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Review article

Wheat Production and Research in Canada

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Introduction

The Ninth International Wheat Genetics Symposium will be held in Canada at the University of Saskatchewan, Saskatoon, August 2-7, 1998. This paper is intended to provide wheat researchers with background information about wheat production and wheat research in Canada.

Wheat Production

The major wheat growing area of Canada is the central prairie or great plains area, primarily the provinces of Alberta, Saskatchewan and Manitoba. The area is noted for its hot, dry summers, short growing season and very cold winters. Precipitation ranges from about 300 to 450 cm in different regions. Unfortunately, water resources are limited and a relatively small area is irrigated. In this area, most of the wheat produced has a spring growth habit. A small area of winter wheat has been grown in southwestern Alberta for many years. In most of the rest of the area, the winters were considered to be too cold to permit the regular survival of even the hardiest winter wheat cultivars. However, over the last 20 years the development of appropriate production methods has resulted in an increase in the acreage of winter wheat. The key step is the planting of winter wheat early and in stubble to trap snow and protect the young plants.

The other major wheat producing area is Ontario (eastern Canada) where production has been largely soft, white winter wheat, but increasing amounts of soft red winter wheat are being grown. The winters in Ontario are much less harsh and many winter wheat cultivars will survive.

For the past five years, about 11-12 million hectares have been planted to wheat in Canada. Production has been about 25-30 million tonnes per year. Of this, just over 2 million hectares and 3.3 to 4.6 million tonnes have been durum wheat. In Ontario production has been about 1 million tonnes on about 0.3 million hectares.

Wheat Exports

For many years Canada has been noted for its production and export of high protein, hard red spring wheat. It is particularly valuable for mixing with softer, lower protein, wheats for the

making of bread. Western Europe, and particularly Great Britain, was the major market. However, the agricultural policies of the European Economic Community resulted in the loss of much of this market. Fortunately, other markets have opened up in Asia (particularly China, Japan and Iran), north Africa and eastern Europe (particularly Russia until recently). Canada is also the world's major exporter of durum wheat, particularly to countries around the Mediterranean.

Wheat Classes

As a result of the broadening of Canada's wheat exports, Canadian wheat is now used for a wide range of products. The traditional hard red spring wheat is not necessarily the best type for all purposes. Consequently, in the last 25-years Canadian wheat breeders have been developing several new classes of wheat, with different quality characteristics. Traditionally, Canadian hard red spring wheats had to meet very specific requirements for protein content and protein strength. For many years the cultivar Marquis was the standard, but now it is Neepawa. By relaxing the standards, particularly for protein content, it has been possible for Canadian wheat breeders to produce higher-yielding cultivars with quality characteristics better suited for other uses such as noodles, steam bread, falt breads, etc. Since it is not desirable to have different classes of wheat mixed in the export delivery system, they must be distinguishable on the basis of kernel characteristics. The classes of wheat now being grown in the central prairies are:

1. Canada Western Red Spring (CWRS)
CWRS wheat is the traditional high protein spring wheat and is still the most widely grown. Its protein content varies from year to year depending on the weather. In most years the crop matures under hot, dry conditions which reduce the yield but increase the protein content. In a "normal" year the protein content averages about 13.5%. CWRS wheat is sold on the basis of a guaranteed protein content with premiums being paid for higher protein content.

2. Canada Prairie Spring (CPS)
The CPS wheat class has somewhat lower protein and weaker gluten than CWRS wheat. Cultivars in this class generally yield 20-30% more than CWRS cultivars. Because some markets prefer white wheats for their higher flour extraction, both white and red cultivars have been developed.

3. Canada Western Extra Strong (CWES)
Cultivars in this class may have slightly lower protein than the CWRS cultivars but the gluten is extra strong. Wheats of this type are particularly valuable for blending with weaker gluten, lower protein wheats.

4. Canada Soft White Spring (SWS)
Relatively small amounts of SWS wheats are grown under irrigation in southern Alberta. They are used mainly for cake and pastry flour.

5. Hard Red Winter
The production of hard red winter wheat has fluctuated widely in recent years. Because winter

wheat heads and matures earlier than spring wheat, it makes better use of the normal May and June rains and yields are often higher.

6. Canada Western Amber Durum
Durum wheat is well adapted to the southern prairie area, particularly in Saskatchewan. The area planted to durum wheat fluctuates substantially depending on current prices.

Registration

Canada has a strict registration process for wheat cultivars. For a new wheat cultivar to be registered in a particular class, it must meet the quality and kernel distinguishability requirements for the class and be at least equal to the current cultivars in agronomic characters. These requirements have made it very difficult for prairie wheat breeders to produce new cultivars. However, registration has been important in maintaining the reputation of Canadian wheat. When buyers purchase a cargo of wheat of a particular class, they know exactly what they are going to receive.

Wheat Breeding and Research

In the early years, wheat breeding and research were carried out by what is now Agriculture and Agri-Food Canada (AAFC). As Colleges of Agriculture developed at the universities, several of them initiated wheat breeding programs. All three provincial universities on the prairies, Manitoba, Saskatchewan and Alberta, carry out wheat research. Appropriately, the major wheat-growing province, Saskatchewan has the strongest program. The University of Guelph in Ontario has a winter wheat breeding program.

When Plant Breeders Rights were enacted in Canada in 1991, it provided a stimulus for wheat breeding by private companies. Several now have programs in Canada, often as an offshoot of their programs in the U.S.A. Nevertheless, Agriculture and Agri-Food Canada is still the largest player in wheat research in Canada. On the prairies, AAFC's wheat research centres are at Lethbridge, Alberta, Swift Current, Saskatchewan (to be visited on the post-conference tour) and Winnipeg, Manitoba.

Rust Research

Leaf and stem rust are major diseases of wheat wherever the crop is grown in North America, and particularly in the central great plains. Stripe rust is a problem in the western states of the U.S.A. but in Canada it is of minor importance only in southwestern Alberta and southern British Columbia.

The centre for rust research in Canada is the world renowned Dominion Rust Laboratory (Agriculture and Agri-Food Canada) established in Winnipeg in 1925. The early scientists at the Rust Lab did pioneering work on the life cycle, epidemiology, biological specialization and inheritance of resistance, particularly for stem rust. Over the years the Rust Lab (now the Cereal Research Centre) has produced most of the rust resistant wheat cultivars grown on the prairies.

In more recent years, the Centre has developed strong programs in molecular biology and genetic engineering. It is also a centre for work on other wheat diseases such as smut, bunt, leaf diseases and scab.

In 1952, Canada Agriculture provided a grant to the University of Saskatchewan to study resistance to a devastating new race of stem rust, 15B-1. Essentially all Canadian cultivars of common and durum wheat at that time were susceptible. A major epidemic of both leaf and stem rust occurred in 1954. The program at the University of Saskatchewan focussed on identifying genes for resistance, transferring genes to wheat from its relatives and producing near-isogenic lines carrying single genes for resistance.

Wheat Stem Sawfly

In the drier areas of the prairies, southwestern Saskatchewan and southern Alberta, the wheat stem sawfly can be a major problem. The sawfly deposits eggs in the stem, the larvae move down to the base of the plant and girdle the stem. The stems then break over and are almost impossible to pick up and harvest. The solution is to breed cultivars with solid stems which inhibit the movement of the larvae and cause them to starve. Breeding for resistance began at the Lethbridge Research Station and was later transferred to the Swift Current Research Station. With the development of resistant cultivars, the insect is now under control.

The Wheat Midge

The wheat midge had been present on the prairies for many years without causing any real problems. However, in the 1980s the population suddenly increased dramatically and began to cause serious losses in eastern Saskatchewan and Manitoba. It is still not clear whether the increase resulted from some change in the environment or the loss of a parasite on the midge. Resistance to the midge is difficult to find but breeding work is underway.

Wheat Research Centres in Saskatchewan, Manitoba and Alberta

Agriculture and Agri-Food Canada
AAFC has three major wheat research centres–the Cereal Research Centre, Winnipeg, Manitoba, the Lethbridge Research Centre, Lethbridge, Alberta, and the Semi-Arid Prairie Agricultural Research Centre (SPARC), Swift Current, Saskatchewan.
The work of the Cereal Research Centre, Winnipeg has been outlined above.
SPARC is located in one of the driest areas of Saskatchewan. In addition to the sawfly resistance program mentioned above, it has major breeding programs for Canada Prairie Spring and Canada Western Amber Durum wheats. The Centre is also known for its soils and agronomic work on wheat production under semi-arid conditions.

Although the Lethbridge Research Centre did pioneering work on sawfly resistance, its wheat research now involves breeding new cultivars of Soft White Spring Wheat for production under irrigation and Hard Red Winter Wheat.

University of Saskatchewan

The Crop Development Centre at the University of Saskatchewan has large breeding programs for Canada Western Red Spring, Canada Prairie Spring and Canada Western Amber Durum. It has also been the leader in developing production methods and new cultivars for Hard Red Winter Wheat. In addition to work on rust resistance, research on leaf diseases is being carried out.

University of Alberta

The University of Alberta is the most northern of the wheat research centres and has always been interested in developing early cultivars. It is also near the only sizeable area of acidic soils on the prairies and is carrying out research on and breeding for resistance to aluminum toxicity.

University of Manitoba

The University of Manitoba produced Glenlea, the first cultivar in the Canada Western Extra Strong class. It is continuing to develop CWES wheats and also winter-hardy, rust-resistant Hard Red Winter Wheats.

Alberta Agriculture

The Alberta government funds a breeding program aimed at developing red and white-seeded winter wheats adapted to the regions where snow mold is a problem.

Visits

Participants in the Ninth International Wheat Genetics Symposium who wish to visit one or more of the research centres before or after the Symposium should contact the centre ahead of time. Arrangements can then be made for their visit.

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Research article

Genetic control of supernumerary spikelet in common wheat line LYB

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Summary

The supernumerary spikelet(SS) is abnormal spike morphology of wheat (*Triticum* L.) having additional spikelets per spike. The common wheat (*T. aestivum* L.) selection, LYB stably showed SS character. Monosomic analysis was used to determine the chromosomal location of genes for the SS character of LYB. F_2 monosomic analysis indicated that SS character was controlled by three genes on chromosomes 2A, 2D and 4A. Results also showed that two recessive genes on chromosomes 2A and 4A of LYB promoted the development of SS character, and that a dominant inhibitor of SS on chromosome 2D of Chinese Spring prevented the expression of SS character. These conclusions were confirmed by the data of progenies derived from backcrossing monosomic F_1 hybrids to LYB.

Key words: Branched spike, gene localization, supernumerary spikelet, *Triticum aestivum*, wheat.

Introduction

The normal spike of wheat (*Triticum* L.) plant has spikelets which attached to the rachis in a distichous pattern. The supernumerary spikelets(SS) character is a genetically conditioned abnormal wheat spike morphology. The term SS, often referred to as branched spike, embraces additional sessile spikelets at a rachis node and additional spikelets on an extended rachilla.

The low kernel weight (Koric 1966) has hindered development of SS cultivars (Yen et al. 1993). However, because SS character conditions additional spiklets, the possibility of utilizing SS character to increase yield of wheat has been suggested (Koric 1966, 1969; Pennell and Halloran 1983; Rawsan and Ruwali 1972; Salunke and Asana 1971). Moreover, it is practical to utilize SS gene to create multispikelet wheat lines (Huang and Yen 1988; Koric 1969; Yen 1965), and

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multispikelet was regarded as an ideal spike type of high-yielding wheat by breeders (Millet 1983; Yen et al. 1993).

Cytogenetical analysis of SS character development has been conducted in common wheat (*T. aestivum* L.). Sears (1954) observed that plants nullisomic for chromosome 2A or 2D produced twin spikelets, and the arm locations of these genes were identified as 2AL and 2DS. Swaminathan et al. (1966) found that a deletion caused the SS character in a common wheat mutant. Singh and Joshi (1983) found that all ear-branched plants were trisomic (2n=43) in a population containing ear-branching segregates, and the trisome was subsequently identified as 5A (Singh 1986).

It was found that the environmental factors significantly affect the expression of SS in some lines (Sharman 1944; Pennell and Halloran 1984). Fortunately, some lines with stable expression of SS character are obtained, which provide the feasibility to map the genes for SS character. The present study aims to localize the genes for SS character on certain chromosomes in a common wheat line.

Materials and methods

LYB (an ear branching selection selected from a common wheat cultivar, Liying No. 3) stably showed abnormal spikes with additional spikelets on extended rachilla. The Chinese Spring monosomic series with normal spikes were used for monosomic analysis of LYB's SS character. Three-five monosomic plants were selected from each the 21 monosomic line, and were artificially pollinated with LYB. At the same time, euploid Chinese Spring was crossed with LYB. A part of F_1 monosomic plants and F_1 disomic plants was selfed to obtain F_2 seeds, other F_1 monosomic plants and F_1 disomic plants were backcrossed to LYB to obtain corresponding BC_1 seeds.

On 3 Nov. 1995, the F_1 and F_2 seedlings were separately planted. The seeds of BC_1 of each combination were sowed in the field. At harvest, all the spikes were observed carefully to determine whether they were SS spikes or normal spikes, and the plants were classified into SS spike type (with at least one SS spike) and normal spike type (with normal spike only). The F_2 population which derived from F_1 disomic plants was taken as a control in F_2 monosomic analysis.

Result and discussion

The F_2 monosomic analysis showed that 2A, 2D and 4A F_2 populations significantly surpassed the control population in frequency of SS spike plants (Table 1). The progenies which derived from backcrossing F_1 hybrids monosomic for 2A, 2D or 4A to LYB exhibited higher frequency of SS spike plants than other backcross combinations (Table 2). These results mean that chromosomes 2A, 2D and 4A were responsible for SS character.

Koric (1973) found that two genes promoting development of SS and a dominant epistatic inhibitor of SS (*Nr*) exist in common wheat, and that these genes were independently inherited. The F_2 progenies which derived from F_1 monosomic plants were homozygous (disomic) or

Table 1. The result of F_2 monosomic analysis for SS character of common wheat line LYB*

Population	No. of plants investigated	No. of plants with SS spike	Frequency	χ^2 (1:3)
1A	187	19	0.102	
1B	186	21	0.113	
1D	188	17	0.096	
2A	184	44	0.239**	0.065
2B	183	18	0.0984	
2D	185	75	0.405**	23.007
3A	186	20	0.108	
3B	187	18	0.096	
3D	182	18	0.099	
4A	185	39	0.211**	1.314
4B	184	21	0.114	
4D	183	20	0.109	
5A	186	21	0.113	
5B	188	22	0.117	
5D	187	18	0.096	
6A	185	20	0.108	
6B	186	20	0.108	
6D	187	18	0.096	
7A	187	23	0.124	
7B	185	22	0.120	
7D	184	20	0.109	
CK	191	20	0.105	

*data of nullisomics in F_2 populations was not involved

** χ^2 analysis showed that the significance of difference from the control F_2 population reached 0.01 level

hemizygous (monosomic) corresponding chromosome (s) of LYB. Thus, if a chromosome of LYB carries the gene promoting development of SS, the plants in its corresponding F_2 population would be homozygous (disomic) or hemizygous (monosomic) for the gene promoting development of SS. However, according to Koric's conclusion (1973), these plants show SS only when the dominant *Nr* gene on other chromosome is absent in their genome. So, the segregation for spike type in the corresponding F_2 population would be identical with single gene (*Nr*) segregation, and the expected segregation ratio would be 1:3 (SS:normal). Only the F_2 population which did not

Table 2. Segregation for spike type in the progenies derived from backcrossing F_1 plants to LYB, and goodness of fit to three gene model

Used F_1 plants monosomic for	No. of plants with normal spike	No. of plants with SS spike	Frequency of SS spike plants	Goodness of fit to three gene-model Ratio	χ^2_c
1A	82	44	0.349	5:3	0.256
1B	88	40	0.313	5:3	1.875
1D	80	40	0.323	5:3	1.239
2A	59	67	0.532**	1:1	0.388
2B	79	46	0.368	5:3	0.005
2D	36	88	0.710**	1:3	0.871
3A	85	41	0.325	5:3	1.120
3B	82	45	0.354	5:3	0.152
3D	85	41	0.325	5:3	0.120
4A	60	64	0.516*	1:1	0.073
4B	80	47	0.370	5:3	0.001
4D	83	43	0.341	5:3	0.477
5A	80	48	0.375	5:3	0.000
5B	76	50	0.397	5:3	0.171
5D	71	45	0.357	5:3	0.104
6A	82	42	0.339	5:3	0.551
6B	80	45	0.360	5:3	0.065
6D	76	49	0.392	5:3	0.090
7A	75	49	0.395	5:3	0.138
7B	71	50	0.397	5:3	0.171
7D	85	43	0.336	5:3	0.675
disomic	82	46	0.359	5:3	0.075

*and ** χ^2 analysis showed that the significance of difference from the progeny which derived from backcrossing F_1 disomic plants to LYB reached 0.05 and 0.01 levels, respectively

possess *Nr* may show more than 1/4 SS plants. Therefore, to determine whether *Nr* gene exists or not, chi-square analysis was used to test for the goodness of fit to the segregation ratio of 1:3 in F_2 populations. The result showed that F_2 progenies of mono-2A and -4A fitted the single -gene segregation ratio well (Table 1), and the SS character was recessive. The segregation of monosomics and disomics in 2A and 4A F_2 populations could not account for the segregation of spike types, because both disomic and monosomic plants segregated for spike type in these two F_2 populations.

As more than two chromosomes were responsible for the SS character in this cross, the segregation ratio of 1:3 (SS:normal) in 2A and 4A F_2 populations could not be interpreted as the act of two recessive complementary genes. The most acceptable explanation is that chromosomes 2A and 4A carry genes promoting development of SS, and a dominant strong inhibitor of SS (*Nr*) exists on other chromosome. Chromosome 2D should be the location of *Nr* gene, because only it was responsible for the SS character except chromosomes 2A and 4A. The fact that only 2D F_2 population showed more than 1/4 SS spike plants supported this conclusion. Obviously, LYB itself could not carry the dominant allele of *Nr* gene, because it stably showed SS phenotype. Chinese Spring must carry the dominant allele of *Nr* gene, while LYB should carry its recessive allele(*nr*) or delete this locus.

Since 2D F_1 monosomic plants carried no chromosome 2D from Chinese Spring, there was no *Nr* in their genomes. In addition, 2D F_1 monosomic plant was heterozygous for genes promoting development of SS. Therefore, all or part of 2D F_1 monosomic plants should exhibit SS phenotype, if the genes promoting development of SS are dominant or incompletely dominant. However, the F_1 monosomic analysis indicated that all 2D F_1 monosomic plants exhibit only normal spikes, as the other F_1 plants did. So, the genes on chromosomes 2A and 4A which promote the development of SS are recessive, and the gene symbol *ss* was used to represent them in this paper. The conclusion of Koric (1973) and Dencic (1988) that dominant or incompletely dominant genes promoted the development of SS is not valid for present experiment. In this aspect, the *ss* gene is synonym of the *bh* (branching head) gene which was first used by Sharman (1944) in emmer wheat.

Based on the result of F_2 monosomic analysis, we conclude that the SS character in this cross is controlled by three genes, i.e., two recessive *ss* genes on chromosomes 2A and 4A which promoted development of SS character, and a strong dominant inhibitor of SS (*Nr*) on chromosome 2D which prevented the expression of this character. In the light of this conclusion, the segregation ratio of spike type in progenies which derived from backcrossing F_1 disomic or monosomic plants to LYB could be predicted. For convenience, we adopt the symbol *ss1* and *ss2* to represent the genes on chromosomes 2A and 4A respectively. Clearly, the genotype of LYB is *ss1ss1ss2ss2nrnr*, and that of Chinese Spring is *SS1SS1SS2SS2NrNr*. According to Mendel's laws, F_1 disomic plant (*SS1ss1SS2ss2Nrnr*), or F_1 plant monosomic for chromosome other than 2A, 2D and 4A (the genotype is *SS1ss1SS2ss2Nrnr* too), is expected to produce 8 different genetic constitutions of gametes, among them, 1/8 gametes is *ss1ss2nr*, 1/8 gametes is *ss1SS2nr* and 1/8 gametes is *SS1ss2nr*. These three types of gametes (total proportion is equal to 3/8) combine with male gamete (*ss1ss2nr*) of LYB to form the genotypes *ss1ss1ss2ss2nrnr*, *ss1ss1SS2ss2nrnr* and *SS1ss1ss2ss2nrnr* for SS phenotype. So, the expected segregation ratio of spike type in the BC_1 population which derived from backcrossing F_1 disomic plants, or F_1 plants monosomic for chromosome other than 2A, 2D and 4A, to LYB would be 5:3 (normal :SS). Among the female gametes formed by 2A F_1 monosomic plant (*ss1SS2ss2Nrnr*), those having the genetic constitution *ss1ss2nr*, *ss1SS2nr*, *Oss2nr* (O: delete chromosome 2A and thus delete *SS1* locus) or *OSS2nr* combine with male gamete of LYB to form genotypes *ss1ss1ss2ss2nrnr*, *ss1ss1SS2ss2nrnr*, *ss1ss2ss2nrnr* and *ss1SS2ss2nrnr* for SS phenotype, and frequency of each the 4 types of female

gametes is 1/8. Thus the BC_1 population which derived from backcrossing 2A F_1 monosomic plants to LYB should exhibit 1/2 SS spike plants. In the same way, the BC_1 population which derived from backcrossing 4A F_1 monosomic plants (*SS1ss1ss2Nrnr*) to LYB should exhibit 1/2 SS spike plants too. The 2D F_1 monosomic plant (*SS1ss1SS2ss2nr*), produces only 1/4 female gametes (*SS1SS2*) which combine with male gametes (*ss1ss2nr*) of LYB to form genotype *SS1ss1SS2ss2* for normal spike. Therefore, the expected segregation ratio of spike type in the BC_1 population which derived from backcrossing 2D F_1 monosomic plants to LYB is 1:3 (normal:SS). Chi-square analysis showed a good fit to the expected segregation ratio in BC_1 progenies (Table 2), indicating that the result of the backcross test supported the three gene inheritance pattern based on the data of F_2 monosomic analysis.

Klindeworth et al. (1990) concluded that the SS character was primarily conditioned by the group 2 chromosomes. The presence of genes controlling SS character on chromosomes 2A and 2D in this cross supported this conclusion. Moreover, the finding that chromosome 4A carried ss gene indicated that the SS character is also controlled by chromosome other than group 2.

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References

Dencic S, (1988) Genetic analysis of different structures of sink capacity in wheat. Proc 7th Intern Wheat Genet Symp, Cambridge UK 499-502.

Huang G and Yen C (1988) Studies on the developmental genetics of multiple spikelet per spike in wheat. Proc. 7th Intern Wheat Genet Symp, Cambridge UK 527-532.

Klindworth DL, Williams ND and Joppa LR (1990) Chromosomal location of genes for supernumerary spikelet in tetraploid wheat. Genome 33: 515-520.

Koric S (1966) Productivity of branched ears of vulgare wheat. Savrem Poljopr 14: 545-552.

Koric S (1969) Utilization of branched genic complex for increasing productivity of *Triticum aestivum* ssp. *vulgare*. Savrem Poljopr 17: 151-158.

Koric S (1973) Branching genes in *Triticum aestivum*. Proc 4th Intern Wheat Genet Symp, Columbia Mo USA 283-288.

Millet E (1983) Breeding for large number of spikelets per spike in wheat. Proc 6th Intern Wheat Genet Symp, Kyoto Japan 623-628.

Pennell AL and Halloran GM (1983) Inheritance of supernumerary spikelets in wheat. Euphytica 32: 767-776.

Pennell AL and Halloran GM (1984) Influence of vernalisation and photoperiod on supernumerary spikelet expression in wheat. Ann Bot 53: 828-831.

Rawson HM and Ruwali KN (1972) Ear branching as a means of increasing grain uniformity in wheat. Aust J Agric Res 23: 551-559.

Salunke NR and Asana RD (1971) Comparative study of the grain in normal- and branched-ear types of wheat (*Triticum aestivum* L.). Indian J Agric Sci 41: 1050-1053.

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

Sharman BL (1944) Branched head in wheat and wheat hybrids. Nature (London) 153: 497-498.

Singh D (1986) Location of gene(s) for branched spike character of bread wheat. Wheat Inf Serv 64: 16-18.
Singh D and Joshi BC (1983) Cytogenetics of branched spike in bread wheat. Wheat Inf Serv 56: 1-2.
Swaminathan MS, Chopra VL and Ststry GRK (1966) Expression and stability of induced mutation for branching in bread wheat. Curr Sci 35: 91-92.
Yen C (1965) On the developmental genetics of spike appearances in *Triticum aestivum* L. Genet Sinica 6: 116-129.
Yen C, Zheng YL and Yang JL (1993) An ideal type for high yield breeding, in theory and practice. Proc 8th Intern Wheat Genet Symp, Beijing China, 1113-1117.

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Research article

Chromosomal distribution of genes in diploid *Lophopyrum elongatum* (Host) A. Löve that influences crossability of wheat with rye

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Summary

Triticum aestivum L. lines with added or substituted chromosomes of *Lophopyrum elongatum* were hybridized with rye to identify chromosomes in *L. elongatum* that influenced crossability of wheat with rye. The results indicated that chromosome $4E^e$ in *L. elongatum* suppressed crossability of wheat with rye. It was suggested that homoeologous chromosome distribution of crossability genes in *L. elongatum* was different from that of wheat.

Key words: Chromosome distribution, Crossability, *Lophopyrum elongatum*, Wheat

Introduction:

The study on the crossability of wheat with rye dates back to the work of Backhouse (1916). Lein (1943) and Riley and Chapman (1967) showed that alleles at *Kr* loci control crossability and that *Kr1* and *Kr2* are located on chromosome 5B and 5A, respectively. Krolow (1970) suggested that chromosome 5D also carries a gene *Kr3* influencing crossability with rye. Luo et al. (1989) and Zheng et al. (1992) reported, besides the *Kr1*, *Kr2* and *Kr3* loci, a new gene, *Kr4* located on chromosome 1A.

Dominant alleles of crossability genes in wheat, *Kr1*, *Kr2*, *Kr3* and *Kr4* are known to reduce crossability with rye (Riley and Chapman 1967; Krolow 1970; Zheng et al. 1992). The *Kr* loci also influences on the crossability of wheat with other species in the Triticeae (Snape et al. 1979; Falk and Kasha 1981; Thomas et al. 1980). There is a strong correlation between crossability with rye and other species in the Triticeae tribe.

Most European wheat varieties carry dominant *Kr* alleles and thus have very low crossability with rye (Zeven 1987). However, wheat landraces from China, Japan, East Siberia and Iran are rich in high crossability resources (Zeven 1987; Luo et al. 1994; Ma et al. 1996). It is known that Chinese Spring, a strain of a landrace in Sichuan province of China, has been selected as a

standard cultivar in the genetic study of wheat primarily for its easy crossability with rye, which carries high crossability genes *Kr1, Kr2, Kr3*. Some Chinese landraces of wheat were found that had even better crossability than Chinese Spring and possess a new crossability gene *Kr4* (Luo et al. 1994).

Genetic variability for crossability occurs not only in wheat but also has been reported in alien species. Rye has a single dominant gene for crossability with wheat (Tanner and Falk 1981). *Hordeum spontaneum* carries a crossable genetic factor(s) similar to the *Kr* alleles in wheat (Snape et al. 1979; Taketa et al. 1995). Cheng (1997) found the crossability of octoploid triticale with common wheat was controlled by a pair of allelic genes. Moreover, genetic variability for crossability also exists in other species, such as *Psathyrostachys juncea*, *Thinopyrum trichophorum*, etc. (Sharma 1995). However, which homoeologous chromosome(s) in these species influence(s) the crossability with wheat is still needed to be answered.

To advance the understanding of the evolution of genes that regulate crossability in wheat and its relatives in general, more information is needed about the presence and distribution of chromosomes influencing crossability in genomes of the diploid species. *Lophopyrum* is closely related to the genus *Triticum* and contains species that are the closest extant relative to the ancestors of *Triticum* (Dvorak et al. 1984). The seven chromosomes of *Lophopyrum elongatum* (Host) Löve (2n=2x=14, E^eE^e) show close genetic correspondence to the seven wheat homoeologous groups (Dvorak 1980). The objective of this study is to identify chromosomes in *L. elongatum* that influence crossability of wheat with rye.

Materials and methods

T. aestivum L. cv. Chinese Spring (CS), the 41 disomic substitutions in which each of A and B genome chromosome pairs of Chinese Spring was replaced by a homoeologous pair from the E^e genome of *L. elongatum*, and the seven disomic additions of single *L. elongatum* chromosome in Chinese Spring were kindly provided by Dr. J. Dvorak, University of California, Davis, CA, USA (Table 1). All the above additions and substitutions are in a uniform cv. Chinese Spring background. These substitutions, additions and Chinese Spring were used as female parent in crosses with rye, *Secale cereale* L. cv. Qinling (a Chinese landrace).

The crosses were made in the field condition in the 1996-1997 growing season. Crosses were made using two outermost florets. Emasculated spikes were bagged to avoid pollination with other plants. After 2-3 days, the stigmas of emasculated florets were pollinated with fresh pollen of rye, then bagged again.

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

Results and discussion

The crossability of the 41 disomic substitutions and the seven disomic additions were compared with that of control, disomic Chinese Spring (Table 1). Disomic substitutions DS4E^e(4A), DS4E^e(4B), DS4E^e(4D), DS5E^e(5B), DS6E^e(6B) and disomic addition DA4E^e displayed a pronounced reduction in crossability percentages in comparison with that of control whereas the remaining 36 substitutions and six additions had no statistically significant difference from the control.

Table 1. Crossability of Chinese Spring (CS), disomic substitutions (DS) or disomic additions (DA) of *L. elongatum* in cv. Chinese Spring with rye

Wheat lines	No. of florets pollinated	No. of seed-sets	Crossability percentage
DS1E^e(1A) DV83-1-(3)	148	115	77.7
DS1E^e(1A) DV83-1-(4)	112	86	76.8
DS1E^e(1A) DV83-1-(5)	192	145	75.5
DS1E^e(lB) DV84-2	178	133	74.7
DS1E^e(1D) DV60-2-3-(2)	167	136	81.4
DS1E^e(1D) DV60-2-3-(3)	120	90	75.0
DA1E^e-2-1-5-2-1-(3)	130	100	76.9
DA1E^e-2-1-5-2-1-(4)	143	117	81.8
DS2E^e(2A) DV62-2-3-(1)	130	105	80.8
DS2E^e(2A) DV62-2-3-(4)	112	100	89.3
DS2E^e(2A) DV62-2-3-(5)	122	102	83.6
DS2E^e(2B) DV63-3-1-(3)	145	130	89.7
DS2E^e(2D) DV64-2-4-(1)	122	108	88.5
DS2E^e(2D) DV64-2-4-(2)	114	97	85.1
DS2E^e(2D) DV64-2-4-(3)	154	135	87.7
DS2E^e(2D) DV64-2-4-(4)	106	92	86.8
DS2E^e(2D) DV64-2-4-(5)	144	130	90.3
DA2E^e New-8-9-4-3-6-(1)	164	143	87.2
DS3E^e(3A) DV65-2-1-1-(2)	132	106	80.3
DS3E^e(3A) DV65-2-1-1-(6)	108	87	80.6
DS3E^e(3A) DV65-2-1-1-(7)	122	108	88.5
DS3E^e(3A) DV65-2-1-1-(8)	136	123	90.4
DS3E^e(3A) DV65-2-1-1-(10)	130	113	86.9
DS3E^e(3A) DV65-2-1-1-(11)	128	111	86.7

(continued)

(continued)

Wheat lines	No. of florets pollinated	No. of seed-sets	Crossability
DS3E^e(3A) DV65-2-1-1-(12)	92	79	85.9
DS3E^e(3A) DV65-2-1-1-(13)	136	122	89.7
DS3E^e(3B) DV66-2-2-2-(1)	120	99	82.5
DS3E^e(3B) DV66-2-2-2-(2)	165	145	87.9
DS3E^e(3B) DV66-2-2-2-(3)	150	134	89.3
DS3E^e(3B) DV66-2-2-2-(4)	109	100	91.7
DS3E^e(3D) DV67-1-1-(1)	142	125	88.0
DS3E^e(3D) DV67-1-1-(2)	114	101	88.6
DS3E^e(3D) DV67-1-1-(4)	150	126	84.0
DS4E^e(4A) DV893-5-(1)	142	96	67.6**
DS4E^e(4B) DV85-2-1-(1)	186	127	68.3*
DS4E^e(4D) DV87-3-2-(3)	174	116	66.7**
DA4E^e-15-6-2-3-6-(3)	104	70	67.3**
DS5E^e(5B) DV824-5-(2)	188	129	68.6**
DS5E^e(5D) DV72-1-2-(2)	322	262	81.4
DA5E^e-4456-4-2	134	108	80.6
DS6E^e(6A) DV88-3-(5)	150	116	77.3
DS6E^e(6B) DV76-3-(3)	146	37	25.3**
DS6E^e(6D) DV89-3-(3)	134	110	82.1
DA6E^e-2-4-12-4-2-(5)	141	130	92.2
DS7E^e(7A) DV79-2-1-(1)	175	150	85.7
DS7E^e(7B) DV80-2-1-(4)	143	121	84.6
DS7E^e(7D) DV82-2-1-(1)	134	118	88.1
DA7E^e New-(3)	132	114	86.4
CS DV418 (control)	130	115	88.5

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

DS5E(5A) was not available.

