XksuH1-5A* (9685).'

Pathogenic Disease/Pest Reaction

Reaction to *Diuraphis noxia*

Following *Dn2*, add the following comment:

According to Saidi & Quirk (834), *Dn1* and *Dn2* are probably allelic. Reference stocks with each gene showed allelism with a gene in PI 262605.

Dn4 (834).			
Dn5.	7DL (7623).	**v:**	STARS - 9302 W-sib (9621).
Dn6 (834).		**v:**	PI 243781 (834,9621).

Reaction to *Erysiphe graminis* DC.
Disease: Powdery mildew

Pm1. **ma:** Co-seg. with *Xcdo347-7A* using NILs (9615).

Pm2.	**v:**	XX186 = *T. durum* 'Santa Marta'/*Aeg. squarrosa* BGRC 1458 (1189). Compal *Pm4b* (9624).
	dv:	*Aeg. squarrosa* BGRC 1458 (1189). Forty accessions of *T. tauschii* (9630).
	ma:	*Xbcd1871-5D* 3.5 cM using F_2s (9615).
Pm3.	**ma:**	*Xwhs179* 3.3 cM (9650).
Pm3a & Pm3b.	**ma:**	*Xbcd1434-1A* 1.3 cM using NILs (9615).
Pm3c.	**v:**	Borenos (9624).
Pm4a.	**ma:**	Co-seg with *Xbcd1231-2A.2 & Xcdo678-2A* using F2s (9615). *Xbcd1231-2A.1* and*Xbcd292-2A* flank gene, both at 1.5 cM (9615).
Pm4b.	**v:**	Botri (heterogeneous) (9624); Fakon (9624); Facta (9624); Factor (heterogeneous) (9624); Fazit (9624). Compal *Pm2* (9624).
Pm5.	**v:**	Alidos (9624); Kontrast (9624).
Pm8.		

Suppressor of *Pm8*

SuPm8 (9651). 1AS (9651). **v:** Wheats with *Gli-A1a* (9651).

Pm12 (723). Replace '$6S^{1}S$ (429). **v:** Wembley derivative #31 (723). **al:** *Ae. speltoides* (723).

Pm12 was mapped to a translocated $6S^{1}S$ segment proximal to *Xpsr551-6B* (429).'

Pm17.	T1BL·1RS (9646).	**v:**	Helami 105 *Pm5* (9646).
Pm19 (1189).	7D (1189).	**v:**	*T. durum* 'Moroccos 183'/*Aeg. squarrosa* AE 457/78 (1189).
Pm22 (9642).	1D (9642).	**v:**	Virest (9642).

Note: It was not possible to test *Pm22* for possible allelism with *Pm10.*

Temporary designations

Mlar (9624).	**v:**	Abo (9614); Aristide (9614); Courtot (9614).
Ml-Br (9624).	**v:**	Bretonischer Bartweizen (9624).
Ml-Ga (9624).	**v:**	Garnet (9624); many old German cultivars (9624).
Ml-Ad (9624).	**v:**	Adlungs Alemannen (9624).

Lists in 9614 (French wheats), 9625 (Chinese wheats).

Reaction to *Mayetiola destructor*

H3.	**i:**	Carol = Newton-207*5/Larned (9601).
H6.	**i:**	Erin = Newton-207*7/Arthur 71 (9601).
H6.	**i:**	Flynn = Newton-207*7/Knox 62 (9601).
H9.	**i:**	Iris = Newton-207*7/Ella (9601).

H10. **i:** Joy = Newton-207*3/IN76529A5-3-3 (9601).

H11. **i:** Karen = Newton-207*4/IN916-1-3-1-47-1 (9601).

H12. **i:** Lola = Newton-207*4/Luso (9601).

H13. **i:** Molly = Newton-207*7/3/KU221-19/Eagle//KS806 (9601).

Reaction to *Phaeosphaeria nodorum*

Snb3 (9643). 5DL (9643). **s:** CS*/Synthetic 5D (9643).
v: Synthetic (9643).
al: *T. tauschii* (9643).

Reaction to *Pseudocercosporella herpotrichoides*

Pch2 (9617). 7A (508,9617). **s:** CS (Cappelle Desprez 7A) (508, 9617).
v: Cappelle Desprez (508, 9617).
Pch3 (9634). **ad:** CS + 4V (9635).

Reaction to *P. graminis*

Sr24. 1BL [T1BL·1BS-3Ae#1L] (9604).
v: Amigo (1060,9604); Teewon (9604).

Sr27. T3AS·3RS (9605). T3AL·3RS and T3BL·3RS stocks were generated (9605).

Sr44 (9644). 7DS [T7DS-7Ai#1L·7Ai#1S] (9644).
v: Line 86.187.
su: Group 7 alien substitution lines with 7Ai#1 and 7Ai#1S (660).
ad: TAF2 = L1 (9645).

Temporary designations

SrA (9620). **v:** SW55-1 (9620); SW56-1 (9620). SW33-5 *Sr9a Sr13* (9620). SW54-3 *Sr9d Sr13* (9620).

YrZdar (9627). 1B (9627). **v:** Zdar (9627).

Genotype lists: 9620, 9647.

Reaction to *P. recondita*

Lr1 **ma:** Co-seg. with *Xpsr567-5D* and *Xglk621-5D* in a Frisal x *Lr1* resistant line. pTAG621 was converted to a diagnostic STS (9667).

Lr9. **ma:** Co-seg with *XksuD27-6B* (9631).

Lr13. To first sentence add:..'especially at high temperatures (660,6609).
v: Yecora *Yr1* (9611). Lerma Rojo 64 *Lr17* (9610). Oasis 86 *Lr19* (9610). Cumpas 88 *Lr26* (9610). Frontana *Lr34* (9611); Parula *Lr34* (9611). Inia 66 *Lr14a Lr17* (9610).

Lr14a. **v:** Inia 66 *Lr13 Lr17* (660).

Lr16. **v:** Ciano 79 (9610); Imuris 79 (9610); Papago 86 (9610).

Lr17. **v:** Lerma Rojo 64 *Lr13* (9610). Inia 66 *Lr14a Lr13* (9010).

Lr18. **v:** FTF (9602); Several Sabikei lines including Sabikei 12 (9602).

Independently derived lines with *Lr18* possess a unique N band terminally located in chromosome 5BL (9602). Low seedling responses conferred by *Lr18* are most effective at 15-18°C. With increasing temperatures the response becomes less effective and ineffective at 25-27°C (666, see also 9602).

Lr19. **v:** Oasis 86 *Lr13* (9610).
ma: Co-seg. with 8 RFLP markers (9631). *Ep-D1c* 0.33 cM (9626).

Lr23. **tv:** Altar 84 (9636).
Suppressor of *Lr23*

SuLr23 (9636). 2DS (9636). **v:** Altar 84/*T. tauschii* 219 (9636)

suLr23 (9636). **v:** Opata 85 (9336).

Lr24. **ma:** Co-seg. of *Lr24* in Agent with 8 RFLP markers; segment in Sears' 3D-3Ag#1 is shorter (9631). Tagged with *Xpsr1203-3D* (9676).
1BL [T1BL·1BS-3Ae#1L] (9604).
v: Amigo (1060, 9604); Teewon (9604).

Lr26. **v:** Bacanora 88 (9610). Cumpas 88 *Lr13* (9610).

Lr27 + Lr31. **v:** Ocoroni 86 (9610).

Lr29. **i:** RL6080 = Tc*6/Sears' 7D/Ag#11 (9068).

Lr32. **ma:** *Xbcd1278 -3D* 3.6 cM, *Xcdo395-3D* 6.9cM (9631).

Lr34. **v:** Frontana *Lr13* (9611); Parula *Lr13* (9611).

Lr37. **i:** RL6081 = Tc*8/VPM1 (9608).

Complex resistances: Mango *Lr1 Lr13 Lr26 Lr34* (9611). Trap *Lr1 Lr3 Lr10 Lr13 Lr34* (9611).

Genotype tests: 9610 (Mexican cultivars), 9618 (cultivars from the former USSR), 9647.

Reaction to *P. striiformis*

Yr2. **v:** Laketch (9507).

Yr3a.		1B (9628).	**v:** Druchamp (9628); Stephens (9628).
Yr3.	Undesignated allele.		**v:** Enkoy (9507).
Yr4a.		6B (9628).	**v:** Yamhill *Yr2* (9628).
Yr4.	Undesignated allele.		**v:** Kenya Kubangu (9507).
Yr9.			**v:** See also 9507.
Yr24	(9633).	1BS (9633).	**v:** Meering*3//K733/*T. tauschii* AUS18911 (9633). **tv:** K733 (9633).

Temporary designations:

Yrcv	(660).		**i:** Avocet S*4/Carstens V (9647); Cook*6/Carstens V (9647). **v:** Caribo (9648); Cyrano (9648); Okapi (9648). Felix *Yr3* (9648). Zdar *Yr3a Yr4a* (9627).
YrD	(9628).	6A (9628).	**v:** Druchamp (9628).
YrDru	(9628).	6B (9628).	**v:** Druchamp (9628).
YrS	(9628).	3B (9628).	**v:** Stephens (9628).
YrSk	(9649).	2BL (9649).	**v:** Selkirk (9649). Opata 81 (9649). Common in CIMMYT materials (9649).
YrSte	(9628).	2B (9628).	**v:** Stephens (9628).
YrYam	(9628).	4B (9628).	**v:** Yamhill (9628).

Genotype lists: 9619, 9647.

Reaction to *Pyrenophora tritici-repentis*

Disease: Tan spot, yellow spot.

Tan spot produces two types of genetically determined symptoms, viz. extensive chlorosis and tan necrosis. Pathotypes with the ability to inflict tan spot necrosis (TSN) produce a host gene-specific toxin in culture.

Reaction to *Septoria nodorum*

Temporary designation ***SnbTM***	(9686).	3A.	**dv:** S3-6, S9-10, S12-1 derived from *T. timopheevii* (PI290518).

Insensitivity to tan spot toxin

Insensitivity (disease resistance) is recessive.

tsn (9629).	5BL (9629).	**v:**	Synthetic W-7976 = Cando/R143//Mexicali 'S'/3/*Aegilops squarrosa* C122.
Tsn		**v:**	Kulm (9629).

Reaction to *Tilletia indica* Mitra

Disease: Karnal bunt.

Kb1 (9640).	**v:**	Chris (9640). CMH77.308 *Kb2* (9640).
Kb2 (9640).	**v:**	PF7113 (9640). CMH77308 *Kb1* (9640). Shanghai #8 *Kb4* (9640).
Kb3 (9640).	**v:**	Amsel (9640).
Kb4 (9640).	**v:**	Shanghai #8 *Kb2* (9640).
Kb5 (9640). Recessive (9640).	**v:**	Pigeon *Kb6*. (9640).
Kb6 (9640). Recessive (9640).	**v:**	Pigeon *K65* (9640).

Reaction to wheat streak mosaic virus

Wsm1 (9637).	**i:**	Karl*4/C.I. 17884 = PI 583794 = KS93WGRC27 (9637).

Genetic linkages

Chromosome 6B

6BS	*Pm11*	-	Cent.	1cm (9616).

Chromosome 7A

7AL	*Ep-A1b*	-	*Xpsr121-7A*	3.8 ± 2.1% (9617).
		-	*Pch2*	15 ± 4.0% (9617).
	Xpsr121-7A	-	*Pch2*	11.2 ± 3.5% (9617).

Chromosome 7D

7DS	*Pm15*	-	Cent.	I (9616).
7DL	Cent.	-	*Dn5*	I (9623).

References

Amendments.

161. Change year to '1990' and correct misspelling of 'dehydrins'.

200. Du Toit F. 1989. Inheritance of resistance in two *Triticum aestivium* lines to Russian wheat aphid (*Homoptera : Aphididea*). Journal of Economic Entomology 82: 1251-1253.

323. Gulli M, Maestri E, Hartings H, Raho G, Perrotta C, Devos KM & Marmiroli N. 1995. Isolation and characterization of abscisic acid inducible genes in barley seedlings and their

responsiveness to environmental stress. Plant Physiology (Life Science Advances). 14:89-96.
337. Change 'Plant Molecular Biology' to 'Plant Physiology'.
344. Replace with 9547.
429. Jia J, Miller TE, Reader SM, Devos KM & Gale MD. 1996. RFLP-based maps of homoeologous group-6 chromosomes of wheat and their application in the tagging of *Pm12*, a powdery mildew resistance gene transferred from *Aegilops speltoides* to wheat. Theoretical and Applied Genetics 92: 559-565.
703. Metakovsky EV. 1991. Gliadin allele identification in common wheat II. Catalogue of gliadin alleles in common wheat. Journal of Genetics and Breeding 45: 325-344.
834. Saidi A & Quick JS. Inheritance and allelic relationships among Russian wheat aphid resistance genes in winter wheat. Crop Science (Manuscript).
868. Rogers WJ, Payne PI, Seekings JA & Sayers EJ. 1991. Effect on bread-making quality of x-type and y-type high-molecular-weight subunits of glutenin. Journal of Cereal Science 14: 209-221.
1179. Xie DX, Devos KM, Moore G, & Gale MD. 1993. RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 87: 70-74.
1189. Lutz J, Hsam SLK, Limpert E & Zeller FJ. 1995. Chromosomal location of powdery mildew resistance genes in *Triticum aestivum* L. (common wheat) 2. Genes *Pm12* and *Pm19* from *Aegilops squarrosa* L. Heredity 74: 152-156.
9430. Arbuzova VS. 1994. Chromosome localization of genes *Pp* for purple grain pigmentation introgressed into common wheat. Genetika 30: 9 (Supplement).
9441. McIntosh RA, Hart GE & Gale MD. 1995. Catalogue of gene symbols for wheat. Proceedings 8th International Wheat Genetics Symposium, Beijing, 1993 (Li ZS & Xin ZY eds.): 1333-1500.
9504. Hussain T, Bowden RL, Gill BS & Cox TS. 1994. Chromosomal location of wheat leaf rust resistance gene *Lr43* derived from *Triticum tauschii*. Phytopathology 84: 1116.
9522. Ma Z-Q, Zhao Z-H & Sorrells ME. 1995. Inheritance and chromosomal location of a male fertility restoring gene transferred from *Aegilops umbellulata* Zhuk. to *Triticum aestivum* L. Molecular and General Genetics 247: 351-357.
9524. Euphytica 82: 141-147.
9528. 1995. Crop Science 35: 1237.
9541. Devos KM, Dubcovsky J. Dvorák J, Chinoy CN & Gale MD. 1995. Structural evolution of wheat chromosomes 4A, 5A and 7B and its impact on recombination. Theoretical and Applied Genetics 91: 282-288.
9542. Galiba G, Quarrie SA, Sutka J, Morgunov A & Snape JW. 1995. RFLP mapping of the vernalisation (*Vrn1*) and frost resistance (*Fr1*) genes on chromosome 5A of wheat. Theoretical and Applied Genetics 90: 1174-1179.
9543. Devos KM, Chao S, Li QY, Simonetti MC & Gale MD. 1994. Relationship between chromosome 9 of maize and wheat homoeologous group 7 chromosomes. Genetics 138: 1287-1292.
9544. Quarrie SA, Gulli M, Calestani C, Steed A & Marmiroli N. 1994. Location of a gene regulating drought-induced abscisic acid production on the long arm of chromosome 5A of wheat. Theoretical and Applied Genetics 89: 794-800.
9545. Bonhomme A, Gale MD, Koebner RMD, Nicolas P, Jahier J & Bernard M. 1995. RFLP analysis of an *Aegilops ventricosa* chromosome that carries a gene conferring resistance to leaf rust (*Puccinia recondita*) when transferred to hexaploid wheat. Theoretical and Applied Genetics 90: 1042-1048.
9546. Flintham JE & Humphray SJ. 1993. Red coat genes and wheat dormancy. Aspects Applied Biology 36: 135-141.
9547. Gale MD, Atkinson MD, Chinoy CN, Harcourt RL, Jia J, Li QY & Devos KM. 1995. Genetic maps of hexaploid wheat. In: Proceedings 8th International Wheat Genetics Symposium (Li ZS, Xin ZY eds.). China Agricultural Scientech Press, Beijing: 29-40.

9555. Ainsworth CC, Hosein F, Tarvis M, Weir F, Burrell M, Devos KM & Gale MD. 1995. Adenosine diphosphate glucose pyrophosphorylase genes in wheat: differential expression and gene mapping. Planta 197: 1-10.

New.

9601. Patterson FL, Maas FB, Foster JE, Ratcliffe RH, Cambron S, Safranski G, Taylor PL & Ohm HW. 1994. Registration of eight Hessian fly resistance common winter wheat germplasm lines (Carol, Erin, Flynn, Iris, Joy, Karen, Lola and Molly). Crop Science 34: 315-316.
9602. Yamamori M. 1994. An N-band marker for gene *Lr18* for resistance to leaf rust in wheat. Theoretical and Applied Genetics 89: 643-646.
9603. Koval SF. 1994. Genetic analysis of isogenic lines of spring wheat variety Novosibirskaya 67: I. Location of the gene determining the brown colour of the glume in chromosome 1D. Genetica 30: 569-570. (English translation from Russian Journal of Genetics 30: 508-509).
9604. Jiang J, Friebe B & Gill BS. 1994. Chromosome painting of Amigo wheat. Theoretical and Applied Genetics 89: 811-813.
9605. Marais GF & Marais AS. 1994. The derivation of compensating translocations involving homoeologous group 3 chromosomes of wheat and rye. Euphytica 79: 75-80.
9606. Laurie DA, Pratchett N, Benzant JH & Snape JW. 1994. Genetic analysis of a photoperiod response gene on the short arm of chromosome 2 (2H) of *Hordeum vulgare*. Heredity 72: 619-627.
9607. Badebo A, Stubbs RW, van Ginkel M & Gebeyehu G. 1990. Identification of resistance genes to *Puccinia striiformis* in seedlings of Ethiopian and CIMMYT bread wheat varieties and lines. Netherlands Journal of Plant Pathology 96: 199-210.
9608. Dyck PL & Lukow OM. 1988. The genetic analysis of two interspecific sources of leaf rust resistance and their effect on the quality of common wheat. Canadian Journal of Plant Science 68: 633-639.
9609. Pretorius ZA, Wilcoxson RD, Long DL & Schafer JF. 1984. Detecting leaf rust resistance gene *Lr13* in seedlings. Plant Disease 68: 585-586. Cited in Plant Breeding Abstracts 54: 8760, p. 880.
9610. Singh RP & Rajaram S. 1991. Resistance to *Puccinia recondita* f. sp. *tritici* in 50 Mexican bread wheat cultivars. Crop Science 31: 1472-1479.
9611. Singh RP & Rajaram S. 1992. Genetics of adult-plant resistance to leaf rust in 'Frontana' and three CIMMYT wheats. Genome 35: 24-31.
9612. Gill BS. 1993. Molecular cytogenetic analysis in wheat. Crop Science 33: 902-908.
9613. Gulyaeva JB. 1984. Localization of the genes for pubesence of the glumes and coloration of the auricles in the leaf sheath in winter wheat variety Ulyanovka. Trudy po Prikladnoi Botanike, Genetikei Selektsii 85: 85-86.
9614. Zeller FJ, Lutz J, Reimlein EI, Limpert E & Koenig J. 1993. Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L.) II. French cultivars. Agronomie 13: 201-207.
9615. Ma ZQ, Sorrells ME & Tanksley SD. 1994. RFLP markers linked to powdery mildew resistance genes *Pm1*, *Pm2*, *Pm3* and *Pm4a* in wheat. Genome 37: 871-875.
9616. Tosa Y & Tsujimoto H. 1994. Telosomic mapping of wheat genes for resistance to inappropriate formae speciales of *Erysiphe graminis*. Wheat Information Service 79: 33-36.
9617. De La Pena RC, Murray TD & Jones SS. 1995. Linkage relations among eyespot resistance gene *Pch2*, endopeptidase *Ep-A1b* and RFLP marker *Xpsr121* on chromosome 7A of wheat. Plant Breeding (In press).
9618. Singh RP, Morgunov A & Huerta-Espino J. 1995. Genes conferring low seedling reaction to Mexican pathotype of *Puccinia recondita* f. sp. *tritici*, and adult-plant responses of recent wheat cultivars from the former USSR. Euphytica 81: 225-234.
9619. Sharma S, Louwers JM, Karki CB & Snijders CHA. 1995. Postulation of resistance genes to yellow rust in wild emmer wheat derivatives and advanced wheat lines from Nepal. Euphytica 81: 271-277.

9620. Dyck PL & Sykes EE. 1995. The inheritance of stem rust and leaf rust resistance in some Ethiopian wheat cultivars. Euphytica 81: 291-297.
9621. Saidi A & Quick JS. Inheritance of Russian wheat aphid resistance in three winter wheats. Proceedings of the 6th Russian Wheat Aphid Conference. Fort Collins, Colorado, USA. (In press, see 9622).
9622. Dong H & Quick JS. 1995. Inheritance and allelism of resistances to the Russian wheat aphid in seven wheat lines. Euphytica 81: 299-303.
9623. Du Toit F, Wessels WG & Marais GF. 1995. The chromosome arm location of Russian wheat aphid resistance gene *Dn5*. Cereal Research Communications 23: 15-17.
9624. Lutz J, Katzhammer M, Stephan U, Felsenstein FG, Oppitz K & Zeller FJ. 1995. Identification of powdery-mildew-resistance genes in common wheat (*Triticum aestivum* L. em Thell.). V. Old German cultivars and cultivars released in the former GDR. Plant Breeding 114: 29-33.
9625. Xia XC, Hsam SLK, Stephan U, Yang TM & Zeller FJ. 1995. Identification of powdery-mildew-resistance genes in common wheat (*Triticum aestivum* L.). VI. Wheat cultivars grown in China. Plant Breeding 114: 175-175.
9626. Winzeler M, Winzeler H & Keller B. 1995. Endopepidase polymorphism and linkage of the *Ep-D1c* null allele with the *Lr19* leaf-rust-resistance gene in hexaploid wheat. Plant Breeding 114: 24-28.
9627. Bartos P & Kosner J. 1995. Monosomic analysis of resistance to stem rust in the winter wheat cultivar Zdar (Boheme). Cereal Rusts and Powdery mildews Bulletin 23: 1-4.
9628. Chen XM, Line RF & Jones SS. 1994. Chromosomal location of genes for resistance to *Puccinia sriiformis* in wheat cultivars Druchamp, Stephens, and Yamhill. Phytopathology 84: 1116.
9629. Faris J. 1995. Personal communication.
9630. Lutz J, Hsam SLK, Limpert E & Zeller FJ. 1994. Powdery mildew resistance in *Aegilops tauschii* Coss. and synthetic hexaploid wheats. Genetic Resources and Crop Evolution 41: 151-158.
9631. Autrique E, Singh RP, Tanksley SD & Sorrells ME. 1995. Molecular markers for four leaf rust resistance genes introgressed into wheat from wild species. Genome 38: 75-83
9632. Reikhel, NV & Wilkes TA. 1987. Differentiation between homoeologous chromosomes 1A of wheat and $1A^m$ of *Triticum monococcum* and its recognition by the wheat *Ph1* locus. Proc. Natl. Acad. Sci. 92: 6745-6749.
9633. McIntosh RA et al. 1995. In preparation.
9634. Jones SS. 1995. Personal communication.
9635. Murray TD, de la Pena RC, Yildirim A & Jones SS. 1994. A new source of resistance to *Pseudocercosporella herpotrichoides*, cause of eyespot disease of wheat, located on chromosome 4V of *Daspyrum villosum*. Plant Breeding 113: 281-286.
9636. Singh RP. 1995. Personal communication.
9637. Gill BS, Friebe B, Wilson DL, Martin DJ & Cox TS. 1995. Registration of KS93WRC27 wheat streak mosaic virus resistant T4DL.4Ai#25 wheat germplasm. Crop Science 35: 1236-1237.
9638. Yamamori M, Nakamura T & Nagamine T. 1995. Polymorphism of two waxy proteins in the emmer group of tetraploid wheat, *Triticum dicoccoides*, *T. dicoccum*, and *T. durum*. Plant Breeding 114: 215-218.
9639. Yamamori M, Nakamura T, Endo TR & Nagamine T. 1994. Waxy protein deficiency and chromosomal location of coding genes in common wheat. Theoretical and Applied Genetics 89: 178-184.
9640. Fuentes-Davila G, Rajaram S & Singh G. 1995. Inheritance of resistance to Karnal bunt (*Tilletia indica* Mitra) in bread wheat (*Triticum aestivum* L.). Plant Breeding 114: 250-252.
9642. Peusha H, Hsam SLK & Zeller FS. 1995. Chromosomal location of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.) 3. Gene *Pm22* in cultivar Virest. Manuscript.

9643. Worland AJ. 1995. Personal communication.
9644. Friebe B, Jiang J, Raupp WJ, McIntosh RA & Gill BS. 1996. Characterization of wheat-alien translocations conferring resistance to diseases and pests: current status. Manuscript.
9645. Cauderon Y, Saigne B & Dauge M. 1973. The resistance to wheat rusts of *Agropyron intermedium* and its use in wheat improvement. Proceedings of the 4th International Wheat Genetics Symposium. (Sears ER & Sears LMS eds.). University of Missouri, Columbia, USA. : 401-407.
9646. Hsam SLK, Cermeno M-C, Friebe B & Zeller FJ. 1995. Transfer of Amigo wheat powdery mildew resistance gene *Pm17* from T1AL.1RS to the T1BL.1RS wheat-rye translocated chromosome. Heredity 74: 497-501.
9647. McIntosh RA, Wellings CR & Park RF. 1995. Wheat Rusts: An Atlas of Resistance Genes. CSIRO Australia.
9648. Stubbs RW. 1985. Stripe rust. In: The Cereal Rusts II: (Roelfs AP and Bushnell WR, eds.). Academic Press, Orlando, Florida, U.S.A.: 66-101.
9649. McDonald D & McIntosh RA. 1995. Personal communication.
9650. Hartl L, Weiss H, Zeller FJ & Jahoor A. 1993. Use of RFLP markers for the identification of alleles at the *Pm3* locus conferring powdery mildew resistance in wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics 86: 959-963.
9651. Ren SX, McIntosh RA, Sharp PJ & The TT. 1995. A storage protein marker associated with the suppressor of *Pm8* for powdery mildew resistance in wheat. Manuscript.
9652. Nelson JC, Van Deynze AE, Autrique E, Sorrells ME, Lu YH, Merlino M, Atkinson M & Leroy P. 1995. Molecular mapping of wheat. Homoeologous group 2. Genome 38: 516-524.
9653. Goldmark P, Curry J, Morris CG & Walker-Simmons MK. 1992. Cloning and expression of an embryo-specific mRNA up-regulated in hydrated dormant seeds. Plant Molecular Biology 19: 433-441.
9654. Walker-Simmons MK. 1995. Personal communication.
9655. Nelson JC, Van Deynze AE, Autrique E, Sorrells ME, Lu YH, Negre S, Bernard M & Leroy P. 1995. Molecular mapping of wheat. Homoeologous group 3. Genome 38: 525-533.
9656. Bethards LA, Skadsen RW & Scandalios JG. 1987. Isolation and characterization of a cDNA clone for the *Cat2* gene in maize and its homology with other catalases. Proceedings National Academy Science 84: 6830-6834.
9657. Nelson JC, Sorrells ME, Van Deynze AE, Lu YH, Atkinson MD, Bernard M, Leroy P, Faris JD & Anderson JA . 1995. Molecular mapping of wheat: Major genes and rearrangements in homoeologous groups 4, 5 and 7. Genetics 141: 721-731.
9658. Cassidy BG & Dvorák J. 1991. Molecular characterization of a low-molecular-weight glutenin cDNA clone from *Triticum durum*. Theoretical and Applied Genetics 81: 653-660.
9659. Breiman A. 1995. Personal communication
9660. Meadows JW, Hulford A, Raines CA & Robinson C. 1991. Nucleotide sequence of a cDNA clone encoding the precursor of the 33 kDa protein of the oxygen-evolving complex from wheat. Plant Molecular Biology 16: 1085-1087.
9661. Ainsworth C. 1995. Personal communication
9662. Weng J, Wang Z-F & Nguyen HT. 1991. Nucleotide sequence of a *Triticum aestivum* cDNA clone which is homologous to the 26 kDa chloroplast-localized heat shock protein gene of maize. Plant Molecular Biology 17: 255-258.
9663. Elkeles A, Devos KM, Graur D, Zizi M & Breiman A. 1995. Multiple cDNAs of wheat voltage-dependent anion channels (VDAC): Isolation, differential expression, mapping and evolution. Plant Molecular Biology 29: 109-124.
9664. Gautier M-F, Alary R & Joudrier P. 1990. Cloning and characterisation of a cDNA encoding the wheat (*Triticum durum* Desf.) CM16 protein. Plant Molecular Biology 14: 313-322.