The disomic substitution lines are designated DS which is followed by a designation of the E^e-genome chromosome replacing a cv. Chinese Spring chromosome (in parentheses). Thus, a disomic substitution line with a substituted chromosome 1E^e for 1B is designated DS1E^e(1B). The disomic addition lines are designated DA which is followed by a designation of the E^e-genome chromosome. Thus, a disomic addition line with a added chromosome 1E^e is designated DA1E^e. Different line number indicates different substitutions with same substituted chromosome or different additions with same added chromosome.

All the disomic substitutions and disomic addition of homoeologous 4, i.e. DS4E^e(4A), DS4E^e(4B), DS4E^e(4D) and DA4E^e showed significantly lower crossability than control Chinese Spring. The results indicated that chromosome 4E^e in *L. elongatum* suppressed crossability of wheat with rye.

The substitution line DS5E^e(5B) showed significantly lower crossability than Chinese Spring, while DS5E^e(5D) and DA5E^e showed similar crossability to Chinese Spring. DS6E^e(6A), DS6E^e(6D) and DA6E^e showed similar crossability to Chinese Spring, while DS6E^e(6B) showed significantly lower than Chinese Spring. Since only one of the substitution line DS5E^e(5B) or DS6E^e(6B) was involved in this experiment and showed reduction of crossability, it was not assured that the reduction was caused by the suppressing effect of chromosome 5E^e or 6E^e on crossability, respectively. The reduction of DS5E^e(5D) or DS6E^e(6D) could be also caused by technical error or other factors in the experiment, such as partial sterility associated with these substitution lines.

Though the effect of the gene *Kr3* was very weak (Riley and Chapman 1967; Falk and Kasha 1983), crossability genes in wheat, *Kr1*, *Kr2*, *Kr3* and *Kr4* were located on chromosome 5B, 5A, 5D and 1A, respectively (Riley and Chapman 1967; Krolow 1970; Zheng et al. 1992). According to the results of this study, it was demonstrated that chromosomes 4E^e in *L. elongatum* involved in the crossability of wheat with rye. It was suggested that homoeologous chromosome distribution of crossability genes in *L. elongatum* was different from that of wheat.

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References

Backhouse OW (1916) Note on inheritance of crossability. J. Genet 6: 91-94.

Cheng ZJ (1997) The gene influencing crossability of cross-combination between octoploid triticale and short-straw common wheat used as male parents. Sci Agri Sinica 30(2): 16-20.

Dvorak J (1980) Homoeology between *Agropyrum elongatum* chromosomes and *Triticum aestivum* chromosome. Can J Genet Cytol 23: 481-492.

Dvorak J, McGuire PE and Mendlinger S (1984) Inferred chromosomes morphology of the ancestral genome of *Triticum*. Plant System Evol 144: 209-220.

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

Falk DE and Kasha KJ (1983) Genetic studies of the crossability of hexaploid wheat with rye and *Hordeum bulbosum*. Theor Appl Genet 64: 303-307.

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

Lein A (1943) Die genetische Grundlage der Kreuzbarkeit zwischen Weizen und Roggen. Z Indukt Abstamm Vererblehre 81: 28-61.

Luo MC, Yen C and Yang JL (1989) The crossability of landraces of common wheat in Sichuan with *Aegilops tauschii* and rye. J Sichuan Agric Univ 7: 77-81.

Luo MC, Yen C, Yang JL and Yang ZL (1994) The evaluation on crossability of Chinese wheat landraces. Proc 2nd Intern Triticeae Symp, Utah U.S.A. 83-85.

Ma R, Zheng DS and Fan L (1996) The crossability of 96 bread wheat landraces and cultivars from Japan with rye. Euphytica 92: 301-303.

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

Sharma HC (1995) How wide can a wide cross be ? Euphytica 82: 43-46.

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

Taketa S, Kato J and Takeda K (1995) High crossability of wild barley (*Hordeum spontaneum* C. Koch) with bread wheat and the differential elimination of barley chromosomes in the hybrids. Thoer Appl Genet 91: 1203-1209.

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

Thomas JB, Kaltsikes PJ and Anderson G (1980) Relation between wheat-rye crossability and seed set of common wheat after pollination with other species in the *Hordeae*. Euphytica 30: 121-127.

Zeven AC (1987) Crossability percentages of some 1400 bread wheat varieties and lines with rye. Euphytica, 36: 299-319.

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

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Research article

Genetic control of oligo-culms in common wheat

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Summary

Genetic analysis of oligo-culms was carried out in the bread wheat (*Triticum aestivum*) line "88F2185" by using the regular cultivar Chinese Spring (CS) monosomic series. The difference of culm number per plant between reciprocal crosses was nonsignificant, which means that cytoplasmic differences for culm number per plant is absent. The result of test-cross experiment revealed that the difference between "88F2185" and CS in culm number per plant was due to only one gene, and the oligo-culms was a dominant character. Based on the result of F_2 monosomic analysis, the gene for oligo-culms of "88F2185" was located on chromosome 2A. The symbol *Tin2* is suggested to represent this dominant gene.

Key words: Gene location, monosomic analysis, oligo-culms, restricted tiller number, *Triticum aestivum*, wheat

Introduction

The culms of wheat (*Triticum* L.) comprise one main stem and more or less fertile tillers. The production of tillers which are destined to die constitutes a wastage of resources, since relocation of nitrogen, minerals and carbon compounds from sterile tiller to the rest of the plant is thought to be incomplete (Donald 1968). The uniculm habit was first proposed by Donald (1968) as a mechanism to avoid the formation of unproductive tillers, and this design was in many breeders' mind. The potential to increase yield by restricted tillering is supported by results from detillering experiments both on barley (Jones and Kirby 1977; Kirby and Jones 1977; Yen 1964) and on wheat (Islam and Sedgley 1981; Yen 1964).

Breeding toward to the ideotype of Donald (1968), breeders have created a few uni- and oligo-

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culms common wheat (*T. aestivum* L.) materials. The uniculm habit is associated with some bad agronomy characters (Yen et al. 1993), and the gene for uniculm of common wheat was located on chromosome 1AS by Richards (quoted from McIntosh et al. 1993). But the genetic control of oligo-culms is unknown. To evaluate the value of oligo-culms in wheat breeding, genetic analysis on it is necessary.

The present study was concerned with inheritance of oligo-culms, and the chromosomal location of the gene for this character in common wheat.

Materials and Methods

Prior to initiating this study, the Chinese Spring (CS) monosomic series (kindly provided by Dr. E.R. Sears) was identified using the modified C-banding technique of Endo (1986). The seedlings of CS monosomic series were planted in autumn 1994. Three to five monosomic plants in each monosomic line were selected by cytological examination of root-tip cells, and were pollinated by the common wheat oligo-culms line, "88$F_2$185" (provided by X.L. Zhang, agronomist in Xianyang Agricultural Institute, China). Three disomic CS plants were crossed reciprocally with "88$F_2$185". Data on culm number per plant were recorded and evaluated in the following analysis:
(1) test-cross analysis: F_1 seeds of reciprocal crosses between CS (euploid line) and "88$F_2$185" were planted in Markang city for summer propagation. A part of reciprocal F_1 plants backcross to CS to obtain BC_1 seeds. Other F_1 hybrids were selfed to obtain F_2 seeds. On 3 Nov. 1995, seeds of "88$F_2$185", euploid CS, BC_1 and the reciprocal F_1 and F_2 were sowed separately in the same experimental field in Dujiangyang city. The distances between plants were kept 10cm apart.
(2) F_2 monosomic analysis: 24 different populations comprising 21 F_2 populations that derived from F_1 plants monosomic for different chromosomes, the F_2 population that derived from disomic F_1 plants and the two euploid parental lines were analyzed. In all, 128 seeds of each population were planted in four randomized double rows, 1.5m long each. The distances between plants were kept 10cm apart in every rows, and the rows were spaced 30cm apart. The sowing date was 3 Nov. 1995.

Some F_2 populations that derived from F_1 monosomic plants needed grouping according to whether they were monosomic or disomic. So, seeds of plants in these F_2 populations were individually harvested, and chromosome counts of five F_3 seeds was carried out at mitosis. The F_2 plant was considered as disomic if all the five F_3 seeds that derived from it had 42 chromosomes, or as monosomic if one or more seeds possessed 41 chromosomes in somatic cell.

In 1996, the culm number per plant and the final plant height were investigated at harvest. The total tiller number was investigated at jointing stage, when the tiller number per plant reached the maximum for the materials in the present experiment. The F_2 population derived from F_1 disomic plants was taken as check population in F_2 monosomic analysis. The significance of differences between the mean values were detected by t-test, and F-test was adopted to detect the significance of the differences between the variances.

Results and discussion

Test-cross analysis:

The F_1 population of the cross ($88F_2185$ x CS) showed 4.15 culms per plant, whereas the F_1 population of cross (CS x $88F_2185$) showed 4.18 culms per plant. However, statistic analysis showed the difference of culm number per plant between the reciprocal F_1 populations was not significant (P=0.912). In addition, two F_2 populations that derived from the reciprocal F_1 hybrids segregated for culm number per plant, with mean culm number per plant of 5.90 and 5.96 respectively. Statistic analysis of the two reciprocal F_2 populations indicated homogeneity in culm number per plant (P=0.874). These results indicated that cytoplasmic differences for the oligo-culms was absent, and that data from reciprocal crosses could be pooled.

The result of test-cross was shown in Fig. 1. F_1 progeny showed similar culm number to "$88F_2185$". This result means that the oligo-culms is a dominant character. So, the suggestion of Richards that a recessive gene inhibit the tillering capacity is not valid for the present experiment.

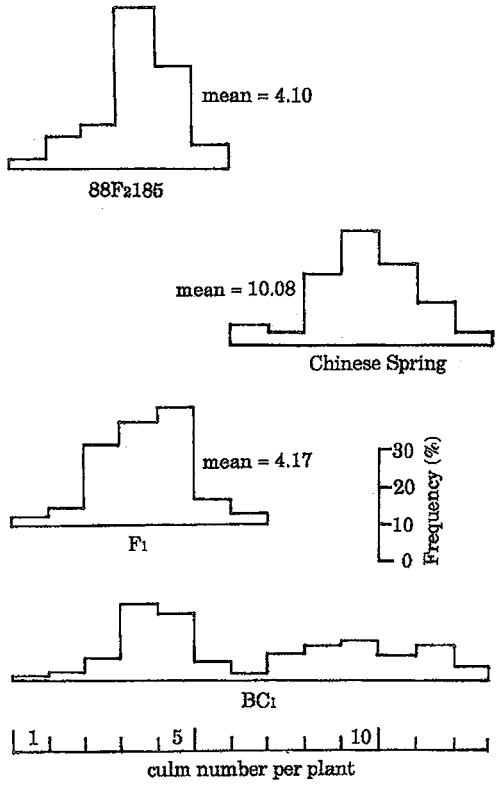

Fig. 1. Frequency distributions of the culm number per plant of the lines $88F_2185$ and Chinese Spring, and the F_1 (Chinese Spring x $88F_2185$) and BC_1 (F_1 x Chinese Spring)

The BC_1 frequency distribution figure of culm number per plant could be divided into two parts. One part comprised 133 (52.4%) plants with 1-6 culms, the other comprised 121 (47.6%) plants with 7-13 culms. If we arbitrate the plants with 1-6 culms per plant as oligo-culms plants, and the others as regular ones, the segregation of BC_1 population was fitted to the ratio of 1:1 (χ^2=0.476, P=0.493). Therefore, the BC_1 frequency distribution of culm number per plant could be interpreted as one gene segregation.

F_2 monosomic analysis:

Besides the disomic and monosomic plants, nullisomic plants existed in every F_2 populations that derived from F_1 monosomic plants. Among them, most of or all of the nullisomic plants died before flowering in some F_2 populations. Some nullisomic plants could survive to harvest in some other F_2 populations. Nullisomic plants deleted a part of chromosomes, and were stunted and nonvigorous, consequently they showed less culms than

the disomic plants in the same population. This was due to the nullisomic effect, and did not related to whether the corresponding chromosome carried gene for this character or not. So, nullisomics were excluded after determination by meiosis observation. Thus, the data of nullisomics was not involved in the means and variances of F_2 populations in Table 1.

As 4A, 7A and 7B F_2 populations surpassed the check F_2 population in variance, they were grouped into disomic and monosomic subpopulations. The 4A, 7A and 7B F_2 disomic subpopulations exhibited statistically similar culm number per plant to the check F_2 population. This result means that chromosomes 4A, 7A and 7B could not be the location of gene coding for oligo-culms. Thus, the low culm numbers of 4A, 7A and 7B F_2 monosomic subpopulations could be attributed to their hemizygous state of corresponding chromosome. This hemizygous effect was previously observed in Bersee monosomic series (Law et al. 1987).

In all the 21 F_2 populations that derived from F_1 monosomic plants, only the 2A F_2 population showed a considerable and significant low culm number per plant with small variance among plants (Table 1). 2A F_2 population was similar to "88F2185" in the mean value of culm number per plant. Therefore, the gene for oligo-culms of "88F2185" is on chromosome 2A.

In 2A F_2 population, monosomic plants possessed only one dose of "88F2185"s' chromosome 2A, and the disomic ones possessed two doses of this chromosome. However, statistic analysis showed no correlation between the culm number per plant and the dosage of chromosome 2A. Thus, the gene on chromosome 2A is hemizygous effective and dosage-independent.

Table 1. Means and variances of culm number per plant of lines "88F2185", CS and of the F_2 populations derived from crosses of "88F2185" with the monosomic series of CS

Population	Mean	Variance	Population	Mean	Variance	Population	Mean	Variance
88F2185	4.06	1.16						
CS	10.12	1.99						
check F_2	5.94	9.15						
F_2 monosomic for								
1A	6.06	8.95	1B	5.88	9.76	1D	5.94	9.14
2A	4.15**	1.27**	2B	5.76	8.47	2D	5.82	9.86
3A	6.07	9.77	3B	6.11	10.22	3D	5.84	9.37
4A disomic	6.11	10.08	4B	5.97	8.55	4D	6.14	10.16
monosomic	5.24*	8.63						
5A	6.18	8.95	5B	6.01	9.32	5D	5.94	8.69
6A	6.21	8.67	6B	6.03	9.88	6D	6.17	9.07
7A disomic	5.89	9.24	7B disomic	6.10	8.42)	7D	5.80	8.79
monosomic	5.17*	8.76	monosomic	5.35*	8.53			

*: $p<0.05$, **: $p<0.01$

Considering that *Rht7* gene on chromosome 2A had pleiotropic effect reducing culm number per plant (Worland et al. 1980), and "88F2185" was a semi-dwarfing line, to determine whether the gene for oligo-culms of "88F2185" was *Rht7* or not, the final height of plants in 2A F_2 population were investigated. The result (Table 2) showed that the height of disomic plants in 2A F_2 population was similar to that of the check F_2 population, indicating that chromosome 2A of "88F2185" did not carry any dwarfing gene. Thus, the gene on chromosome 2A of "88F2185" for oligo-culms could not be *Rht7*.

As we known, tiller number is often related to flowering date, earlier flowering genotypes having fewer fertile tillers. The low culm number of 2A F_2 population could have been attributed to the presence of day length sensitivity gene, *ppd3* which was located on chromosome 2A. However, heading date investigation indicated that 2A F_2 disomic plants was similar to the check F_2 population in the time to ear emergency (Table 2), indicating that "88F2185" is similar to CS in chromosome 2A's effect on heading date. So, the gene for oligo-culms on chromosome 2A of "88F2185" did not belong to *Ppd3* gene locus.

At spaced condition, the productive culm number of "88F2185" (4.1 ± 1.08) was little lower than its total tiller number (3.4 ± 1.44) plus one (main stem). So, the oligo-culms character of "88F2185" observed at harvest was due to its restricted tillering capacity. Richards had located a recessive gene, *tin* (tiller inhibitor) on chromosomal arm 1AS, which inhibited tillering in a bread wheat uniculm line (quoted from McIntosh et al. 1993). But in this experiment, the 1A, 1B and 1D F_2 populations showed similar culm number to the check F_2 population, indicating that group 1 chromosomes did not contribute to the oligo-culms of "88F2185". Whereas, the gene which reduced significantly the tiller number of "88F2185" was on chromosome 2A. Thus it belongs to a new gene locus. So, it is suggested that the gene symbol, *Tin2* is designated to denote the dominant gene on chromosome 2A of "88F2185".

Table 2. Final plants heights and the heading date of "88F2185", CS and the hybrid populations derived from crossing "88F2185" to disomic and monosomic 2A of CS respectively, grouped according to whether they were monosomic or disomic.

Population	Disomics or monosomics	Final plant height (cm)		Heading date*	
		Mean	Variance	Mean	Variance
CS mono. 2A x 88F2185	disomic	115.7	167.24	15.5	16.94
	monosomic	104.3**	148.51	16.2	17.71
CS disomics x 88F2185	disomic	117.1	138.21	15.8	16.25
CS	disomic	129.7	28.20	22.0	2.02
88F2185	disomic	95.0	18.87	3.6	1.90

* days from a desingnated date

**: $p<0.01$

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References

Endo TR (1986) Complete identification of wheat chromosomes by mean of a C-banding technique. Jpn J Genet 61: 89-93.

Donald CM (1968) The breeding of crop ideotypes. Euphytica 17: 385-403.

Islam TMT and Sedgley KH (1981) Evidence for a uniculm effect in spring wheat (*Triticum aestivum*) in a Mediterranean environment. Euphytica 30: 277-282.

Jones HG and Kirby EJM (1977) Effects of manipulation of number of tillers and water supply on grain yield in barley. J Agric Sci 88: 391-397.

Kirby EJM and Jones HG (1977) The relations between the main shoot and tillers in barley plants. J Agric Sci 88: 381-389.

Law CN, Snape TW and Worland AJ (1987) Aneuploidy in wheat and its uses in genetic analysis. In: Lupton FGH (ed) Wheat Breeding-its scientific basis, Chapman and Hall Ltd England, pp 71-108.

McIntosh RA, Hart GE and Gale MD (1993) Catalogue of symbols for wheat. Proc. 8th Intern Wheat Genet Symp, Beijing China: 1396

Worland AJ, Law CN and Shakoor A (1980) The genetical analysis of an induced height mutant in wheat. Heredity 45(1): 61-67.

Yen C (1964) The studies of detillering treatment I: The influence of repeated treatment in successive generations of wheat and barley. Genet Sinica 5: 14-28.

Yen C, Zheng YL and Yang JL (1993) An ideotype for high yield breeding, in theory and practice. Proc. 8th Intern Wheat Genet Symp, Beijing China: 1113-1117.

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Research article

Chromosome assignment and polymorphism of a wheat cDNA encoding protein disulfide isomerase

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Summary

Chromosomal location, cytological mapping and the assessment of variability of a cDNA encoding protein disulfide isomerase (PDI) in wheat are reported. Three PDI homoeoloci were mapped to chromosome arms 4AL, 4BS and 4DS. Deletion mapping localized PDI sequences at the distal 0.3 length fraction of 4DS, in a region, thus far, poor in other DNA markers. RFLP pattern detected by PDI probes were extremely conserved among hexaploid wheats. Some polymorphism was observed among tetraploid wild wheats, and among A-genome and S-genome diploids, making PDI probes useful to monitor introgressions from these lines into common wheat.

Key words: PDI (protein disulfide isomerase), cytological mapping, *Triticum* sp., *Aegilops* sp.

Introduction

Mapping of plant genomes has been attracting considerable attention in the past two decades (reviewed by Dean and Schmidt 1995). In this respect, combining the recombinational and cytological maps is of particular importance (Warner et al. 1992). Inspection of a number of cytological maps of wheat chromosomes reveals that considerable length fractions (up to 15%) currently lack cloned DNA markers, while other chromosomal regions are relatively rich in such markers (Hohmann et al. 1994; Mickelson-Young et al. 1995; Delaney et al. 1995). Therefore, it is important to obtain new chromosomal landmarks for regions in which DNA markers are scarce.

Protein disulfide isomerase (PDI EC 5.3.4.1) is an enzyme involved in the formation of disulfide bonds required for correct protein folding (Shimoni et al. 1995). Following its recent cloning and characterization in common wheat (therein) we hereby describe its cytological location and possible usefulness as a genetic marker in wheat.

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Materials and methods

Source of the probe

Aneuploid analysis was done using the *Nco*I-*Eco*RI 335 bp DNA fragment encoding amino acid residues 67-178 from the deduced open reading frame of wheat protein disulfide isomerase (PDI) cDNA (Shimoni et al. 1995). In addition, for RFLP studies of wheat and related species, we have also used the 3' untranslated region (3'UTR) of the same cDNA which was a 234 bp *Sac*I-*Xho*I fragment, from the first nucleotide 5' of the stop codon to the cloning site.

Results and discussion

Chromosomal location, deletion mapping and copy number

Hybridization experiments conducted under high stringency using the PDI coding probe revealed three fragments of similar signal intensity on Southern blots of the common hexaploid wheat cv. Chinese Spring (CS). Southern analysis of wheat nullisomic-tetrasomic and ditelosomic lines of

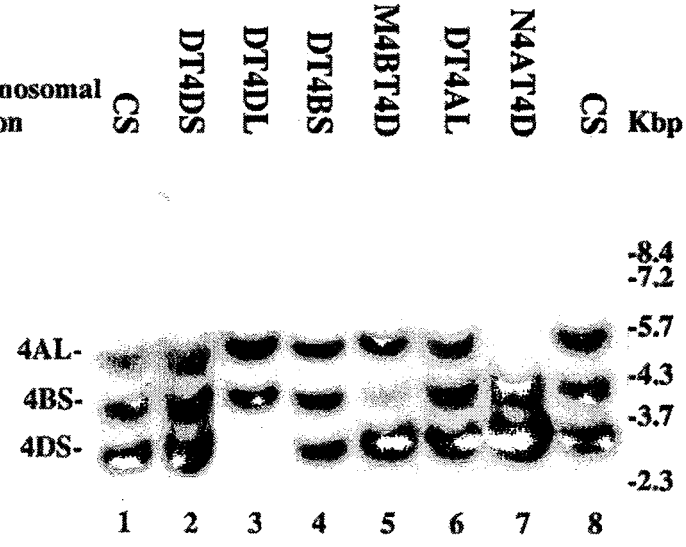

Fig. 1. Chromosomal arm assignment of wheat PDI genes. EcoRI-digested DNA of a set of chromosome group 4- ditelosomic lines or suitable nullisomic-tetrasomic lines of common wheat CS was hybridized with the PDI coding probe. Lanes 1 and 8: hexaploid wheat cultivar Chinese Spring. Lane 2: ditelosomic 4DS. Lane 3: ditelosomic 4DL. Lane 4: ditelosomic 4BS. Lane 5: monosomic 4B-tetrasomic 4D. Lane 6: ditelosomic 4AL. Lane 7: nullisomic 4A-tetrasomic 4D. The deduced chromosomal location of the observed bands is indicated on the left.

CS allowed us to assign these fragments to chromosome arm 4AL, 4BS and 4DS (Fig. 1). Wheat chromosome 4A is known to have undergone complex rearrangements (Naranjo et al. 1987; Devos et al. 1995). We inferred that PDI maps proximal to the 4AL/5AL translocation breakpoint, since it remained on chromosome 4A.

The physical location of the PDI genes on chromosome 4D was studied by deletion mapping, using DNA isolated from Endo's (1988) deletion stocks. The sequence from the 4DS chromosome arm (Fig. 2) was missing in lines 4DS-1 and 4DS-3, with fraction length (FL, the chromosome

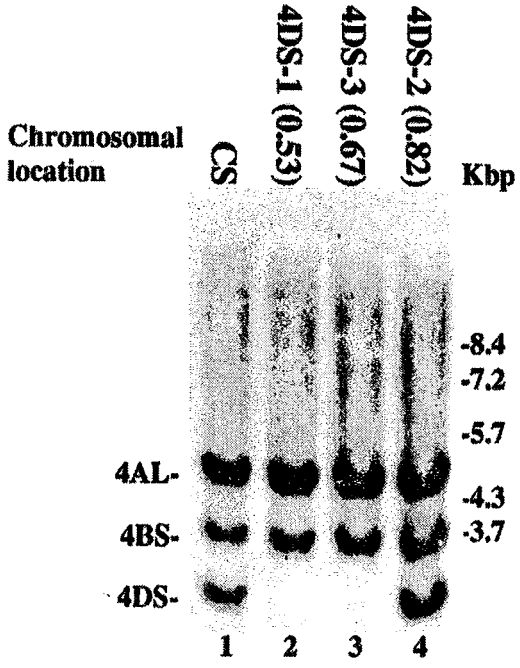

Fig. 2. Physical location of wheat PDI genes. Autoradiogram of a Southern analysis of DNA extracted from 4DS deletion lines and CS hybridized with PDI coding probe. The identity and fraction lengths (between parenthesis) of the deletion lines are shown.

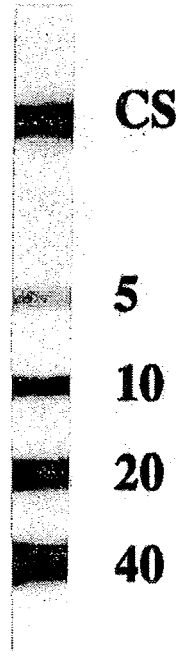

Fig. 3. Determination of copy number of PDI wheat genes. Five μg of nuclear DNA from the common hexaploid wheat Chinese Spring (CS) were digested with EcoRI, denatured and slot-blotted together with proportional amounts of target DNA corresponding to 5-40 copies. Hybridization was carried out with the PDI coding probe.

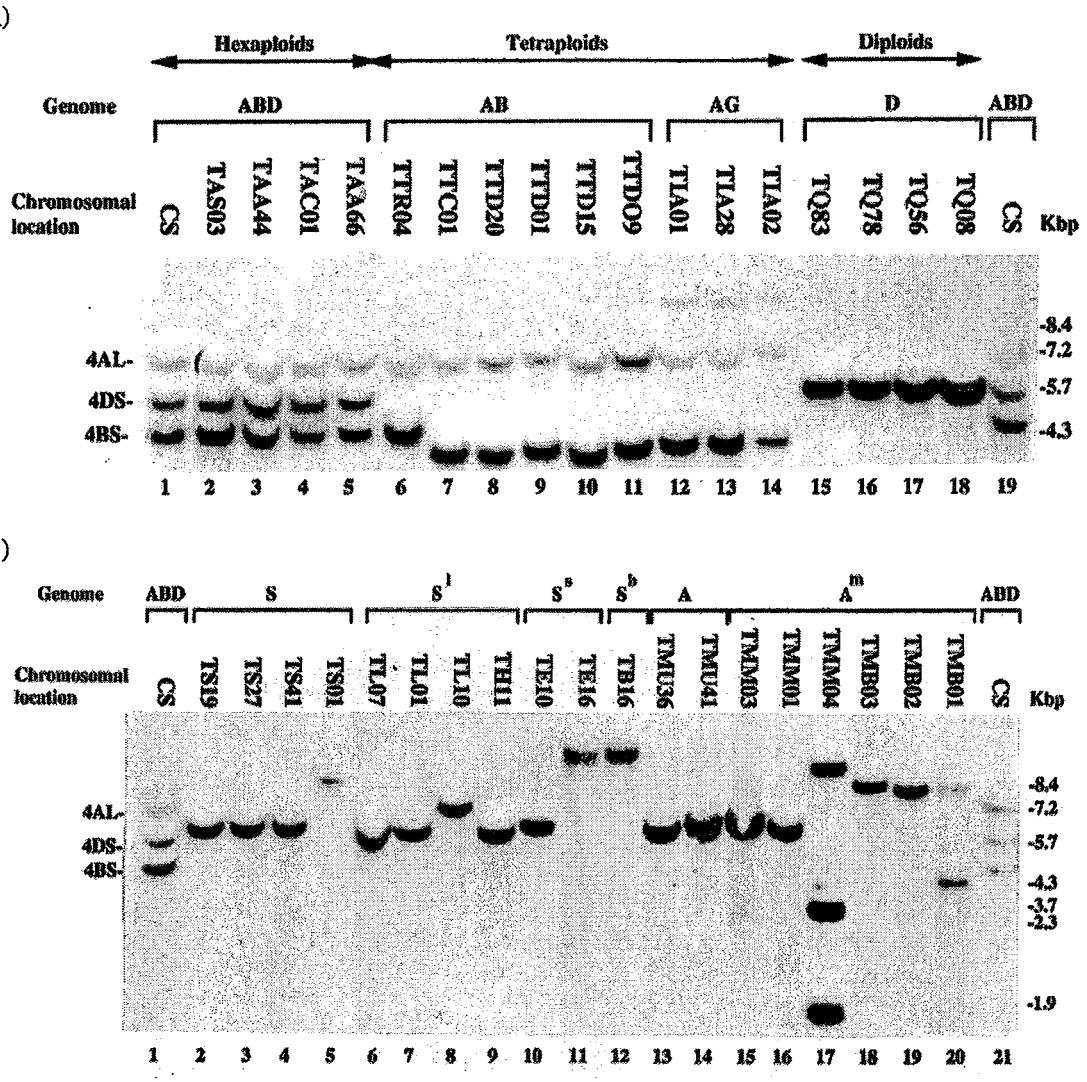

Fig. 4. Southern analysis of *Bam*HI-restricted DNA from wheat lines and their diploid progenitors and related species hybridized with the PDI coding probe. A) Hexaploids: CS= *T. aestivum* ssp. *vulgare* cv. Chinese Spring, TAS03= ssp. *spelta*, TAA44= ssp. *vulgare* cv. Thatcher, TAC01= ssp. *compactum*, TAA66= ssp. *vulgare* cv. Bethlehem. Tetraploids: Genome AB, TTR= *T. turgidum* var. *durum* cv. Inbar, TTC= ssp. *dicoccum* cv. Farum Körn, TTD= ssp. *dicoccoides*. Genome AG, TIA= *T. timopheevii* ssp. *araraticum*. Diploids: Genome D, TQ= *Ae. squarrosa*. B) Sitopsis group, TS= *Ae. speltoides*. TL= *Ae. longissima*. TH= *Ae. sharonensis*, TE= *Ae. searsii*. TB= *Ae. bicornis*. Genome A, TMU= *T. urartu*, TMM= *T. monococcum* ssp. *monococcum*, TMB= ssp. *boeoticum*.

arm length in the deletion line relative to the standard length) of 0.53 and 0.67 respectively, whereas it was present in line 4DS-2, with FL of 0.82. This indicates that the corresponding PDI locus resides on the distal third of chromosome arm 4DS, between FL values 0.67 and 0.82. Inspection of the cytological map of wheat chromosome 4D (Mickelson-Young et al. 1995) indicates that this sub-chromosomal region, encompassing 15% of the arm length, currently lacks any molecular markers.

Comparison of the hybridization intensities of CS total DNA and known amounts of plasmid DNA corresponding to 5-40 copies of PDI (Fig. 3) suggests that this sequences are present in ca. 30 copies in hexaploid wheat, or 5-6 copies per wheat constituent genome. This indicates that the number of PDI loci in wheat is similar to that in alfalfa (Shorrosh and Dixon 1991), barley (Chen and Hayes 1994) and maize (Li and Larkins 1996).