9665. Green R. 1991. Isolation and characterisation of genes induced in barley during powdery mildew infection. PhD thesis, Cambridge University.
9666. Van Deynze AE, Dubcovsky J, Gill KS, Nelson JC, Sorrells ME, Dvorák J, Gill BS, Lagudah ES, McCouch SR & Appels R. 1995. Molecular-genetic maps for group 1 chromosomes of Triticeae species and their relation to chromosomes in rice and oat. Genome 38: 45-59.
9667. Feuillet C, Messmer M, Schachermayr G & Keller B. 1995. Genetic and physical characterisation of the *LR1* leaf rust resistance locus in wheat (*Triticum aestivum* L.). Molecular and Genetical Genetics 248: 553-562.
9668. Dubcovsky J, Luo M-C & Dvorák J. 1995. Differentiation between homoeologous chromosomes 1A of wheat and $1A^m$ of *Triticum monococcum* and its recognition by the wheat *Ph1* locus. Proceedings National Academy Science 92: 6645-6649.
9669. Quarrie SA, Steed A, Semikhodski A, Lebreton C, Calestani C, Clarkson DA, Tuberosa R, Sanguineti MC, Melchiorre R & Prioul J-L. 1995. Identification of quantitative trait loci regulating water and nitrogen-use efficiency in wheat. In: Proceedings Second STRESSNET Conference. (Leigh RA, Blake-Kalff MMAM eds.). European Commission. Ref F.II.3-MOR/0001, Brussels: 175-180.
9670. Forde BG, Kreis M, Williamson MS, Fry RP, Pywell J, Shewry PR, Bunce N & Miflin BJ. 1985. Short tandem repeats shared by B- and C-hordein cDNAs suggest a common evolutionary origin for two groups of cereal storage protein genes. EMBO J 4: 9-15.
9671. Rohde W, Dorr S, Salamini F & Becker D. 1991. Structure of a chalcone synthase gene from *Hordeum vulgare*. Plant Molecular Biology 16: 1103-1106.
9672. Dvorák J, Dubcovsky J, Luo MC, Devos KM & Gale MD. 1995. Differentiation between wheat chromosomes 4B and 4D. Genome 38: 1139-1147.
9673. Dubcovsky J, Luo M-C & Dvorák J. 1995. Linkage relationships among stress-induced genes in wheat. Theoretical and Applied Genetics 91: 795-801.
9674. Morris CF, Anderberg RJ, Goldmark PJ & Walker-Simmons M. 1991. Molecular cloning and expression of abscisic acid-response genes in embryos of dormant wheat seeds. Plant Physiology 95: 814-821.
9675. Hurkman WJ, Lane BG & Tanaka CK. 1994. Nucleotide sequence of a transcript encoding a Germin-like protein that is present in salt-stressed barley roots. Plant Physiology 104: 803-904.
9676. Schachermayr GM, Messmer MM, Feuillet C, Winzeler H, Winzeler M & Keller B. 1995. Identification of molecular markers linked to the *Agropyron elongatum*-derived leaf rust resistance gene *Lr24* in wheat. Theoretical and Applied Genetics 90: 982-990.
9677. Weng J, Wang Z-F & Nguyen HT. 1993. Molecular cloning and sequence analysis of cDNA encoding cytoplasmic low molecular weight heat shock proteins in hexaploid wheat. Plant Science 92: 35-46.
9678. Weng J, Wang Z-F & Nguyen HT. 1991. A *Triticum aestivum* cDNA clone encoding a low-molecular-weight heat shock protein. Plant Molecular Biology 17: 273-275.
9679. Berkelman T, Houtchens KA & DuPont FM. 1994. Two cDNA clones encoding isoforms of the B subunit of the vacuolar ATPase from barley roots. Plant Physiology 104: 287-288.
9680. DuPont FM. 1995. Personal communication.
9681. Espelund M, Sæboe-Larssen S, Hughes DW, Galau GA, Larsen F & Jakobsen KS. 1992. Late embryogenesis-abundant genes encoding proteins with different numbers of hydrophilic repeats are regulated differentially by abscisic acid and osmotic stress. Plant Journal 2: 241-252.
9682. King SW, Joshi CP & Nguyen HT. 1992. DNA sequence of an ABA-responsive gene (*rab 15*) from water-stressed wheat roots. Plant Molecular Biology 18: 119-121.
9683. Litts JC, Simmons CR, Karrer CF, Huang RL & Rodriguez RL. 1990. The isolation and characterization of a barley 1,3-1,4-β-glucanase gene. European Journal of Biochemistry 194: 831-838.

9685. Ma Z-Q & Sorrells ME. 1995. Genetic analysis of fertility restoration in wheat using restriction fragment length polymorphism. Crop Science 35: 1137-1143.
9686. Ma H & Hughes GR. 1995. Genetic control and chromosomal location of *Triticum timopheevii*-derived resistance to *septoria nodorum* blotch in durum wheat. Genome 38: 332-338.
9687. Mundy J & Chua NH. 1988. Abscisic acid and water stress induce the expression of a novel rice gene. EMBO Journal 7: 2279-2286.
9688. Singh N, Donovan GR, Carpenter HC, Skerrit JH & Langridge P. 1993. Isolation and characterization of wheat triticin cDNA revealing a unique lysine-rich repetitive domain. Plant Molecular Biology 22: 227-237.
9689. Anderson OD, Greene FC, Yip RE, Halford NG, Shewry PR & Malpica-Romero J-M. 1989. Nucleotide sequence of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, *Triticum aestivum* L. cv. Cheyenne. Nucleic Acids Research 17: 461-462.
9690. Barkardottir RB, Jensen BF, Kreiberg JD, Nielsen PS & Gausing K. 1987. Expression of selected nuclear genes during leaf development in barley. Developmental Genetics 8: 495-511.
9691. D'Ovidio R, Masci S & Porceddu E. 1995. Development of a set of oligonucleotide primers specific for genes at the *Glu-1* complex of wheat. Theoretical and Applied Genetics 91: 189-194.
9692. William MDHM, Peña RJ & Mujeeb-Kazi A. 1993. Seed protein and isozyme variations in *Triticum tauschii* (*Aegilops squarrosa*). Theoretical and Applied Genetics 87: 257-263.
9693. Ciaffi M, Lafiandra D, Porceddu E & Benedettelli S. 1993. Storage-protein variation in wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) from Jordan and Turkey. I. Electrophoretic characterization of genotypes. Theoretical and Applied Genetics 86: 474-480.
9694. Knackstedt MA. 1995. Personal communication.
9695. Lookhart GL, Hagman K & Kasarda DD. 1993. High-molecular-weight glutenin subunits of the most commonly grown wheat cultivars in the U.S. in 1984. Plant Breeding 110: 48-62.
9696. Zhong G.-Y. & Qualset CO. 1993. Allelic diversity of high-molecular-weight glutenin protein subunits in natural populations of *Dasypyrum villosum* (L.) Candargy. Theoretical and Applied Genetics 86: 851-858.
9697. Wang G, Snape JW, Hu H & Rogers WJ. 1993. The high-molecular-weight glutenin subunit compositions of Chinese bread wheat varieties and their relationship with bread-making quality. Euphytica 68: 205-212.
9698. Ruiz M & Carrillo JM. 1993. Linkage relationships between prolamin genes on chromosomes 1A and 1B of durum wheat. Theoretical and Applied Genetics 87: 353-360.
9699. Gupta RB & Shepherd KW. 1993. Production of multiple wheat-rye 1RS translocation stocks and genetic analysis of LMW subunits of glutenin and gliadins in wheats using these stocks. Theoretical and Applied Genetics 85: 719-728.
96100. Metakovsky EV & Baboev SK. 1992. Polymorphism and inheritance of gliadin polypeptides in *T. monococcum* L. Theoretical and Applied Genetics 84: 971-978.
96101. Metakovsky EV & Baboev SK. 1992. Polymorphism of gliadin and unusual gliadin alleles in *Triticum boeoticum*. Genome 35: 1007-1012.
96102. Nieto-Taladriz MT, Branlard G & Dardevet M. 1994. Polymorphism of omega-gliadins in durum wheat as revealed by the two-step APAGE/SDS-PAGE technique. Theoretical and Applied Genetics 87: 1001-1005.
96103. Metakovsky EV, Ng PKW, Chernakov VM, Pogna NE & Bushuk W. 1993. Gliadin alleles in Canadian western red spring wheat cultivars: use of two different procedures of acid polyacrylamide gel electrophoresis for gliadin separation. Genome 36: 743-749.

96104. Redaelli R, Pogna NE, Dachkevitch T, Cacciatori P, Biancard AM & Metakovsky EV. 1992. Inheritance studies of the 1AS/1DS chromosome translocation in the bread wheat variety 'Perzivan-1'. Journal of Genetics and Breeding 46: 253-262.
96105. Pogna NE, Metakovsky EV, Redaelli R, Raineri F & Dachkevitch T. 1993. Recombination mapping of *Gli-5*, a new gliadin-coding locus on chromosomes 1A and 1B in common wheat. Theoretical and Applied Genetics 87: 113-121.
96106. Metakovsky EV & Sozinov AA. 1987. Organization, variability and stability of the family of the gliadin-coding genes in wheat: genetic data. Gluten proteins - Proceedings of the 3rd International Workshop, Budapest, Hungary (Lastity R & Bekes F eds.): 30-45.
96107. Metakovsky EV. 1990. Organization of gliadin-encoding genes which are genetic markers in wheat. Molecular mechanisms of genetic processes, Nauka, Moscow (Sozinov AA & Schuppe NG eds.): 157-168.
96108. Krugman T, Rubin B, Levy O, Snape JW & Nevo E. 1995. RFLP mapping of chlorotouron resistance gene *Su1*, in bread wheat (*Triticum aestivum*) and wild wheat (*Triticum dicoccoides*). Proceedings Herbicide Resistance Conference, Cordoba, Spain 1994.
96109. Graner A, Jahoor A, Schondelmaier J, Siedler H, Pillen K, Fischbeck G, Wenzel G, & Herrmann RG. 1991. Construction of an RFLP map of barley. Theoretical and Applied Genetics 83: 250-256.
96110. Kleinhofs A, Kilian A, Saghai MA, Biyashev RM, Hayes P, Chen FQ, Lapitan N, Fenwick A, Blake TK, Kanazin V, Ananiev E, Dahleen L, Kudrna D, Bollinger J, Knapp SJ, Liu B, Sorrells M, Heun M, Franckowiak JD, Hoffman D, Skadsen R & Steffenson BJ. 1993. A molecular, isozyme and morphological map of barley (*Hordeum vulgare*) genome. Theoretical and Applied Genetics 86: 705-712.
96111. Causse M, Fulton TM, Cho YG, Ahn SN, Chunwongse J, Wu K, Xiao J, Yu Z, Ronald PC, Harrington SB, Second GA, McCouch SR, & Tanksley SD. 1994. Saturated molecular map of the rice genome based on an interspecific backcross population. Genetics 38: 1251-1274.
96112. Mickelson-Young L, Endo TR & Gill BS. 1995. Cytogenetic ladder-maps of the wheat homoeologous group-4 chromosomes. Theoretical and Applied Genetics 90: 1007-1011.
96113. Marino CL, Nelson JC, Lu YH, Sorrells ME, Leroy P, Tuleen NA, Lopes, CR and Hart GE. 1996. Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (*Triticum aestivum* L. em. Thell.). Genome 39: 359-366.
96114. Gill KS, Gill BS & Endo TR. 1993. A chromosome region-specific mapping strategy reveals gene-rich telomeric ends in wheat. Chromosoma 102: 374-381.
96115. Hart GE. 1996. Personal communication.
96116. Werner JE, Endo TR & Gill BS. 1992. Toward a cytogenetically based physical map of the wheat genome . Proceeding of the National Academy of Sciences USA. 89: 11307-11311.
96117. Kota RS, Gill KS, Gill BS & Endo TR. 1993. A cytogenetically based physical map of chromosome 1B in common wheat. Genome 36: 548-554.
96118. Hohmann U, Endo TR, Gill KS & Gill BS. 1994. Comparison of genetic and physical maps of group 7 chromosomes from *Triticum aestivum* L. Molecular and General Genetics 245: 644-653.
96119. Dubcovsky J, Luo, M-C, Zhong G-Y, Bransteitter R, Desai A, Kilian A, Kleinhofs A & Dvorak J. 1996. Genetic map of diploid wheat, *Triticum monococcum* L., and its comparison with maps of *Hordeum vulgare* L. Genetics 143: 983-999.
96120. Rohde W, Dorr S, Salamini F & Becker D. 1991. Structure of a chalcone synthase genes from Hordeum vulgare. Plant Molecular Biology 16: 1103-1106.
96122. Chandler P. 1995. Personal communication.
96123. Kilian A, Kleinhofs A, Villand P, Thorbjornsen T, Olsen O-A & Kleczkowski L. 1994. Mapping of the ADP-glucose phosphorylase genes in barley. Theoretical and Applied Genetics 87: 869-871.

96124. Heun M, Kennedy AE, Anderson JA, Lapitan NLV, Sorrells ME & Tanksley SD. 1991. Construction of a restriction fragment length polymorphism map for barley (*Hordeum vulgare*). Genome 34: 437-447.
96125. Devos KM. 1996. Personal communication.
96126. Delaney DE, Nasuda S, Endo TR, Gill BS & Hulbert SH. 1995. Cytologically based physical maps of the group-2 chromosomes of wheat. Theoretical and Applied Genetics 91: 568-573.
96128. Dubcovsky J, Santa Maria G, Epstein E, Luo M-C & Dvorak J. 1996. Mapping of the K^+/Na^+ discrimination locus *Kna1* in wheat. Theoretical and Applied Genetics (In press).
96129. Delaney DE, Nasuda S, Endo TR, Gill BS & Hulbert SH. 1995. Cytologically based physical maps of the group 3 chromosomes of wheat. Theoretical and Applied Genetics 91: 780-782.

Wheat Information Service
Number 83: 106-116 (1996)

V. Abstracts of the 25th Japanese wheat genetics symposium

The 25th Japanese Wheat Genetics Symposium was held in July 19-20, 1996 at Takigawa Memorial Hall, Kobe University. A main thema of the Symposium was "Reorganization and new development of genetic research in Granimeae". Ninety-three researchers including fourty graduate students participated the Symposium. The Symposium was organization by Chiharu Nakamura, Laboratory of Plant Genetics, Department of Biological and Environmental Science, Faculty of Agriculture, Kobe University and partly sponsored by Kihara Memorial Yokohama Foundation and Rikuso-kai (an alumuni association of the Faculty of Agriculture, Kobe University).
The followings are the Symposium program and abstracts of the papers presented.

July 19 (Fri)
Openning Remarks by C. Nakamura (Kobe Univ.)
Session 1: Towards the new develoment of genetic research in Gramineae
Chaired by T. R. Endo (Kyoto Univ.) and T. Kinoshita (Hokkaido Univ.)
K. Tsunewaki (Fukui Pref. Univ.) Trends in wheat genetics.
K. Takeda (Okayama Univ.) Genetical studies in barley.
Chaired by M. Murata (Okayama Univ.) and Y. Mukai (Osaka Kyoiku Univ.)
A. Kilian (Washington State Univ.) Fine mapping of barley *Rpg1* based on barley and rice microsynteny.
A. Saito (Kyushu Agr. Exp. Station) Specificity of genomes in cereal plants: some motifs of repetitive sequence in Gramineae.
Session 2: Information networks of Gramineae genetic resources
Chaired by T. Sasakuma (Yokohama city Univ.) and H. Tsujimoto (Yokohama City Univ.)
K. Nishikawa (Kihara Memorial Yokohama Foundation) Planning oa a new network fo r wheat genetic resources.
Y. Yamasaki (National Inst. of Genetics) Wheat genetic resources database in Japan.
Y. Ogihara (Yokohama City Univ.) DNA repository in wheat.
S. Nasuda (Kyoto Univ.) An introduction to the GrainGenes database for Triticeae and relatives.
Reception at Rokko Mountain Hotel

July 20 (Sat)
Session 3: Cytoplasmic genomes and nucleus-cytoplasm interaction
Chaired by T. Kawahara (Kyoto Univ.) and N. Miyashita (Kyoto Univ.)
T. Terachi (Kyoto Sangyo Univ.) Evolution of mitochondrial genomes in Gramineae
G.-Z. Wang (Kyoto univ.) Plasmon analysis of *Triticum* and *Aegilops*
N. Asakura (Kobe Univ.) A nucleus-cytoplasm compatibility gene of *Triticum timopheevi* restoring viability and male fertility of an alloplasmic hybrid with *Aegilops squarrosa* cytoplasm.

Chaired by T. Koba (Chiba Univ.)

K. Murai (Ishikawa Agr. College) Photoperiod-sensitive cytoplasmic male sterility in wheat

Y. Ogihara (Yokohama City Univ.) Molecular basis of nuclear-cytoplasm hybrids showing photoperiod-sensitive cytoplasmic male sterility in wheat.

Lunch Session: Exploration report

Chaired by Y. Furuta (Gifu Univ.)

S. Ohta (Fukui Pref. Univ.) A short report on the field research in Spain and Morocco by the Gifu University Scientific Exploration in the Mediterranean Region in 1995 (GSEM95).

N. Mori (Kobe Univ.) A brief report on the field research project in Egypt, Tunisia, Sardinia, Corsica and Southern Italy by GSEM96.

T. Morikawa (Osaka Pref. Univ.) Survey of genetic resources of the genus *Avena* in the Canary Islands and Morocco by GSEM95.

K. Kato (Okayama Univ.) A report on the wheat field research in the central Tibet, China.

Session 4: Genome analysis

Chaired by N. Nakata (Tottori Univ.)

K. Nagaki (Yokohama City Univ.) The repetitive sequences in wheat and barley.

S. Taketa (Okayama Univ.) Cytogenetical analysis of wheat-barley hybrids.

Chaired by J. Fijigaki (Tokyo Agr. College)

T. Sasanuma (Kyoto Univ.) Analysis of the small subunit of ribulose-1,5-bisphosphate carboxylase (*rbcS*) multigene family in the tribe Triticeae.

M. Murata (Okayama Univ.) Attempts to clone alien chromosome-specific genes in wheat (*Triticum aestivum*).

Session 5: Haploid production, transformation and retrotransposons in wheat

Chaired by K. Noda (Okayama Univ.) and T. Shimada (Ishikawa Agr. College)

M. Ohtani (Ishikawa Agr. College) Recent advances in wheat anther culture.

S. Takumi (Ishikawa Agr. College) Production and characterization of transgenic wheat through particle bombardment.

Y. Matsuoka (Fukui Pref. Univ.) Wheat retrotransposon families in cereal genomes: their distribution and evolutionary rate.

Business session

Chaired by T. Sasakuma (Yokohama City Univ.)

Abstracts

K. Tsunewaki (Dept. Biosci., Fukui Pref. Univ.)

Trends in wheat genetics

Development of genome analysis (or polyploid genetics), aneuploid genetics, cytoplasmic genetics

and molecular genetics in wheat after the corresponding epoch-making discovery was reviewed, and the contributions of these fields to our understanding of wheat evolution and to wheat breeding were mentioned. Genome analysis clarified the interspecific relationship in the *Triticum* and *Aegilops* complex, and stimulated triticale breeding. Aneuploid genetics contributed in establishing the homoeology first between the chromosomes then between the genes. At the same time, it facilitated the development of various means of chromosome manipulation. Comparative gene analysis of common wheat and its ancestors, that was facilitated by the use of aneuploid methods of gene analysis, yielded rich information on the phylogenetic differentiation and origin of polyploid wheats. Cytoplasmic genetics, represented by the plasmon analysis, allowed the determination of maternal lineage of the polyploids on one hand and stimulated hybrid wheat breeding on the other. The newest field of molecular genetics already achieved construction of the synteny map of cereal chromosomes, and steady development of biotechnology is now apparent through integration of various *in vitro* culture techniques and DNA delivery methods. Then the perspective of wheat genetics was discussed, pointing out the followings as the important problems, unsolved or remained; (1) need of unification of taxonomical system and genome symbol, (2) molecular mechanism of the homologous chromosome pairing, (3) origin of the clusters of modified genomes at the diploid level, (4) amplification of the repeated sequences in specific chromosomes and genomes, (5) molecular changes in genes which are closely related to wheat domestication, (6) entire structure and function of the complex loci, (7) targeting a gene to a specific chromosome site and to a specific organelle, and (8) regeneration of wheat plant from the protoplast.

T. Takeda (Res. Inst. Bioresources, Okayama Univ.)

Genetical studies in barley

In 1940's Dr. R. Takahashi started genetical studies in barley at the Ohara Institute of Agriculture. For this half century he and his successors continued their efforts to collect barley germplasm and to analyze the phylogeny and genetical constitution of the materials. At present we keep ca. 10,000 barley accessions including wild relatives, local varieties, mutants, isogenic lines, linkage testers, trisomics, tetraploids, doubled haploids, recombinant inbreds, wheat-barley addition lines etc. In this symposium I will introduce a histry of barley genetic study in our Institute, an outline of the germplasm collection, and some topics on the stress tolerance of barley and QTL analysis of the agronomic traits.

A. Kilian[1] and A. Kleinhofs[2] ([1]Dept. Crop & Soil Sci. and [2]Dept. Genetics and Cell Biol., Washington State Univ.)

Fine mapping of barley *Rpg1* region by using rice-barley microsynteny

The barley stem rust resistance genes *Rpg1* and *rpg4* were mapped in barley on chromosomes

1P and 7M, respectively and syntenous rice chromosomes identified as 6P and 3P by mapping common probes in barley and rice. Rice yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC) and cosmid clones were used to isolate probes mapping to the barley *Rpg1* region. A high resolution map of the *Rpg1* region was established with 1400 gametes yielding a map density of 3.6 markers per 0.1 cM. These experiments confirm the validity of using large insert rice clones as probe sources for saturation mapping in large genome cereals.

A. Saito[1] and Y. Ogihara[2] ([1]Kyusyu National Agric. Exp. Station, [2]Kihara Inst. Biol. Res., Yokohama City Univ.)

Specificity of genomes in cereal plants: some motifs of repetitive sequence in the Gramineae.

A number of cereal molecular maps were constructed as based on RFLP markers. We characterized some rice RFLP markers to be homologous or heterologous to other cereal genomes. We found that some regions in rice genome might be putative ancestral genome in cereal. On the other hand, four RFLP markers being a few copied clones exhibited moderately repetitive sequences in most of the Gramineae. Northern analyses revealed these clones to be expressed in cereal leaves. These sequences had no homology to each other and reported genes. RNA folding analyses, revealed that all four clones contain remarkable stem (loop) structure in their sequences.

K. Nishikawa (Kihara Mem. Yokohama Found. Adv. Life Sci.)

Planning on a new network for wheat genetic resources

Agreements at the meeting held three times in 1994 for planning a new network for wheat genetic resources were reported as follows: 1) The network is organized from a center and stations, 2) it is concerned only genetic and experimental lines of *Triticum, Aegilops* and *Avena*, 3) The center operates general amnagement, 4) Station does registration, actual preservation, distribution, and assembling and updating data base, of the lines, 5) DNA clones are expected to be included in the network. Nineteen institutes or laboratories have agreed participation as a station in the network.

Y. Yamazaki (Genetic Stocks Res. Center, National Inst. of Genetics)

Wheat genetic resources database in Japan

The first phase of the Genetic Resources Databank Project for wheat has been initiated in this laboratory in cooperation with Wheat Networking Group of Japan. The database is composed of ca. 70 entities including the biological and molecular biological features of each strain, as well as

bibliographical information. The working group plans to continue the work on the database in several directions, such as incorporation of the wheat DNA repository database and of image data and cross referencing with related databases. The development of a data management system through which researcher can constantly update their own data by connecting to the remote computer runnning the databases is also an ongoing project.

Y. Ogihara (Kihara Inst. Biol. Res., Yokohama City Univ.)
DNA repository in wheat

It has been well recognized that DNA repository is essential not only for practical use, but also for basic research work. In order to set up DNA repository for wheat species, I presented and discussed on, what kinds of DNAs should be collected, and how those DNAs could be maintained, in connection to genome database of Japan. Based on the assessment of DNA clones related to wheat species in Japan, I have written to the researchers who keep the wheat DNA clones and/or DNA itself, so as to register those information. At the next step, DNA repository office should collect those DNA materials and maintain in the DNA repository center.

S. Nasuda (Lab. of Genetics, Fac. of Agr., Kyoto Univ.)
An introduction to the GrainGenes database for Triticeae and relatives

A brief review on GrainGenes, the database for Triticeae and relatives assembled by the United States Department of Agriculture, was presenterd. The method how to obtain the information of interest was shown. The author also intended to introduce "Mugi-net", a communication tool based on the E-mail system. "Mugi-net" is a mailing list for the researchers working on wheat, barley and relatives. To date, 75 researchers are subscribing "Mugi-net". Additionally, useful URLs on internet were summarized. The URLs are linked by Dr. Eiji Domon and can be connected through the following address; http//infofar,.affrc.go.jp/%7Edomon/mugi-links.htm

T. Terachi (Dept. Biotech., Fac. of Eng., Kyoto Sangyo U.)
Evolution of the mitochondrial genome in Triticeae

In 1984, a multicircular structural model for the plant mitochondrial genome was proposed (Palmer and Shields 1984, Lonsdale et al. 1984). Although the model has been widely accepted, it is even unclear whether "a master chromosome" is present or not. Peculiar features of the genome such as "sublimon" and "RNA editing" also make it difficult to study on the evolution of the plant mitochondrial genome. Little is known about mitochondrial genome of Triticeae other than wheat. However, comparative studies on the *rrn18/rrn5* repeat between rye and wheat (Coulhart et al.

1990, 1993) showed a possible history of the repeated sequences in grass species. A contradictory nature of the plant mitochondrial genome, represented by the slow rate of base-substitution and the high rate of rearrangement, is emphasized.

G.-Z. Wang[1], N. T. Miyashita[1] & K. Tsunewaki[2] ([1]Fac. Agric., Kyoto Univ.; [2]Dept. Biosci., Fukui Univ.)