Gene nomenclature (McIntosh et al. 1993)
Xpdi (4A, 4B, 4D)

Polymorphism and presence of PDI sequences in wheat and related species
Southern analyses of DNA from 34 cultivars of bread wheat digested with four restriction enzymes (*Eco*RI, *Bam*HL *Hind*III and *Dra*I) did not detect any restriction fragment polymorphism, with both coding region and 3'UTR probes (data not shown). When the PDI coding probe was hybridized to DNAs extracted from wheat and related species of various origins and ploidy, digested with *Bam*HI (Fig. 4), 1-3 bands were detected. Hexaploid wheats (Panel A, lanes 1-5) presented three monomorphic bands. Tetraploid wheats with genome AABB (lanes 6-11) showed two bands. With the exception of durum wheat, they shared a B-genome fragment of higher mobility than the one from hexaploid wheat. *T. timopheevi* var. *araraticum* (lanes 12-14) presented an additional band and showed no intraspecific variation. Among the diploids, one band was observed in all accessions except for *T. monococcum* var. *monococcum* accession TMM04 (Panel B, lane 17) and *T. monococcum* var. *boeoticum.*, accession TMB01 (Panel B, lane 20), which showed three and two fragments, respectively. *T. tauschii* accessions (Panel A, lanes 15-18) were monomorphic, with restriction fragments similar in size to the CS D-genome bands. Polymorphisms were evident between and within species of the S-genome Sitopsis group (Panel B, lanes 2-12), which is related to the B genome of hexaploid wheat. The A genome diploids (lanes 13-20) also showed interspecific and intraspecific variation, with no variant closely matching the gel mobility of the A-genome PDI band in CS.

Despite limited polymorphism between bread wheat cultivars, the cytological location of the PDI locus, the absence of nearby cloned markers and observed variation in tetraploid wheat could make PDI an useful marker when analyzing DNA transfer from emmer wheat into hexaploid wheat.

Acknowledgments

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References

Chen F and Hayes PM (1994) Nucleotide sequence and developmental expression of duplicated genes encoding protein disulfide isomerase in barley (*Hordeum vulgare* L.). Plant Physiol. 106: 1705-1706.

Dean C and Schmidt R (1995) Plant genomes: a current molecular description. Ann. Rev. Plant Physiol. Plant Mol. Biol. 46: 395-418.

Delaney DE, Nasuda S, Endo TR, Gill BS and Hulbert SH (1995) Cytologically based physical maps of the group 3 chromosomes of wheat. Theor. Appl. Genet. 91: 780-782.

Devos KM, Dubcovsky J, Dvorak J, Chinoy CN and Gale MD (1995) Structural evolution of wheat chromosomes 4A, 5A and 7B and its impact on recombination. Theor. Appl. Genet. 91: 282-288.

Endo TR (1988) Induction of chromosomal structural changes by a chromosome of *Aegilops cylindrica* L. in common wheat. J. Hered. 79: 366-370.

Hohmann U, Endo TR, Gill KS and Gill BS (1994) Comparison of genetic and physical maps of group 7 chromosomes from Triticum aestivum L. Mol. Gen. Genet. 245: 644-653.

Li CP and Larkins B (1996) Expression of protein disulfide isomerase is elevated in the endosperm of the maize floury-2 mutant. Plant. Mol. Biol. 30: 873-882.

McIntosh R, Hart G and Gale MD (1995) Catalogue of gene symbols for wheat. In: Proc. 8th Int. Wheat Genet. Symp., Beijing, China, Vol 2, pp 1333-1500.

Mickelson-Young L, Endo TR and Gill BS (1995) A cytogenetic ladder-map of the wheat homoeologous group-4 chromosomes. Theor. Appl. Genet. 90: 1007-1011.

Naranjo T, Roca A, Goicoechea PG and Giraldez R (1987) Arm homoeology of wheat and rye chromosomes. Genome 29: 873-882.

Shimoni Y, Segal G, Zhu X-Z and Galili G (1995) Nucleotide sequence of a wheat cDNA encoding protein disulfide isomerase. Plant. Physiol. 107: 281.

Shorrosh BS and Dixon RA (1991) Molecular cloning of a putative plant endomembrane protein resembling vertebrate protein disulfideisomerase and a phosphatidylinositol-specific phospholipase C. Proc. Natl. Acad. Sci. USA 88: 10941-10945.

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

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Research article

Cytoplasmic diversity in *Triticum* and *Aegilops* evaluated by the respiratory electron flows in seedlings of alloplasmic hybrids of common wheat

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Summary

Fifteen cytoplasms of *Triticum* and *Aegilops* species were characterized by the respiratory electron flows through the cytochrome and alternative paths under normal and NaCl salinity conditions using 3-day-old seedlings of common wheat (*T. aestivum* L.) cv. Chinese Spring (CS) and the alloplasmic hybrids of CS. Under the normal condition, five plasm types of C, Sl, Sb, Mt and Mt2 showed respiratory path activities equivalent to those of B plasm type of the euplasmic CS. NaCl salinity caused significant increases in the total and cytochrome path activities but no detectable changes in the alternative path activity in CS. Plasm types of Sl and Mt showed a similar salinity response to the euplasmic CS. These results and a cluster analysis suggested that Sl plasm type of *Ae. sharonensis* is most closely related to B plasm type of CS.

Key words: cytoplasmic diversity, respiratory electron flow, NaCl salinity, *Triticum* and *Aegilops*, B plasm donor

Introduction

In *Triticum* and *Aegilops*, the evolution of plasmons has been studied extensively using cytoplasm substitution lines or alloplasmic hybrids in which given nuclei of common wheat and/or tetraploid wheat are combined with alien cytoplasms from various species in these genera (for reviews see Tsunewaki 1980, 1989, 1993, 1995; Ohtsuka 1991; Maan 1995). Plasmon diversity in *Triticum* and *Aegilops* has been studied primarily based on the nucleus-cytoplasm interactions affecting fertility and other physiological and agronomical characteristics in the alloplasmic hybrids (Kihara 1954; Tsunewaki 1980, 1993, 1995; Ohtsuka 1991; Maan 1995; Tsunewaki et al. 1996). The

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organellar DNA polymorphisms in the alloplasmic hybrids also have provided important information on the cytoplasmic diversity and maternal lineage in *Triticum* and *Aegilops* (Ogihara and Tsunewaki 1982, 1988; Tsunewaki and Ogihara 1983; Terachi and Tsunewaki 1986, 1992; Terachi et al. 1990; Miyashita et al. 1994; Ohsako et al. 1996; Wang et al. 1997).

However, information on the physiological contribution of the alien cytoplasms in the two major organellar functions, *i. e.* photosynthesis in chloroplasts and respiration in mitochondria, has been limited in the alloplasmic hybrids. A considerable amount of information is available on the photosynthetic components and activities in *Triticum* and *Aegilops* species (Chen et al. 1975; Austin et al. 1984; Evans 1986; Evans and Austin 1986; Terachi et al. 1987; Nakamura et al. 1991; Kasai et al. 1997), but a very few studies have been reported on the effects of alien cytoplasms on the respiratory characteristics in the alloplasmic hybrids (Iwanaga et al. 1978; Nakamura et al. 1991).

In this paper we report the cytoplasmic diversity evaluated by the respiratory electron flows in seedlings of common wheat cv. CS and 14 alloplasmic hybrids of CS under normal and NaCl salinity conditions. Based on the data and the estimated taxonomic relationship, it was suggested that Sl plasm type of *Ae. sharonensis* is most closely related to B plasm type of CS.

Materials and methods

Plant materials

Fourteen alloplasmic hybrids used in this study (Table 1) were originally produced by Prof. K. Tsunewaki (presently Fukui Prefectural University). CS served as control. Seeds were imbibed for 5hr under tap water, placed in 4°C overnight and germinated on filter papers in petri dishes supplied with either 0 (normal condition) or 0.15 M NaCl solution (salinity condition).

Respiratory measurements

Three-day-old whole seedlings (3 days after imbibition) were used in the following study of respiration. The rate of oxygen consumption was measured polarographically using a Klark-type oxygen electrode (Rank Brothers, Cambridge) according to Nakamura et al. (1991). Briefly, the whole seedlings were incubated at 25°C in 3 ml of buffer (pH 6.6) containing 50 mM N-[2-hydroxyethyl] piperazine-N'-2-ethanesulfonic acid and 10 mM 2-[N-morpholino]-ethanesulfonic acid inside the sample cell. Effects of respiratory inhibitors, *i.e.*, 1 mM KCN for the cytochrome path and 1 mM salicylhydroxamic acid (SHAM) for the alternative path, were studied singly and in combination. The data were taken from at least 9 samples per line and the activity of each path was calculated according to a model equation developed by Bahr and Bonner (1973). The residual rate of oxygen consumption which is resistant to both KCN and SHAM was subtracted to estimate the total path activity. Average taxonomic distances among all the alloplasmic hybrids and CS were calculated based on standardized values and a dendrogram was constructed by UPGMA (Sneath and Sokal 1973).

Results and discussion

The total respiratory path activity at the 3-day-old seedling stage was significantly higher in 6 alloplasmic hybrids and lower in 3 others than CS under the normal condition (Table 1). D plasm type of *Ae. squarrosa* and Mh of *Ae. heldreichii* showed higher cytochrome path activities than CS, while the cytochrome path activity of Sv plasm type of *Ae. kotschyi* was lower. Only Cu plasm type of *Ae. umbellulata* showed a higher alternative path activity than CS. Under the normal condition, as a whole, five plasm types (C of *Ae. caudata*, Sl of *Ae. sharonensis*, Sb of *Ae. bicornis* and Mt and Mt2 of *Ae. mutica*) showed the respiratory path activities equivalent to those of CS.

Under the salinity condition, coefficients of variation of a majority of parameters were larger than those under the normal condition (Table 1). Cu plasm type showed significantly lower total path and cytochrome path activities than CS, and C and Sv plasm types showed lower total path activities. It was noted that the alternative path activities of six plasm types were higher than CS under the salinity condition. The alternative path is known to be operative uniquely in plants under the conditions of energy oversupply or limited cytochrome path capacity (Moore and Siedow 1991). The path is resistant to cyanide and the electron flow through this path is considered to be energetically wasteful because of the uncoupling with ATP production. Although physiological significance of this path remains unclear, it has been suggested that the path plays a role in maintaining the homeostasis of plant cells in relation to cellular energy states (Lambers 1982). The observed higher alternative path activity in one half of the alloplasmic hybrids than CS under the salinity condition suggests that the energy overflow through this path is associated with the limited capacity of the cytochrome path in these alloplasmic hybrids. The response of plasm types to NaCl salinity, i.e., increases or decreases in the respiratory path activities relative to those under the normal condition, is shown in Fig. 1. NaCl salinity caused significant increases in the total and cytochrome path activities in CS. The observation is consistent with the report that the cytochrome path activity increases in wheat plants subjected to NaCl salinity, possibly to cope with the increased energy demand under salinity conditions (Zagdanska 1995). Similarly, Sl, Mt, Mt2 and Sv plasm types showed increases in both total and cytochrome path activities under the salinity condition. On the other hand, the salinity condition caused significant decreases in the total path activity and/or cytochrome path activity in D, Mh and G plasm types.

Based on the average taxonomic distances estimated by the respiratory electron flows under both normal and NaCl salinity conditions, a dendrogram showing the phylogenetic relationships was constructed. In this dendrogram, B plasm type of CS was clustered with Mu, G, S, Sl and Mt plasm types (Fig. 2). Among these five plasm types, Mu, G and S showed higher total activities than CS under the normal condition and higher alternative path activities under the salinity condition and Mt plasm type showed higher total and alternative path activities under the salinity condition. Only Sl plasm type showed the respiratory activity equivalent to that of CS under both conditions. The results suggested that Sl-palsm type of *Ae. sharonensis* is most closely related to B palsm of CS.

A large volume of research results have been accumulated on the interspecific variations in the nuclear and organellar DNAs of *Triticum* and *Aegilops* species, suggesting that *Ae. speltoides*

Table 1. Comparison of respiratory electron flows between euplasmic CS and 14 NC hybrids under normal and NaCl salinity conditions.

Cytoplasm donor (Plasma type)		Normal condition						NaCl salinity condition					
		Total		Cytochrome		Alternative		Total		Cytochrome		Alternative	
Triticum aestivum cv. CS	(B)	16 ± 2.8		8 ± 3.0		6 ± 2.8		19 ± 3.9		15 ± 6.1		5 ± 2.5	
Aegilops caudata	(C)	15 ± 2.1		7 ± 1.9		8 ± 1.9		13 ± 5.3	–	7 ± 6.5		8 ± 7.1	
Ae. umbellulata	(Cu)	20 ± 5.8	+	8 ± 1.2		12 ± 4.4	+	16 ± 4.0	–	6 ± 1.5	–	9 ± 5.1	
Ae. squarrosa	(D)	31 ± 3.2	+	25 ± 1.4	+	6 ± 1.7		21 ± 5.9		19 ± 3.7		5 ± 5.2	
Ae. heldreichii	(Mh)	29 ± 3.0	+	22 ± 3.6	+	5 ± 2.5		19 ± 3.4		14 ± 2.0		5 ± 1.7	
Ae. uniaristata	(Mu)	19 ± 5.2	+	10 ± 2.0		5 ± 4.1		20 ± 3.0		9 ± 0.7		9 ± 1.8	+
Ae. speltoides	(S)	20 ± 3.1	+	10 ± 3.2		9 ± 2.2		18 ± 3.1		11 ± 3.3		8 ± 0.5	+
Ae. sharonensis	(Sl)	17 ± 4.4		6 ± 3.0		8 ± 2.9		21 ± 4.7		12 ± 4.3		8 ± 4.2	
Ae. bicornis	(Sb)	15 ± 4.4		11 ± 1.0		5 ± 2.9		24 ± 4.5	+	14 ± 3.1		11 ± 4.7	+
Ae. mutica	(Mt)	15 ± 3.8		5 ± 1.5		8 ± 2.5		24 ± 6.0	+	14 ± 2.4		9 ± 1.6	+
Ae. mutica	(Mt2)	14 ± 4.7		8 ± 3.1		5 ± 2.0		27 ± 2.5	+	14 ± 0.4		15 ± 2.7	+
T. timopheevi	(G)	23 ± 5.7	+	12 ± 2.3		7 ± 3.1		18 ± 4.4		10 ± 1.5		10 ± 4.2	+
Ae. ovata	(Mo)	11 ± 1.7	–	5 ± 1.2		5 ± 2.1		17 ± 3.0		7 ± 1.7		9 ± 4.3	
Ae. kotschyi	(Sv)	11 ± 2.7	–	4 ± 1.2	–	6 ± 1.6		14 ± 3.1	–	8 ± 1.6		7 ± 1.4	
Ae. crassa 4X	(D2)	14 ± 2.4	–	6 ± 2.2		7 ± 2.7		18 ± 3.4		9 ± 2.0		9 ± 2.5	

Three-day-old seedlings were used in the experiment. Figures represent nmol/hr/mg FW±standard deviation.
+ and – indicate the significantly higher and lower mean values than CS at the 5% level, respectively.

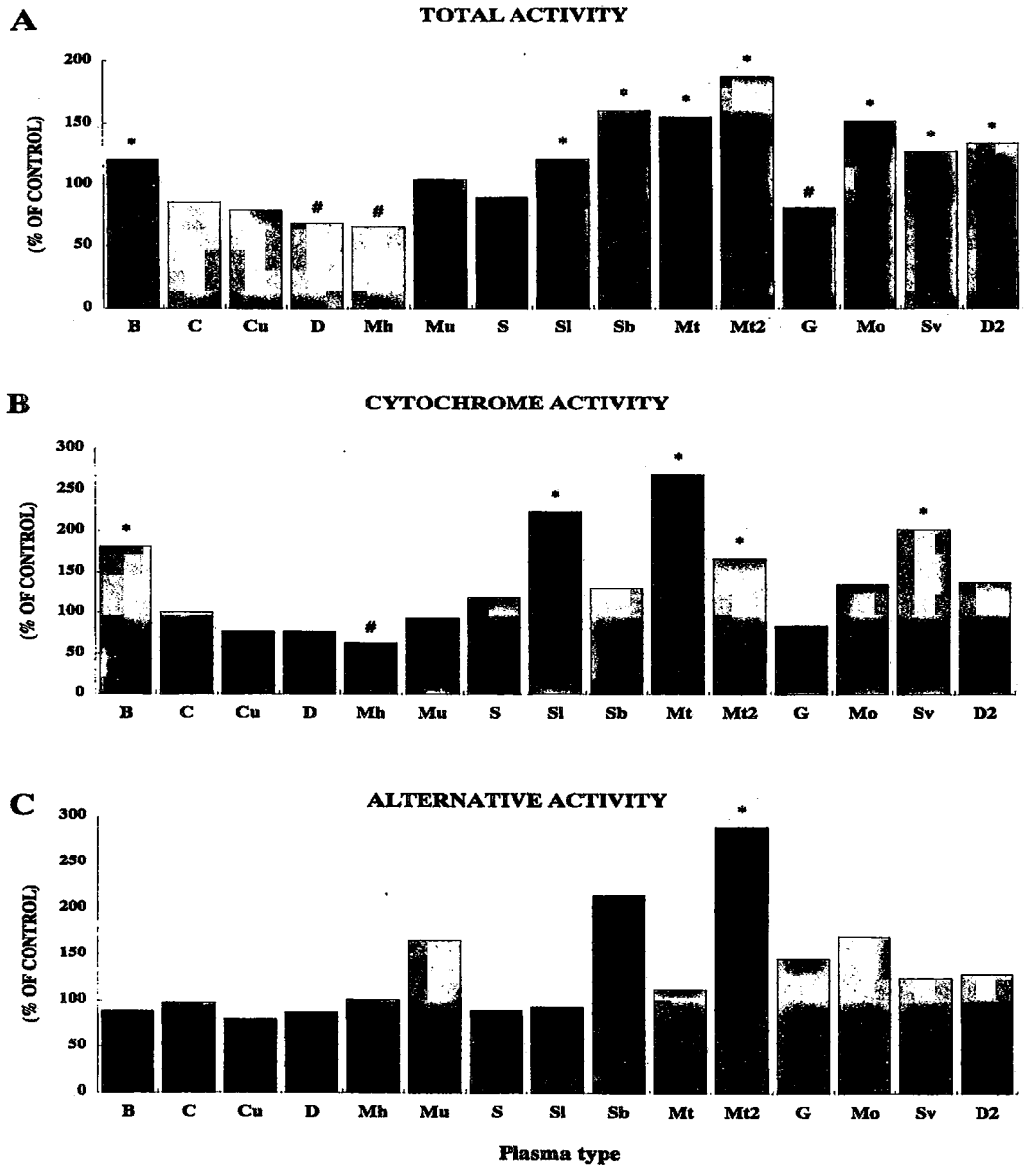

Fig. 1. Changes in the respiratory electron flows under NaCl salinity condition as compared with those under the normal condition. * and # indicate the lines showing significantly higher and lower mean values respectively under the salinity condition than the normal condition. For the abbreviations of the plasm types, see Table 1.

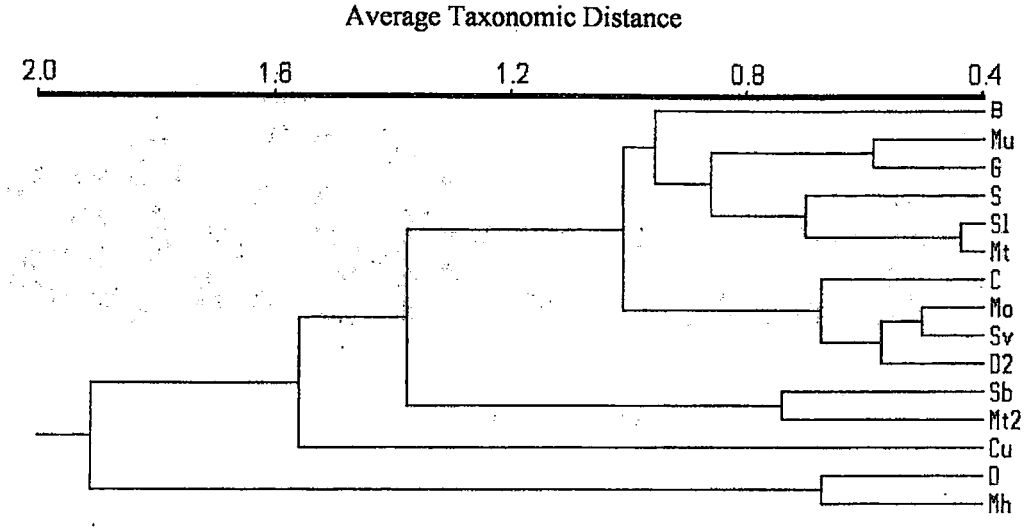

Fig. 2. A dendrogram showing the taxonomic relationship of 15 palsm types based on the respiratory electron flows. A dendrogram was constructed using the data obtained under the normal and NaCl salinity conditions. For the abbreviations of the plasm types, see Table 1.

is the cytoplasm donor of polyploid wheat (Tsunewaki et al. 1976; Breiman 1987; Ogihara and Tsunewaki 1988; Dvorak and Zhang 1990; Terachi and Tsunewaki 1992; Miyashita et al. 1994; Tsunewaki 1995; Ohsako et al. 1996; Wang et al. 1997). However, there are several reports suggesting that *Ae. sharonensis*, *Ae. searsii* and/or *Ae. longissima* are the cytoplasm donor(s) of B plasm type (Sears 1956; Feldman 1978; Kushnir and Halloran 1981, 1982; Nishikawa and Furuta 1978; Nath et al. 1983, 1984). Although some major discrepancy can be seen between the phylogenetic relationships constructed based on the respiratory electron flows (Fig. 2) and those based on various agronomic characteristics and organellar DNA polymorphisms (for a review see Tsunewaki 1995), our results pointed out the possibility that *Ae. sharonensis* might have played a role in the evolution of B palsm type of polyploid wheat.

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References

Austin RB, Ford MA, Morgan CL, Laminski A and Miller TE (1984) Genetic constraints on photosynthesis and yield in wheat. In : Sybesma C (ed) Advances in photosynthesis research IV Junk The Hague pp 103-110.

Bahr JT and Bonner WD Jr (1973) Cyanide-insensitive respiration. J Biol Chem 248: 3441-3445.

Breiman A (1987) Mitochondrial DNA diversity in the genera of *Triticum* and *Aegilops* revealed by Southern blot hybridization. Theor Appl Genet 73: 563-570.

Chen K, Gray JC and Wildman SG (1975) Fraction 1 protein and the origin of polyploid wheat. Science 190: 1304-1306.

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

Evans JR (1986) The relationship between carbon-dioxide-limited photosynthetic rate and ribulose-1,5-bisphosphate carboxylase content in two nuclear-cytoplasm substitution lines of wheat, and the coordination of ribulose-1,5-bisphosphate-carboxylation and electron-transport capacities. Planta 167: 351-358.

Evans JR and Austin RB (1986) The specific activity of ribulose-1,5-bisphosphate carboxylase in relation to genotype in wheat. Planta 167: 344-350.

Feldman M (1978) New evidence on the origin of the B genome of wheat. Proc 5th Int Wheat Genet Symp, New Delhi: 120-132.

Iwanaga M, Mukai Y, Panayatov I and Tsunewaki K (1978) Genetic diversity of the cytoplasm in *Triticum* and *Aegilops*. VII. Cytoplasmic effects on respiratory and photosynthetic rates. Jpn J Genet 53: 387-396.

Kasai K, Nakamura C, Mori N and Uchida N (1997) Rubisco activity vs photosynthetic CO_2 assimilation rate in the alloplasmic hybrids of common wheat cv. Chinese Spring. Wheat Inf Serv 85: 25-30.

Kihara H (1954) Considerations on the evolution and distribution of *Aegilops* species based on the analyser-method. Cytologia 19: 336-357.

Kushnir U and Halloran GM (1981) Evidence for *Aegilops sharonensis* Eig as the donor of the B genome of wheat. Genetics 99: 495-512.

Kushnir U and Halloran GM (1982) Quantitative studies of the amphiploid (*Aegilops sharonensis* x *Triticum monococcum*) and the origin of the B genome of wheat. Wheat Inf Serv 54: 12-16.

Lambers H (1982) Cyanide-resistant respiration: A non-phosphorylating electron transport pathway acting as an energy overflow. Physiol Plant 55: 478-485.

Maan SS (1995) The species-cytoplasm-specific gene hypothesis. In: Raupp WJ and Gill BS (ed) Classical and Molecular Cytogenetic Analysis (Proc US-Japan Symp) Kansas State Univ Press, Manhattan, Kansas pp 165-174.

Miyashita NT, Mori N and Tsunewaki K (1994) Molecular variation in chloroplast DNA regions in ancestral species of wheat. Genetics 137: 883-889.

Moore AL and Siedow JN (1991) The regulation and nature of the cyanide-resistant alternative oxidase of plant mitochondria. Biochem Biophys Acta 1059: 121-140.

Nakamura C, Kasai K, Kubota Y, Yamagami C, Suzuki T and Mori N (1991) Cytoplasmic diversity in alloplasmic common wheats with cytoplasms of *Triticum* and *Aegilops* revealed by photosynthetic and respiratory characteristics. Jpn J Genet 66: 471-483.

Nath J, McNay JW, Paroda CM and Culati SC (1983) Implication of *Triticum searsii* as the B-genome donor to wheat using DNA hybridizations. Biochem Genet 21: 745-760.

Nath J, Hanzel JJ, Thompson JP and McNay JW (1984) Additional evidence implicating *Triticum searsii* as the B-genome donor to wheat. Biochem Genet 22: 37-50.

Nishikawa K and Furuta Y (1978) DNA content of nucleus and individual chromosomes and its evolutionary significance. Proc 5th Int Wheat Genet Symp, New Delhi: 133-138.

Ogihara Y and Tsunewaki K (1982) Molecular basis of the genetic diversity of the cytoplasm in *Triticum* and *Aegilops*. I. Diversity of the chloroplast genome and its lineage revealed by the restriction pattern of ctDNAs. Jpn J Genet 57: 371-396.

Ogihara Y and Tsunewaki K (1988) Diversity and evolution of chloroplast DNA in *Triticum* and *Aegilops* as

revealed by restriction fragment analysis. Theor Appl Genet 76: 321-332.
Ohtsuka I (1991) Genetic differentiation in wheat nuclear genomes in relation to compatibility with *Aegilops squarrosa* cytoplasm and application to phylogeny of polyploid wheats. J Fac Agric Hokkaido Univ, part 2: 127-198.
Ohsako T, Wang GZ and Miyashita NT (1996) Polymerase chain reaction-single strand conformational polymorphism analysis of intra- and interspecific variations in organellar DNA regions of *Aegilops mutica* and related species. Genes Genet Syst 71: 281-292
Sears ER (1956) The B genome of *Triticum*. Wheat Inf Serv 4: 8-10.
Sneath PA and Sokal RR (1973) Numerical taxonomy. Freeman, San Francisco.
Terachi T and Tsunewaki K (1986) The molecular basis of genetic diversity among cytoplasms of *Triticum* and *Aegilops*. 5. Mitochondrial genome diversity among *Aegilops* species having identical chloroplast genomes. Theor Appl Genet 73: 175-181.
Terachi T and Tsunewaki K (1992) The molecular basis of genetic diversity among cytoplasms of *Triticum* and *Aegilops*. VIII. Mitochondrial RFLP analyses using cloned genes as probes. Mol Biol Evol 9: 917-931.
Terachi T, Ogihara Y and Tsunewaki K (1987) The molecular basis of genetic diversity among cytoplasms of *Triticum* and *Aegilops*. VI. Complete nucleotide sequences of the *rbcL* genes encoding H- and L-type Rubisco large subunits in common wheat and *Ae. crassa* 4x. Jpn J Genet 62: 375-387.
Terachi T, Ogihara Y and Tsunewaki K (1990) The molecular basis of genetic diversity among cytoplasms of *Triticum* and *Aegilops*. 7. Restriction endonuclease analysis of mitochondrial DNAs from polyploid wheats and their ancestral species. Theor Appl Genet 80: 366-373.
Tsunewaki K (1980) Genetic diversity of the cytoplasm in *Triticum* and *Aegilops*. Jpn Soc Promot Sci, Tokyo. pp 290
Tsunewaki K (1989) Plasmon diversity in *Triticum* and *Aegilops* and its implication in wheat evolution. Genome 31: 143-154.
Tsunewaki K (1993) Genome-plasmon interaction in wheat. Jpn J Genet 68: 1-34.
Tsunewaki K (1995) Plasmon differentiation in *Triticum* and *Aegilops* revealed by the cytoplasmic effects on wheat genome manifestation. In: Raupp WJ and Gill BS (ed) Classical and Molecular Cytogenetic Analysis (Proc US-Japan Symp) Kansas State Univ Press, Manhattan, Kansas pp 38-48.
Tsunewaki K and Ogihara Y (1983) The molecular basis of genetic diversity among cytoplasm of *Triticum* and *Aegilops* species. II. On the origin of polyploid wheat cytoplasms as suggested by chloroplast DNA restriction fragment patterns. Genetics 104: 155-171.
Tsunewaki K, Mukai Y, Endo TR, Tsuji S and Murata M (1976) Genetic diversity of the cytoplasm in *Triticum* and *Aegilops*. VI. Distribution of the haploid-inducing cytoplasms. Jpn J Genet 51: 193-200.
Tsunewaki K, Wang GZ and Matsuoka Y (1996) Plasmon analysis of *Triticum* (wheat) and *Aegilops*. 1. Production of alloplasmic common wheats and their fertilities. Genes Genet Syst 71: 293-311.
Wang GZ, Miyashita NT and Tsunewaki K (1997) Plasmon analyses of *Triticum* (wheat) and *Aegilops*: PCR-single-strand conformational polymorphism (PCR-SSCP) analyses of organellar DNAs. Proc Natl Acad Sci USA 94: 14570-14577.
Zagdanska B (1995) Respiratory energy demand for protein turnover and ion transport in wheat leaves upon water deficit. Physiol Plant 95: 428-436.

Wheat Information Service
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Research information

Genomic constitution of a partial *Triticum aestivum* x *Thinopyrum intermedium* amphiploid

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Zhong 2 is a partial amphiploid (2n=56) between *Triticum aestivum* and *Thinoyrum intermedium*. Meiotic metaphase I in the hybrids between *Triticum aestivum* Chinese Spring and Zhang 2 usually has 21 bivalents and 7 univalents (Table 1), suggesting that Zhong 2 may carry all the chromosomes of common wheat and seven pairs of chromosomes from *Th. intermedium*. *Th. intermedium* is a hexaploid species, its genome constitution is revised as $E_1E_1E_2E_2XX$(Dewey 1984; Friebe et al. 1992). In order to determine which set of *Th. intermedium* chromosomes Zhong 2 contains, we made crossing between F_1 hybrids from *T. durum* x *Th. intermedium* and Zhong 2, and crossing between Zhong 2 and *T. durum*. Chromosome pairing of the hybrids was studied in this paper .

In all the combinations, the PMCs of the hybrids exhibited trivalents and quadrivalents. A high level of trivalents was observed in hybrids between (*T. durum* x *Th. intermedium*)F_1 and Zhong 2, five trivalents were observed in some cells. Quadrivalent and pentavalent can also be observed in some cells, these mutivalents may be due to chromosome translocation or chromosome structural variation in Zhong 2.

The genomic constitution of the partial amphiploids of *T. aestivum* x *Th. intermedium* should

Table 1. Chromosome pairing at meiotic metaphase I of PMCs of the hybrids.

Cross combination	Number of cells	Uinvalents	Bivalents	Trivalents	Quadrivalents
(*T. durum* x *Th. intermedium*)F_1 x Zhong 2	64	17.2+0.48	17.9+0.26	2.4+0.13	0.4+0.06
T. aestivum CS x Zhong2	48	8.2+0.20	19.4+0.18	0.4+0.07	0.2+0.05
Zhong 2 x *T. durum*	34	13.4+0.26	12.8+0.22	0.9+0.13	0.1+0.02

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be AABBDDE$_1$E$_1$ or AABBDDE$_2$E$_2$ and AABBDDXX. The genomic constitution of hybrids of (*T. durum* x *Th. intermedium*) x Zhong 2 (2n=63) is AABBDXE$_1$E$_2$C (the C represents one genome in Zhong 2 that comes from *Th. intermedium*). If C=X, the genomic constitution of the hybrids (2n=63) is AABBDXE$_1$E$_2$X, they should have 28 bivalents and 7 univalents at meiotic metaphase I. If C=E$_1$ or E$_2$, the genomic constitution of the hybrids (2n=63) is AABBDXE$_1$E$_1$E$_2$ or AABBDXE$_1$E$_2$E$_2$, they should show 14 bivalents, 7 trivalents and 14 univalents in the PMC. From the actual observed results, chromosome pairing averaged 17.2I+17.9II+2.4III+0.4IV+0. 1V in the hybrids (2n=63), but the average of trivalents per cell in Zhong 2 x *T. durum* and C S x Zhong 2 hybrids were 0.9 and 0.4, respectively. These results indicated that the genomic constitution of Zhong 2 may be AABBDDE$_1$E$_1$ or AABBDDE$_2$E$_2$. A slightly low frequency of trivalents in the hybrids (2n=63) might be due to a tendency of chromosome pairing towards bivalentization. This result is similar to the frequency of trivalents in the triploid hybrids between diploid *Th. elongatum* (EE) and tetraploid. *Th. elongatum* (E$_1$E$_1$E$_2$E$_2$). Chromosome pairing averaged 5.6II+2.2III and 4.2II+2.8III in the triploid hybrids as reported by Dvorak(1981)and Charpentier et al. (1986), respectively.