Plasmon analysis of *Triticum* and *Aegilops*

To study genetic diversity of organellar genomes of *Triticum* and *Aegilops*, 47 alloplasmic lines of the 34 species were analyzed with respect to phenotypic and molecular variations. From the analysis of the phenotypic variations of 22 traits, it was shown that plasmons had a large variation and were calssified into 16 groups. SSCP analysis was conducted to study the molecular variations and the phylogenetic relationship of the genera. A strong evidence that *Ae. speltoides* is the B genome donor of the common wheat was obtained. In addition, the relationship between the phenotypic traits and the detected molecular variations was investigated.

N. Asakura[1], C. Nakamura[1] & I. Ohtsuka[2] ([1]Kobe Univ., [2]Kanagawa Univ.) **A nucleus-cytoplasm compatibility gene of *T. timopheevi* that restors viability and male fertility of an alloplasmic hybrid with *Ae. squarrosa* cytoplasm**

Kihara (1973) was the first to introduce the cytoplasm of *Ae. squarrosa* into common wheat. Based on the result that *Ae. squarrosa* cytoplasm causes early maturity and yield increase in some genetic backgrounds, Kihara proposed the nucleus-cytoplasm heterosis (Kihara 1980, 1982). A systematic attempt of introducing *Ae. squarrosa* cytoplasm into a large number of tetraploid wheat species revealed that 1D chromosome of *Ae. squarrosa* is required for the NC hybrids to be viable and produce functional pollen (Ohtsuka 1991). It was shown that *T. timopheevi* and *T. araraticum* possess a gene or genes functionally similar to that on 1D chromosome. We produced a euploid alloplasmic hybrid of *T. durum* with *Ae. squarrosa* cytoplasm by introgressing such nucleus-cytoplasm compatibility (*ncc*) gene from *T. timopheevi*. In attempt to tag *ncc* four RAPD markers were detected that are tightly linked and highly conserved in Timopheevi group of wheat.

K. Murai (Res. Inst. Agr. Resources, Ishikawa Agr. Coll.)

Photoperiod-sensitive cytoplasmic male sterility caused by *Aegilops crassa* cytoplasm

Photoperiod-sensitive cytoplasmic male sterility (PCMS) has been found to be caused by interaction between the *Aegilops crassa* cytoplasm and the nuclear genomes of some Japanese wheat (*Triticum aestivum*) cultivars (Murai and Tsunewaki 1993, 1995). Based on PCMS, a 'two-line system' for

hybrid wheat production can be proposed. Eleven F_1 hybrids have been produced using the PCMS system and examined for their yield performance (Murai 1995). PCMS gives us several interesting subjects for investigation, e.g., the genome-plasmon interaction induced by photoperiod and occurrence of pistilody. Studies on the molecular mechanism of PCMS are required to elucidate these problems.

Y. Ogihara[1], K. Futami[1], K. Tsuji[1] & K. Murai[2] ([1]Kihara Inst. Biol. Res., Yokohama City U. & Res. [2]Inst. Agr. Resources, Ishikawa Agr. Col.)

Molecular basis of nuclear-cytoplasm hybrids showing photoperiod-sensitive cytoplasmic male sterility in wheat

Analyses of structure and transcription patterns of mitochondrial genes in alloplasmic wheats showing photoperiod-sensitve cytoplasmic male sterility (PCMS) were carried out, to assess the molecular basis of that phenomenon. The RFLP and transcription patterns of *orf25* gene in alloplasmic wheats differed from those of their parental speices, i.e., *Aegilops crassa*, suggesting that the transcriptions of *orf25* are associated with PCMS phenomenon. The analyses of DNA sequencing and primer extension of *orf25* in both of alloplasmic and euplasmic lines indicate that the promoter of the gene in *Ae. crassa* was replaced by that of *rps7* and the transcript of *Ae. crassa* pure line was shorter about 300 nucleotides than that of alloplasmic lines.

S. Ohta[1], M. Morikawa[2], T. Tominaga[3] & Y. Furuta[4] ([1]Fukui Pref. Univ., [2]Osaka Pref. Univ., [3]Shinsu Univ., [4]Gifu Univ.)

A short report on the field research in Spain and Morocco by the Gifu University Scientific Exploration in the Mediterranean Region in 1995 (GSEM95)

Three years' field research project in the Mediterranean region, supported by the Ministry of Education, Science, Sports and Culture, Japan (Grant-in-Aid for International Scientific Research Program: Field Research No. 07041133), was schemed to calrify close relationships among man, crops and weeds in the agricultural system based on wheat and barley. Spain and Morocco were surveyed from May 24 to September 1 as the first year research work of the project. The research in Spain was carried out as a cooperative work with Dr. R. Ponz Ascaso, CRF-INIA. A total of 373 samples, including *Triticum spelta*, *T. dicoccum*, *Aegilops ventricosa*, *Avena* spp. etc., were collected from the Canary Islands, Cuenca and Asturias. In Morocco, a cooperative field research with INRA collected a total of 1,346 samples of plant materials from the north-western coastal plain, the High Atlas Mountains and the Rif Mountains. *T. monococcum*, *Ae. ventricosa*, *Ae. ovata* ssp. *atlantica*, *Haynaldia hordeasea* and endemic *Avena* spp. were successfully collected during the trip. A detailed report is now being prepared and will be published elsewhere.

N. Mori[1], T. Tominaga[2], M. Morikawa[3], S. Ohta[4] & Y. Furuta[5] ([1]Kobe Univ., [2]Shinshu Univ., [3]Osaka Pref. Univ., [4]Fukui Pref. Univ. [5]Gifu Univ.)

A brief report on the field research project in Egupt, Tunisia, Sardinia, Corsica and Southern Italy by GSEM96

Egypt, Tunisia, Sardinia, Corsica and Southern Italy were surveyed from April 1 to June 4. This was the second year research work of the GSEM supported by the Ministry of Education, Science, Sports and Culture, Japan (Grant-in-Aid for International Scientific Research Program: Field Research No. 07041133). The research was carried out as a cooperative research work with Drs. R. Sayed (Assiut Univ., Egypt), M. Harrabi (Inst. National d'Agronomie de Tunis). A total of about 1,010 samples of wheat, barley, oat and the weed in their filed were collected. More detailed report is now in preparation.

T. Morikawa (Fac. of Agric., Osaka pref. Univ.)

Survey of genetic resources of the genus *Avena* in the Canary Islands and Morocco by GSEM95

All the biological species of *Avena* coexist in the area roughly between Southern Spain, Morocco and the Canary Islands. The genetic resources of the genus *Avena* were surveyed in the Canary Island (La Gomera, Tenerife, Fuerteventura and Lanzarote) and Morocco from May 14th to Luly 1st 1995 by the Gifu University Scientifc Exploration in the Mediterranean Region (GSEM95). A total of 61 accessions including 7 species (*Avena canariensis, A. hirtula, A. strigosa, A. barbata, A. sterilis, A. fatua and A. atherantha* were collected from the Canary Islands. In Morocco, a total of 193 accessions including 14 species (*A. eriantha, A. agadiriana, A. atlantica, A. barbata, A. damascena, A. hirtula, A. longiglumis, A. prostrata, A. maroccana, A. murphyi, A. fatua, A. sativa, A. byzantiana* and *A. strilis*) were collected.

K. Kato[1], H. Tsujimoto[2], Y.-H. Zhou[3] and C. Yen[4] ([1]Fac. Agric., Okayama Univ.; [2]Kihara Inst. Biol. Res., Yokohama City Uni.; [3]Dept. Basic Sci, Sichuan Agric. Univ., Yaan, Sichuan, China; [4]Triticeae Res. Inst., Sichuan Agric. Univ., Dujiangyan, Sichuan, China)

A report of the wheat field research in the central Tibet, China

Field research on wheat and its wild relatives was carried out in August, 1995, as one of the projects on 'Evaluation and basic research in Chinese crop germplasm' sponsored by the Ministry of Education, Science, Sports and Culture, Japan (Grant-in-Aid for International Scientific Research Program: Field Research No. 07041154). In Tibet two major crops, wheat as a cash plant and barley for self consumption, are cultivated. Because of its economical importance,

wheat landraces (spring type) had been mostly replaced by modern varieties (winter type). Wheat samples were collected from both wheat and barley fields, and totaled 320 samples. Those from spring wheat or barley fields proved to be of spring growth habit, while those from winter wheat fields were mostly of winter growth habit. Among them, one accession could not be classified as *T. aestivum*, and was considered as hybrid origin between emmer wheat and common wheat.

K. Nagaki, H. Tsujimoto & T. Sasakuma (Kihara Inst. Biol. Res., Yokohama City Unvi.)
The repetitive sequences in wheat and barley

Synteny maps of Triticeae species indicated that the structures of these genomes are well conserved. We here analyzed the repetitive DNA sequences in these species, especially in wheat and barley. *Afa* family repetitive sequence that was originally isolated as the D genome-specific sequence *(pAs1;* Rayburn and Gill, 1988) was found in all the Triticeae species investigated. The molecular evolutionary studies of the sequences clearly showed that amplification events took place relatively suddenly using a single unit as the master of amplification. One clone including sub-family sequence of barley could be a good chromosome marker to identify each barley chromosome just like a clone *pAs1* is a good marker for the wheat D genome chromosome identification.

S. Taketa & K. Takeda (Res. Inst. Bioresources, Okayama Univ.)
Cytogenetical analysis of wheat-barley hybrids

Bread wheat cultivars were crossed as the female parent with cultivated barley (*Hordeum vulgare*) and wild barley (*H. spontaneum*). Some barley accessions showed enhanced crossability with bread wheat. Variation in the patterns of chromosome elimination in the hybrids was recognized. Some morphological marker genes of the barley parent expressed their characteristics in the hybrids. All barley chromosome 5 so far tested caused sterility when introduced to bread wheat. A cytogenetical scheme to remove this sterility factor(s) are proposed. A partial amphiploid between bread wheat and barley, which carries all barley chromosomes except chromosome 5 in disomic condition (2n=54), was successfully produced.

T. Sasanuma (Fac. of Agric., Kyoto Univ.)
Analysis of the small subunit of ribulose-1,5-bisphosphate carboxylase (*rbcS*) multigene family in the tribe Triticeae

To study the evolution of multigene family in plants, *rbcS* was chosen. Fifteen species of the Triticeae and its relative tibes were analyzed. The sequences were classified into three types (a, b and c) based on the differences in the intron. *Triticum* and *Aegilops* species have both a and b

types. The c type was found only in *Agropyron*. The difference between a and b types was larger than the interspecific difference within each type. It was concluded that the differentiation of a and b types of *rbcS* occurred before the formatrion of Triticeae.

M. Murata (Res. Inst. Bioresources, Okayama Univ.)
Attempts to clone alien chromosome-specific genes in wheat (*Triticum aestivum*)

Wheat has large genome size (16,000 Mb/haploid), more than 100 times as much as that of *Arabidopsis thaliana* (145 Mb/haploid), and also involves a large proportion of repetitive DNA sequences in the genome. These make it difficult to isolate wheat genes by the strategies that are being commonly used in *A. thaliana* and other plant species. By using genomic subtraction, we attempted to isolate genes from the midget chromosome in a common wheat with rye cytoplasm. However, repetitive DNA and rye-chloroplast DNA were preferentially cloned, and no low-copy sequences were obtained. We also applied the differential screening to identify rye-specific cDNA in the wheat strain carrying the midget chromosome, since it has been shown that the midget chromosome had originated from rye. Almost all cDNAs screened by this strategy were those corresponding to the photosynthesis-related genes such as *rbcL*, *rbcS*, and *cab*. Other few cDNAs showed rye-specificity, but their functions are unknown.

M. Otani & T. Shimada (Res. Inst. of Agrc. Resources, Ishikawa Agr. Coll.)
Recent advances in wheat anther culture

Efficient methods for pollen embryo production from cultured anthers of common and emmer wheat have been established. Filter sterilized W14 medium (Ouyang et al. 1988) and C17 medium (Wang et al. 1986) containing 0.26M maltose were effective for the pollen embryo production in all genotypes tested. The pollen embryos were produced at high frequency when anthers were cultured in these media at 28 °C in the dark. We cultured the anthers of various genotypes containing some aneuploid lines of common and emmer wheat to investigate the genetic factors for the anther culture ability. The genetic factors of the pollen embryo formation, regeneration from pollen embryos and the green plant production were revealed to be controlled by a few individual major genes.

S. Takumi (Res. Inst. Agr. Resources, Ishikawa Agr. Coll.)
Production and characterization of transgenic wheat through particle bombardment

Transformation system in wheat was developed by using particle bombardment. Transgenic wheat plants were produced from scutellar tissues of immature embryos bombarded with the bar

selectable marker gene, and this transformation frequency was influenced by pre-culture duration and genotype. To study the mobility of maize transposable elements in wheat, the *Ac*/*Ds* elements were introduced into two cultured cell lines. By the phenotypic assay and the following molecular analyses, the transposition of the elements were confirmed. Moreover, transgenic plants with both the *Ac* transposase gene and *Ds* element were produced, and the integration and expression of Ac/Ds in the T1 generation were confirmed.

Y. Matsuoka & K. Tsunewaki (Fac. of Biosci., Fukui Pref. Univ.)

Wheat retrotransposon families in cereal genomes: their distribution and evolutionary rate

We addressed (1) the family structure of wheat retrotransposons and (2) their distribution in cereal genomes. Seven wheat retrotransposon families were identified by analyses of the 243 bp reverse transcriptase domain. All these families were common to the genomes of ancestral diploid species of common wheat, and barely and rye. Family 1 retrotransposons were detected in rice and three millets from tribe Paniceae, indicating their very ancient origin. The nucleotide sequence comparison between Family 1 retrotransposons and other nuclear genes from wheat and rice suggested that Family 1 retrotransposons evolved at similar rate to that of nuclear genes.