Reference

Charpentier A, Feldman M and Cauderon Y (1986) Genetic control of meiotic chromosome pairing in tetraploid *Agropyron elongatum*. I. Pattern of pairing in natural and induced tetraploid and in F$_1$ tetraploid hybrids. Can J Genet Cytol 28: 783-788.

Dewey D R (1984) The genomic system of classification as a guide to intergeneric hybridization within the perennial Triticeae. In: Gustafson J P (ed) Gene manipulation in plant improvement. Plenum Publishing, New York, PP 209-279.

Dvorak J (1981) Genome relationships among *Elytrigia* (=*Agropyron*) *elongata*, *E. stipifolia*, "*E. elongata* 4x", *E. caespitosa*, *E. intermedium*, and "*E. elongata* 10x" . Can J Genet Cytol 23: 481-492.

Friebe B, Mukai Y, Gill BS and Cauderon Y (1992) C-banding and in situ hybridization analyses of *Agropyron intermedium*, a partial wheat x *Ag. intermedium* amphiploid, six derived chromosome addition lines. Theor Apll Genet 84: 899-905.

Wheat Information Service
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Research information

Crossability percentages of some improved wheat cultivars (lines) from China with rye

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Many papers have reported the crossability of bread wheat landraces from China with rye (Luo et al. 1992, 1993a, 1993b, 1994), however, few of them has excellent agronomic traits, so landraces with high crossability were less useful in wheat breeding by distant cross than those with both high crossability and excellent agronomic traits. With the artificial evolution of wheat cultivars, more and more cultivars or lines with high-yielding, multi-resistance, semi-dwarf and so on appears in China, but little work has been done to test their distant crossability, we so selected some improved wheat cultivars or lines, most of them are being grown in China, to cross with rye in order to reveal their distant crossability, this would be more helpful in wheat breeding by distant cross.

Of 69 wheat materials (*Triticum aestivum* L.), the landrace Chinese Spring from Sichuan Province was as the check, the improved cultivars or lines were kindly provided by Professor Bao Wen-Yi and Mr. Wang Yong. Of 68 wheat cultivars or lines, most of them were from Shandong Province, the others were from Shanxi, Shaanxi, Henan, Hebei provinces and Beijing City. Rye (*Secale cereale*) was used as male tester in the crosses. In each wheat material about 400 florets were emasculated and pollinated by brush with large amount of fresh pollen of rye at the appropriate stage of stigma receptivity at Taian farm in Shandong Province, China in 1993. The crossability percentage was expressed in terms of the % seed-set out of the florets pollinated in each cross.

Of 69 wheat materials (Table 1), Chinese Spring showed the highest crossability (82. 3%) with the rye, no cultivar or line expressed higher or similar crossability than or to the check, and only 3 cultivars had a crossability more than 50%, 3 ones with 30—50%, 5 ones with 10—30%, and 57 cultivars or lines with less than 10% crossability.

In comparison with the previous studies (Luo et al. 1992, 1993a, 1993b, 1994) on the crossability of bread wheat landraces from China, there were less cultivars or lines with high crossability than that of landraces and no cultivar or line were with higher or similar crossability than or to Chinese Spring. The results revealed that with artificial evolution of wheat cultivars, wheat

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cultivars or lines are losing their crossability with rye despite their improving agronomic traits, so it is very important to transfer the high crossability genes into the improved wheat cultivars or lines in wheat breeding.

Table 1. Four groups of wheat cultivars (lines) from China as classified by crossability with rye

Group 1: >50.0%
Chinese Spring (Sichuan), Bima No. 4 (Shaanxi) Youzimai (Henan), Mazhamai (Shaanxi)

Group 2: ≥30%<50%
Qida No. 195 (Shandong), Huixianhong (Henan),Jinan No. 10 (Shandong)

Group 3: ≥10% <30%
Yannong No. 15 (Shandong), Shannong No. 587 (Shandong), 8641012 (Shandong), Jinan No. 2 (Shandong), Laizhou No. 953 (Shandon

Group 4: <10
Lumai No. 2 (Shandong), Lumai No. 1 (Shandong), Lumai No. 8 (Shandong), Lumai No. 4 (Shandong), Tai No. 856903 (Shandong), 215953 (Shandong), Wei No. 4311 (Shandong), Fu No. 63 (Shandong), Lumai No. 17 (Shandong), Lumai No. 20 (Shandong), Hongtutou (Shandong), 80 -36 (Shandong),Jinan No. 6 (Shandong), Lumai No. 7 (Shandong), Lumai No. 11 (Shandong), Yumai No. 14 (Henan), 864990 (Shandong), Lumai No. 14 (Shandong), Yan No. 1936 (Shandong), Zinong No. 033 (Shandong), Jinmai No. 31 (Shanxi), Taishan No. 8 (Shandong), Lumai No. 12 (Shandong), Lumai No. 15 (Shandong), Hongyoubao (Shandong), Yumai No. 13 (Henan), Lin No. 85-14 (Shandong), Taishan No. 5 (Shandong), Honggao No. 38 (Shandong), Fengchan No. 3 (Shaanxi), Jinghua No. 1 (Beijing), Jinghua No. 3 (Beijing), Lumai No. 10 (Shandong), Lumai No. 19 (Shandong), Ju No. 8408(Shandong), Lumai No. 13 (Shandong), Linfen No. 6010 (Shanxi), Ji No. 84-5418 (Hebei), Baiyoubao (Shandong), Jihe No. 02 (Shandong), Jinan No. 13 (Shandong), Zao No. 1 (Shandong), PH85-88-3 (Shandong), Jinan No. 8 (Shandong), Taishan No. 4 (Shandong), Yumai No. 17 (Henan), Baigao No. 38 (Shandong), Lumai No. 5 (Shandong), Taishan No. 1 (Shandong), PH90-3 (Shandong), PH85-4 (Shandong), Lumai No. 16 (Shandong), Longkou No. 7915 (Shandong), Jinmai No. 33 (Shanxi), Yumai No. 2 (Henan), Jinmai No. 37 (Shanxi), FengKang 13 (Beijing)

References

Luo MC, Yen C and Yang JL (1992) Crossability percentages of bread wheat landraces from Sichuan Province, China with rye. Euphytica 61:1-7.

Luo MC, Yen C and Yang JL (1993a) Crossability percentages of bread wheat landraces from Shaanxi and Henan Provinces ,China with rye. Euphytica 67:1-8.

Luo MC, Yen C and Yang JL (1993b) Crossability percentages of bread wheat collections from Tibet, China with rye. Euphytica 70:127-129.

Luo MC, Yen C and Yang JL (1994) Crossability percentages of bread wheat landraces from Hunan and Hubei provinces, China with rye. Wheat Inf Serv 78: 34-38.

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Research information

Crossability percentages of bread wheat landraces from Shandong Province, China with rye

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The previous studies (Luo et al. 1992; 1993a; 1993b; 1994) reported the crossability percentages of landraces from Sichuan, Shanxi, Henan, the Tibet Region, Hunan and Hubei, China and their geographical distribution, and revealed that landraces with high crossability widely exist in the regions of Sichuan, Shanxi, Henan, Hunan and Hubei, but rare in the Tibet Region. Our paper reports the crossability percentages of bread wheat landraces from Shandong province in eastern China with rye and their geographical distribution.

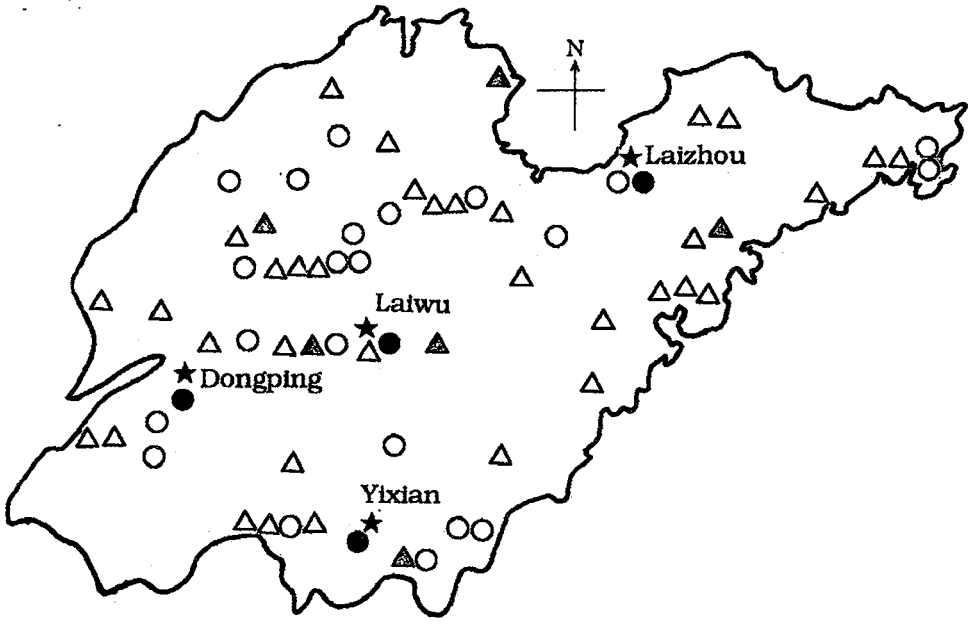

Fig. 1 The geographical distribution of crossability of 65 wheat landraces in comparison with CS in Shandong Province, China
△: Group 1, ○: Group 2, ▲: Group 3, ●: Group 4

Table 1. Four groups as classified by crossability percentages of 65 wheat landraces from Shandong Province, China with rye

Group 1 (no or very low: 0% <5%)
Hongtutou (2096) Juxian, SilengBaimai (077) Wudi, Silengzibaimai (175) Tengxian, Hongxingmai (190) Liaocheng, Hongkangliangmai (374) Jimi, Lougouding (246) Licheng, Hongtutou (359) Boxing, HuangXiandalibanmang(12007) HuangXian, Xianmai (437) Fushan, Baipiansui (354) Wendeng, Damangmai (368) Huangxian, Xiaohongmang (410) Juancheng, Yulinbai (034) Licheng, Hongtubailixiaomai (304) Lushan, Zijelumai (096) Jimi, Baikangyangmai (373) Jimi, Biansui (361) Qufu, Dahongmang (104) Juancheng, Hongbanmang (288) Zhucheng, Hongmazhatou (191) Yucheng, Baiguozitou (183)Taian, Honghuomai (280) Licheng, Toulingzi (111) Pingyin, Banjemang (213) Fushan, Zhuganqing (378) Guanxian, Xiaobaimang (007)B i n x i a n , Dabaimang (078) Guangrao, Dabaimang (009) Guangrao, Hongtutouxiaomai (285) Laiyang, Wutongmang (089) Weibei, Baitutou (265) Gaomi, Yaozhuhong (162) Shouguang, Gaoliaomai (315) Laiwu

Group 2 (significantly lower than CS: ≥5% <50%)
Daqingke (122) Tengxian, Baiguozitou (177) Taian, Tanglangzi (237) Zhangqiu, Laolaixia (107) Changqing, Banjiemang (219) Pingyi, Ertutou (244) Rongcheng, Silengbaimai (058) Zoucheng, Yulinbai (034) Licheng, Toulingbai (053) Licheng, Yaoguodu (232) Huantai, Baitutou (343) Rongcheng, Honglibanmeng (211) Changyi, Honghuomai (117) Guangrao, Hongqisiwu (414) Linyi, Xiaoshimai (094) Yexian, Feichenghemai (153) Feicheng, Baiqisiwu (404) Linyi, Baisuihongmai (405) Cangshan, Jianmai (429) Liangshan, Jianmai (428) Pingyuan, Yejiling (137) Yexian

Group 3 (high but lower than CS: ≥50% <86.4)
Yangmai (233)Yucheng, Zijiebai (178) Taian, Baitutouxiaomai (275) Laiyang, Xiaobaimang (076) Bohai Farm, Baitutou (349) Cangshan, Changmangbai (047) Yiyuan

Group 4 (same level as CS)
Xiaomangmai (143) Yexian, Mazhatouhuomai (106) Dongping, Changmangtoulongbai (004)Laiwu, Baitutou (210)Yixian, Chinese Spring Sichuan

Sixty-five accessions of wheat landraces (*Triticum aestivum* L.) were kindly provided by Mr. Ma Lishen of Crop Institute of Shandong Academy of Agricultural Sciences, rye (*Secale cereale* L.) was used as male tester in the crosses. In each wheat material about 200 florets were emasculated and pollinated by brush with large amount of fresh pollen of rye at the appropriate stage of stigma receptivity at Taian farm in Shandong Province, China in 1993. The crossability percentage was expressed in terms of the % seed-set out of the florets pollinated in each cross. The t-test were used to detect the difference of crossability between a wheat landrace and Chinese Spring.

Of 65 bread wheat landraces from Shandong Province, 10 showed high crossability (50%)

with rye and 4 of them had similar crossability (≒86.4%) to Chinese Spring, 22 presented lower crossability (≥5% <50%) than Chinese Spring did, and 33 landraces had no or very low crossability (0% <5%) with rye (see Table 1). The landraces with high crossability or similar crossability to Chinese Spring occurred widely in the province (Fig. 1).

From the investigation, we found that the geographical distribution of high crossability landraces in Shandong Province is continuous with that in Sichuan, Shanxi, Henan, Hunan and Hubei (Luo et al. 1992; 1993a; 1994), and no landraces had higher crossability than Chinese Spring did, only 4 showed similar crossability to Chinese Spring in this area.

References

Luo MC, Yen C and Yang JL (1992) Crossability percentages of bread wheat landraces from Sichuan Province, China with rye. Euphytica 61: 1-7.

Luo MC, Yen C and Yang JL (1993a) Crossability percentages of bread wheat landraces from Shaanxi and Henan Provinces, China with rye. Euphytica 67: 1-8.

Luo MC, Yen C and Yang JL (1993b) Crossability percentages of bread wheat collections from Tibet, China with rye. Euphytica 70: 127-129.

Luo MC, Yen C and Yang JL (1994) Crossability percentages of bread wheat landraces from Hunan and Hubei provinces, China with rye. Wheat Inf Serv 78: 34-38.

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Research information

Effect of delayed sowing on some parameters of photosynthesis in wheat (*Triticum aestivum* L.)

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Wheat is the staple food of the people of Pakistan and is cultivated on large area. However in the face of ever growing population, crop production in the country is limited and could be attributed among other factors to the forced late sowing because of delay in the harvesting of the preceding Kharif crops e.g. rice and cotton. As a result, the grain filling period (Mid March to first week of April) of the late sown wheat experiences higher temperature (35-45°C) as well as a longer photoperiod. In addition the crop receives less total photosynthetically active radiant energy than its early sown counterparts resulting in a reduction in biomass and the grain yield (Panelia et al. 1993). The duration of grain filling period is relatively more affected than the period from sowing to anthesis and occasionally the crop is prematurely ripened.

Besides many other factors, productivity of a crop depends on the photosynthetic efficiency which is regulated by gaseous exchange capacity, leaf area and their chlorophyll contents (Ashraf, Azmi et al. 1994; Ashraf, Khan et al. 1992). We, therefore, investigated the effect of three sowing times on the leaf area and chlorophyll contents of 16 wheat genotypes.

A field experiment was conducted during 1994-1995 season, to study the effect of different sowing times on chlorophyll contents and leaf area of six wheat genotypes. The experiment consisted of three treatments i.e. T_1 (normal, 13-11-1994), T_2 (1-12-1994) and T_3 (15-12-1994) with five replications and 16 wheat genotypes. Fertilization was done @ 100 kg N/ha, 115 kg P_2O_5/ha and 5.3 kg K/ha and normal cultural practices were followed as and when required. Ninety days after sowing leaf area (LI-3100 Area meter, LI-COR, inc, USA) and chlorophyll content were determined (Arnon, 1949). At maturity grain yield per plant was determined. Analysis of variance was applied to determine the significance of differences among the treatments and/or genotypes. Differences compared by Duncan's Multiple Range Test (DMRT) at 5% probability (Steel and Torrie 1980).

Chlorophyll content in all genotypes decreased with late sowing (Fig. 1). Under normal conditions, Mehran-89, Sarsabz form one group with the highest chlorophyll content, Soghat-90, PN-9086, PN-9041, PN-9005, SH-9044, SI-9077, SP-89128, SH-8921, SH-8918, SI-8927 second group and PN-9111, PN-9083, SI-90157 and SP-89126 the third group with lowest chlorophyll content. Under T_2 treatment, genotypes form four groups and PN-9005 having the highest chlorophyll content. Under T_3 conditions Sarsabz competed to all genotypes (Fig. 1 a).

Leaf area (LA) also decreased with late sowing (Fig. 1 b) but the differences between T_2 and

T_3 were nonsignificant. Under normal conditions, genotype SH-8921 had the highest and SP-89128, PN-9005 and SI-8927 had the lowest LA. Under T_2 SH-8921 had the highest LA and SP-89128, SI-9077, SH-9044 and PN-9005 had the lowest LA. But under T_3 Sarsabz was on the top and SI-9077 on the bottom of the list. Genotypic means showed that SH-8921 had greater LA than all other genotypes.

Grain yield per plant in all genotypes was reduced due to late sowing (Fig. 1 c). However, the differences between T_1 and T_2 are nonsignificant. Under T_1 the highest grain yield per plant was recorded in SH-8918 while under late sowing it lost its top position. Under T_2, Mehran had the maximum grain yield per plant which nonsignificantly differed from Sarsabz, PN-90111, PN-9086, SI-90157 and SP-89126. But under T_3, the maximum grain yield per plant was obtained in PN-90111 and SH-8918 and the second group with high grain yield per plant was formed by Sarsabz, Mehran-89, PN-9041, PN-9005, SI-9077 and SP-89128, while others remained beyond these. Genotypic means again showed that SH-8918 had the highest grain yield per plant (Fig. 1 c). The correlations between grain yield per plant, chlorophyll contents and leaf area were positive but nonsignificant.

The results showed reduction in chlorophyll content (Fig. 1 a) and leaf area (Fig. 1 c) of plants subjected to delayed sowing. The role of chlorophyll and leaf area in photosynthesis is well known. Leaf is a major plant organ where all photosynthetic activities take place, and photosynthesis is the process by which radiant energy from the sun is converted into chemical energy necessary for vital functions of living organisms. The reduction in leaf area and chlorophyll contents in plants may affect the photosynthetic activity of plants adversely. The end product of photosynthesis is utilized by man as the cereal grain the yield of which was reduced in the present experiment due to late sowing of the crop (Fig. 1 c). The reduction in chlorophyll may be due to enhanced chlorophyllase activity (Garcia et al. 1987) due to rise in temperature. But according to others (Ashraf and Khan 1994; Ashraf, Azmi et al. 1994; and Kuroda et al. 1990) the reduction in chlorophyll may be due to higher peroxidase activity and accumulation of some phenolic compounds which might occur in the late sown crop due to temperature (25-35°C) favourable for them. As a result of reduced leaf area the crop intercepted less photosynthetically active radiant energy resulting in reduction in the grain yield (Ashraf et al. 1989): our results supported this conclusion (Fig. 1 c).

It has been suggested that in wheat the increase in the rate of grain growth, due to higher temperature experienced by late sown crop, does not compensate for the loss in grain yield caused by reduced duration of grain growth (Bagga and Tandon 1991). The ideal condition would be to develop varieties having faster rates of grain growth in a shorter period. Since the rate of grain growth (increase in weight) is dependent on starch forming enzymes, with a narrow range of temperatures (15-30°C) for activity, large differences in grain growth rate are not expected among wheat varieties with similar sink size. Improvement of wheat genotypes for faster rates of grain growth would therefore, be restricted within narrow limits. The duration of the grain amenable growth period, on the other hand appears to be of great relevance since a number of wheat varieties are known to maintain relatively longer durations of grain growth under increasing temperatures. Bagga and Tandon (1991) suggested the use of medium to long duration varieties for late sowing

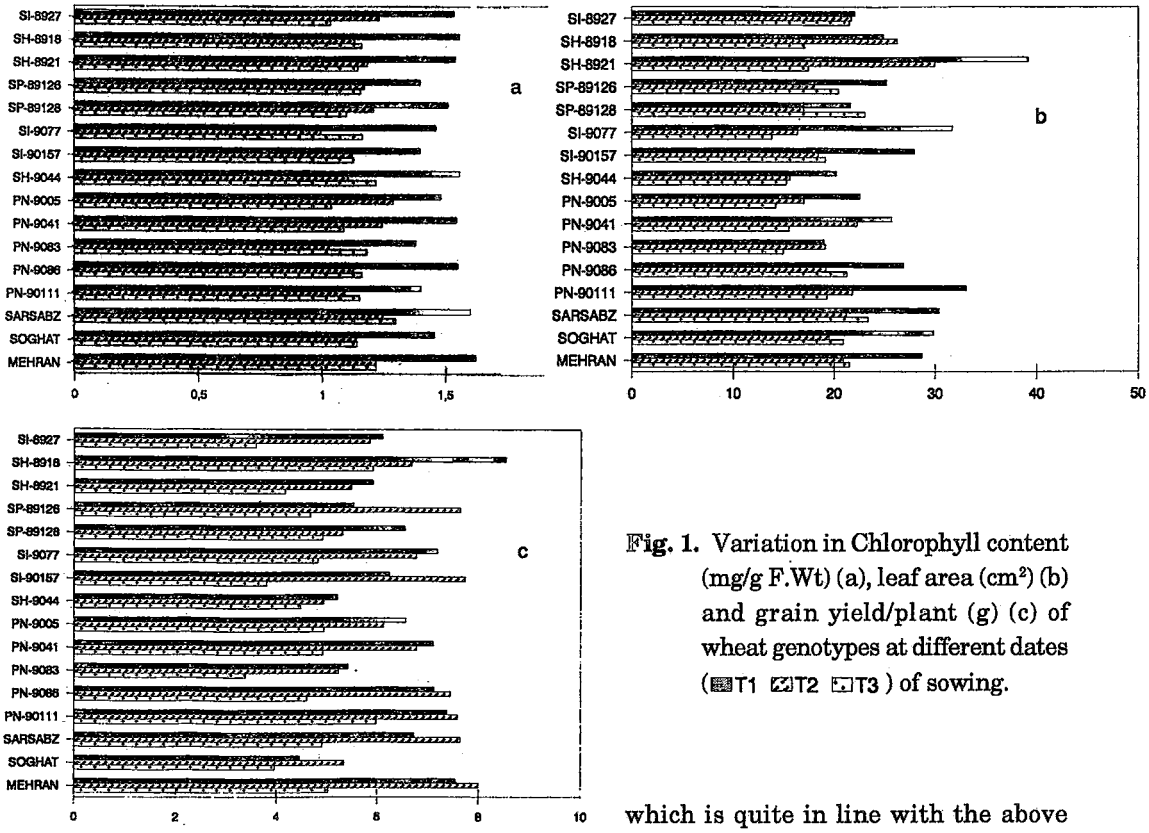

Fig. 1. Variation in Chlorophyll content (mg/g F.Wt) (a), leaf area (cm^2) (b) and grain yield/plant (g) (c) of wheat genotypes at different dates (▩T1 ▨T2 □T3) of sowing.

which is quite in line with the above contention.

References

Arnon DT (1949) Copper enzymes in isolated chloroplast. Poly-phenoloxidase in *Beta vulgaris*. Plant Physiol 24: 1-15.

Ashraf MY and Khan AH (1994) Characterization of induced high temperature chlorophyll mutant of rice (*Oryza sativa* L.). Sci Intl 6(1): 73-75.

Ashraf MY, Azmi AR, Khan AH and Ala SA (1994) Effect of water stress on total phenol, peroxidase activity and chlorophyll contents in wheat. Acta Physiol Plant 16(3):185-191.

Ashraf MY, Khan AH and Azmi AR (1992) Cell membrane stability and its relation with some physiological processes in wheat. Acta Agron. Hung. 41 (3 -4): 183-191.

Ashraf MY, Baig NA and Baig F (1989) Response of wheat (*Triticum aestivum* L.) treated with cycocel under water stress conditions. Acta Agron Hung 38(3-4): 265-269.

Bagga AK and Tandon JP (1991) Productivity of wheat under late sown condition. A report on collaborative work, In: Plant Physiology Research at IARI, Division of Plant Physiology, IARI New Delhi. pp. 31-40.

Garcia AL, Torrecillas A, Leon A and Ruiz-Sanchez MC (1987) Biochemical indicators of the water stress in maize seedlings. Biol Plant 29: 45-48.

Kuroda M, Ozawa T and Imagawa H (1990) Changes in chloroplast peroxidase activities in relation to chlorophyll loss in barley leaf segments. Physiol Plant 80: 555-560.

Penelia JR, Bagga AK and Wasnik KG (1993) Effect of late sown conditions on productivity and nitrogen status in wheat. Indian J. Plant Physiol 36: 178-184.

Steel RGD and Torrie JH (1980) Principles and procedures of statistics. McGraw-Hill, New York.

Wheat Information Service
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Proposal

Taxonomic Issues in *Triticum* L. and *Aegilops* L.

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In two recent issues of WIS, Yen et al. (No. 84:56-59) and Gupta (No. 85: 52-55) discussed nomenclatural and classification problems in the wheat complex. Yen et al. reviewed the nomenclature of the wild diploid D-genome species, establishing that the name is *Aegilops tauschii* Coss. or *Triticum tauschii* (Cosson) Schmalh., depending on the classification followed. Gupta recommended that the illegitimate name *Ae. squarrosa* L. be conserved to avoid further confusion given its popular usage among wheat researchers. Using this nomenclatural issue as a launching point, Gupta also discussed the problems of wheat taxonomy, particularly those resulting from Bowden's (1959) lumping of *Aegilops* into *Triticum*. He also recommended that a taxonomy workshop be held at the 9th International Wheat Genetics Symposium (IWGS) in Saskatoon, Canada (August 2-7, 1998). I have several comments to offer on the issues raised in each of these articles.

Nomenclature and Classification

When Bowden revised the classification of the wheats, he argued that "a correct nomenclature" required him to lump *Aegilops* into an enlarged genus *Triticum*. As I have pointed out elsewhere (Morrison, 1993, 1994), Bowden's argument is flawed because the rules of the International Code of Botanical Nomenclature (ICBN: Greuter, 1994) govern only the naming of taxonomic entities, playing no role in the construction of classifications. In short, Bowden's decision for an emended *Triticum* was based on his own assessment of how to show evolutionary relationships (via hybridization) within a taxonomic treatment of the wheats. This very important procedural point is relevant to the debate over the names, *Ae. tauschii* versus *Ae. squarrosa*.

Nomenclature for the D-genome species has a long, complicated history as discussed by Yen et al. (1997) and also by Slageren (1994). I will review several facts as they relate to Gupta's conservation proposal. The name *Ae. squarrosa* L. (Linnaeus, 1753) was originally associated with a Linnaean specimen of *Ae. triuncialis* which Linnaeus had labeled "*3 squarrosa*". Although in disagreement with the original Linnaean concept, the name *Ae. squarrosa* did become associated with the D-genome species. In 1850, Cosson corrected the nomenclature by introducing the name *Ae. tauschii*. Due to mistakes of other botanists, usage of the name *Ae. squarrosa* for the D-

genome species continued into this century. In his emendment of *Triticum*, Bowden (1959) adopted an early *Triticum* concept of the species and accordingly used the name *T. aegilops* P. Beauv. ex Roem. & Shult. Upon discovering that the name *T. aegilops* was based on the misidentified Linnaean specimen of *Ae. triuncialis* (= *T. triunciale*), Bowden (1966) changed the name to *T. tauschii* (Coss.) Schmalh. Revisions to Bowden's treatment by Morris and Sears (1967), Kimber and Sears (1987), and Kimber and Feldman (1987) have maintained the name *T. tauschii*, which a review of the genetic literature will show is now in common use. The name *Ae. squarrosa* persists among researchers who ignore the current monographs of *Aegilops* by Hammer (1980a,b) and Slageren (1994), choosing instead to follow the outdated classifications of Zhukovsky (1928) and Eig (1929), or other genetic and germplasm-oriented treatments with nomenclatural errors such as those of Kihara (1954), Chennaveeraiah (1960), and the IBPGR (now IPGRI) Wheat Programme identification guide authored by J.R. Witcombe (1983).

The name issue is not yet settled. According to Slageren (1994), the diploid D-genome species in *Triticum* is, as originally proposed by Bowden, *T. aegilops*. Here, Slageren gives priority to the epithet *aegilops* which predates *tauschii*. Because a species name cannot repeat the name of the genus, *Aegilops aegilops* is not allowed. The next available name must be selected, i.e., *Ae. tauschii*. Thus, following Slageren, there are two legitimate names for the D-genome species, *T. aegilops* and *Ae. tauschii*. It is doubtful that wheat researchers, who use the genomic classification of *Triticum* sensu Bowden, will drop the name *T. tauschii* for *T. aegilops*. This and other nomenclatural problems should be addressed by a monographic revision of *Triticum* as already recommended by the 1st IWGS Taxonomy Workshop (see below). Until a revision project is underway, the easiest remedy for maintaining some degree of nomenclatural consistency is for researchers to abandon the enlarged *Triticum* classification concept, which is filled with nomenclatural errors, and return to the traditional concepts of *Triticum* and *Aegilops* as separate genera. For *Aegilops*, the nomenclatural issues are mostly resolved and two current classifications are available. Slageren's move of *Ae. mutica* into the monotypic genus *Amblyopyrum* may cause some researchers to prefer Hammer's classification. Unfortunately, there is no agreement on how to classify *Triticum* sensu stricto. The wide disparity between the genomic treatment of Mac Key (1966) and the morphological treatment of Dorofeev and Migushova (1979) exemplifies the problematic complexities of handling a genus with domesticated taxa. Reaching a consensus will require a collaborative effort supervised under the banner of an international revision project which can deal directly and expertly with the classification controversy as well as with difficult nomenclatural issues.

In my opinion, a formal proposal under Art. 14 of the ICBN to conserve *Ae. squarrosa* is ill-advised. In support of his recommendation, Gupta argues that usage of the "popular, though illegitimate name" *Ae. squarrosa* has declined due to Bowden's introduction of the name *T. tauschii*. This reasoning confuses issues of nomenclature with those of classification. As pointed out by Yen et al. (1997), nomenclatural rules establish both the legitimacy and priority of the name *Ae. tauschii*. These rules operate independent of classification, whether the issue is an enlarged *Triticum* sensu Bowden or any other conceptual treatment approach taken by the various researchers and botanists who have dealt with *Triticum* and *Aegilops*. Despite Gupta's claims to

the contrary, the name *Ae. tauschii* has an established historical precedence which will be difficult to challenge in a conservation proposal. The argument that *Ae. tauschii* will cause a "futile" and "disadvantageous nomenclatural change" does not account for the recent monographic work of Hammer (1980a,b) and Slageren (1994) and ignores current use of *Ae. tauschii* by wheat researchers and botanists. A conservation proposal of *Ae. squarrosa* against *Ae. tauschii* is sure to fail because stability of the nomenclature for this species is not threatened (see ICBN, Art. 14.2).

2nd IWGS Taxonomy Workshop

Regarding Gupta's call for a workshop, I would like to invite those members of the wheat research community who have an interest in the taxonomy of the wheats to participate in the 2nd IWGS Taxonomy Workshop with discussions initiated in 1993 at the 1st IWGS taxonomy workshop. The report of the 1993 workshop, which was not included in the 8th IWGS Proceedings volume, is presented in the following section. J.G. Waines (University of California, Riverside) and I will co-chair the 2nd IWGS taxonomy workshop. In addition to the issues of nomenclature and classification, this workshop will consider a recommendation to accept the recent Slageren monograph of *Aegilops* L. (1994) as a first step towards an overall monographic revision of wheat taxonomy.

1st IWGS Taxonomy Workshop Report

The 1st IWGS Taxonomy Workshop committee consisted of A.B. Damania, formerly ICARDA; M. Feldman, Weizmann Institute of Science; T.E. Miller, John Innes Centre; L.A. Morrison, Oregon State University, and J.G. Waines, University of California, Riverside.

The workshop noted that the state of classification and nomenclature of the genus *Triticum* is such that they do not well serve the research community who need to use them.

There is confusion in the research community about the circumscription of the genus *Triticum*, whether it is *Triticum* L. defined narrowly, or *Triticum* L. emend. defined broadly to include *Triticum* and *Aegilops*.

There is confusion about the number of species in the genus *Triticum*.

There is confusion about the correct names of the species.

There is confusion about the status and nomenclature of the subspecies and botanical varieties.

There is confusion about how to classify the domesticated varieties and varietal groups.

There is a lack of workable keys and descriptions that many different people, such as botanists, geneticists, agronomists, and lay persons, can use.

The present state of taxonomy and nomenclature in *Triticum* is confusing for people who collect germplasm, for people who maintain genebanks, and for wheat breeders and geneticists who use the seed held by these genebanks.

The workshop agreed that this situation needs to be rectified.

The workshop committee proposed that there should be a monographic revision of the genus

Triticum, and that a professionally-trained taxonomist be asked to do this revision. The workshop recognized that there would be a need to attract outside funding to finance this revision which, because of the magnitude of the task, would take several years. The revision might necessitate consultation among interested taxonomists familiar with Russian, German, English, and French, even though there should be one person who would direct the project. There may be a need to consult experimental taxonomists about the significance of genetic differences among domesticated and wild forms.

Monographic Revision Project

These nomenclatural discussions in WIS illustrate the pressing need to resolve the complicated issues of *Triticum* taxonomy. It is timely that the 2nd IWGS Workshop will take place this year. The workshop will primarily focus on establishing guidelines for setting up a monographic revision project. Interested researchers who are unable to attend the workshop can forward their comments and suggestions directly to me.

References

Bowden WM (1959) The taxonomy and nomenclature of the wheats, barleys, and ryes and their wild relatives. Can J Bot 37: 657-684.

Bowden WM (1966) Chromosome numbers in seven genera of the Tribe Triticeae. Can J Genet Cyto. 8: 130-137.

Chennaveeraiah MS (1960) Karyomorphologic and cytotaxonomic studies in *Aegilops*. Acta Hort Gotoburg 23:85-178.

Cosson ES-Ch (1850) Notes sur quelques plants critiques, rares ou nouvelles. 1(2b): 68-69.

Dorofeev VF and Migushova EF (1979) Wheat vol 1. In: V.F. Dorofeev and O.N. Korovina (ed) Flora of cultivated plants. Leningrad [St. Petersburg] [in Russian].

Eig A (1929) Monographisch-kritische Übersicht der Gattung *Aegilops*. Feddes Repert Spec Nov Reg Veg, Beih. 55: 1-228.

Greuter W et al. (1994) International code of botanical nomenclature (Tokyo Code), adopted by the 15th In. Bot Cong, Yokohama. Koeltz Scientific Books, Konigstein.

Gupta PK (1998) Nomenclature in Triticeae with emphasis on D genome diploid species. Wheat Inf Serv 85: 52-55.

Hammer K (1980a) Vorarbeiten zur monographischen Darstellung von Wildpflanzensortimenten: *Aegilops* L. Kulturpflanze 28: 33-180.

Hammer K (1980b) Zur Taxonomie und Nomenklatur der Gattung *Aegilops* L. Feddes Repert Spec Nov Reg Veg. 91: 225-258.

Kihara H (1954) Considerations on the evolution and distribution of *Aegilops* species based on the analyser-method. Cytologia 19: 336-357.

Kimber G and Feldman M (1987) Wild wheat: an introduction. Spec Rpt 353. College of Agri, Univ of Missouri, Columbia.

Kimber G and Sears ER (1987) Evolution in the genus *Triticum* and the origin of cultivated wheat. In: Heyne EG (ed) Wheat and wheat improvement (2 ed) Am Soc Agron, Madison WI, pp154-164

Linnaeus C (1753) Species plantarum. Stockholm.

MacKey J (1966) Species relationship in *Triticum*. Proc 2nd Int Wheat Genet Symp, Lund Sweden. Hereditas Suppl. 2: 237-276.

Morris R and Sears ER (1967) The cytogenetics of wheat and its relatives. In: Quisenberry KS and Reitz LP (ed) Wheat and Wheat Improvement. Am Soc Agron, Madison WI, pp. 19-87

Morrison LA (1993) *Triticum-Aegilops* systematics: taking an integrative approach. In Damania AB (ed) Biodiversity and wheat improvement. ICARDA Sayce Pub, Exeter, UK. pp. 59-66

Morrison LA (1994) Taxonomy of the wheats: a commentary. Proc 8th Int Wheat Genet Symp, vol 1. Beijing, China : 65-72.

Slageren MW van (1994) Wild wheats: a monograph of *Aegilops* L. and *Amblyopyrum* (Jaub. & Spach) Eig. Wageningen Agric Univ Pap. 1994(7).

Witcombe JR (1983) A guide to the species of *Aegilops* L.: their taxonomy, morphology and distribution. IPBGR/83/77. IPBGR Secretariat, Rome.

Yen C, Yang JL and Yen Y (1997) The history and the correct nomenclature of the D-genome diploid species in Triticeae (Poaceae). Wheat Inf Serv 84: 56-59.

Zhukovsky PM (1928) Kritiko-systematischeskii obzor vydov roda *Aegilops* L. Trudy Prikl Bot, Ser 2 Genet. Rast [Bull Appl Bot Gen & Pl Breeding] [in Russian with English summary] 18: 417-609.

Wheat Information Service
Number 86: 54-91 (1998)
Gene symbol

Catalogue of gene symbols for wheat: 1998 Supplement

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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 and 1996 Supplements.

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 revise past entries. Researchers and readers are encouraged to advise updatings and errors to make the Catalogue more useful to others.

Revisions of and additions to 'Summary Table 1' of the 1995 Catalogue of Gene Symbols for Wheat:

Revise title of table to
'Symbols for wheat loci, including loci of known function, loci detected with 'known-function' DNA clones, and loci detected by PCR-amplification of DNA using primers'.

Symbol		Character
Add:		
ACCc	sets	Acetyl CoA carboxylase - cystolic form
ACCp	sets	Acetyl CoA carboxylase - plastid form
Chr		Hybrid chlorosis Type 1 gene in rye
GluTR	set	Glutamyl-tRNA reductase
Mtase	set	DNA (cytosine-5)-methyltransferase
Pina		Puroindoline a
Pinb		Puroindoline b
Rep	set	DNA replication regulating gene
sc		Seedling chlorosis
scs		Nuclear-cytoplasmic compatability enhancer
Tria	set	Pollen allergen encoding gene
Vgw		Temperature-sensitive winter variegation
Vi		Restorer for cytoplasmic male sterility, *T. longissimum* cytoplasm
Wcs		Wheat cold-specific genes
Revise:		
X		Basic symbol for DNA markers of unknown function

Revision of 'Summary Table 2'

Add footnote c to 7DS:
c 7DS is cytogenetically the longer arm {9841}.

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Aluminium tolerance

Alt1 {9869}. **v:** ET3 = Carazinho/4*Egret {9869}.

alt1 {9869}. **v:** ES3 = Carazinho/4*Egret {9869}.

Alt2 : Change the reference for the synonym 'Alt_{BH}' to {9835} and revise the previous *Alt2* 'ma:' entry to, '*Alt2* - 1.1 cM - *Xbcd1230-4D* {9835}.'

Anthocyanin Pigmentation

3. Red/purple coleoptiles
Revise the previous *Rc3* 'ma:' entry to '*Rc3* (distal) - 3 cM - *Xpsr108 -7D* {140}.'

4. Purple/red culm/straw/stem.
Revise the previous *Pc1* 'ma:' entry to '*Pc* (proximal) - 5.7 cM - *Xpsr490(Ss1)-7B* {9739}[2].'

Blue Aleurone

The *Ba* allele in *T. monococcum* spp. *aegilopoides* acc. G3116 determines a half-blue seed phenotype and is different from the allele present in *Elytrigia pontica* {96119} that determines a solid-blue seed phenotype. They are treated as different genes.

Ba1 {461}. [*Ba* {461}]. Derived from *Elytrigia pontica* (2*n*=70). 4B [4BS-4el2 {461}]. **tr:** UC66049B {425}.
Ba2. $4A^{m}L$ {96119}[3]. **dv:** G3116 {96119}. **ma:** *Ba2* cosegregated with *Xcdo1387-4A*, *Xmwg677-4A* and *Xbcd1092-4A* {96119}.

For review see {1210}.

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

Add {9848} to 'The *kr* genes influence crossability with *H. vulgare*.'
List of crossabilities {9801}.

DNA Markers

In the preamble, following 'b', substitute "Designates loci detected by hybridization with DNA clones whose sequences are largely homologous with known genes in the EMBL database {9754}.' for 'Designates loci whose functions were identified through homology with known genes in the EMBL database {9754}.' Also, in the statement entitled 'STS's from RFLP clones:', revise the second sentence to 'The convention adopted is to add a *'p'* to the laboratory designator.'

Revise all previously-listed 'WMS' primer desigations by inserting an open space immediately after the basic symbol, e.g, change 'WMS30F/WMS30R' to 'WMS 30F/WMS 30R'.

Temporary DNA-marker designations are identified with an asterisk (*).

Replace *'Xwms'* with *'Xgwm'* throughout the DNA Markers section.

Group 1S
Add:

Xbcd98-1B,D {98139}.		BCD98.	(1A, 7A,D).
Xcdo534-1B.1,.2 {98139}.	[*cdo534a,b* {98139}].	CDO534.	(6A, 6D, 7A).
Xfba8-1D {98105}.		FBA008.	(2A, 3B, 4B, 6A, 7D).
Xfba26-1A [{98105}].	[*Xfba26b-1A* {98105}].	FBA026.	(6D).
Xfba250-1D {98105}.		FBA250.	
Xfba285-1A [{98105}].		FBA285.	
Xfba298-1A {98105}.		FBA298.	
Xfba299-1A {98105}.		FBA299.	
Xfba383-1D [{98105}].	[*Xfba383a-1D* {98105}].	FBA383.	
Xfba393-1A [{98105}].	(5B,D).	FBA393.	
Xfbb196-1A,D [{98105}].	[*Xfbb196b-1A*, *Xfbb196a-1D* {98105}].	FBB196.	
Xfbb234-1B {98105}.		FBB234.	
Xfbb250-1D [{98105}].	[*Xfbb250a-1D* {98105}].	FBB250.	
Xfbb260-1B,D [{98105}].			

[*Xfbb260a-1B, Xfbb260b-1D* {98105}]. FBB260.
Xglk558-1D {594,98105}. pTag558. (2B,D).
Note: The arm location of *Xglk558-1D* was not reported in {594}.
Xgwm106-1D [{98119}]. WMS 106F/WMS 106R.
Xgwm164-1A [{98119}]. WMS 164F/WMS 164R.
XksuD14-1B.1,.2,.3{98139}.
[*ksud14a,b,c* {98139}]. pTtksuD14.
Xmta14(Gli-1) {98105}. MTA14 {98129}.
Xmtd161-1B,D [{98105}].
[*Xmtd161a-1B, Xmtd161b-1D* {98105}]. MTD161 {98129}.
Xmwg36-1A,B,D {98139}. MWG36.
XNor9 {98134}[3]. [*Nor9* {98134}]. pTa71.
XpsrX-1A,B,D {98140}. PSRX.
Xsfr1(Lrk10)-1A [{98102}].
[*Lrk10* {98102}]. Lrk10.
Xsfrp1(Lrk10)-1A [{98106}].
[*STSLrk10-6* {98106}]. Lrk10D1/Lrk10D2.
Xutv10(Glu-3)-1B [{98150}]. UTV7F/UTV10R.
Xutv17(Glu-3)-1B [{98151}]. UTV17F/UTV7R.

Revise:
Xbcd98-1A.2; delete '5A' and add '1B,D, 7A' to the last column.
Xbcd1434; add '*-1B* {98139},[{98105}]' in the first column, '[*bcd1434* {98139}, *Xbcd1434b-1B* {98105}', in the second column and '(2B)' in the last column.
Xcdo99; add '*-1B* {98105}' in the first column.
Xcdo618-1B {9666}; add '*Xcdo618-1A,D* {98139}' in the first column.
Xcdo658-1A {9668}[3,5]; add '*Xcdo658-1B,D* {98139}[1]' in the first column.
Xcdo1173-1A {9668}[3,5]; *1B* {9666}[1]; add '*Xcdo1173-1D* {98139}[1]' in the first column.
Xcdo1188-1A {9668}[3,5]; add '*Xcdo1188-1B,D* {98139}[1]' in the first column.
Xgwm30; add '(2D)' in the last column.
XksuE19-1B,D; add '*-1A* [{98105}],{98139}' in the first column and '[*XksuE19b-1A* {98105}].' in the second column.
XksuF42-1B.1,.2.; add '*XksuF43-1A,D* {98139}' in the first column.
Xwg789-1A {9668}[5], *1D* {9666}[4]; add '*Xwg789-1B* {98139}[1]' in the first column.

Group 1L
Add:
Xbcd310-1B {98139}. BCD310. (7B).
Xcdo844-1A {98139}. [*cdo844* {98139}]. CDO844.
Xcmwg649 {98154}[2]. cMWG649 {96109}. (2A).
Xcmwg701-1A .1,.2 {98154}[2]. cMWG701 {96109}. (5A).
Xfba34-1B.1,.2 [{98105}].
[*Xfba34a-1B, Xfba34b-1B* {98105}]. FBA034.
Xfba92-1A {98105}. FBA092.
Xfba177-1B [{98105}]. [*Xfba177a-1B* {98105}]. FBA177. (5A,4B,D).
Xfba178-1B [{98105}]. [*Xfba178b-1B* {98105}]. FBA178. (2A).
Xfba234-1A {98105}. FBA234. (6A, 7A).
Xfba266-1A.1,.2 [{98105}].
[*Xfba266a-1A, Xfba266b-1A* {98105}]. FBA266.

Xfba309-1B [{98105}]. FBA309.
Xfba316-1A {98105}. FBA316.
Xfbb35-1B {98105}. FBB035.
Xfbb180-1B [{98105}]. [*Xfbb180a-1B* {98105}]. FBB180.
Xfbb255-1A,B [{98105}].
[*Xfbb255c-1A*, *Xfbb255a-1B* {98105}].
FBB255. (4B, 6A).
Xglk163-1B {594, 98139}. pTag163.
The arm location of *Xglk163-1B* was not reported in {594}.
Xglk431-1B {98105}. pTag431 {594}. (2D, 4B).
Xgwm135-1A [{98119}]. WMS 135F/WMS 135R.
Xgwm337-1D [{98119}]. WMS 337F/WMS 337R.
XksuA1-1B [{98105}]. [*XksuA1c-1B* {98105}]. pTtksuA1 {309}. (5B, 7D).
Xmta17(Glu-1) {98105}. MTA17 {98129}.

Revise:
Xabc160-1A {9668}; add '*Xabc160-1B,D* {98139}' in the first column.
Xabg387-1A.1,.2 {96119}[3]; add '*Xabg387-1B,D* {98139}[1]' in the first column.
Xbcd207; add '(5A)' in the last column.
Xbcd265-1A; add '*Xbcd265-1B,D* {98139}[1]' in the first column.
Xbcd304-1A {9668}[5]; *1B* {9666}[1]; add '*Xbcd304-1D* {98139}[1]' in the first column.
Xbcd386-1A {9668}[5]; *1B* {9666}[1]; add '*Xbcd386-1D* {98139}[1]' in the first column.
Xbcd738-1A {9668}[5]; add '*Xbcd738-1B* {98139}[1]' in the first column.
Xbcd921; add '*Xbcd921-1D* {98139}[1]' in the first column.
Xbcd1562-1B; add '*Xbcd1562-1D* {98139}' in the first column.
Xcsd19(Adh)-1A,B,D; change to '*Xcsc19(Adh)-1A,B,D* '.
Xcdo393; add '*-1B* {98105}' in the first column.
Xcdo572-1A {9668}[3,5]; add '*Xcdo572-1B,D* {98139}[1]' in the first column.
Xglk163; add '*-1B* {98105}' in the first column.
Xglk558; add '*Xglk558-1B* {98139}' in the first column and '[*tag588* {98139}.' in the second column.
XksuE3; add '(2B, 3AL, 3BS, 6AS, 6DL)' and delete '(3A, 6A)' in the last column.
XksuE11; add '*XksuE11-1D* {98139}' in the first column.
XksuG30; add '(3B, 5A)' in the last column.
XksuH14-1A; add '*XksuH14-1B,D* {98139}' in the first column.
Xmwg710-1A [{9668}][1,3]; add '*Xmwg710-1B,D* {98139}[1]' in the first column.
Xwg241; add '*Xwg241-1B* {98139}' in the first column.
Xwg605-1A {9666}[1],{9668}[5], *1B* {9666}[1]; add '*Xwg605-1D* {98139}[1]' in the first column.

Group 1
Note:
The following markers was moved to 1S.
Xglk558
The following marker was moved to 1L.
Xglk163-1B

Add:
Xgwm232-1D [{98119}]. WMS 232F/WMS 232R.
Xipk2(Rep)-1A,B,D [{98101}].
[*XRep* {98101}]. Rep.

Revise:
Xglk549; add '*-1A* {98125}' in the first column and '(7A,D)' in the last column.

Group 2S

Add:

Xbcd1434-2B [{98105}].
[*Xbcd1434a-2B* {98105}]. BCD1434 {96124}. (1A,B,D).

Xfbb75-2B.1 {9652}[{98105}].
[*Xfbb75b-2B* {98105}]. FBB075. (2BL).

The arm location of *Xfbb75-2B* was not reported in {9652}.

Xfbb171-2B {98105}. FBB171.

Xfbb185-2B {98105}. FBB185. (3B).

Xfbb353-2A {9652}, *-2B* {98105}. FBB353. (3A).

The arm location of *Xfbb353-2A* was not reported in {9652}.

Xgwm55-2B {98121}. WMS 55F/WMS 55R.

Xgwm71-2A.1 [{98121}].
[*gwm71a* {98121}]. WMS 71F/WMS 71R.

Xgwm71-2A.2 [{98121}].
[*gwm71b* {98121}]. WMS 71F/WMS 71R.

Xgwm102-2D {98121}. WMS 102F/WMS 102R.

Xgwm129-2B {98121}. WMS 129F/WMS 129R.

Xgwm148-2B {98121}. WMS 148F/WMS 148R.

Xgwm210-2D {98121}. WMS 210F/WMS 210R.

Xgwm249-2D {98121}. WMS 249F/WMS 249R.

Xgwm257-2B {98121}. WMS 257F/WMS 257R.

Xgwm261-2D {98118}. WMS 261F/WMS 261R.

Xgwm296-2A,D [{98121}].
[*gwm296a,b* {98121}]. WMS 296F/WMS 296R.

Xgwm319-2B {98121}. WMS 319F/WMS 319R.

Xgwm339-2A {98121}. WMS 339F/WMS 339R.

Xgwm372-2A {98121}. WMS 372F/WMS 372R.

Xgwm374-2B {98121}. WMS 374F/WMS 374R.

Xgwm410-2B {98121}. WMS 410F/WMS 410R.

Xgwm425-2A {98121}. WMS 425F/WMS 425R.

Xgwm429-2B {98121}. WMS 429F/WMS 429R.

Xgwm455-2D {98121}. WMS 455F/WMS 455R.

Xgwm484-2D {98121}. WMS 484F/WMS 484R.

Xgwm512-2A {98121}. WMS 512F/WMS 512R.

Xgwm515-2D {98121}. WMS 515F/WMS 515R.

Xgwm636-2A {98121}. WMS 636F/WMS 636R.

Xgwm95-2A [{98119}]. WMS 95F/WMS 95R.

Xgwm148-2B [{98119}]. WMS 148F/WMS 148R.

Xgwm261-2D [{98119}]. WMS 261F/WMS 261R.

Revise:

Xfba65; add '(5B)' in the last column.

Xfba83; add '*-2B* {98105}' in the first column.

Xfba88; add '*-2A* {98105}' in the first column.

Xfba178; add '(1B)' in the last column.

Xfbb61; add '(6B)' in the last column.

Xfbb62-2B; delete reference '9641'.

XksuD18; add '*-2B* {98105}' in the first column, and add '(7B)' in the last column.

Group 2L

Add:

Xcdo770-2A {98105}. CDO770 {96124}.

Xcrc4-2B {98131}. [*Xcrc4.2* {98131}]. CRC4F/CRC4R.

Xfba71-2A [{98105}]. [*Xfba71b-2A* {98105}]. FBA071. (7A).

Xfbb75-2B.2 [{98105}].
[*Xfbb75a-2B* {98105}]. FBB075. (2BS).
Xfbb278-2B [{98105}]. [*Xfbb278a-2B* {98105}]. FBB278. (7A).
Xfbb324-2B [{98105}]. [*Xfbb324a-2B* {98105}]. FBB324. (3D, 7B).
Xglk554-2A {594,98105},*B* {594}.
[*Xglk554a,c* {594}]. pTag554. (5B).
The arm locations of *Xglk554-2A,B* were not reported in {594}.
Xglk594-2A [{98105}],*2B* {594}[{98105}].
[*Xglk594a-2A*, *Xglk594b-2B* {98105}]. pTag594.
The arm location of *Xglk594-2B* was not reported in {594}.
Xgwm16-2B {98121}. WMS 16F/WMS 16R.
Xgwm47-2B {9736,98121}. WMS 47F/WMS 47R.
Xgwm55-2B {98121}. WMS 55F/WMS 55R.
Xgwm120-2B [{98119}]. WMS 120F/WMS 120R.
Xgwm157-2D [{98119}]. WMS 157F/WMS 157R.
Xgwm189-2B [{98119}]. WMS 189F/WMS 189R.
Xgwm191-2B {98121}. WMS 191F/WMS 191R.
Xgwm265-2A {98121}. WMS 265F/WMS 265R.
Xgwm294-2A [{98119}]. WMS 294F/WMS 294R.
Xgwm301-2D {98121}. WMS 301F/WMS 310R.
Xgwm312-2A {98121}. WMS 312F/WMS 312R.
Xgwm328-2A {98121}. WMS 328F/WMS 328R.
Xgwm349-2D {98121}. WMS 349F/WMS 349R.
Xgwm356-2A {98121}. WMS 356F/WMS 356R.
Xgwm382-2A,D {98121}. WMS 382F/WMS 382R.
Xgwm388-2B {98121}. WMS 388F/WMS 388R.
Xgwm445-2A {98121}. WMS 445F/WMS 445R.
Xgwm501-2B {98121}. WMS 501F/WMS 501R.
Xgwm526-2B {98121}. WMS 526F/WMS 526R.
Xgwm539-2D {98121}. WMS 539F/WMS 539R.
Xgwm558-2A {98121}. WMS 558F/WMS 558R.
Xgwm608-2D {98121}. WMS 608F/WMS 608R.
Xgwm619-2B {98121}. WMS 619F/WMS 619R.

Revise:
Xabc153-2A; add '*2B.1, .2* {98131}' in the first column and add '[*Xcrc153-2B.1, Xcrc153- 2B.2*{98131}].' in second column
Xcmwg649-2A; add '(1A).' in the last column.
Xfba8; add '(1D)' in the last column.
Xfba62-2B; delete reference '9641'.
Xfba359; add '(5A)' in the last column.
XksuD22; add '-*2B* {98105}' in the first column.
XksuE3; add '-*2B* [{98105}]' in the first column, add '[*XksuE3c-2B* {98105}].' in the second column, add '(3AL, 3BS, 6AS, 6DL)' in the last column and delete (3A, 6A) in the last column.
XksuF2; add '(7B)' in the last column.
XksuF43; add '1B,D' in the last column.
XksuG30; add '(3B, 5A)' in the last column.
Xfba61; add '-*2A* [{98105}]' in the first column and '[*Xfba61a-2A* {98105}].' in the second column.
Xfba62; add '-*2A* [{98105}]' in the first column and '[*Xfba62a-2A* {98105}].' in the second column.
Xfba64; add '-*2A,B* [{98105}]' in the first column and '[*Xfba64a-2A*, *Xfba64b-2B* {98105}].' in the second column.

Xfba209-2D.1; add '*-2B.1* [{98105}]' in the first column and '[*Xfba209a-2B* {98105}].' in the second column.
Xfba209-2D.2; add '*-2A, B.2* [{98105}]' in the first column and '[*Xfba209b-2A*, *Xfba209c-2B* {98105}].' in the second column.
Xfba314; add '*-2B* [{98105}]' in the first column and '[*Xfba314a-2B* {98105}].' in the second column.
Xfba345; add '*-2A* [{98105}]' in the first column and '[*Xfba345b-2A* {98105}].' in the second column.
Xgwm30; add '(1A)' in the last column.
XksuF1; add '*-2B* [{98105}]' in the first column and '[*XksuF1b-2b* {98105}].' in the second column.
Xwg645; add '*-2B* [{98105}]' in the first column and '[*Xwg645a-2B* {98105}].' in the second column.

Group 2
Note: The following markers were moved to the 2S group.
Xfbb75, *Xfbb353*
Note: The following markers were moved to the 2L group.
Xglk554, *Xglk594*, *Xgwm47*

Add:

Xglk370-2B {594},*2D* {98125}.		pTag370.	(4A).
Xglk744-2A,B,D {98125}.		pTag744 {98126}.	(6B).
Xkuj64-2A,B,D {98125}.		pTac64 {98127}.	
Xucg1(ACCp)-2A,2B,2D {9847}.		UCG1 {9847}.	

Revise:
Xglk407; add '(5A)' in the last column.
Xglk431; add '(1B)' in the last column.
Xglk653; add '*-2D* {98125}' in the first column.
XksuF36; add '(4A)' in the last column.
XksuG49; add '(4A, 6A)' in the last column.

Group 3S
Add:

Xfba189-3B [{98105}].	[*Xfba189b-3B* {98105}]. (3BL).	FBA189.	
Xfbb156-3B [{98105}].	[*Xfbb156a-3B* {98105}]. (3BL, 5D,	FBB156.	6B, 7A).
Xglk538-3B,D.1 [{98105}].	[*Xglk538a-3B*, *Xglk538b-3D* {98105}].	pTag538 {594}.	
Xglk538-3D.2 [{98105}].	[*Xglk538c-3D* {98105}].	pTag538 {594}.	
Xgwm161-3D [{98119}].		WMS 161F/WMS 161R.	
Xgwm218-3A [{98119}].		WMS 218F/WMS 218R.	
XksuE3-3B [{98105}].	[*XksuE3b-3B* {98105}]. 3AL,4A, 6AS,	pTtksuE3 {309}.	(1A, 2A,B,D, 6DL, 7A,D).
XksuG30-3B [{98105}].	[*XksuG30a-3B* {98105}].	pTtksuG30 {309}.	(1A, 2D, 4A,

5A,

6A,B).
Xmtd120-3D [{98105}]. MTD120 {98129}.

Revise:
Xbcd15; add '(4B)' in the last column.
Xfba127; add '(6B)' in the last column.
Xfbb24; add '(4B)' in the last column.
Xfbb185; add '(2B)' in the last column.
XksuE2; add '(5A)' in the last column.

Group 3L
Add:
Xbcd358-3A {98105}. BCD358 {96124}.
Xcdo113-3A {98105}. CDO113 {96124}.
Xfba189-3B [{98105}]. [*Xfba189a-3B* {98105}]. (3BS). FBA189.
Xgwm52-3D [{98119}]. WMS 52F/WMS 52R.
Xgwm108-3B [{98119}]. WMS 108F/WMS 108R.
Xgwm340-3B [{98119}]. WMS 340F/WMS 340R.
Revise:
Xabg387; add '1B,D' in the last column.
Xfba8; add'(1D)' in the last column.
Xfba213; add '*-3D* {98105}' in the first column.
Xfba214; add '*-3D* {98105}' in the first column.
Xfba242; add '*-3A* {98105}' in the first column.
Xfbb156; add '(3BS, 6B)' in the last column.
Xfbb353; add '(2B)' in the last column.
XksuE2; add '(5A)' in the last column.
XksuE3; add '(2B, 3BS, 6AS, 6DL)' and delete '(6A)' in the last column.

Group 3
Add:
Xgwm144-3B [{98119}]. WMS 144F/WMS 144R.
Xkuj72-3B,D {98125}. pTac72 {98127}.

Revise:
Xfbb324; add '(2B,7B)' in the last column.
Xglk221; add '*-3D* {98125}' in the first column.
Xglk577; add '*-3B,D* {98125}' in the first column.
Xucg(ACCc)-3A,3B,3D.1,.2,.3 {9846}. Clone name not stated in {9846}.

Group 4S (4AL:4BS:4DS)
Add:
Xglk556-4B {594,98105}. pTag556.
Note: The arm location of *Xglk556-4B* was not reported in {594}.
Xgwm165-4B [{98119}]. WMS 165F/WMS 165R.
Xgwm160-4A [{98119}]. WMS 160F/WMS 160R.
Xwg909-4B {98105}. WG909 {96124}.

Revise:
Xabg387; add '1B,D' in the last column.
Xbcd265; add '1B,D' in the last column.
Xfba8; add '(1D, 6A, 7D)' in the last column.
XksuE3; add '(2B, 3AL, 3BS, 6AS, 6DL)' and delete '(3A, 6A)' in the last column.
XksuG12; add '(6B)' in the last column.
Xmwg634; add '*-4B* {98117}' in the first column.

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

Xfba137-4A {98105}.		FBA137.	(5D).
Xfbb120-4A {98105}.		FBB120.	
Xfbb248-4A {98105}.		FBB248.	
Xgwm149-4B {98117}.		WMS 149F/WMS 149R.	
Xgwm165-4D {98117}.		WMS 165F/WMS 165R.	
Xgwm375-4B [{98119}].		WMS 375F/WMS 375R.	

Note: The following markers were moved to the 5AL:4BL:4DL group
Xfba41.

4A^{m}L
Revise:
XksuG30; add '(3B, 5A)' in the last column.

Group 5AL:4BL:4DL

Add:

Xfba1-4B {98105}.		FBA001.	(6D).
Xfbb24-4B [{98105}].	[*Xfbb24b-4B* {98105}].	FBB024.	(3B).
Xfba41-4B {9657,98105}.		FBA041.	
Xgwm179-5A,4D {9839}.		WMS 179F/WMS 179R.	
Xgwm291-5A {9839}.		WMS 291F/WMS 291R.	
Xgwm410-5A {9839}.		WMS 410F/WMS 410R.	
Xmwg616-5A {9839}.		MWG616 {96109}.	
Xipk1(Tria)-4B, 4D, 5A [{98101}].			
	[*XTria* {98101}].	Tri a III {98103}.	
XksuG30-5A [{98105}].			
	[*XksuG30b-5A* {98105}].	pTtksuG30 {309}.	(1A, 2D, 3B, 4A, 6A,B).

Revise:
Xbcd15; add '*-4B* [{98105}]' in the first column and '[*Xbcd15a-4B* {98105}].' in the second column.
Xfba177; add '*-5A* [{98105}]' in the first column, '[*Xfba177b-5A* {98105}].' in the second column, and '(1B)' in the last column.
Xfbb255; add '(1A,B, 6A)' in the last column.
XksuE2; add '*-5A* {98105}' in the first column.

Group 4
Add:

Xglk575-4B,D {98125}.	pTag575 {98126}.	
Xgwm149-4B [{9839}].	WMS 149F/WMS 149R.	
Xgwm198-4A [{98119}].	WMS 198F/WMS 198R.	

Revise:
Xfba43; add '(5A)' in the last column.
Xfba359; add '(5A)' in the last column.
Xglk370; add '(2D)' in the last column.
Xglk431; add '(1B)' in the last column
Xglk694; add '*-4D* {98125}' in the first column.
XksuD18; add '(2B, 7B)' in the last column.
XksuF43;add '1B,D' in the last column.

Group 5S

Add:

Xbcd207-5A {98105}.		BCD207 {96124}.	(1A).
Xfbb238-5B {98105},*5D* {9657}.		FBB238.	(7A).
Note: The arm location of *Xfbb238-5D* was not reported in {9657}.			
Xglk407-5A {98105}.		pTag407 {594}.	(2B).
Xglk424-5A {594,98105}.		pTag424.	
Note : the arm location of *Xglk424-5A* was not reported in {594}.			
Xgwm129-5A [{98119}].		WMS 129F/WMS 129R.	
Xgwm234-5B [{98119}].		WMS 234F/WMS 234R.	
Xgwm304-5A [{98119}].		WMS 304F/WMS 304R.	
Xmtd116-5B {98105}.		MTD116 {98129}.	