Wheat Information Service
Number 83: 117-128 (1996)

VI. Recent publications on wheat genetics

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

1995

---

(59)
ACCN:001545481 CTLN:3797572
ABSJ:G (Genetics Abstracts); D (Ecology Abstracts)
AUTH:Sallares, R.;Allaby, R.G.;Brown, T.A.*
AFFN:Dep. Biochem. Appl. Mol. Biol., UMIST, Manchester M60 1QD, UK
TITL:PCR-based identification of wheat genomes
HTIL:MOL. ECOL.
HSSN:0962-1083
HYER:1995
HCOL:vol. 4, no. 4, pp. 509-514

---

(60)
ACCN:001548246 CTLN:3800825
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts); D (Ecology Abstracts)
AUTH:De Leij, F.A.A.M.;Sutton, E.J.;Whipps, J.M.;Fenlon, J.S.;Lynch, J.M.
AFFN:Sch. Biol. Sci., Univ. Surrey, Guildford, Surrey GU2 5XH, UK
TITL:Impact of field release of genetically modified Pseudomonasfluorescens on indigenous microbial populations of wheat
HTIL:APPL. ENVIRON. MICROBIOL.
HSSN:0099-2240
HYER:1995
HCOL:vol. 61, no. 9, pp. 3443-3453

---

(61)
ACCN:001553303 CTLN:3806543
ABSJ:G (Genetics Abstracts)
AUTH:Cuadrado, A.;Jouve, N.*
AFFN:Dep. Cell Biol. and Genet., Univ. Alcala de Henares, E-28871, Alcala de Henares, Madrid, Spain
TITL:Fluorescent in situ hybridization and C-banding analyses of highly repetitive DNA sequences in the heterochromatin of rye (Secale montanum Guss.) and wheat incorporating S. montanum chromosome segments
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 4, pp. 795-802

---

(62)
ACCN:001553304 CTLN:3806544
ABSJ:G (Genetics Abstracts)
AUTH:Anderson, J.A.;Maan, S.S.
AFFN:Plant Sci. Dep., North Dakota State Univ., Fargo, ND 58105-5051, USA
TITL:Interspecific nuclear-cytoplasmic compatibility controlled by genes on group 1 chromosomes in durum wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 4, pp. 803-808

---

(63)
ACCN:001553320 CTLN:3806560
ABSJ:G (Genetics Abstracts)
AUTH:Symillides, Y.;Henry, Y.;De Buyser, J.
AFFN:Agric. Univ. Athens, Plant Breed. and Biom., Iera Odos 75, 11855 Athens, Greece
TITL:Analysis of Chinese spring regenerants obtained from short- and long- term wheat somatic embryogenesis
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1995
HCOL:vol. 82, no. 3, pp. 263-268

---

(64)
ACCN:001553417 CTLN:3806657
ABSJ:G (Genetics Abstracts)
AUTH:Chen, J.M.*Gustafson, J.P.
AFFN:USDA-ARS, Plant Genet. Res. Unit, and Plant

Sci. Unit, Univ. Missouri, Columbia, MO 65211, USA
TITL:Physical mapping of restriction fragment length polymorphisms (RFLPs) in homoeologous group 7 chromosomes of wheat by in situ hybridization
HTIL:HEREDITY
HSSN:0018-067X
HYER:1995
HCOL:vol. 75, no. 3, pp. 225-233

---

(65)
ACCN:001553949 CTLN:3807189
ABSJ:G (Genetics Abstracts)
AUTH:Gosink, M.M.;Vierstra, R.D.*
AFFN:Dep. Hortic., Univ. Wisconsin, Madison, WI 53706, USA
TITL:Redirecting the specificity of ubiquitination by modifying ubiquitin- conjugating enzymes
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1995
HCOL:vol. 92, no. 20, pp. 9117-9121

---

(66)
ACCN:001557292 CTLN:3809548
ABSJ:G (Genetics Abstracts)
AUTH:Porter, D.R.;Nguyen, H.T.;Burke, J.J.
AFFN:USDA-ARS, Plant Sci. and Water Conserv. Res. Lab., 1301 N. Western, Stillwater, OK 74075, USA
TITL:Genetic control of acquired high temperature tolerance in winter wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1995
HCOL:vol. 83, no. 2, pp. 153-157

---

(67)
ACCN:001558722 CTLN:3811123
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Ma, H.;Singh, R.P.;Mujeeb-Kazi, A.
AFFN:Int. Maize and Wheat Improv. Cent. CIMMYT, Lisboa 27, Apdo. Postal 6- 641, 06600 Mexico, D.F., Mexico
TITL:Suppression/expression of resistance to stripe rust in synthetic hexaploid wheat (Triticum turgidum x T. tauschii)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1995
HCOL:vol. 83, no. 2, pp. 87-93

---

(68)
ACCN:001559126 CTLN:3811615
ABSJ:G (Genetics Abstracts)
AUTH:Szakacs, E.;Barnabas, B.
AFFN:Agric. Res. Inst. Hungarian Acad. Sci., H-2462 Martonvasar, Hungary
TITL:The effect of colchicine treatment on microspore division and microspore-derived embryo differentiation in wheat (Triticum aestivum L.) anther culture
HTIL:EUPHYTICA
HYER:1995-2336
HCOL:vol. 83, no. 3, pp. 209-213

---

(69)
ACCN:001559129 CTLN:3811618
ABSJ:G (Genetics Abstracts)
AUTH:Labuschagne, M.T.;Van Deventer, C.S.
AFFN:Dep. Plant Breed., Univ. Orange Free State, PO Box 339, Bloemfontein, South Africa
TITL:The effect of Glu-B1 high molecular weight glutenin subunits on biscuit-making quality of wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1995
HCOL:vol. 83, no. 3, pp. 193-197

---

(70)
ACCN:001559130 CTLN:3811619
ABSJ:G (Genetics Abstracts)
AUTH:Yau, S.K.;Nachit, M.M.;Ryan, J.;Hamblin, J.
AFFN:Intl. Cent. Agric. Res. Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria
TITL:Phenotypic variation in boron-toxicity tolerance at seedling stage in durum wheat (Triticum durum)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1995
HCOL:vol. 83, no. 3, pp. 185-191

---

(71)
ACCN:001559131 CTLN:3811620
ABSJ:G (Genetics Abstracts)
AUTH:Slafer, G.A.;Rawson, H.M.
AFFN:Crop Improv. Cent., Dep. Agric., Univ. Melbourne, Parkville, Vic. 3052, Australia
TITL:Intrinsic earliness and basic development rate assessed for their response to temperature in wheat
HTIL:EUPHYTICA

HSSN:0014-2336
HYER:1995
HCOL:vol. 83, no. 3, pp. 175-183

---

(72)
ACCN:001561542 CTLN:3814186
ABSJ:G (Genetics Abstracts)
AUTH:Aniol, A.M.
AFFN:Dep. Plant Biochem. and Physiol., Plant Breed. and Acclim. Inst., Radzikow, PO Box 1019, 00-950 Warszawa, Poland
TITL:Physiological aspects of aluminium tolerance associated with the long arm of chromosome 2D of the wheat (Triticum aestivum L.) genome
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 3, pp. 510-516

---

(73)
ACCN:001561548 CTLN:3814192
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Pagnotta, M.A.;Nevo, E.*;Beiles, A.;Porceddu, E.
AFFN:Inst. Evol., Univ. Haifa, Haifa 31905, Israel
TITL:Wheat storage proteins: Glutenin diversity in wild emmer, Triticum dicoccoides, in Israel and Turkey. 2. DNA diversity detected by PCR
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 3, pp. 409-414

---

(74)
ACCN:001561549 CTLN:3814193
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Nevo, E.;Pagnotta, M.A.;Beiles, A.;Porceddu, E.
AFFN:Inst. Evol., Univ. Haifa, Mt. Carmel, Haifa 31905, Israel
TITL:Wheat storage proteins: Glutenin DNA diversity in wild emmer wheat, Triticum dicoccoids, in Israel and Turkey. 3. Environmental correlates and allozymic associations
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 3, pp. 415-420

---

(75)
ACCN:001583068 CTLN:3835748
ABSJ:G (Genetics Abstracts)
AUTH:Friebe, B.;Tuleen, N.A.;Gill, B.S.
AFFN:Dep. Plant Pathol., Wheat Genet. Resour. Cent., Throckmorton Hall, Kansas State Univ. Manhattan, KS 66506-5502, USA
TITL:Standard karyotype of Triticum searsii and its relationship with other S-genome species and common wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 2, pp. 248-254

---

(76)
ACCN:001583072 CTLN:3835752
ABSJ:G (Genetics Abstracts)
AUTH:Devos, K.M.;Dubcovsky, J.;Dvorak, J.;Chinoy, C.N.;Gale, M.D.
AFFN:John Innes Cent., Norwich Res. Park, Colney, Norwich NR4 7UH, UK
TITL:Structural evolution of wheat chromosomes 4A, 5A, and 7B and its impact on recombination
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 2, pp. 282-288

---

(77)
ACCN:001583085 CTLN:3835765
ABSJ:G (Genetics Abstracts)
AUTH:Talbert, L.E.;Blake, N.K.;Storlie, E.W.;Lavin, M.
AFFN:Dep. Plant, Soil and Environ. Sci., Montana State Univ., Bozeman, MT 59717, USA
TITL:Variability in wheat based on low-copy DNA sequence comparisons
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 5, pp. 951-957

---

(78)
ACCN:001583086 CTLN:3835766
ABSJ:G (Genetics Abstracts)
AUTH:Zhang, J.;Friebe, B.;Gill, B.S.*
AFFN:Dep. Plant Pathol. and Wheat Genet. Resour. Cent., Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:Detection of maize DNA sequences amplified in wheat
HTIL:GENOME
HSSN:0831-2796

HYER:1995
HCOL:vol. 38, no. 5, pp. 946-950
---
(79)
ACCN:001583097 CTLN:3835777
ABSJ:G (Genetics Abstracts)
AUTH:Nelson, J.C.;Sorrells, M.E.;Deynze, A.E.V.;Lu, Y.H.;Atkinson, M.; Bernard, M.;Leroy, P.;Faris, J.D.;Anderson, J.A.
AFFN:Dep. Plant Breed. and Biom., 252 Emerson Hall, Cornell Univ., Ithaca, NY 14853, USA
TITL:Molecular mapping of wheat: Major genes and rearrangements in homoeologous groups 4, 5, and 7
HTIL:GENETICS
HSSN:0016-6731
HYER:1995
HCOL:vol. 141, no. 2, pp. 721-731
---
(80)
ACCN:001583103 CTLN:3835783
ABSJ:G (Genetics Abstracts)
AUTH:Lee, S.J.;Penner, G.A.*;Devos, K.M.
AFFN:Agric. and Agri-Food Canada, Winnipeg Res. Cent., 195 Dafoe Rd., Winnipeg, MB R3T 2M9, Canada
TITL:Characterization of loci containing microsatellite sequences among Canadian wheat cultivars
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 5, pp. 1037-1040
---
(81)
ACCN:001583105 CTLN:3835785
ABSJ:G (Genetics Abstracts)
AUTH:Limin, A.E.;Houde, M.;Chauvin, L.P.;Fowler, D.B.;Sarhan, F.
AFFN:Crop Dev. Cent., Univ. Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada
TITL:Expression of the cold-induced wheat gene Wcs120 and its homologs in related species and interspecific combinations
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 5, pp. 1023-1031
---
(82)
ACCN:001583370 CTLN:3836062
ABSJ:G (Genetics Abstracts)
AUTH:Campenhout, S.V.;Vander Stappen, J.;Sagi, L.;Volckaert, G.*
AFFN:Lab. Gene Technol., Catholic Univ. Leuven, Willem de Croylaan 42, B- 3001 Leuven, Belgium
TITL:Locus-specific primers for LMW glutenin genes on each of the group 1 chromosomes of hexaploid wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 2, pp. 313-319
---
(83)
ACCN:001583395 CTLN:3836087
ABSJ:G (Genetics Abstracts)
AUTH:Delaney, D.E.;Nasuda, S.;Endo, T.R.;Gill, B.S.*;Hulbert, S.H.
AFFN:Dep. Plant Pathol., Kansas State Univ., Manhattan, KS 66506, USA
TITL:Cytologically based physical maps of the group-2 chromosomes of wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 4, pp. 568-573
---
(84)
ACCN:001583400 CTLN:3836092
ABSJ:G (Genetics Abstracts)
AUTH:Hohmann, U.;Endo, T.R.;Herrmann, R.G.;Gill, B.S.
AFFN:Bot. Inst. Ludwig-Maximilians-Univ. Muenchen, Menzinger Str. 67, D-80638 Munich, FRG
TITL:Characterization of deletions in common wheat induced by an Aegilops cylindrica chromosome: Detection of multiple chromosome rearrangements
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 4, pp. 611-617
---
(85)
ACCN:001583401 CTLN:3836093
ABSJ:G (Genetics Abstracts)
AUTH:Hohmann, U.;Graner, A.;Endo, T.R.;Gill, B.S.;Herrmann, R.G.
AFFN:Bot. Inst. Ludwig-Maximilians-Univ. Muenchen, Menzinger Str. 67, D-80638 Munich, FRG
TITL:Comparison of wheat physical maps with barley linkage maps for group 7 chromosomes
HTIL:THEOR. APPL. GENET.