Revise:
Xfba342; add '*-2A* {98105}' in the first column.
Xfba393; add '(1A)' in the last column.
XksuA3; add '(7B)' in the last column.

XNor 10 {98134}[3].	[*Nor10* {98134}].	pTa71.	

Group 5L
Add:

Xfba43-5A {98105}.		FBA043.	(4A).
Xfba65-5B {98105}.		FBA065.	(2D, 4A, 6A, 7A).
Xfba359-5A {98105}.		FBA359.	(2B, 4A, 6B).
Xfbb292-5B {98105}.		FBB292.	
Xglk510-5A [{594,98105}],*5B* [{594,98105}].	[*Xglk510a* {594,98105}, *Xglk510b* {594,98105}].	pTag510.	
Note: The arm locations of *Xglk510-5A,B* were not reported in {594}.			
Xgwm118-5B [{98119}].		WMS 118F/WMS 118R.	
Xgwm129-5A {9839}.		WMS 129F/WMS 129R.	
Xgwm174-5D [{98119].		WMS 174F/WMS 174R.	
Xgwm186-5A {9839}.		WMS 186F/WMS 186R.	
Xgwm272-5D [{98119}].		WMS 272F/WMS 272R.	
Xtam75-5A {179,98105},*5B,D* {179}.		TAM75.	
Note: The arm locations of *Xtam75-5A,B,D* were not reported in {179}.			
Xwpg15-5B [{98108}].	[*WPG15* {98108}].	WPG15.	
Xwpg35-5B [{98108}].	[*WPG35* {98108}].	WPG35.	
Xwpg79-5B [{98108}].	[*WPG79* {98108}].	WPG79.	
Xwpg90-5B [{98108}].	[*WPG90* {98108}].	WPG90.	
Xwpg176-5B [{98108}].	[*WPG176* {98108}].	WPG176.	
Xwpgp90-5B [{98109}].		WPG90F/WPG90R.	

Revise:
Xabg387 add '1B,D' in the last column.
Xbcd265; add '1B,D' in the last column.
Xfba127; add '(6B)' in the last column.
Xfbb156; add (3BS, 3BL, 6B)' and delete '(3B)' in the last column.
XksuA1; add '(1B)' in the last column.
XksuG12; add '(6B)' in the last column.
Xwg909; add '(4B)' in the last column.

Group 5
Note: The following markers were moved to the 5S group.
Xglk424

Note: The following markers were moved to the 5L group.
Xtam75, Xglk510

Add:
Xfba259-5B {98107}. FBA259. (7B).
Xmta9-5D {98107}. MTA9 {98129}.

Revise:
Xfba137; add '(4A)' in the last column.
Xglk251; add '*-5B* {98125}' in the first column.
Xglk510; add '*-5D* {98125}' in the first column.
Xglk587; add '*-5B* {98125}' in the first column.
XksuF43; add '1B,D' in the last column.

Group 6S
Add
Xfbb95-6A {96113,98105}. FBB095.
Note: The arm location of *Xfbb95-6A* was not reported in {96113}.
Xfbb255-6A [{98105}]. [*Xfbb255b-6A* {98105}]. FBB255. (1A,B, 4B).
Xglk547-6D {98105}. pTag547 {594}.
Xgwm193-6B [{98119}]. WMS 193F/WMS 193R.
Xgwm334-6A [{98119}]. WMS 34F/WMS 334R.
Xmtd15(Gli-2) {98105}. MTD15 {98129}.
Xmtd184-6A {98105}. MTD184 {98129}.
Xwg487-6A {98105}. WG487 {96124}.

Revise:
Xcdo534-6D; add '1B' in the last column.
Xfba1; add '(4B)' in the last column.
Xfba65; add '(5B)' in the last column.
Xfba234; add '(1A)' in the last column.
Xfba359; add '(5A)' in the last column.
Xfbb222; add '(7A)' in the last column.
XksuE3; add '(2B, 3AL, 3BS, 6AS, 6DL)' and delete '(3A, 6A)' in the last column.
XksuF43-6D; add '1B,D' in the last column.
XksuH14-6B; add '1B,D' in the last column.

Group 6L
Add:
Xfba26-6D [{98105}]. [*Xfba26a-6D* {98105}]. FBA026. (1A).
Xfba76-6D {98105}. FBA076.
Xfba127-6B [{98105}]. [*Xfba127a-6B* {98105}]. FBA127. (3A, 5B, 7A).
Xfbb250-6B [{98105}]. [*Xfbb250b-6B* {98105}]. FBB250.
Xgwm58-6B [{98119}]. WMS 58F/WMS 58R.
Xgwm169-6A [{98119}]. WMS 169F/WMS 169R.
Xgwm200-6A [{98119}]. WMS 200F/WMS 200R.
XksuE3-6D [{98105}]. [*XksuE3a-6D* {98105}]. pTtksuE3 {309}. (1A, 2A,B,D, 3AS, 3BL, 4A, 6AS, 7A,D).
XksuG12-6B [{98105}].

[*XksuG12a-6B* {98105}].

pTtksuG12 {309}. (4A, 5D, 7A).

XksuG49-6A [{98105}].

[*XksuG49b-6A* {98105}].

pTtksuG49 {309}. (2D, 4A).

Xmtd11(Dhn9.6)-6A {98105}. MTD11 {98129}.

*XWcs1-6A,B,D** {98146}. pWcs120.

Revise:

Xcdo836; add '*-6B.1,.2* [{98105}]' in the first column and '[*Xcdo836c,a-6B* {98105}].' in the second column.

Xcsb112(Dhn5)-6A,B[9596][2]; change reference for clone 'pHv5' from '9599' to '9597'.

Xfba8; add '(1D)' in the last column.

XksuG30; add '(3B, 5A)' in the last column.

Group 6

Note: The following markers were moved to 6S.

Xfbb95

Add:

Xfbb61-6B {98105}. FBB061. (2A).

Xfbb156-6B [{98105}]. [*Xfbb156b-6B* {98105}]. FBB156. (3BS, 3BL, 5D, 7A).

Xgwm325-6D [{98119}]. WMS 325F/WMS 325R.

Xkuj77-6A,B,D {98125}. pTac77 {98127}.

Revise:

Xcdo534-6B; add '1B' in the last column.

Xglk744; add '(2A,B,D)' in the last column.

Substitute '*XksuE19-6D* {309}[4]' for '*XksuF19-6D* {309}[4].

XksuF36; add '(4A)' in the last column.

Group 7S

Add:

Xfbb53-7B {98105}. FBB053.

Xfbb324-7B [{98105}]. [*Xfbb324b-7b* {98105}]. FBB324. (2B, 3D).

Xgwm60-7A [{98119}]. WMS 60F/WMS 60R.

Xgwm68-7B [{98119}]. WMS 68F/WMS 68R.

Xgwm130-7D [{98119}]. WMS 130F/WMS 130R.

Xgwm260-7A [{98119}]. WMS 260F/WMS 260R.

Xgwm297-7B [{98119}]. WMS 297F/WMS 297R.

XksuD18-7B [{98105}]. [*XksuD18a-7B* {98105}]. pTtksuD18 {309}. (2A,B,D, 4D).

Revise:

Xbcd98-7B,D; add '1B,D' to the last column.

Xbcd310-7B; add '(1B).' in the last column.

Xcdo534-7A; add '1B' in the last column.

Xglk61-7A; substitute '(7BL).' for '(7DL).' in the last column

XksuA1; Replace '*XksuA1-1D* {309}' with '*XksuA1-7D* {309}', and add '(1B, 5B)' in the last column.

Group 7AS:4AL:7DS

Add:
XksuF36-4A {98105}. pTtksuF36. (2D, 6D).
XksuG49-4A [{98105}]. [*XksuG49c-4A* {98105}]. pTtksuG49. (2D, 6A).

Revise:
Xbcd1438; add '*-7A* {98105}' in the first column.
Xfba8; add '(1D)' in the last column.
Xfba65; add '(5B)' in the last column.
Xfba127; add '(6B)' in the last column.
Xfba231; add '*-7A* {98105}' in the first column.
Xfba243; add '*-7A,4A* [{98105}]' in the first column, and '[*Xfba243a-7A, Xfba243b-4A* {98105}].' in the second column.
Xfbb156; add '(3BS, 3BL, 6B)' and delete '(3B)' in the last column.
Xfbb278; add '(2B)' in the last column.
Xmwg710; add '1B,D' in the last column.

Group 7L
Add:
Xfba71-7A [{98105}]. [*Xfba71a-7A* {98105}]. FBA071. (2A).
Xfbb222-7A {98105}. FBB222. (6D).
Xfbb366-7A,D [{98105}]. [*Xfbb366a-7A, Xfbb366b-7D* {98105}]. FBB366.
XGlu-7A [{98154}][3]. pTdUCD1 {9658}.
XksuA1-7D [{98105}]. [*XksuA1b-7D* {98105}]. pTtksuA1 {309}. (1B, 5B).
XksuA3-7B {98105}. pTtksuA3 {309}. (5D).
XksuF2-7B {98105}. pTtksuF2 {309}. (2A,D).
Xtam51-7A {179,98105}. TAM51. (4A,B).
Note: The arm location of *Xtam51-7A* was not reported in {179}.
Xwg232-7A [{98105}]. [*Xwg232a-7A* {98105}].' WG232 {96124}. (1A, 4A, 5A).

Revise:
Xfba234; add '(1A)' in the last column.
Xfba259; add '(5B)' in the last column.
Xfba382; add '*-7B* {98105}' in the first column.
Xfbb79; add '*-7A* {98105}' in the first column.
Xfbb238; add '(5B)' in the last column.
XksuE3; add '(2B, 3AL, 3BS, 6AS, 6DL)' and delete '(3A, 6A)' in the last column.
XksuG12; add '*-7A* [{98105}]' in the first column, '[*XksuG12b-7A* {98105}].' in the second column, and '(6B)' in the last column.
Xglk478; add '*7A* [{98105}]' in the first column, and '[*Xglk478a-7A* {98105}].' in the second column.
Xpsr311-7A,B,D; change reference from '1168' to '869'.

Group 7
Add:
Xipk3(Mtase)-7A,B,D [{98101}]. [*XMtase* {98101}]. Mtase.

XSbeI-7A,B,D *{98145}. wSBE I-D2 clone 7.8.

Revise:
Xglk549; add '*-7A,B* {98125}' in the first column and '(1A)' in the last column.

Gametocidal Genes

1. Gametocidal activity
Revised to:

Gc1-B1a {9849}.	*Gc1a* {1084}, *Gc1* {1081}.	2B {1084}.	**i:**	CS*8/*Aegilops speltoides* {1081}.
Gc1-B1b {9849}.	*Gc1b* {1084}.	2B {1084}.	**i:**	CS*8/*Ae. speltoides* subsp. *ligustica* {1084}.
Gc1-S^{l}1 {9849}.	*Gc-S^{l}3* {9849}.	2S^{1} {9850}.	**ad:**	CS/*Ae. sharonensis* {9850}.
Gc2-S^{l}1a {9849}.	*Gc-S^{l}1* {9849}.	4S^{1} {9851}.	**ad:**	CS/*Ae. longissima* {9851}.
Gc2-S^{l}1b {9849}.	*Gc-S^{l}2* {9849}.	4S^{1} {9852}.	**ad:**	CS/*Ae. sharonensis* {9852}.
Gc3-C1 {9849}.	*Gc-C* {9849}.	3C {9853}.	**ad:**	CS/*Ae. triuncialis* {9854}.

Gc1-B1a, Gc1-B1b and *Gc1-S^{l}*, classified in the same functional group, are hypostatic to the genes *Gc2-S^{l}1a* and *Gc2-S^{l}1b*. *Gc3-C1* does not interact with the *Gc* genes in the other two groups. In addition to these genes, chromosomes carrying gametocidal genes occur in *Ae. caudata* {9855} and *Ae. cylindrica* {9856} and other strains of *Ae. longissima* and *Ae. sharonensis* {9857,9858}.

Genes with gametocidal activity (*Sd1* {1211} and *Sd2* {9868}) in wheat are present in homoeologous group 7 chromosomes of *Thinopyrum elongatum* {471,1211}.

Sd1 {1211}.		7D {1211}.	**v:**	*Agatha Sd2* {1211,9868}.
Sd2 {9868}.		7BL {9867}.	**v:**	88M22-149 {9867,9868}.

In the presence of both *Sd1* and *Sd2*, *Lr19* is transmitted preferentially in heterozygotes, the degree of distortion being determined by genetic background. In heterozygotes with the same background, and in the presence of only *Sd2*, *Lr19* shows strong self-elimination. Based on these results, it seems likely that the Sears' translocation 7D-7Ag#7 does not carry *Sd1* {660}.

Glaucousness

Add:
Orthology among *gs1, gs6, gs8* of barley (2HS){96109}, *wa1* of rye (7RL){9837} and *gl2* of maize {98114} was indicated in {9837}.

W3^{I} [{98154}].	*I3-W* {98154}.	1BL {98154}.	**tv:**	*T. turgidum* var. *dicoccoides*.

Glume Colour

1. Red (brown/bronze)
Rg3 : Add '{9862}' to symbol and chromosome location references and add '**v:** L'govskaya-47 {9861}.'

Move paragraph beginning 'The majority ...' to top and add 'The 1A gene, *Rg3*, was eventially identified linked to *Gli-A1* {9861} and shown to cosegregate with *Hg* {9860}. A linkage order of *Glu-A1* - cent - *Gli-A1* - *Hg* - *Rg3* was reported {9860}.
Replace sentence '*Rg3* was ...' with '{9861} reports a further block of 30 international varieties which, by inference from their *Gli-A1* alleles, probably also carry *Rg3*.'

2. Black
Revise the *'Bg'* listing to the following:

'Bg {916}.	1A {916}, 1AS {96119}.	**s:** CS*7/Indian 1A {916}.
		dv: G1777, G3116 {96119}.
Bga {96119}.	[*Bg(a)* {96119}].	**dv:** G1777.
Bgb {96119}.	[*Bg(b)* {96119}].	**dv:** G3116.
bg {96119}.		**dv:** DV92, G2528.

Bga and *Bgb* and are dominant and cause a solid black glume and a black line at the margins of the glume, respectively. *bg* is recessive and causes a non-black glume.'

6. **Chocolate Chaff**
cc; add '7BS {9701}' in the third column and 'PI349056 {9701}' in the fourth column.

Grain Hardness

Insert prior to listing of the *Gsp-1* set:
'Friabilin consists mainly of puroindoline a and puroindoline b and, although both soft and hard wheats possess them, distinction between the two textural types depends upon the manner in which the friabilin binds to starch. See Puroindoline (Proteins 5. VIII).'

Hairy/Pubesent Auricles

Pa {add 9884}. 4BS {add 9884}.

Hairy glume

Add:
'hg1 {9861}. **v:** Ulyanovkn {9861}; Pionerskaya {9861,98124}.
The likelihood of three alleles, *hg* (hairless), *Hg1* (weakly hairy) and *Hg* (very hairy), with *hg1* being recessive to *Hg* and causing a short (weak) hairy phenotype, was mentioned in {9861}.'

Height

Ht is the general symbol.

Reduced Height : GA-insensitive
Rht1, see *Rht-B1b*; *Rht2*, see *RhtD1b*; *Rht3*, see *Rht-B1c*; *Rht10*, see *Rht-D1c* .
Rht-1.
Rht-B1 {9748}. 4B {87,284,736}, 4BS {69; see also 9748}. **ma:tv:** *Gai1/Rht-B1b* - 1.8cM - *Xpsr622-4B*{9739}.
Rht-B1a {9748}. **v:** Tall wheats {9748}, e.g. Chinese Spring.
Rht-B1b {9748}. [*Rht1, Sd1* {12}]. Partially recessive {21}, recessive {242}, semi-dominant {289}. **i:** See {289, 279}. **v:** Frontier {1173}; Guardian {1173}; Selection 14-53/Burt, 5 {12}; Siete Cerros {285}; Wren {831}; WW15

{285}. Norin 10-Brevor, 14 *Rht-D1b* {12}; Oleson *Rht-D1b* {242}; Selection D6301 *Rht-D1b* {242}, Shortim *Rht-D1b* {178}. See {285, 287, 747}. **tv:** Cocorit 71 {87,286}; Creso {87,286,311}; Malavika {1042}; Mida {312}; Sansone {87}; Valgerado {87,286}; Valnova {312}; Valselva {312}.

Rht-B1c {9748}. [*Rht3, Sd3*{402}]. Semi-dominant {736}. **i:** Tom Thumb/7* Kharkov//Lancer {736}. See {289}. **v:** Minister Dwarf {282}; Selection D6899 (Tom Thumb-Sonora 64/Tacuari) {242}; Tom Thumb {283}; Tom Pouce Blanc {285,1199}; Tom Pouce Barba Rouge {285,1199}; Topo; Tordo. **ma:** *Xmwg634-4B* (distal) - 30.6 cM - *Rht-B1c* - 11.9 cM *Xpsr144 -4B* (proximal) {98117}.

Rht-B1d {9748}. [*Rht1S* {1175}]. Semi-dominant {1175,9748}. **v:** Saitama 27 {1175}. Occurs frequently in Italian and Yugoslavian wheats {1175}: Argelato, Centauro, Chiarano, Etruria, Farnesse, Gallo, Gemini, Lario, Pandas, Produttore, Orlandi, Orso, Salvia, Sprint, Strampelli.

RhtB1e {9748}. [*RhtKrasnodari 1* {9822}, *Rht1(B-dw)*{9745}]. **v:** Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezostaya 1 {9745}).

Rht-B1f {9748}. [*RhtT.aethiopicum* {9748}]. Semi-dominant {9748}. **tv:** *T. aethiopicum* accessions W6824D {9748}, W6807C {9748}.

Rht-D1 {9748}. 4D {281,414,1132}, 4DS {698,896, see also 9748}. **ma:** *Xpsr1871(Pki)-4D* - 4cM - *Rht-D1* - 6 cM - *Xubc821(PhyA)-4D* {9547}.

Rht-D1a {9748}. **v:** Tall wheats {9748}, e.g. Chinese Spring.

Rht-D1b {9748}. [*Rht2, Sd2* {12}]. Partially recessive {21}, recessive {242}, semi-dominant {289}. 4D {281}, 4DS {698}. **i:** See {289, 279}. **v:** Combe {405}; Era {285}; Gaines Sib 2 {12}; Jaral {285}; Kite {831}; Maris Hobbit {281}; Pitic 62 {405}; Songlen {178}. Oleson *Rht-B1b* {242}; Norin 10-Brevor 14 *Rht-B1b* {12}; Selection D6301 *Rht-B1b* {242}.

Rht-D1c {9748}. [*Rht10* {896}]. Dominant {89}. **v:** Ai-bian {1132,896}. **ma:** *Xpsr921-4D* (4DS) - 0.8 cM - *Rht-D1c* - 28 cM - *Xgwm165-4D* (4DL) {98117}.

Rht-D1d {9748}. [*RhtAi-bian 1a* {9749}]. Semi-dominant {9748}. **v:** Ai-bian 1a (spontaneous mutant of Ai-bian 1) {9749}.

Reduced Height : GA-sensitive

Rht4 {404}. Recessive. **v:** Burt *ert* 937, CI 15076 {403,518}.

Rht5 {518}. **v:** Marfed *ert* 1, M1, CI 13988 {518,519,1168}.

Rht6 {519}. Recessive. **v:** Brevor {406}; Burt {406,519}; Norin 10-Brevor 14 *Rht-B1b Rht-D1b* {406}.

Rht7 {1172}. 2A {1172}. **v:** Bersée Mutant A {1172}; Bersée Mutant C {1172}.

Rht8. 2D {555,1171,1170}, 2DL. **s:** Capelle-Desprez*/ Mara 2D {1171}. **v:** Novasadska Rana 1 {1176}; Sava {1171,279}, Akakomugi *Rht9* {840}; Mara *Rht9* {840}. **ma:** *Xgwm484-2D* (proximal) - 19.9 cM - *Rht8* - 0.6 cM - *Xgwm261-2D* (distal) {98118}.

Rht9. 7BS {555,1171}. **s:** Capelle-Desprez*/Mara 5BS-7BS {1171}. **v:** Acciao {519}; Forlani {519}. Akakomugi *Rht8* {1171}; Mara *Rht8* {1171}.

Rht11 {519}. **v:** Karlik 1 {519}.

Rht12 {519}. Dominant. 5A {1045,9531}. **v:** Karcagi 522M7K {522}. **ma:** *Rht12* is located distally on 5AL cosegregating with the gene *B1* and closely linked to *β-Amy-A1* {9531}. *Xgwm291-5A* - 5.4cM - *Rht12* {9839}.

Rht13 {519}. **v:** Magnif 41M1, CI 17689 {519}.

Rht14 {519}. **v:** Cp B 132 {94} = Castelporziano, PI 347331 {519}.

Rht15 {519}. **tv:** Durox {519}.

Rht16 {519}. **v:** Edmore M1 {519}.

Rht17 {519}. **v:** Chris Mutant, CI 17241 {800}.

Rht18 {519}. **tv:** Icaro {519}.

Rht19 {519}. **tv:** Vic M1 {519}.

Rht20 {519}. **v:** Burt M860 {519}.

Börner et al. {9748} found no evidence of orthologous GA-insensitive genes in rye, but reviewed evidence for orthologous GA-insensitive genes.

Herbicide Response

3. Chlortoluron Insensitivity

Add:

Su1. **tv:** B-35 {98104}.

su1. **tv:** B-7 {98104}.

Revise the previous 'ma:' entry to '*Xpsr312-6B* - 5.3 cM - *Su1* - 6.8 cM - *Xpsr477(Pgk2)-6B* {96108}.'
Add to the 'ma:' section:
'*Nor2* (6BS) - 2.7 cM - *Su1* {98142} - 5.2 cM - *Xpsr371-6B* (6BL) {98104}.'

Hybrid Weakness

2. Hybrid Chlorosis Type 1

Add at end of section: 'A gene, *Chr1*, in rye produces chlorosis symptoms in hybrids with wheats possessing *Ch2*, such as C306, HD2939 and NI5439 {9816}. Evidence for multiple alleles of *Chr1* was also presented {9816}.'

Chr1 {9816}. **dv:** Cereal rye lines, EC179188 = WSP527A{9816}; EC143825 = WSP506A {9816}; EC338685 = Blanco {9816}; others {9816}.

chr1 {9816}. **dv:** EC179178 {9816}; EC179185 SAR/SWPY5{9816}.

Lack of Ligules

Add:
'Evidence for orthology of *lg1* and *lg2* with *lg* of rice {96111}, *lg1* of maize {98116}, *li* of barley {98111} and *al* of rye was presented in {9837}.'

Nuclear-Cytoplasmic Compatability Enhancers

scs {98138}. 1A {98136}, 1AL {98137}. **v:** *T. timopheevi* {98138}.

ma: A number of RAPD completely linked makers were identified {9812}.

Asakura *et al.* {9812} used the symbol *Ncc* as a synonymn for *scs*, pointing out that the effects of the gene are not limited to a single species.

Nucleolar Organizer Regions

18S - 5.8S - 26S rRNA genes

Nor-B2: change 6BS reference '252' to '251'.

Osmoregulation

Revise the previous 'ma:' entry to '*Or* (proximal in 7AS) - 13 cM - *Xpsr119-7A* {9740}.'

Proteins

1. Grain Protein Content

Revise the previous *QGpc.ndsu* 'ma:' entries to include the complete symbol for each DNA marker, as follows:

'***QPro.mgb-4B*** associated at P≤0.001 with *Gai1* and *Xpsr622-4B* {9739}[2].
QPro.mgb-5A associated at P≤0.05 with *Xpsr911-5A* {9739}[2].
QPro.mgb-6A.1 associated at P≤0.01 with *Xpsr167-6A* and *XksuG8-6A* {9739}[2].
QPro.mgb-6A.2 associated at P≤0.05 with *Xmgb56-6A* {9739}[2].
QPro.mgb-7B associated at P≤0.01 with *Xpsr490(Ss1)-7B* and *Pc* {9739}[2].'

2. Enzymes

III. Aminopeptidase
Amp-M^{v}2 {9836}. 4M^{v} {9836}. **su:** H-93-33 {9836}.

VII. Esterase
Est-R6; in the last column, add 'rye popn' after 'DS2 x RxL10'.
Est-R8; change the last-column entry to '**ad**: CS/Imperial, CS/KingII.'

VIII. Glucosephosphate isomerase
Add comment: 'GPI zymogram phenotypes observed in *Triticum* and *Aegilops* species were reported in {98147, 98148}.'

XV. Phosphogluconate dehydrogenase
Delete the previous listing and substitute the following:

'***Pgd1*** [{96119}]. [***Pgd3*** {96119}, ***Pgd-A3*** {98156}].
7A^{m}S {96119}.'
v: *T. monococcum.*

XXVIII. β-Glucosidase

β–Gls {96119}.	2A^{m}L.	**dv:** DV92.
β–Glsa {96119}.		**dv:** DV92.
β–Glsb {96119}.		**dv:** G3116 (Null).

3. Endosperm storage proteins
I. Glutenins

In the preamble, after the sentence that ends '...the transcribed portion of the gene {255}.', add the following, '(Definitive evidence that subunit 21* {98152}, which has a mobility close to that of subunit 21, is a 'x-type' protein rather than a 'y-type' protein has not been obtained, however.)'

After *'Glu-A1s'*, add
Glu-A1t [{98152}]. 21* {98152}. **v:** W29323, W 3879, W 31169.

After *'Glu-A1-1s'*, add
Glu-A1-1t {98152}. 21* {98152}. **v:** W29323, W 3879, W 31169.
Glu-A1-1t' is a provisional designation because definitive evidence that subunit 21*, which has a mobility similar to that of subunit 21, is a 'x-type' and not a 'y-type' protein has not been obtained.

After *'Glu-H^{t}1'*, delete the sentence that begins 'The symbol *Glu-2*, formerly used...' and add the following:

Glu-B2 {98155, 98154}.
[*XGlu-B2* {98154}].
1BS. **s:** CS*/Cheyenne 1B, Langdon*/*T. turgidum* var. *dicoccoides* 1B{98154}.

Gli-B3 was designated*Glu-B2* {420} until the name of the locus was changed in {792}.

II. Gliadins
Add the following paragraphs at the end of the preamble:

'Recombination was observed within the gliadin multigene family at *XGli-A1* {98154}. These closely linked genes may correspond to *Gli-A1* and *Gli-A5*, but they were temporarily designated *XGli-A1.1* and *XGli-A1.2* until orthology with *Gli-A1* and/or *Gli-A5* is established.
A number of novel gliadin alleles were reported in {98153}; they will be included in the next supplement to the catalogue'.

Add the following comment after *Gli-A4:* 'Dubcovsky et al. {98154} did not find evidence for the simultaneous presence of both *Gli-A3* and *Gli-A4* in five 1A or 1A^m mapping populations and concluded that *Gli-A4* should be considered to be *Gli-A3* until conclusive evidence for the former is obtained.'

4. Water-soluble proteins

Wsp-D1c {9840}. **v:** T4 = Agatha {9840,639}; Indis {639,641}.

5. Other proteins

VI. Waxy protein
To first sentence in parenthesis add: '= ADP glucose glycosyl tranferase, EC2.4.1.21 = GBSS.' Change second sentence to 'Waxy proteins, characterised by starch granules containing increased amylopectin and reduced amylose, are preferred for Japanese white salted or "udon" noodles {9897}.'
Add to preamble: 'Waxy phenotypes are controlled by orthologous genes in barley, maize and rice, but are not known in rye {9837}.'

Wx-B1b . Add: '**v:** For list of Australian wheats, see {9897}.'

VIII. Puroindolines
Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). Hard wheats result from unique changes in the puroindoline amino acid sequence or (currently) a null form of one of the completely linked genes (max. map distance 4.3 cM) {9822}.

Pina-D1a {9822}. 5DS {9822}. **v:** CS {9822}; Heron {9823}.
Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pinb-D1b* mutation {9822, 9823}.

Pina-D1b {9823}. **v:** Falcon {9823}; Butte 86 {9823} (null).
Pina-D1b may be present in all hard hexaploid wheats not carrying the *Pinb-D1b* mutation {9822, 9823}.

Pinb-D1a{9822}. 5DS {9822}. **v:** CS {9822}; Hill 81 {9822}.

Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pina-D1b* mutation {9822,9823}.

Pinb-D1b {9822}. 5DS {9823}. **s:** CS (Cheyenne 5D) {9822}.

v: Wanser {9822}.

Pinb-D1b may be present in all hard hexaploid wheats not carrying the *Pina-D1b* (null) mutation {9822,9823}. Wheats with *Pinb-D1b* contain a Gly-46 to Ser-46 change in amino acid sequence {9822}.

Wx-B1b . Add: '**v:** For list of Australian wheats, see {9897}.'

Response to Salinity

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

Kna1 {9810}. 4DL {9810}. **v:** hexaploid wheats {9810}.

4BS.4BL-4DL {96128}. **tv:** **tr:** Various lines {9810}.

4BS.4BL-4DL-4BL {9811}. **tv:** **tr:** Selection 3*5-4 {9811}.

ma: *Kna1* was found to be completely linked with *Xabc305-4B, Xabc305-4D, Xbcd402-4B, Xbcd402-4D, Xpsr567-4B, Xpsr567-4D, Xwg199-4B and Xwg199-4D* in recombined *T. turgidum* 4B and *T. aestivum* 4D chromosomes {96128, 9811}.

Response to Tissue Culture

QTL loci mapped include:

Qtcr.ipk-2B.1 [{98110}]. [*Tcr-B1* {98110}]. Is weakly associated with *Xpsr102-2B.*

Qtcr.ipk-2B.2 [{98110}]. [*Tcr-B2* {98110}]. Is linked closely and distal to *Ppd2.*

Qtcr.ipk-2B.3 [{98110}]. [*Tcr-B3* {98110}]. Is linked to *Yr7/Sr9g.*

Response to Vernalization

Vrn-1 {9880}.
Orthologous series in long arms of chromosomes of homoeologous Group 5.

Vrn-A1 {9880}. [*Vrn1* {829}, *Sk* {2}]. 5AL {558,633}. **i:** Triple Dirk {828,829}. **s:** Kharkov 22MC*/Rescue 5A {243}; Winalta*8/Rescue 5A {626}. Rescue*/Cadet 5A *Vrn-D1 Vrn-B1* {860}. **v:** Cadet {860}; Conley {828}; Diamant II {625}; Falcon {829}; Koga II {1181}; Kolben {1,828,829}; Konosu 25 {315}; Marquis {1}; Reward {828}; Saitama 27 {315}; Saratov 29 {633}; Saratovskaya 29 {635}; Saratovskaya 210 {633}; Shabati Sonora {635}; Thatcher {828}; WW15 {829}. Shortandinka *Vrn-B1* {635}; Takari *Vrn-B1* {253}. Hope *Vrn-B4* {1026}. **ma:** *Vrn-A1* - 7.5cM - *Xwg644-5A* {9839}.

Cultivars possessing *Vrn-A1* are insensitive to vernalization. *Vrn-A1* is epistatic to other genes. According to {860}, *Vrn-A1* is not always fully dominant and not always epistatic. Kuspira et al. {531} attributed single gene variation in *T. monococcum* to the *Vrn-A1* locus. Multiple recessive alleles were suggested {531}.

Vrn-A^{m}1 was mapped on the long arm of chromosome 5A^m closely linked to the same RFLP markers as *Vrn-1* {9877}.

Vrn-1 should be orthologous to *Vrn-H1* {*Sh2/Sgh2*} of barley {9839,9873,9874} and *Vrn-R1 {Sp1}* of rye {9839,9875} based on map locations using common RFLP markers.

Vrn-B1 {9880}. The literature indicates this gene is located in chromosome 5BL. Because the previously designated genes *Vrn4* and *Vrn2* are probably the same, or allelic, the listing of information will follow earlier formats under the previous synonymns. Stelmakh {1026} doubted the existence of *Vrn4*.

[*Vrn4* {830}]. 5B {635}, 5D {9438}, 5BL {635}. **s:** Rescue*/Cadet 5A *Vrn-A1 Vrn-D1* {635}. **v:** Mara {1181}; Pirourix 28 {635}. Shortandinka *Vrn-A1* {860}.

[*Vrn2* {829}, *Ss* {2}]. 5B {9428,9433}, 5BL or 7BL {9438}. Earlier location of 2B {625} was not correct. **i:** Triple Dirk B {829}. Brown Schlanstedt {1,2,828,829}; Bersee {396}; Cadet {860}; Festiguay {829}; Milturum 321 {635}; Milturum 553 {635}, Noe {2}; Spica {396}. Borsum *Vrn1* {1}; Dala *Vrn1* {1}; Diamant 1 *Vrn1* {1}; Halland *Vrn-A1* {1}; Haruhikari *Vrn-A1* {633}; Rubin *Vrn-A1* {1}; Triple Dirk *Vrn-A1* {830}. Gabo *Vrn4* {829}.

In some studies, genotypes were subdivided. Carriers of *Vrn2a* did not react to 15 and 30 days vernalization. Carriers of *Vrn2b* showed accelerated heading after 15 and 30 days vernalization {9428,9433}.

[*Vrn2a* = *Vrn2* {9428,9433}]. **i:** Ank-18 {9428,9433}. **s:** Saratovskaya 29*8/Mironovskaya 808 {9433}; Saratovskaya 29*8/Odesskaya 51 5A {9433}. **v:** Pirothrix 28 {9433}. Saratovskaya 29 *Vrn-A1* {9433}.

[*Vrn2b* = *Vrn2* {9428,9433}]. **s:** Diamant 1*8/Mironovskaya 808 5A {9433}; Diamant 1*8/Skorospelka 35 5A {9433}. **v:** Magali; Milturum 321 {9433}; Milturum 553 {9433}; Ulyanovka 9 {9433}. Diamant 1 *Vrn-A1* {9433}; Novosibirksaya 67 *Vrn-A1* {9433}.

Vrn-D1 {9880}. [*Vrn3* {829}]. 5DL {558,633}. **i:** Triple Dirk E {829}. **s:** Rescue*/Cadet 5A *Vrn-A1 Vrn4* {860}. **v:** Chinese Spring {829}; Norin 61 {315}; Shinchunaga {315}; Shirasagi Komugi {315}; Ushio Komugi {315}. Rescue *Vrn-B1* {860}.

Vrn-2 {9877}.

Orthologous series in chromosomes of homoeologous group 4. *Vrn-A^{m}2* was located in *T. monococcum* {9877} on chromosome 5A^m on the 4A^m translocated region. *Vrn-H2 (sh/sgh1)* occurs in barley chromosome 4H {9876} and is probably orthologous to *Vrn-A^{m}2* based on comparative maps {9877,9874}.

Vrn2a {9877}. Winter habit - dominant in diploid wheat. **dv:** G1777 {9877}; G3116 {9877}.

Vrn2b {9877}. Spring habit. **dv:** DV92 {9877}.

Vrn-3 {9880}.

Orthologous series in chromosomes of homoeologous group 1 predicted from orthology with *Vrn-H3 (Sh3)* in barley chromosome 1H {9876,9878}. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {9879}.

Vrn-4 {9880}.

To date, only *Vrn-B4* has been detected.

Vrn-B4 {9880}. [*Vrn5, eHi* {557} {552}]. 7BS {553,557}. The distal region of 7BS has been translocated with a chromosome segment with homoeology to the distal region of 5AL. It is not known if *Vrn-4* is located in the region homoeologous to 5L or 7S. **s:** CS*/Hope 7B *Vrn-D1* {553}. **v:** Hope *Vrn-A1* {1026}.

References to additional studies are given in {1026}.

Stock	Genotype	Vernalization Response
Triple Dirk	*Vrn-A1 vrn-B1 vrn-D1*	No
Kolben	*Vrn-A1 vrn-B1 vrn-D1*	No
Festiguay	*vrn-A1 vrn-B1 vrn-D1*	Yes
Gabo	*vrn-A1 vrn-B1 vrn-D1*	Yes
Chinese Spring	*vrn-A1 vrn-B1 Vrn-D1*	Yes

Winter cultivars carry recessive alleles at all loci. Differences among winter wheats with respect to vernalization requirements seem to be due to multiple recessive alleles {830}. Two genes may determine differences between winter wheats requiring 20 days and 60-65 days of vernalization {316}.

Restorers for Cytoplasmic Male Sterility

2. Restorers for *T. longissimum* cytoplasm

Vi {98135}. 1B{98136}, 1BS {98137}. **v:** *T. turgidum*{98135}. Probably derived from a cv. Selkirk *T. aestivum* line with *T. cylincricum* cytoplasm {98135}.

3. Restorers for photoperiod-sensitive *Aegilops crassa* cytoplasm

Morai & Tsunewaki {9898} described photoperiod-sensitive CMS caused by *Aegilops crassa* cytoplasm in bread wheat cv. Norin 26. Almost complete sterility occurred when plants were grown in photoperiods of 15h or longer.

Rfd1 {9899}. 7BL{9899}. **v:** Chinese Spring{9899}.

A different system of restoration occurs in cv. Norin 61, where at least four chromosomes, 4A, 1D, 3D and 5D, appear to be involved {9899}.

Ribosomal RNA

5S rRNA genes

5S-Rrna-A1. Add 'v: Chinese Spring {98133}' in the last column.

Add the following comments at the end of the '5SrRNA genes' section:
'The *5S-Rrna-1* loci were physically mapped in 1AS, 1BS, and 1DS and the *5S-Rrna-2* loci were physically mapped in 5AS, 5BS, and 5DS of Chinese Spring using deletion lines {98133}.
Table 1 in {98134} lists the chromosome or chromosome arm locations of rRNA loci in 12 Triticeae species.'

Pathogenic Disease/Pest Reaction

Reaction to *Diuraphis noxia*

Dn2 7DL {98132}. **v:** PI262660 {98132}.
ma: *XksuA1-7D* - 9.8 cM - *Dn2* {98132}.

Dn4 1DL {98132}. **v:** CORWA1 {9866}; CI2401 {9866}; {9866}; PI151918 PI372129 {98132}.

ma: *Xabc156-1D* - 11.6 cM - *Dn4* {98132}

Dn5 **i:** Palmiet derivative 92RL28 {9623}.

Dn6 **v:** CI6501 {9866}.

Reaction to *Erysiphe graminis*

Pm1. **v:** Zhengzhou 871124 {9870}.

ma: Co-segregation or close linkage with three RAPDs; one RAPD converted to a STS {9870}.

Lists in {9883} (Western Siberia).

Pm1a {9862}. *Pm1* {9862}. **v:** See earlier lists.

Pm1b {9862}. **v:** MocZlatka {9862}.

Pm1c {9862}. *Pm18* {1189,9862}. **v:** M1N (see earlier *Pm18*).

Pm1d {9862}. **v:** *T. spelta* var *duhamelianum* TRI2258 {9862}.

Pm2. **v:** Orestis {98158}.

Pm3. Revise '**ma:**' listing to'*Pm3* - 3.3 cM - *Xwhs179-1A* {9650}.'

Pm4b. **v:** Ronos {98158}.

Pm5. **v:** Kormoran {98158}.

Pm6. **v:** Coker747 {98158}.

Pm8. **v:** Others: {9809}.

Crosses between three lines with *Pm8* and Helami-105, a 1BL.1RS line with *Pm17*, indicated that *Pm8* and *Pm17* were allelic {9628}. Earlier, these genes were reported to be genetically independent {1060}.

Su-Pm8. *Su-Pm8* occurs at high frequency in CIMMYT-generated wheats {9863,9809}. Further genotypes are identified in {9865}.

Pm12. 6BS-6SS.6SL {429}.

Pm13. 3B {135}, T3BL.3BS-3S^{l}#1S {9844}.**tv:** *T. longissimum* derivative R1A {136}.

3D {135}, T3DL.3DS-3S^{l}#1S {9644}.**tv:** *T. longissimum* derivative R1D {136}.

Pm17. 1AL.1RS {9628}. **v:** Amigo {9628}; Century {9894}; {9894}; TAM107 TAM200 {9894}; TAM201 {9894}.

Pm18. See *Pm1c*.

Pm21. **ma:** RAPD *OPH17$_{1900}$* (synonym 'OPH17-1900') was associated with *Pm21* and RAPD *OPH17$_{1000}$* (synonym 'OPH17-1000') with its absence {9803}.

Pm24 {9805}. 6D {9805}. **v:** Chiyacao {9805}.

Lists in {9844} (Chinese wheats).

Temporary designations:

PmTmb {9802}. **v:** NC94-3778 {9802}.

dv: *T. monococcum* PI427662 {9802}.

ma: Associated with 3 RAPDs {9802}.

Reaction to *Fusarium graminearum*

Disease : Fusarium head scab (= Fhs).
Fhs1 {9888}. **v:** Line A {9888}. Ning 7840 *Fhs2* {9888}.
Fhs2 {9888}. **v:** Line B {9888}. Ning 7840 *Fhs1* {9888}.

Reaction to *Heterodera avenae*
Cre1. **i:** AP = Prins*8/AUS10894 {9845}.
ma: *Xglk605-2B* - 7.3cM - *Cre1* - 8.4cM - *Xcdo588-2B/Xabc451-2B* {9845}.

Reaction to *Mayetiola destructor*
H3. **ma:** Cosegregation of *H3* and a RAPD {98141}.
H5. **ma:** Cosegregation of *H5* and two RAPDs {98141}.
H6. **ma:** Cosegregation of *H6* and three RAPDs {98141}.
H9. **ma:** Cosegregation of *H9* and two RAPDs {98141}.
H10. **ma:** Cosegregation of *H10* and one RAPD and close linkage of *H10* to another RAPD {98141}.
H11. **ma:** Close linkage of *H11* to two RAPDs {98141}.
H12. **ma:** Cosegregation of *H12* and one RAPD and close linkage of *H12* to another RAPD {98141}.
H13. **ma:** Cosegregation of *H13* and a RAPD {98141}.
H14. **ma:** Cosegregation of *H14*and a RAPD {98141}.
H16. **tv:** IN80164 {9885}.
ma: Cosegregation of *H16* and a RAPD {98141}.
H17. **ma:** Cosegregation of *H17* and a RAPD {98141}.
H19. **tv:** IN84702 {9885}.
PI422297 *H29* {9885}.
H23. **ma:** *H23* - 6.9 cM - *XksuH4-6D* {9815}.
H24. 6DL {9815}.
ma: *H24* - 5.9 cM - *Xbcd451-6D/Xcdo482-6D* {9815}.
H27 {9836}. $4M^{v}$ {9836}.**su:** H-93-33 {9836}.
al: *Ae. ventricosa* No. 10 {9836};
Ae. ventricosa No. 11 {9836}.
H28 {9886}. 5A {9886}. **tv:** PI59190 {9886}.
H29 {9887}. [*H27* {9886}]. 5A {9885}. **tv:** PI422297 *H19* {9885}.

Reaction to *Pseudocercosporella herpotrichoides*

Phc2. Add '7AL {98144}' in the third column.
ma: *Xcdo347-7A* (distal) - 11 cM - *Pch2* - 18.8 cM - *Xwg380-* *7A* (proximal){98144}.

Temporary Designation:
PchDv {9808}. 4V {9808}. **ad:** Wheat + 4V {9808}.
s: Wheat 4V (group IV) {9808}.

Reaction to *Puccinia graminis*
Sr21. See also *Sr45.*
Sr22. **i:** Others {9817}.
v: Others {9817}.
ma: Hexaploid derivatives with *Sr22* carried "alien" segments of varying lengths; the shortest segment was distal to *Xpsr129-7A* {9817}.
Sr24. Add '**ma:** All lines with *Sr24* also possess *Lr24;* see *Lr24.*'

Sr25. Add 'Refer to *Lr19* for linkage information.'

Sr32. 2A {660, 916}, T2AL.2S#1L-2S#1S {9644}.

v: C95.24 {9644}.

2B {916}, T2BL/2S#1S {9644}.

v: C82.1 = P80-14.1-2 {9644}.

2D {916}, T2DL-2S#1L.2S#1S

v: C82.2 = P80-139.1-4 {9644}.

2D {916}. **v:** C82.3 = P80-132.2-2 {660,916}; C82.4 = P80-153.1-2 {660,916}.

Sr34. 2D {689}, T2DS-2M#1L.2M#1S {9644}.

2A {689}, T2AS-2M#1L.2M#1S {9644}.

2M {689}.

v: Others {9644}.

Sr36.

Sr40. Derived from *T. araraticum* T2BL/2G#2S {9644}.

Sr45 {9831}. *SrD* {9832}; *SrX* {1805}.

1D {9881},1DS {9831}.

v: 87M66-2-1 {9831}. 87M66-5-6 {9881}Thatcher + *Lr21*, RL5406 {9831,9832}.

Various backcross derivatives developed at PBI Cobbitty {1058}.

dv: *T. tauschii* RL5289 {9831,9832}.

Tests of natural and induced mutants of *P. graminis* f. sp. *tritici* indicated that *Sr45* has identical specificity to *Sr21* {9832}.

Reaction to *Puccinia recondita*

Lr9. T6BS.6BL-6U#1L {9644}.

The structures of additional translocations are given in {9644}.

Lr10. **ma:** *Xcdo426-1A* - 5.1cM - *Lr10* {9636}; *Lr10* - 8 cM -*Glu-A3* {9818}.

ma: Completely linked with *Lrk10* ,which encodes a protein kinase {9864}.

ma: Cosegregation with *Xsfr1(Lrk10)* and *Xsfrp1(Lrk10)* {98106}.

Lr17a {9891}. [*Lr17*].

Lr17b {9891}. [*LrH* {9647}, WBR2 {9892}]. **v:** Harrier {9891}; Norin 10 - Brevor, 14 {9891}; Maris Fundin {9891}. Hobbit Sib = Dwarf A *Lr13* {9891}.

Lr18. T5BS.5BL-5G#1L {9644}.

Lr19. 7BL {9867}. **v:** 88M22-149 {9867}; L503 {9843}; Sunnan {9843}; L513 {9895}.

ma: Cosegregation with *Ep-D1d* {9826}.

ma: Prins et al. {9872} studied 29 deletion mutants in Indis to determine the gene order: *Sd-1 - Xpsr105 - Xpsr129 - Lr19 - Wsp- D1 - Sr25 -* Y.
Replace the note at the end of the section with 'Knott {489} obtained two mutants (28 and 235) of Agatha possessing *Lr19*, but with reduced levels of yellow pigment in the flour. Marais {639,641} obtained mutants and recombined lines with intermediate levels of, or no, yellow pigment. It was shown that in recombinant line 88M22-149 lacking yellow pigment, *Lr19* was transferred to chromosome 7BL {9867}.'
The chromosome with *Lr19* in Indis is probably identical to that in Agatha {9872}.

Lr21. **v:** AC Cora *Lr13* {9824}.

Lr22a. **v:** AC Minto *Lr11 Lr13* {9824}.

Lr24. 1B {9628}. **v:** Amigo {9628}.
ma: Cosegregation with RAPD marker that was converted to a SCAR {9871}.

Lr25. **ma:** Cosegregation with a RAPD {98130}.

Lr27. **ma:** Positive association with *XksuG53-3B* {9636}.

Lr28. T4AS.4AL-7S#2S {9644}.
ma: *Lr28* was tagged using STS primer OPJ-02_{378} {9896}.

Lr29. 7DL-7e#1L.7Ae#1S {9644}.
ma: Cosegregation with two RAPDs {98130}.

Lr31. **ma:** A positive association with *XksuG10-4B* {9636}.

Lr43. 7DS (98159}.

Lr46 {9821}. 1B {9821}. **s:** Lalbahadur (Pavon 1B) *Lr1* {9821}.
v: Pavon F76 *Lr1 Lr10 Lr13* {9821}.

Complex genotypes: AC Domain *Lr10 Lr16 Lr34* {9859}; Grandin *Lr2a Lr3 Lr10 Lr13 Lr34* {9627}; Opata 85 *Lr10 Lr37 + Lr31 Lr34* {9636}; Roblin *Lr1 Lr10 Lr13 Lr34* {9824}.
Genotype Lists: {9825} (U.S.A.)
Temporary Symbols:
LrTb {9859}. Adult plant resistance {9859}. **v:** AC Taber *Lr13 Lr14a* {9859}.

Reaction to *Puccinia striiformis*

Yr2.	7B {9830}.	Yamhill *Yr4a* {9830}.
Yr3a.	1B {9830}.	Druchamp {9830}; Stephens {9830}.
Yr3c.	1B {9830}.	Minister {9830}.
Yr4a.	6B {9830}	Vilmorin 23 {9830}. Yamhill *Yr2* {9830}.
Yr4b.	6B {9830}.	Hybrid 46 {9830}.

Yr15. **tv:** D447 derivatives B1,B2,B9,B10 {9806}.
ma:tv: $OPB13_{1420}$ - 27.1cM - *Yr15* - 11.0cM - *Nor-B1* {9806}.

Yr26 {9807}. 6AS (6AL.6VS) {9807}. **v:** Yangmai-5 {9807}.
Derived from *Haynaldia villosa (Daspyrum villosum).*

Yr27 {9889}. [*YrSk* {9649}]. 2BS {9889}. **v:** Ciano 79 {9889}; Selkirk {9889}.

Yr27 is present in many CIMMYT wheat lines {9889} and possibly Webster. *Yr27* is closely linked with *Lr13* (repulsion).

Yr28 {9890}. 4DS {9890}. **v:** Synthetic = Altar 84/*T. tauschii* 85 W-219. Synthetic/Opata SSD.

dv: *T. tauschii* W-219 {9890}.

Yr22 was also reported for chromosome 4D but in the absence of an appropriate single gene stock and the unavailability of avirulent cultures in most laboratories, tests of linkage with *Yr28* data are unlikely to be available in the foreseeable future.

Temporary Symbols:

YrDru.	5B {9830}.	Druchamp {9830}.
YrDru2.	6A {9830}.	Druchamp {9830}.
YrH46.	6A {9830}.	Hybrid 46 {9830}.

Not the same gene as *YrDru2* {9830}.

YrMin.	4A {9830}.	Minister {9830}.
YrND.	4A {9830}.	Nord Desprez {9830}.

May be the same as *YrMin* {9830}.

YrSte.	2B {9830}.	Stephens {9830}.
YrSte2.	3B {9830}.	Stephens {9830}.
YrV23.	2B {9830}.	Vilmorin {9830}.

Allelic but not the same as *YrSte* {9830}.

YrYam.	4B {9830}.	Yamhill {9830}.

Reaction to *Pyrenophora tritici-repentis*

1. Insensitivity to tan spot toxin

Revise the previous 'ma:' entry to '*Xbcd1030-5B* - 5.7 cM - *tsn1* -16.5 cM - *Xwg583-5B* {9629).'

Reaction to *Schizaphis graminum*

Gb5. 7S {266}. T7S#1L.7S#1S-7AS {9644}.

Reaction to *Tilletia* spp.

Bt10 **v:** Others {9804}.

ma: *Bt10* completely linked with a 590 bp fragment produced by UBC primer 196 {9804}. RAPD - 1.5 cM ± 1.5cM - *Bt10* {9829}.

Reaction to *Ustilago tritici*

Ut-x {98131}. 2BL{98131}. **v:** Biggar BSR {98131}.

ma: *Xcrc4-2B* - 14 cM - *Ut-x* - 10 cM - *Xabc153-2B.2* {98131}. *Xcrc4-2B* (synonym '*Xcrc4-2B.2*') is a SCAR.

Resistance to colonization by *Eriophyes tulipa*

Cmc2. 6A, T6AS.6Ae#2S {9644}.
5B, T5BL.6Ae#2S {9644}. **v:** 875-94-2 {9644}.

Reaction to Wheat Streak Mosaic Virus

Wsm1. 4A {9833}, T4AL-2S {266}. **v:** C1 17766 = B-6-37-1 {266,9833,9834}.

T6AS.4Ai#2L + T6AL-4Ai#2S {9644}. **v:** CI17883 {9644}.

ma: *Wsm1* cosegregated with a STS amplified by the primer set STSJ15 {9819}.

Seedling Leaf Chlorosis

sc {98157}. 3BS{98157}. s: CS*/Hope3B {98157}.
v: Hartog {98157}; Suneca {98157}; wheats with *Sr2* {98157}.

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

Temperature-Sensitive Winter Variegation

This phenotype involves reduced vigour and chlorotic patches on leaves of certain genotypes in *Ae. umbellutata* cytoplasm when grown at low temperatures {9813}.

Vgw {9893}. Variegation is dominant {9813}. [*Vg* {9893}]. 5BL {9893}. v: Bersée {9813}; Cappelle-Desprez {9813}; Hobbit Sib {9813}; Mara {9813}.

vgw {9893}. [*vg* {9893}]. v: Besostaya I {9813}; CS {9813}; Poros {9813}; Sava {9813}; *T. spelta* {9813}.

GENETIC LINKAGES

Chromosome 1A						
1AS	*Rg3*	-	*Hg*	0		{9860}.
	Rg3	-	*Gli-A1*	1.01 %	± 0.56 %	{9860}.
				2 %	± 1.14 %	{9861}.
	Hg	-	*Gli-A1*	0.30 %	± 0.31 %	{9860}.
				0.79 %	± 0.81 %	{9881}.
				2.24 %	± 1.31 %	{9860}.
				2.64 %	± 0.98 %	{9861}.
				3.8 %	± 1.0 %	{9861}.
		-	*Gli-A3*	25.17 %	± 4.27 %	{9860}.
		-	*Glu-A1*	I		{9860}.
	Gli-A1	-	*Gli-A3*	22.73 %	± 4.07 %	{9860}.
				22.42 cM	± 3.61 cM	{9814}.
		-	*Glu-A3*	1.5 cM	± 0.3 cM	{9726}.
		-	*Glu-A1*	I		{9860}.
		-	*Gli-A5*	1.94 cM	± 0.01 cM	{9842}.
	Gli-A3	-	*Glu-A1*	37.55 %	± 5.05 %	{9860}.
Chromosome 1B						
1BS	*Rg1*	-	*Gli-B1*	2.84 %	± 1.39 %	{9861}.
		-		4.05 %	± 1.52 %	{9861}.
		-		0		{9861}.
	Glu-B2	-	*XGli-B3*	0		{98154}.
1BS & L	*Glu-B3*	-	*Glu-B1*	29.9 cM	± 6.0 %	{98149}.
Chromosome 2A						
2AS	*bh*	-	Centromere	8.5 cM	± 2.1 cM	{9701}.
Chromosome 2B						
2BS	*Lr23*	-	Centromere	20 cM		{9636}.
Chromosome 4B						
4BS	*Hl*	-	*Pa*	30 cM		{9884}.

Chromosome 4D						
4DL	*Alt2*	-	*Kna1*	12.5 cM		{9757}.
Chromosome 5A	*H28*	-	*H9*	22 cM		{9886}.
	H29	-	*H16*	Close		{9885}.
Chromosome 5B						
5BL	Centromere	-	*Ne1*	6cM		{9893}.
	Ne1	-	*Vg*	11cM		{9893}.
	Vg	-	*Ibf-B1*	35cM		{9893}.
Chromosome 6A						
6AL	Centromere	-	*Sr26*	0		{9838}.
Chromosome 6B						
6BS tv:	*Nor2*	-	*Xpsr312*	24.8cM		{98104}.
tv:	*Xpsr312-6B*	-	*Su1*	5.5cM		{98104}.
tv:	*Su1*	-	*a-Amy-1*	9.84cM		{98104}.
Chromosome 7A						
7AS	*Xpsr119-7A*	-	*or*	13 cM		{9740}.
7AL	*cn-A1*	-	Centromere	46.6 cM	± 3.8 cM	{9701}.
Chromosome 7B						
7BS	*cc*	-	Centromere	33.5 cM	± 4.1 cM	
7BL	*cn-B1*	-	Centromere	42.6 cM	± 4.3 cM	{9701}.
Chromosome 7D						
7DS	*Lr43*	-	Centromere	I		{98159}.

REFERENCES

Amendments.

429. Revise authors to: Jia J, Devos KM, Chao S, Miller TE, Reader SM & Gale MD.

834. Saidi A & Quick JS. 1996. Inheritance and allelic relationships among Russian wheat aphid resistance genes in winter wheat. Crop Science 36(2): 256-258.

1178. Change to '1179'.

9414. Change to '429'.

9419. Riede CR, Williams ND & Miller JD. 1995. Wheat lines monogenic for resistance to stem rust from the wheat cultivar 'Waldron'. Theoretical and Applied Genetics 90: 1164-1168.

9501. Qi LL, Chen PD, Liu DJ, Zhou B, Zhang SZ, Shang BQ, Xiang QJ, Duang XY & Zhou YL. 1995. The gene *Pm21*- a new source for resistance to wheat powdery mildew. Acta Agriculture Sinica 21: 257-261.

9502. Chromosoma 103: 179-185.

9507. In the 'Reaction to *Puccinia striiformis'* section only, replace with '9607'.

9546. Change to '9551'.

9617. Plant Breeding 115: 273-275.

9636. Nelson JC, Singh RP, Autrique JE & Sorrells ME. 1997. Mapping genes conferring and suppressing leaf rust resistance in wheat. Manuscript .

9646. Change to '1061'.

9651. Ren SX, McIntosh RA, Sharp PJ & The TT. 1996. A storage protein marker associated with the suppressor of *Pm8* for powdery mildew resistance in wheat. Theoretical and Applied Genetics 93: 1054-1060.

96116. Change to '9507'.

9701. 1997. Journal of Heredity 88: 229-232.

9706. Change to '9686'.

9742. Molecular and General Genetics 254: 584-591.
9743. Change '1997' to '1998'.
9751. Crop Science 37: 1586-1589.
9754. Change '1997' to '1998'.
9757. Euphytica 91: 31-35.

New.

9801. Ma R, Zheng DS & Fan L. 1996. The crossability percentages of 96 bread wheat landraces and cultivars from Japan and rye. Euphytica 92: 301-306.
9802. Shi AN, Leath S & Murphy JP. 1996. Transfer of a major gene for powdery mildew resistance from wild einkorn wheat (*Triticum monococcum* var. *boeoticum*) to common wheat (*Triticum aestivum*). Phytopathology 86: 556.
9803. Qi LL, Cao MS, Chen PD, Li EL & Liu DJ. 1996. Identification, mapping, and application of polymorphic DNA associated with resistance gene *Pm21* of wheat. Genome 39: 191-197.
9804. Demeke T, Laroche A & Gaudet DA. 1996. A DNA marker for the *Bt-10* common bunt resistance gene in wheat. Genome 39: 51-55.
9805. Huang XQ, Hsam SLK & Zeller FJ. 1997. Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em. Thell.) 4. Gene *Pm24* in Chinese landrace Chiyacao. 1997. Theoretical and Applied Genetics 95: 950-953.
9806. Sun GL, Fahima T, Korol AB, Turpeinen T, Grama A, Ronin YI & Nevo E. 1997. Identification of molecular markers linked to the *Yr15* stripe rust resistance gene of wheat originated in wild emmer wheat, *Triticum dicoccoides*. Theoretical and Applied Genetics 95: 622-628.
9807. Jones SS. 1997. Personal communication.
9808. Jones SS. 1997. Personal communication.
9809. Ren SX, McIntosh RA & Lu Z. J. 1997. Genetic suppression of the cereal rye-derived gene *Pm8* in wheat. Euphytica 93: 353-360.
9810. Dvorák J & Gorham J. 1992. Methodology of gene transfer by homoeologous recombination into *Triticum turgidum*: Transfer of K^+/Na^+ discrimination from *Triticum aestivum*. Genome 35: 639-646.
9811. Luo M-C, Dubcovsky J, Goyal S & Dvorák J. 1996. Engineering of interstitial foreign chromosome segments containing the K^+/Na^+ selectivity gene *Kna1* by sequential homoeologous recombination in durum wheat. Theoretical and Applied Genetics 93: 1180-1184.
9812. Asakura N, Nakamura C, & Ohtsuka I. 1997. RAPD markers lined to the nuclear gene from *Triticum tiropheevii* that confers compatability with *Aegilops squarrosa* cytoplasm on alloplasmic durum wheat. Genome 40: 201-210.
9813. Worland AJ & Law CN. 1983. Cytoplasmic variation in wheat. 1982 Annual Report, Plant Breeding Institute, Cambridge. Pp. 79-80.
9814. Nieto-Taladriz MT & Carrillo JM. 1996. Complexity of the *Gli-A3* locus in bread wheat. Plant Breeding 115: 192-194.
9815. Ma ZQ, Gill BS, Sorrells ME & Tanksley SD. 1993. RFLP markers linked to two Hessian fly-resistance genes in wheat (*Triticum aestivum* L.) from *Triticum tauschii* (Coss.) Schmal. Theoretical and Applied Genetics 85: 750-754.
9816. Tomar SMS & Singh B. 1998. Hybrid chlorosis in wheat x rye crosses. Eupytica 99: 1-4.
9817. Paull JG, Pallotta MA, Langridge P & The TT. 1994. RFLP markers associated with *Sr22* and recombination between chromosome 7A of bread wheat and the diploid species *Triticum boeoticum*. Theoretical and Applied Genetics 89: 1039-1045.
9818. Feuillet C, Schachermayr G & Keller B. 1997. Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10* disease resistance locus of wheat. The Plant Journal 11: 45-52.
9819. Talbert LE, Bruckner PL, Smith LY, Sears R & Martin TJ. 1996. Development of PCR markers linked to resistance to wheat streak mosiac virus in wheat. Theoretical and Applied Genetics 93: 463-467.

9820. Shi AN, Leath S & Murphy JP. 1996. Indentification of a major gene for powdery mildew resistance from wild einkorn wheat (*Triticum monococcum ssp aegilopoides*) to common wheat *(T. aestivum).* Manuscript.
9821. Singh RP. 1997. Personal communication.
9822. Giroux MJ & Morris CF. 1997. A glycine to serine change in puroindoline b is associated with wheat grain hardness and low levels of starch-surface friabilin. Theoretical and Applied Genetics 95: 857-864
9823. Morris CF & Giroux MJ . 1997. Personal communication.
9824. Kolmer JA. 1997. Virulence in *Puccinia recondita* f. sp. *tritici* isolates from Canada to genes for adult plant resistance to wheat leaf rust. Plant Disease 81: 267-271.
9825. McVey DV & Long DL. 1993. Genes for leaf rust resistance in hard red winter wheat cultivars and parental lines. Crop Science 33: 1373-1381.
9826. McMillin DE, Johnson JW & Roberts JJ. 1993. Linkage between endopeptidase *Ep-Dld* and a gene conferring leaf rust resistance (*Lr19*) in wheat. Crop Science 33: 1201-1203.
9827. Liu JQ & Kolmer JA. 1997. Inheritance of leaf rust resistance in wheat cultivars Grandin and CDC Teal. Plant Disease 81: 505-508.
9828. Hasm SLK & Zeller FJ. 1997. Evidence of allellism between genes *Pm8* and *Pm17* and chromosomal location of powdery mildew and leaf rust resistance genes in the common wheat cultivar 'Amigo'. Plant Breeding 116: 119-122.
9829. Laroche A, Demeke T & Gaudet DA. 1996. Identification of a DNA fragment linked to the bunt *Bt-10* resistance gene and its utilization for marker-assisted selection in hexaploid wheat. Canadian Journal of Plant Pathology 18: 491.
9830. Chen XM, Jones SS & Line RF. 1996. Chromosomal location of genes for resistance to *Puccinia striiformis* in seven wheat cultivars with resistance genes at the *Yr3* and *Yr4* loci. Phytopathology 86: 1228-1233.
9831. Marais GF. 1997. Personal communication.
9832. McIntosh RA. 1981. A gene for stem rust resistance in non-homoeologous chromosomes of hexaploid wheat progenitors. Proceedings XIII International Botanical Congress , Sydney, Australia. Carr DJ (ed.). p. 274.
9833. Liang GH, Wang RC, Niblett CL & Heyne EG. 1979. Registration of B-6-37-1 wheat germplasm. Crop Science 19: 421.
9834. Wang RC, Barnes EE & Cook LL. 1980. Transfer of wheat streak mosaic virus resistance from *Agropyron* to homoeologous chromosome of wheat. Cereal Research Communications 8: 2335-339.
9835. Riede, CR, & Anderson, JA. 1996. Linkage of RFLP markers to an aluminum tolerance gene in wheat. Crop Science 36: 905-909.
9836. Delibes A, Del Morala J, Martín-Sanchez JA, Mejias A, Gallego M, Casado D, Sin E & López-Braña I. 1997. Hessian fly-resistance gene transferred from chromosome $4M^v$ of *Aegilops ventricosa* to *Triticum aestivum.* Theoretical and Applied Genetics 94: 858-864.
9837. Korzun V, Malyshev S, Voylokov A & Börner A. 1997. RFLP-based mapping of three mutant loci in rye (*Secale cereale* L.) and their relation to homoeologous loci within the Gramineae. Theoretical and Applied Genetics 95: 468-473.
9838. Prabhakara Rao MV. 1996. Close linkage of the *Agropyron elongatum* gene *Sr26* for stem rust resistance to the centomere of wheat chromosome 6A. Wheat Information Service 82: 8-10.
9839. Korzun V, Röder M, Worland AJ & Börner A. 1997. Intrachromosomal mapping of genes for dwarfing (*Rht12*) and vernalization response (*Vrn1*) in wheat using RFLP and microsatellite markers. Plant Breeding 116: 227-232.
9840. Marais GF. 1997. Personal communication.
9841. Friebe B, Jellen EN & Gill BS. 1996. Verification of the identity of the Chinese Spring ditelosomic stocks Dt7DS and Dt7DL. Wheat Information Service 83: 31-32.