HSSN:0040-5752
HYER:1995
---
(86)
ACCN:001583443 CTLN:3836135
ABSJ:G (Genetics Abstracts)
AUTH:D'Ovidio, R.;Masci, S.;Porceddu, E.
AFFN:Univ. Tuscia, Dip. Agrobiol. e Agrochim., Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:Development of a set of oligonucleotide primers specific for genes at the Glu-1 complex loci of wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 2, pp. 189-194
---
(87)
ACCN:001583445 CTLN:3836137
ABSJ:G (Genetics Abstracts)
AUTH:Nakamura, T.;Yamamori, M.;Hirano, H.;Hidaka, S.;Nagamine, T.
AFFN:Tohoku Natl. Agric. Exp. Stn., Akahira 4, Morioka, Iwate 020-01, Japan
TITL:Production of waxy (amylose-free) wheats
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1995
HCOL:vol. 248, no. 3, pp. 253-259
---
(88)
ACCN:001588481 CTLN:3841675
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Tosa, Y.;Nakamura, T.;Kusaba, M.
AFFN:Fac. Agric., Kochi Univ., Nankoku, Kochi 783, Japan
TITL:Distribution of genes for resistance to the wheatgrass mildew fungus in Japanese wheat cultivars and of their corresponding genes in the wheat mildew fungus
HTIL:JAP. J. GENET.
HSSN:0021-504X
HYER:1995
HCOL:vol. 70, no. 1, pp. 119-126
---
(89)
ACCN:001588821 CTLN:3842041
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Hetrick, B.A.D.;Wilson, G.W.T.;Gill, B.S.;Cox, T.S.
AFFN:Dep. Biol., Univ. Northern Iowa, Cedar Falls, IA 50614, USA
TITL:Chromosome location of mycorrhizal responsive genes in wheat
HTIL:CAN. J. BOT./REV. CAN. BOT.
HSSN:0008-4026
HYER:1995
HCOL:vol. 73, no. 6, pp. 891-897
---
(90)
ACCN:001594902 CTLN:3847683
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Yu, D.;Kennedy, I.R.*
AFFN:Dep. Agric. Chem. and Soil Sci., Univ. Sydney, Sydney, NSW 2006, Australia
TITL:Nitrogenase activity (C sub(2)H sub(2) reduction) of Azorhizobium in 2,4-D-induced root structures of wheat
CONF:10. Australian Nitrogen Fixation Conference: Genetics, Microbial Ecology and Nitrogen Fixation: Is there a Sustainable Symbiosis?
LOCN:Brisbane (Australia) DATE:7-10 Sep 1993
HTIL:SOIL BIOL. BIOCHEM.
HSSN:0038-0717
HYER:1995
HCOL:vol. 27, no. 4-5, pp. 459-462
---
(91)
ACCN:001594903 CTLN:3847684
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Tchan, Y.T.;Zeman, A.M.M.
AFFN:Dep. Chem. Eng., Univ. Sydney, Sydney, 2006 NSW, Australia
TITL:N sub(2) fixation (C sub(H) sub(2) reduction) in 2,4-dichloro- phenoxyacetic acid (2,4-D) treated wheat inoculated with free-living diazotrophs
CONF:10. Australian Nitrogen Fixation Conference: Genetics, Microbial Ecology and Nitrogen Fixation: Is there Sustainable Symbiosis?
LOCN:Brisbane (Australia) DATE:7-10 Sep 1993
HTIL:SOIL BIOL. BIOCHEM.
HSSN:0038-0717
HYER:1995
HCOL:vol. 27, no. 4-5, pp. 453-457
---
(92)
ACCN:001594904 CTLN:3847685
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Katupitiya, S.;New, P.B.;Elmerich, C.;Kennedy, I.R.*

AFFN:Dep. Agric. Chem. and Soil Sci., Univ. Sydney, Sydney, NSW 2006, Australia
TITL:Improved N sub(2) fixation in 2,4-D treated wheat roots associated with Azospirillum lipoferum: Studies of colonization using reporter genes
CONF:10. Australian Nitrogen Fixation Conference: Genetics, Microbial Ecology and Nitrogen Fixation: Is there aSustainable Symbiosis?
LOCN:Brisbane (Australia) DATE:7-10 Sep 1993
HTIL:SOIL BIOL. BIOCHEM.
HSSN:0038-0717
HYER:1995
HCOL:vol. 27, no. 4-5, pp. 447-452

---

(93)
ACCN:001601007 CTLN:3854381
ABSJ:G (Genetics Abstracts)
AUTH:Deynze, A.E.V.;Nelson, J.C.;Yglesias, E.S.;Harrington, S.E.;Braga, D. P.;McCouch, S.R.;Sorrells, M.E.*
AFFN:Dep. Plant Breed. and Biom., Cornell Univ., Ithaca, NY 14853, USA
TITL:Comparative mapping in grasses. Wheat relationships
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1995
HCOL:vol. 248, no. 6, pp. 744-754

---

(94)
ACCN:001601062 CTLN:3854436
ABSJ:G (Genetics Abstracts)
AUTH:Feuillet, C.;Messmer, M.;Schachermayr, G.;Keller, B.*
AFFN:Dep. Plant Breed., Swiss Fed. Res. Stn. Agron., FAP Reckenholz, Reckenholzstr. 191, 8046 Zuerich, Switzerland
TITL:Genetic and physical characterization of the LR1 leaf rust resistance locus in wheat (Triticum aestivum L.)
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1995
HCOL:vol. 248, no. 5, pp. 553-562

---

(95)
ACCN:001604690 CTLN:3858184
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Baaga, M.;Chibbar, R.N.*;Kartha, K.K.
AFFN:Plant Biotechnol. Inst., Natl. Res. Counc. Canada, 110 Gymnasium Place, Saskatoon, Sask., Canada S7N 0W9
TITL:Molecular cloning and expression analysis of peroxidase genes from wheat
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1995
HCOL:vol. 29, no. 4, pp. 647-662

---

(96)
ACCN:001605271 CTLN:3858807
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Holdsworth, M.J.;Munoz-Blanco, J.;Hammond-Kosack, M.;Colot, V.;Schuch, W.;Bevan, M.W.*
AFFN:Mol. Genet. Dep., John Innes Cent., Coleny Ln., Norwich NR4 7UJ, UK
TITL:The maize transcription factor opaque-2 activates a wheat glutenin promoter in plant and yeast cells
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1995
HCOL:vol. 29, no. 4, pp. 711-720

---

(97)
ACCN:001605292 CTLN:3858828
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:De Leij, F.A.A.M.;Sutton, E.J.;Whipps, J.M.;Fenlon, J.S.;Lynch, J.M.*
AFFN:Sch. Biol. Sci., Univ. Surrey, Guildford, Surrey, GU2 5XH, UK
TITL:Field release of a genetically modified Pseudomonas fluorescens on wheat: Establishment, survival and dissemination
HTIL:BIO/TECHNOLOGY
HSSN:0733-222X
HYER:1995
HCOL:vol. 13, no. 13, pp. 1488-1492

---

(98)
ACCN:001607633 CTLN:3860395
ABSJ:Z (Entomology Abstracts); G (Genetics Abstracts)
AUTH:Brewer, M.J.;Kaltenbach, J.E.
AFFN:Dep. Plant, Soil and Insect Sci., Univ.

Wyoming, P.O. Box 3354, Laramie, WY 82071, USA
TITL:Russian wheat aphid (Homoptera: Aphididae) population variation in response to chlorpyrifos exposure
HTIL:J. KANS. ENTOMOL. SOC.
HSSN:0022-8567
HYER:1995
HCOL:vol. 68, no. 3, pp. 346-354

---

(99)
ACCN:001613443 CTLN:3866607
ABSJ:G (Genetics Abstracts)
AUTH:Bonnard, G.;Grienenberger, J.M.*
AFFN:Institut de Biologie Moleculaire des Plantes du CNRS, Universite Louis Pasteur, 12 rue du General Zimmer, F-67084 Strasbourg, France
TITL:A gene proposed to encode a transmembrane domain of an ABC transporter is expressed in wheat mitochondria
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1995
HCOL:vol. 246, no. 1, pp. 91-99

---

(100)
ACCN:001613485 CTLN:3866649
ABSJ:G (Genetics Abstracts)
AUTH:Roeder, M.S.;Plaschke, J.;Koenig, S.U.;Boerner, A.;Sorrells, M.E.; Tanksley, D.;Ganal, M.W.
AFFN:Institut fuer Pflanzengenetik und Kulturpflanzenforschung, Correnssstrasse 3, 06466 Gatersleben, Germany
TITL:Abundance, variability and chromosomal location of microsatellites in wheat
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1995
HCOL:vol. 246, no. 3, pp. 327-333

---

(101)
ACCN:001613626 CTLN:3866870
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Singh, R.P.;Ma, H.;Rajaram, S.
AFFN:Intl. Maize and Wheat Improvement Cent. (CIMMYT), Lisboa 27, Apdo, Postal 6-641, 06600 Mexico, D.F., Mexico
TITL:Genetic analysis of resistance to scab in spring wheat cultivar Frontana
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:1995
HCOL:vol. 79, no. 3, pp. 238-240

---

(102)
ACCN:001615594 CTLN:3868883
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Donini, P.;Koebner, R.M.D.;Ceoloni, C.*
AFFN:Dep. Agrobiol. and Agrochem., Univ. Tuscia, I-01100 Viterbo, Italy
TITL:Cytogenetic and molecular mapping of the wheat-Aegilops longissima chromatin breakpoints in powdery mildew-resistant introgression lines
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 5, pp. 738-743

---

(103)
ACCN:001622037 CTLN:3875914
ABSJ:G (Genetics Abstracts)
AUTH:Saponaro, C.;Pogna, N.E.*;Castagna, R.;Pasquini, M.;Cacciatori, P.; Redaelli, R.
AFFN:Istituto Sperimentale per la Cerealicoltura, Applied Genet. Sect., via Cassia 176, 00191 Rome, Italy
TITL:Allelic variation at the Gli-A1 super(m), Gli-A2 super(m) and Glu-A1 super(m) loci and breadmaking quality in diploid wheat Tritictum monococcum
HTIL:GENET. RES.
HSSN:0016-6723
HYER:1995
HCOL:vol. 66, no. 2, pp. 127-137

---

(104)
ACCN:001622049 CTLN:3875926
ABSJ:G (Genetics Abstracts)
AUTH:Dubcovsky, J.;Luo, M.-C.;Dvorak, J.
AFFN:Dep. Agronomy and Range Sci., Univ. California, Davis, CA 95616, USA
TITL:Linkage relationships among stress-induced genes in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 5, pp. 795-801

---

(105)

ACCN:001622052 CTLN:3875929
ABSJ:G (Genetics Abstracts)
AUTH:Delaney, D.E.;Nasuda, S.;Endo, T.R.;Gill, B.S.;Hulbert, S.H.
AFFN:Dep. Plant Pathol., 4024 Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506, USA
TITL:Cytologically based physical maps of the group 3 chromosomes of wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 5, pp. 780-782

---

(106)
ACCN:001622054 CTLN:3875931
ABSJ:G (Genetics Abstracts)
AUTH:Joppa, L.R.;Nevo, E.;Beiles, A.
AFFN:Northern Crop Sci. Lab., Box 5677, State Univ. Stn., Fargo, ND 58105, USA
TITL:Chromosome translocations in wild populations of tetraploid emmer wheat in Israel and Turkey
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 5, pp. 713-719

---

(107)
ACCN:001622060 CTLN:3875937
ABSJ:G (Genetics Abstracts)
AUTH:Wang, G.;Hyne, V.;Chao, S.;Henry, Y.;De Buyser, J.;Gale, M.D.;Snape, J. W.*
AFFN:John Innes Cent., Norwich Research Park, Colney, Norwich NR4 7UJ, UK
TITL:A comparison of male and female recombination frequency in wheat using RFLP maps of homoeologous group 6 and 7 chromosomes
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1995
HCOL:vol. 91, no. 5, pp. 744-746

---

(108)
ACCN:001622170 CTLN:3876047
ABSJ:G (Genetics Abstracts)
AUTH:Winfield, M.O.;Schmitt, M.;Loerz, H.;Davey, M.R.;Karp, A.
AFFN:Inst. Arable Crop Res., Long Ashton Res. Stn., Dep. Agric. Sci., Univ. Bristol, Long Ashton, Bristol BS18 9AF, UK
TITL:Nonrandom chromosome variation and morphogenic potential in cell lines of bread wheat (Triticum aestivum L.)
HTIL:GENOME
HSSN:0831-2796
HYER:1995
HCOL:vol. 38, no. 5, pp. 869-878

---

(109)
ACCN:001639536 CTLN:3892528
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Brisbane, P.G.;Neate, S.M.;Pankhurst, C.E.;Scott, N.S.;Thomas, M.R.
AFFN:CSIRO Div. Soils, Private Bag No. 2, Glen Osmond, S.A. 5064, Australia
TITL:Sequence-tagged site markers to identify Rhizoctonia solani AG 4 or 8 infecting wheat in South Australia
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1995
HCOL:vol. 85, no. 11, pp. 1423-1427

---

(110)
ACCN:001640256 CTLN:3893413
ABSJ:G (Genetics Abstracts)
AUTH:Belay, G.;Tesemma, T.;Bechere, E.;Mitiku, D.
AFFN:Dep. Plant Breeding Res., Swedish Univ. Agric. Sci., Box 7003, S-750 07 Uppsala, Sweden
TITL:Natural and human selection for purple-grain tetraploid wheats in the Ethiopian highlands
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:1995
HCOL:vol. 42, no. 4, pp. 387-391

---

(111)
ACCN:001643211 CTLN:3896716
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Rioux, S.;St-Pierre, C.A.;Couture, L.
AFFN:Dep. Phytologie, Univ. Laval, Quebec, PQ G1K 7P4, Canada
TITL:Genetic studies on the resistance of winter wheat to speckled snow mould
HTIL:CAN. J. PLANT SCI./REV. CAN. PHYTOTECH.
HSSN:0008-4220
HYER:1995
HCOL:vol. 75, no. 4, pp. 801-805

---

(112)

ACCN:001645813 CTLN:3899353
ABSJ:G (Genetics Abstracts)
AUTH:Farooq, S.;Shah, T.M.;Asghar, M.
AFFN:Nuclear Inst. for Agric. and Biol. (NIAB), Jhang Rd., Faisalabad, Pakistan
TITL:Intergeneric hybridization for wheat improvement VIII. Variations in chromosome number in backcross-1 derivative of F sub(1) hybrids between wheat and two Aegilops species
HTIL:CYTOLOGIA
HSSN:0011-4545
HYER:1995
HCOL:vol. 60, no. 4, pp. 337-340

---

(113)
ACCN:001653053 CTLN:3906207
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Friebe, B.;Zhang, W.;Raupp, J.W.;Gill, B.S.;Porter, D.R.
AFFN:USDA-ARS, 1301 N. Western St., Stillwater, OK 74075, USA
TITL:Non-homoeologous wheat-rye chromosomal translocations conferring resistance to greenbug
HTIL:EUPHYTICA
HSSN:0014-2336
HCOL:vol. 84, no. 2, pp. 121-125

1996

---

(1)
ACCN:001614484 CTLN:3867730
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Podkowinski, J.;Sroga, G.E.;Haselkorn, R.;Gornicki, P.*
AFFN:Dep. Mol. Genet. and Cell Biol., Univ., Chicago, 920 East 58th St., Chicago, IL 60637, USA
TITL:Structure of a gene encoding a cytosolic acetyl-CoA carboxylase of hexaploid wheat
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1996
HCOL:vol. 93, no. 5, pp. 1870-1874

---

(2)
ACCN:001620772 CTLN:3874645
ABSJ:Z (Entomology Abstracts); G (Genetics Abstracts)
AUTH:Rafi, M.M.;Zemetra, R.S.;Quisenberry, S.S.
AFFN:Dep. Land, Air and Water Resour., Univ. California, Davis, CA 95616- 8627, USA
TITL:Interaction between Russian wheat aphid (Homoptera: Aphididae) and resistant and susceptible genotypes of wheat
HTIL:J. ECON. ENTOMOL.
HSSN:0022-0493
HYER:1996
HCOL:vol. 89, no. 1, pp. 239-246

---

(3)
ACCN:001626911 CTLN:3880060
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Nakase, M.;Hotta, H.;Adachi, T.;Aoki, N.;Nakamura, R.;Masumura, T.; Tanaka, K.;Matsuda, T.
AFFN:Dep. Appl. Biol. Sci., Sch. Agric. Sci., Nagoya Univ., Chikusa Nagoya 464-01 Japan
TITL:Cloning of the rice seed alpha -globulin-encoding gene: sequence similarity of the 5'-flanking region to those of the genes encoding wheat high-molecular-weight glutenin and barley D hordein
PBSR:ELSEVIER SCIENCE B.V.
HTIL:GENE
HSSN:0378-1119
HYER:1996
HCOL:vol. 170, no. 2, pp. 223-226

---

(4)
ACCN:001628623 CTLN:3881792
ABSJ:G (Genetics Abstracts)
AUTH:Jolly, C.J.;Glenn, G.M.;Rahman, S.*
AFFN:CSIRO Div. Plant Ind., GPO Box 1600, Canberra, ACT 2601, Australia
TITL:GSP-1 genes are linked to the grain hardness locus (Ha) on wheat chromosome 5D
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1996
HCOL:vol. 93, no. 6, pp. 2408-2413

---

(5)
ACCN:001630853 CTLN:3884324
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Joshi, C.P.;Kumar, S.;Nguyen, H.T.*

AFFN:Plant Molecular Genet. Lab., Dep. Plant and Soil Sci., Texas Tech Univ., Lubbock, TX-79409, USA
TITL:Application of modified differential display technique for cloning and sequencing of the 3' region from three putative members of wheat HSP70 gene family
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1996
HCOL:vol. 30, no. 3, pp. 641-646

---

(6)
ACCN:001635028 CTLN:3888790
ABSJ:G (Genetics Abstracts)
AUTH:Sharma, H.P.;Bhargava, S.C.
AFFN:Dep. Genet. and Plant Breeding, S. K. N. Coll. Agric., Jobner-303 329 (Jaipur), India
TITL:Relative sensitivity of wheat genotypes under moisture stress conditions
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 1, pp. 39-42

---

(7)
ACCN:001640105 CTLN:3893104
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Marais, G.F.;Pretorius, Z.A.
AFFN:Dep. Genet., Univ. Stellenbosch, Stellenbosch 7600, South Africa
TITL:Gametocidal effects and resistance to wheat leaf rust and stem rust in derivatives of a Triticum turgidum ssp. durum/Aegilops speltoides hybrid
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 88, no. 2, pp. 117-124

---

(8)
ACCN:001640269 CTLN:3893426
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Barakat, M.N.
AFFN:Biotechnol. Lab., Crop Sci. Dep., Fac. Agric., Alexandria Univ., Alexandria, Egypt
TITL:Estimation of genetic parameters for in vitro traits in wheat immature embryo cultures involving high X low regeneration capacity genotypes
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 87, no. 2, pp. 119-125

---

(9)
ACCN:001640272 CTLN:3893429
ABSJ:G (Genetics Abstracts)
AUTH:Matus, A.;Slinkard, A.E.;Van Kessel, C.
AFFN:Dep. Crop Sci. and Plant Ecol., Univ. Saskatchewan, Saskatoon, SK S7N 0W0, Canada
TITL:Carbon isotope discrimination and indirect selection for transpiration efficiency at flowering in lentil (Lens culinaris Medikus), spring bread wheat (Triticum aestivum L.) durum wheat (T. turgidum L.), and canola (Brassica napus L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 87, no. 2, pp. 141-151

---

(10)
ACCN:001645825 CTLN:3899365
ABSJ:G (Genetics Abstracts)
AUTH:Demeke, T.;Laroche, A.*;Gaudet, D.A.
AFFN:Res. Cent., Agric. and Agri-Food Canada, P.O. Box 3000, Lethbridge, AB T1J 4B1, Canada
TITL:A DNA marker for the Bt-10 common bunt resistance gene in wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 1, pp. 51-55

---

(11)
ACCN:001645826 CTLN:3899366
ABSJ:G (Genetics Abstracts)
AUTH:Cai, X.;Jones, S.S.*;Murray, T.D.
AFFN:Dep. Crop and Soil Sci., Washington State Univ., Pullman, WA 99164, USA
TITL:Characterization of an Agropyron elongatum chromosome conferring resistance to cephalosporium stripe in common wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 1, pp. 56-62

---

(12)
ACCN:001645840 CTLN:3899380
ABSJ:G (Genetics Abstracts)
AUTH:Qi, L.;Cao, M.;Chen, P.;Li, W.;Liu, D.
AFFN:Cytogenetics Inst., Nanjing Agric. Univ.,

Nanjing, Jiangsu 210095, People's Rep. China
TITL:Identification, mapping, and application of polymorphic DNA associated with resistance gene Pm21 of wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 1, pp. 191-197

---

(13)
ACCN:001646124 CTLN:3899847
ABSJ:G (Genetics Abstracts)
AUTH:Ma, Z.Q.;Roder, M.;Sorrells, M.E.*
AFFN:Dep. Plant Breeding and Biometry, Cornell Univ., Ithaca, NY 14853, USA
TITL:Frequencies and sequence characteristics of di-, tri-, and tetra-nucleotide microsatellites in wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 1, pp. 123-130

---

(14)
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Shi, Y.L.;Loomis, P.;Christian, D.;Carris, L.M.;Leung, H.*
AFFN:Dep. Plant Pathol., Washington, State Univ., Pullman WA, 99164-6430, USA
TITL:Analysis of the genetic relationships among the wheat bunt fungi using RAPD and ribosomal DNA markers
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 3, pp. 311-318

---

(15)
ACCN:001652300 CTLN:3905452
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Kema, G.H.J.;Sayoud, R.;Annone, J.G.;Van Silfhout, C.H.
AFFN:DLO-Res. Inst. for Plant Prot. (IPO-DLO), P.O. Box 9060, 6700 GW Wageningen, The Netherlands
TITL:Genetic variation for virulence and resistance in the wheat- Mycosphaerella graminicola pathosystem II. Analysis of interactions between pathogen isolates and host cultivars
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 2, pp. 213-220

---

(16)
ACCN:001652306 CTLN:3905458
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Kema, G.H.J.;Annone, J.G.;Sayoud, R.;Van Silfhout, C.H.;Van Ginkel, M.; De Bree, J.
AFFN:DLO-Res. Inst. for Plant Prot. (IPO-DLO), P.O. Box 9060, 6700 GW Wageningen, The Netherlands
TITL:Genetic variation for virulence and resistance in the wheat- Mycosphaerella graminicola pathosystem I. Interactions between pathogen isolates and host cultivars
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 2, pp. 200-212

---

(17)
ACCN:001658461 CTLN:3912005
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Arends, S.;Kraus, J.;Beier, H.*
AFFN:Institut fuer Biochemie, Bayerische Julius-Maximilians-Universitaet, Biozentrum, Am Hubland, D-97074 Wuerzburg, Germany
TITL:The tRNA super(Tyr) multigene family of Triticum aestivum: Genome organization, sequence analyses and maturation of intron-containing pre-tRNAs in wheat germ extract
HTIL:FEBS LETT.
HSSN:0014-5793
HYER:1996
HCOL:vol. 384, no. 3, pp. 222-226

---

(18)
ACCN:001661465 CTLN:3915516
ABSJ:G (Genetics Abstracts)
AUTH:Cullis, B.R.;Thomson, F.M.;Fisher, J.A.;Gilmour, A.R.;Thompson, R.
AFFN:Agric. Res. Inst., Wagga Wagga, N.S.W. 2650, Australia
TITL:The analysis of the NSW wheat variety database. II. Variance component estimation
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 1, pp. 28-39

---

(19)
ACCN:001661466 CTLN:3915517
ABSJ:G (Genetics Abstracts)
AUTH:Cullis, B.R.;Thomson, F.M.;Fisher, J.A.;Gilmour, A.R.;Thompson, R.
AFFN:Agric. Res. Inst., Wagga Wagga, N.S.W. 2650, Australia
TITL:The analysis of the NSW wheat variety database. I. Modelling trial error variance
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 1, pp. 21-27

Wheat Information Service
Number 83: 129 (1996)

V. Information

1. The Second International Triticeae Symposium

(Logan, Utah, USA, June 20-24, 1994)

The participants unanimously accepted a proposal for the Third International Triticeae Symposium to be held in Aleppo, Syria. The International Plant Genetic Resources Institute, West Asia and North Africa Regional Office (IPGRI-WANA) and The International Center for Agricultural Research in the Dry Areas (ICARDA) will serve as hosts.

The purposes of the symposium are: (1) to exchange the latest scientific information and advancements related to annual and perennial Triticeae species; and (2) to promote the exchange of ideas for developing coordinated or collaborative research.

May 4-8, 1997
Aleppo, SYRIA

Program

Plenary lectures will be delivered by invited speakers. Scientific papers may be presented by registered participants orally or as posters. Volunteered papers can be submitted in one of the following topics:

1. Evolutionary Genomic Relationships in the Triticeae
2. Biodiversity and Biogeography
3. Genetic Resources and Core Collections in Breeding and Research
4. Evaluation and Pre-breeding of Cereals and Forages
5. Quality and Utilization

Contact to: A.A. Jaradat
3rd International Triticeae Symposium c/o ICARDA, P.O. Box 5466, Aleppo, SYRIA
E-mail: A.JARADAT@CGNET.COM Fax: 963-21-213-490/225-105

2. 5th International Congress of Plant Molecular Biology

(Singapore; September 21-27, 1997)

The second circular is available: The Secretariat, 5th ISPMB 97, c/o Conference & Travel Management Assoc. Pte Ltd, 425-A Race Course Rd., Singapore 218671. Tel: +65299-8992, Fax: +65-299-8983, E-mail: ctmapl@singnet.com.sg.

The deadline of abstract submission is May 1, 1997.

3. XVIIIth International Congress of Genetics

(Beijing, China; August 22-28, 1998)

The first circular is now available. Mail all correspondence to: Secretariat, XVIIIth International Congress of Genetics, CAS, Datun Rd., Andingmenwai, Beijing 100101, China. Tel: +86-10-64914896, Fax: +86-10-64914896/64913428, E-mail:SYCHEN@MiMi.CNC.AC.CN.

4. 13th International Chromosome Conference

(Ancona, Italy; September 8-12, 1998)

The first circular is available: Istituto di Biologia e Genetica, Universita di Ancona, Via Brecce Bianche, 60131 Ancona, Italy. Fax: +39-71-2204609

Wheat Information Service
Number 83: 130 (1996)

VI. Editorial Remarks

Since the new system of donation for supporting continuous publication of WIS was introduced from in 1996, many contributions have been send to the office, reaching ¥ 300,000 by 74 describers. This amount is about equivalent to the postage for 700 describers over 58 countries. Special thanks for their contribution. Please keep in mind that WIS is not commercial journal, which has been supported by this type of voluntary contribution for mutual research interest.

In the present volume, we have articles more than expected, and because of this, some of information were send for the following issues. Soon or later, we have to consider the increase of volume or frequency of publication. Also, the editorial board is considering to cope with information exchange through computer-network.

Here, I would like to cite a letter from Dr. R. Riley (without his permission, sorry for this); " I write to say how much I admire the editorial work and the presentation of WIS. It now can be viewed as an entirely profession journal and correctly entitled as The International Journal for Wheat Genetics and Breeding but of course that is not so convenient a title as WIS. So I expect that there will be many old-stagers, like me, who will not be able to get out of the habit of referring to WIS!"

Editor: T.S.

WIS No.83

編　集　国際小麦研究連絡会議
　　西　川　浩　三
発行所　木原記念横浜生命科学振興財団
〒244　横浜市戸塚区舞岡町641-12
Tel. (045)825-3487
Fax. (045)825-3307
発行日　1996年12月20日

Wheat Information Service No. 83

Contents