9842. Felix I, Martinant JP, Bernard M & Bernard S. 1996. Genetic characterization of storage proteins in a set of F_1-derived haploid lines in bread wheat. Theoretical and Applied Genetics 92: 340-346.
9843. Sibikeev SN, Kruprov VA, Voronina Sa & Elesin VA. 1996. First report of leaf rust pathotypes virulent on highly effective *Lr*-genes transferred from *Agropyron* species to bread wheat. Plant Breeding 115: 276-278.
9844. Huang XQ, Hsam SLK & Zeller FJ. 1997. Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.). IX. Cultivars, landraces and breeding lines grown in China. Plant Breeding 116: 233-238.
9845. Williams KJ, Fisher JM & Langridge P. 1994. Identification of RFLP markers linked to the cereal cyst nematode resistance gene *(Cre)* in wheat. Theoretical and Applied Genetics 89: 927-930.
9846. Faris J. 1997. Personal communication.
9847. Gornicki P, Faris J, King I, Podkowinski J, Gill B & Haselkorn R. 1998. Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded by a single gene on each of the three ancestral chromosome sets. Proceedings of the National Academy of Sciences U.S.A. 94: 14179-14184.
9848. Koba T, Takumi S & Shimada T. 1997. Isolation, identification and characterization of disomic and translocated barley chromosome addition lines of common wheat. Euphytica 96: 289-296.
9849. Tsujimoto H. 1995. Gametocidal genes in wheat and its relatives. IV. Functional relationships between six gametocidal genes. Genome 38: 283-289.
9850. Endo TR. 1982. Gametocidal chromosomes of three *Aegilops* species in common wheat. Canadian Journal of Genetics and Cytology 24: 201-206.
9851. Maan SS. 1975. Exclusive preferential transmission of an alien chromosome in common wheat. Crop Science 15: 278-292.
9852 Miller TE, Hutchinson J & Chapman V. 1982. Investigation of a preferentially transmitted *Aegilops sharonensis* chromosome in wheat. Theoretical and Applied Genetics 61: 27-33.
9853. Endo TR. On the *Aegilops* chromosome having gametocidal action on common wheat. Proceedings of the 5th International Wheat Genetics Symposium, New Delhi. Ramanujam, S. (ed.) 306-314.
9854. Endo TR & Tsunewaki K. 1975. Sterility of common wheat with *Aegilops triuncialis* cytoplasm. Journal of Heredity 66: 13-18.
9855. Endo TR & Katayama Y. 1978. Finding a selectively retained chromosome of *Aegilops caudata* L. in common wheat. Wheat Information Service 47-48: 32-35.
9856. Endo TR. 1988. Induction of chromosome structural changes by a chromosome of *Aegilops cylindrica* L. in common wheat. Journal of Heredity 79: 366-370.
9857. Endo TR. 1985. Two types of gametocidal chromosomes of *Aegilops sharonensis* and *Ae. longissima.* Japanese Journal of Genetics 60: 125-135.
9858. Tsujimoto H. 1994. Two new sources of gametocidal genes from *Aegilops longissima* and *Ae. sharonensis.* Wheat Information Service 79: 42-46.
9859. Liu JQ & Kolmer JA. 1997. Genetics of leaf rust resistance in Canadian spring wheats AC Domain and AC Taber. Plant Disease 81: 757-760.
9860. Sobkov TA & Sozinov AA. 1997. (Linkage mapping of the loci controlling spike morphological traits and seed storage proteins on the 1A chromosome in winter common wheats). Tsitologiya i Genetika 31(4): 18-26.
9861. Sobko TA & Sozinov AA. 1993. Genetic control of morphologic traits of a spike and the relationship with allelic variation of marker loci of chromosomes 1A and 1B of winter common wheat. Tsitologiya i Genetika (Eng vers) 27(5): 15-22. Russian version: 15-22.
9862. Hsam SLK, Huang XO, Ernst F, Hartl L & Zeller FJ. 1997. Chromosomal location of genes for resistance to powdery mildew in common wheat (*Triticum aestivum* L. em Thell). 5. Alleles at the *Pm1* locus. Manuscript.

9863. Bimb HP & Johnson R. 1996. Expression of the gene *Pm8* for powdery mildew resistance in wheat cultivars with the 1BL/1RS translocation which carries the gene *Yr9* for yellow rust resistance. 1996 Proceedings of the 9th European & Mediterranean Cereal Rusts & Powdery Mildews Conference, Lunteren, The Netherlands (Kema GHJ, Niks RE & Daamen RA, eds.) 247.
9864. Keller B, Schachermayr G & Feuillet C. 1996. Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10*, disease resistance locus of wheat. Proceedings of the 9th European and Mediterranean Cereal Rusts and Powdery Mildews Conference, Lunteren, The Netherlands (Kema GHJ, Niks RE & Daamen, eds.) pp. 34-36.
9865. Hanusová R, Bartos P & Zeller FJ. 1997. Characterization of the suppressor gene of powdery mildew resistance gene *Pm8* in common wheat (*Triticum aestivum* L.) cv. Regina. Journal of Applied Genetics 38: 11-17.
9866. Dong H, Quick JS & Zhang Y. 1997. Inheritance and allelism of Russian wheat aphid resistance in several wheat lines. Plant Breeding 116: 449-453.
9867. Prins R, Marais GF, Pretorius ZA, Janse BJH & Marais AS. 1997. A study of modified forms of the *Lr19* translocation of common wheat. Theoretical and Applied Genetics 95: 424-430.
9868. Prins R & Marais GF. 1997. A genetic study of the gametocidal effect of the *Lr19* translocation of common wheat. Manuscript.
9869. Delhaize E, Craig S, Beaton CD, Bennet RJ, Jagadish VC & Randall PJ. 1993. Aluminim tolerance in wheat (*Triticum aestivum* L.) 1. Uptake and distribution of aluminum in root species. Plant Physiology 103: 685-693.
9870. Hu XY, Ohm HW & Dweikat I. 1997. Identification of RAPD markers linked to the gene *PM1* for resistance to powdery mildew in wheat. Theoretical and Applied Genetics 94: 832-840.
9871. Dedryver F, Jubier MF, Thouvenin J & Goyeau H. 1996. Molecular markers linked to the leaf rust resistance gene *Lr24* in different wheat cultivars. Genome 39: 830-835.
9872. Prins R, Marais GF, Janse BJH, Pretorius ZA & Marais AS. 1996. A physical map of the *Thinopyrum*-derived *Lr19* translocation. Genome 39: 1013-1019.
9873. Galiba G, Quarrie SA, Sutka J, Morgounov A & Snape JW. 1995. RFLP mapping of the vernalization *(Vrn1)* and frost resistance *(Fr1)* genes on chromosome 5A of wheat. Theoretical Applied Genetics 90: 1174-1179.
9874. Laurie DA, Pratchett N, Bezant JH & Snape JW. 1995. RFLP mapping of five major genes and eight quantitative trait loci controlling flowering time in a winter x spring barley (*Hordeum vulgare* L.) cross. Genome 38: 575-585.
9875. Plaschke J, Börner A, Xie DX, Koebner RMD, Schlegel R & Gale MD. 1993. RFLP mapping of genes affecting plant height and growth habit in rye. Theoretical Applied Genetics 85: 1049-1054.
9876. Takahashi R, Yasuda S. 1971. Genetics of earliness and growth habit in barley. In: Proc 2nd International Barley Genetics Symposium, Nilan RA. (ed) Washington State University Press, pp 388-408.
9877. Dubcovsky J, Lijavetzky D, Appendino L, Tranquilli G & Dvorak JD. 1998. Comparative RFLP mapping of *Triticum monococcum* genes controlling vernalization requirement. Theoretical and Applied Genetics. In press.
9879. Law CN, Suarez E, Miller TE & Worland AJ. 1998. The influence of the group 1 chromosomes of wheat on ear-emergence times and their involvement with vernalization and day length. Heredity (In press).
9880. Snape JW, Dubcovsky J & Laurie D. 1998. Personal communication.
9881. Marais GF, Potgieter GF, Roux HS & le Roux J. 1994. An assessment of the variation for stem rust resistance in the progeny of a cross involving the *Triticum* species *aestivum, turgidum* and *tauschii*. South African Journal of Plants and Soil 11: 15-19.
9882. Worland AJ. 1986. Gibberellic acid insensitive dwarfing genes in southern European wheats. Euphytica 35: 857-866.

9883. Paderina EV, Hsam SLK & Zeller FJ. 1995. Identification of powdery mildew resistance genes in common wheat (*Triticum aestivum* L. em Thell.) VII Cultivars grown in Western Siberia. Hereditas 123: 103-107.
9884. Arbuzova VS, Efremova TT, Laikova LI, Maystrenko OI, Popova OM & Pshenichnikova TA. 1996. The development of precise genetic stocks in two wheat cultivars and their use in genetic analysis. Euphytica 89: 11-15.
9885. Ohm HW, Ratcliff RH, Patterson FL & Cambron S. 1997. Resistance to Hessian fly conditioned by genes *H19* and proposed gene *H27* of durum wheat line PI422297. Crop Science 37: 113-115.
9886. Cebert E, Ohm H, Patterson F, Ratcliff R & Cambron S. 1996. Genetic analysis of Hessian fly resistance in durum wheat. Agronomy Abstracts 88: 88.
9887. Ohm HW. 1988a. Personal communication.
9888. Ohm HW. 1988b. Personal communication
9889. McIntosh RA et al. 1998. Personal communication.
9890. Singh RP et al. 1998. Personal communciation
9891. Singh D, Park RF & McIntosh RA. 1998. Personal communication.
9892. Jones ERL & Clifford BC. 1996. Annual Report - U.K. Cereal Pathogen Virulence survey.
9893. Miura H, Parker BB & Snape JW. 1992. The location of major genes associated with quantitative trait loci on chromosome arm 5BL of wheat. Theoretical and Applied Genetics 85: 197-204.
9894. Cox TS. 1991. The contribution of introduced germplasm to the development of U.S. wheat cultivars. In: Use of Plant Introductions in Cultivar Development, Part I, Crop Science Society of America Special Publication No. 17, pp. 25-47.
9895. Knott DR. 1989. The Wheat Rusts - Breeding For Resistance. Springer-Verlag, Berlin.
9896. Naik S, Gill KS, Prakasa VS, Gupta VS, Tamhanka SA, Pujar S, Gill BS & Ranjekar PK. 1998. Identification of a STS marker linked to the *Aegilops speltoides* - derived leaf rust resistance gene *Lr28* in wheat. Theoretical and Applied Genetics (In press).
9897. Zhao XC, Batey IL, Sharp PJ, Crosbie G, Barclay I, Wilson R, Morell MK & Appels R. 1998. A single genetic locus associated with starch granule properties and noodle quality in wheat. Journal of Cereal Science 27: 7-13.
9898. Murai K & Tsunewaki K. 1993. Photoperiod-sensitive cytoplasmic male sterility in wheat with *Aegilops crassa* cytoplasm. Euphytica 67: 41-48.
9899. Murai K. 1997. Genetic analysis of fertility restoration against photoperiod-sensitive cytoplasmic male sterility in *Triticum aestivum* cv. Norin 61. Plant Breeding 116: 592-594.
98101. Korzun V, Balzer H-J, Balzer A, Bäumlein H & Börner A. 1996. Chromosomal location of three wheat sequences with homology to pollen allergen encoding, DNA replication regulating, and DNA (cytosine-5)-methyltransferase genes in wheat and rye. Genome 39: 1213-1215.
98102. Feuillet C, Schachermayr GM & Keller B. 1997. Molecular cloning of a new receptor-like kinase gene encoded at the *Lr10* disease resistance locus of wheat. Plant Journal 11: 45-52.
98103. Balzer H-J, Borysiuk L, Meyer H-M, Matzk F & Bäumlein H. 1998. A pollen allergen encoding gene is expressed in wheat ovaries. Plant Molecular Biology (In Press).
98104. Krugman T, Levy O, Snape JW, Rubin B, Korol A & Nevo E. 1997. Comparative RFLP mapping of the chlorotoluron resistance gene (*Su1*) in cultivated wheat (*Triticum aestivum*) and wild wheat (*Triticum dicoccoides*). Theoretical and Applied Genetics 94: 46-51.
98105. Cadalen T, Boeuf C, Bernard S & Bernard M. 1997. An intervarietal molecular marker map in *Triticum aestivum* L. em. Thell. and comparison with a map from a wide cross. Theoretical and Applied Genetics 94: 367-377.

98106. Schachermayr GM, Feuillet C & Keller B. 1997. Molecular markers for the detection of the wheat leaf rust resistance gene *Lr10* in diverse genetic backgrounds. Molecular Breeding 3: 65-74.
98107. Rouvès S, Boeuf C, Zwickert-Menteur S, Gautier MF, Joudrier P, Bernard M & Jestin L. 1996. Locating supplementary RFLP markers on barley chromosome 7 and synteny with homoeologous wheat group 5. Plant Breeding 115: 511-513.
98108. Liu B, Segal G, Vega JM, Feldman M & Abbo S. 1997. Isolation and characterization of chromosome-specific DNA sequences from a chromosome arm genomic library of common wheat. Plant Journal 11: 959-965.
98109. Segal G, Liu B, Vega JM, Abbo S, Rodova M & Feldman M. 1997. Identification of a chromosome-specific probe that maps within the *Ph1* deletions in common and durum wheat. Theoretical and Applied Genetics 94: 968-970.
98110. Ben Amer IM, Korzun V, Worland AJ & Börner A. 1997. Genetic mapping of QTL controlling tissue-culture response on chromosome 2B of wheat *(Triticum aestivum)* in relation to major genes and RFLP markers. Theoretical and Applied Genetics 94: 1047-1052.
98111. Pratchett N & Laurie DA. 1994. Genetic map location of the barley developmental mutant liguleless in relation to RFLP markers. Hereditas 120: 135-139.
98114. Coe EH & Neuffer MG. 1993. Gene loci and linkage map of corn (maize) (*Zea mays* 2N = 20). In: Genetic maps. (O'Brien SJ ed.). Ed. 6. Cold Spring Harbor Laboratory Press, Cold Spring Harbor: 157-189.
98116. Ahn SN & Tanksley SD. 1993. Comparative linkage maps of the rice and maize genomes. Proceeding of the National Academy of Sciences, USA. 90: 7980-7984.
98117. Börner A, Röder MS & Korzun V. 1997. Comparative molecular mapping of GA insensitive *Rht* loci on chromosomes 4B and 4D of common wheat (*Triticum aestivum*). Theoretical and Applied Genetics (In Press).
98118. Korzun V, Röder MS, Ganal MW, Worland AJ & Law CN. 1997 Genetic analysis of the dwarfing gene *(Rht8)* in wheat. Part I. Molecular mapping of *Rht8* on the short arm of chromosome 2D of bread wheat (*Triticum aestivum*). Theoretical and Applied Genetics (In Press).
98119. Korzun V, Börner A, Worland AJ, Law CN & Röder MS. 1997. Application of microsatellite markers to distinguish inter-varietal chromosome substitution lines of wheat (*Triticum aestivum* L.). Euphytica 95: 149-155.
98121. Röder MS, Korzun VN, Gill BS & Ganal MW. 1997. The physical mapping of microsatellite markers in wheat. Genome (In Press).
98124. Koluchii VT. 1987. Association of gliadin allelic variance with elements of productivity of winter wheat in F_2 hybrids from crossing the varieties Pionerskaya and Mironovskaya 808. In: Molecular Mechanisms of Genetic Processes, Abstracts of Reports of the Sixth All-Union Symposium (In Russian). Moscow: p. 121.
98125. Mori N, Moriguchi T & Nakamura C. 1997. RFLP analysis of nuclear DNA for study of phylogeny and domestication of tetraploid wheat. Genes and Genetic Systems 72: 153-161.
98126. Tsunewaki K. 1998. Personal communication.
98127. Mori N, Liu Y-G & Tsunewaki K. 1995. Wheat phylogeny determined by RFLP analysis of nuclear DNA. II. Wild tetraploid wheats. Theoretical and Applied Genetics 90: 129-134.
98129. Gautier MF & Joudrier P. 1998. Personal communication.
98130. Procunier JD, Townley-Smith TF, Fox S, Prashar S, Gray M, Kim WK, Czarnecki E & Dyck PL. 1995. PCR-based RAPD/DGGE markers linked to leaf rust resistance genes *Lr29* and *Lr25* in wheat (*Tricitum aestivum* L.). Journal of Genetics and Breeding 49: 97-92.

98131. Procunier JD, Knox RE, Bernier AM, Gray MA & Howes NK. 1997. DNA markers linked to a T10 loose smut resistance gene in wheat (*Triticum aestivum* L.). Genome 40: 176-179.
98132. Ma Z-Q, Saidi A, Quick JS & Lapitan NLV. 1998. Genetic mapping of Russian wheat aphid resistance genes *Dn2* and *Dn4* in wheat. Genome (In press).
98133. Mukai Y, Endo TE & Gill BS. 1990. Physical mapping of the 5S rRNA multigene family in common wheat. Journal of Heredity 81: 290-295.
98134. Dubcovsky J & Dvorak J. 1995. Ribosomal RNA multigene loci: nomads of the Triticeae genomes. Genetics 140: 1367-1377.
98135. Maan SS. 1992. A gene for embryo-endosperm compatibility and seed viability in alloplasmic *Triticum turgidum*. Genome 35: 772-7798
98136. Maan SS. 1994. Interactions between the *scs* and *Vi* genes in alloplasmic durum wheat. Genome 37: 210-216.
98137. Anderson JA & Maan SS. 1995. Interspecific nuclear-cytoplasmic compatibility controlled by genes on group 1 chromosomes in durum wheat. Genome 38: 803-808.
98138. Maan SS. 1992. Transfer of a species cytoplasm specific (*scs*) gene from *Triticum timopheevi* to *T. turgidum*. Genome 35:238-243.
98139. Gill K, Gill BS, Endo T & Taylor T. 1996. Identification and high-density mapping of gene-rich regions in chromosome group 1 of wheat. Genetics 144: 1883-1891.
98140. Martinez I, Bernard M, Nicolas P & Bernard S. 1994. Study of androgenetic performance and molecular characterisation of a set of wheat-rye addition lines. Theoretical and Applied Generics 89: 982-990.
98141. Dweikat I, Ohm H, Paterson F & Cambron S. 1997. Identification of RAPD markers for 11 Hessian fly resistance genes in wheat. Theoretical and Applied Genetics 94: 419-423.
98142. Snape JW, Leckie D, Parker BB & Nevo E. 1991. The genetical analysis and exploitation of differential responses to herbicides in crop species. In: Casely JC, Cussans G & Atkin RK (eds). Herbicide Resistance in Weeds and Crops. Butterworth-Heinemann, Oxfordshire, England. Pp. 305-317.
98144. de la Pena RC, Murray TD & Jones SS. 1997. Identification of an RFLP interval containing *Pch2* on chromosome 7AL in wheat. Genome. 40: 249-252.
98145. Rahman S, Abrahams S, Abbott D, Mukai Y, Samuel M, Morell MK & Appels R. 1997. A complex arrangement of genes at a starch branching enzyme I locus in the D-genome of wheat. Genome 40: 465-474.
98146. Limin AE, Danyluk J, Chauvin L-P, Fowler DB & Sarhan F. 1997. Chromosome mapping of low-temperature induced Wcs120 family genes and regulation of cold-tolerance expression in wheat. Molecular and General Genetics 253: 720-727.
98147. Goncharov NP & Konovalov AA. 1996. Inheritance of glucose phosphate isomerase, awnedness, hairy glume, and growth habit in *Aegilops speltoides* and *Aegilops aucheri*. Russian Journal of Genetics (Eng vers) 32: 571-576.
98148. Goncharov NP, Konovalov AA & Chikida NN. 1997. Genetic variation at the *GPI-1* loci among *Aegilops* and *Triticum* genera and phylogeny of polyploid wheat. Zhurnal Obzhckei Biologii 58(2): 75-79.
98149. Goncharov NP, Konovalov AA, Gaidalenok RF, Goryachkovskaya TN, Tseveleva ON, Pel'tek SE, Litkovskaya NP & Khristov YA. 1997. Genetic mapping of the short arm of chromosome 1B in common wheat cultivar Salmon. Russian Journal of Genetics (Eng vers) 33: 387-392.
98150. D'Ovidio R & Porceddu E. 1996. PCR-based assay for detecting 1B-genes for low molecular weight glutenin subunits related to gluten quality properties in durum wheat. Plant Breeding 115: 413-415.
98151. D'Ovidio R, Simeone M, Masci S & Porceddu E. 1997. Molecular characterization of a LMW-GS gene located on chromosome 1B and the

development of primers specific for the Glu-B3 complex locus in durum wheat. Theoretical and Applied Genetics 95: 1119-1126.

98152. Johansson E, Henriksson P, Svensson G & Heneen WK. 1993. Detection, chromosomal location and evaluation of the functional value of a novel high Mr glutenin subunit found in Swedish wheats. Journal of Cereal Science 17: 237-245.

98153. Metakovsky EV & Branlard G. 1998. Genetic diversity of French common wheat germplasm based on gliadin alleles. Theoretical and Applied Genetics 96: 209-218.

98154. Dubcovsky J, Echaide M, Giancola S, Rousset M, Luo MC, Joppa LR & Dvorak J. 1997. Seed-storage-protein loci in RFLP maps of diploid, tetraploid, and hexaploid wheat. Theoretical and Applied Genetics 95: 1169-1180.

98155. Liu C-Y. 1995. Identification of a new low-Mr glutenin subunit locus on chromosome 1B of durum wheat. Journal of Cereal Science 21: 209-213.

98156. McIntosh RA, Hart GE, Devos KM & Gale MD. 1997. Catalogue of gene symbols for wheat: 1997 Supplement. Wheat Information Service 85: 56-81.

98157. Brown GN. 1997. The inheritance and expression of leaf chlorosis associated with gene *Sr2* for adult plant resistance to wheat stem rust. Euphytica 95: 67-71.

98158. Niewoehner AS & Leath S. 1998. Virulence of *Blumeria graminis* f. sp. *tritici* on winter wheat in the eastern United States. Plant Disease 82: 64-68.

98159. Hussein T, Bowden RL, Gill BS & Cox TS. 1998. Chromosome location of leaf rust resistance gene *Lr43* from *Aegilops tauschii* in common wheat. Crop Science 37: 1764-1766.

Wheat Information Service
Number 86: 92–100 (1998)

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.

1997

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(29)
ACCN:001841207 CTLN:4100061
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Seo, Y.W.;Johnson, J.W.;Jarret, R.L.
AFFN:Dep. Agronym, Korea Univ., Anam-Dong, Seongbuk-Gu, Seoul 136-701,Korea
TITL:A molecular marker associated with the H21 Hessian fly resistance gene in wheat
HTIL:MOL. BREED.
HSSN:1380-3743
HYER:19970600
HCOL:vol. 3, no. 3, pp. 177-181

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(30)
ACCN:001843249 CTLN:4102560
ABSJ:G (Genetics Abstracts)
AUTH:Li, Y.-M.;Chaney, R.L.;Schneiter, A.A.;Miller, J.F.;Elias, E.M.; Hammond, J.J.
AFFN:USDA-ARS Environ. Chem. Lab., Beltsville, MD 20705, USA
TITL:Screening for low grain cadmium phenotypes in sunflower, durum wheat and flax
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 1, pp. 23-30

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(31)
ACCN:001843269 CTLN:4102580
ABSJ:G (Genetics Abstracts)
AUTH:Ogihara, Y.;Futami, K.;Tsuji, K.;Murai, K.
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., Yokohama 244, Japan
TITL:Alloplasmic wheats with Aegilops crassa cytoplasm which express photoperiod-sensitive homeotic transformations of anthers, show alterations in mitochondrial DNA structure and transcription
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:19970600
HCOL:vol. 255, no. 1, pp. 45-53

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(32)
ACCN:001843311 CTLN:4102622
ABSJ:G (Genetics Abstracts)
AUTH:Niemeyer, H.M.;Jerez, J.M.
AFFN:Depto. de Cienc. Ecologicas, Fac. de Cienç., Univ. de Chile, Casilla 653, Santiago, Chile
TITL:Chromosomal location of genes for hydroxamic acid accumulation in Triticum aestivum L. (wheat) using wheat aneuploids and wheat substitution lines
HTIL:HEREDITY
HSSN:0018-067X
HYER:19970700
HCOL:vol. 79, no. pt. 1, pp. 10-14

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(33)
ACCN:001845767 CTLN:4105340
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Zantoko, L.;Shukle, R.H.*
AFFN:USDA-ARS, Dep. Entomol., Purdue Univ., West Lafayette, IN 47907, USA
TITL:Genetics of virulence in the Hessian fly to resistance gene H13 in wheat
HTIL:J. HERED.
HSSN:0022-1503
HYER:19970400
HCOL:vol. 88, pp. 120-123

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(34)
ACCN:001846430 CTLN:4106434
ABSJ:G (Genetics Abstracts)
AUTH:Watanabe, N.;Kobayashi, S.;Furuta, Y.
AFFN:Lab. Genet. and Plant Breeding, Fac. Agric., Gifu Univ., Gifu 501-11, Japan
TITL:Effect of genome and ploidy on photosynthesis of wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 3, pp. 303-309

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(35)
ACCN:001846434 CTLN:4106438
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Bozorgipour, R.;Snape, J.W.*
AFFN:JI Cent., Colney Lane, Norwich NR4 7UJ, UK
TITL:An assessment of somaclonal variation as a breeding tool for generating herbicide/tolerant genotypes in wheat (Triticum aestivum L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 3, pp. 335-340

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(36)
ACCN:001846442 CTLN:4106446
ABSJ:G (Genetics Abstracts)
AUTH:Subedi, K.D.;Budhathoki, C.B.;Subedi, M.
AFFN:Plant Environ. Lab., Univ. Reading, Cutbush Lane, Shinfield, Reading RG2 9AD, UK
TITL:Variation in sterility among wheat (Triticum aestivum L.) genotypes in response to boron deficiency in Nepal
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 95, no. 1, pp. 21-26

---

(37)
ACCN:001846447 CTLN:4106451
ABSJ:G (Genetics Abstracts)
AUTH:Taketa, S.;Takeda, K.
AFFN:Res. Inst. for Bioresources, Okayama Univ., Chuo 2-20-1, Kurashiki, Okayama 710, Japan
TITL:Expression of dominant marker genes of barley in wheat-barley hybrids
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19970400
HCOL:vol. 72, no. 2, pp. 101-106

---

(38)
ACCN:001846479 CTLN:4106483
ABSJ:G (Genetics Abstracts)
AUTH:Takumi, S.;Shimada, T.
AFFN:Res. Inst. Agric. Resour., Ishikawa Agric. Coll., Nonoichi-machi, Ishikawa 921, Japan
TITL:Variation in transformation frequencies among six common wheat cultivars through particle bombardment of scutellar tissues
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19970400
HCOL:vol. 72, no. 2, pp. 63-69

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(39)
ACCN:001846483 CTLN:4106487
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Brown, G.N.
AFFN:Univ. Sydney Plant Breeding Inst., Cobbitty, Private Bag 11, Camden, NSW 2570, Australia
TITL:The inheritance and expression of leaf chlorosis associated with gene Sr2 for adult plant resistance to wheat stem rust
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 95, no. 1, pp. 67-71

---

(40)
ACCN:001846487 CTLN:4106491
ABSJ:G (Genetics Abstracts)
AUTH:Ren, S.X.;McIntosh, R.A.;Lu, Z.J.
AFFN:Inst. Genet., Chinese Acad. Sci., Beijing 100101, China
TITL:Genetic suppression of the cereal rye-derived gene Pm8 in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 3, pp. 353-360

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(41)
ACCN:001846491 CTLN:4106495
ABSJ:G (Genetics Abstracts)
AUTH:Brisibe, E.A.;Olesen, A.*;Andersen, S.B.
AFFN:Sect. Plant Breeding and Biotechnol., Dep. Agric. Sci., Royal Veterinary and Agric. Univ., Thorvaldsensvej 40, Copenhagen DK - 1871, Denmark
TITL:Characterization of anther culture-derived cell suspensions exclusively regenerating green plantlets in wheat (Triticum aestivum L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 3, pp. 321-329

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(42)
ACCN:001846494 CTLN:4106498
ABSJ:G (Genetics Abstracts)
AUTH:Anamthawat-Jonsson, K.;Boedvarsdottir, S.K.;Bragason, B.Th.; Gudmundsson, J.;Martin, P.K.;Koebner, R.M.D.

AFFN:Agric. Res. Inst., Keldnaholt, Reykjavik, IS-112, Iceland
TITL:Wide hybridization between wheat (Triticum L.) and lymegrass (Leymus Hochst.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 3, pp. 293-300

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(43)
ACCN:001846751 CTLN:4106755
ABSJ:G (Genetics Abstracts)
AUTH:Mao, L.;Devos, K.M.;Zhu, L.;Gale, M.D.*
AFFN:John Innes Centre, Norwich Research Park, Colney, Norwich NR4 7UH, UK
TITL:Cloning and genetic mapping of wheat telomere-associated sequences
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:19970500
HCOL:vol. 254, no. 5, pp. 584-591

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(44)
ACCN:001846776 CTLN:4106780
ABSJ:G (Genetics Abstracts)
AUTH:Rogers, W.J.;Miller, T.E.;Payne, P.I.;Seekings, J.A.;Sayers, E.J.;Holt, L.M.;Law, C.N.
AFFN:Universidad Nacional del Centro de la Provincia de Buenos Aires, Av. Intendente Giraut s/n, C.C. 178, (7300) Azul, Provincia de Buenos Aires, Argentina
TITL:Introduction to bread wheat (Triticum aestivum L.) and assessment for bread-making quality of alleles from T. boeoticum Boiss. ssp. thaoudar at Glu-A1 encoding two high-molecular-weight subunits of glutenin
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 1, pp. 19-29

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(45)
ACCN:001846779 CTLN:4106783
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Spetsov, P.;Mingeot, D.;Jacquemin, J.M.;Samardjieva, K.;Marinova, E.
AFFN:Institute of Wheat and Sunflower 9520, General Toshevo, Bulgaria
TITL:Transfer of powdery mildew resistance from Aegilops variabilis into bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 1, pp. 49-54

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(46)
ACCN:001846793 CTLN:4106797
ABSJ:G (Genetics Abstracts)
AUTH:Cao, W.;Scoles, G.J.;Hucl, P.
AFFN:Department of Crop Science and Plant Ecology, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N 5A8
TITL:The genetics of rachis fragility and glume tenacity in semi-wild wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 1, pp. 119-124

---

(47)
ACCN:001846799 CTLN:4106803
ABSJ:G (Genetics Abstracts)
AUTH:Ueno, K.;Takahashi, H.
AFFN:Laboratory of Plant Resources, Faculty of Bioindustry, Tokyo University of Agriculture, Abashiri, Hokkaido, 099-24, Japan
TITL:Varietal variation and physiological basis for inhibition of wheat seed germination after excessive water treatment
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 2, pp. 169-173

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(48)
ACCN:001846810 CTLN:4106814
ABSJ:G (Genetics Abstracts)
AUTH:Lukaszewski, A.J.
AFFN:Department of Botany and Plant Sciences, University of California, Riverside, CA 92521-0124, USA
TITL:Further manipulation by centric misdivision of the 1RS.1BL translocation in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 3, pp. 257-261

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(49)
ACCN:001846813 CTLN:4106817
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Ma, H.;Singh, R.P.;Mujeeb-Kazi, A.
AFFN:International Maize and Wheat Improvement

Center (CIMMYT), Lisboa 27, Apdo. Postal 6-641, 06600 Mexico, D.F
TITL:Resistance to stripe rust in durum wheats, A-genome diploids, and their amphiploids
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 3, pp. 279-286

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(50)
ACCN:001846814 CTLN:4106818
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Beharav, A.;Golan, G.;Levy, A.
AFFN:Institute of Field Crops, Israel Gene Bank for Agriculture Crops, Agricultural Research Organization, The Volcani Center, P.O. Box 6, Bet Dagan 50250, Israel
TITL:Evaluation and variation in response to infection with Puccinia striiformis and Puccinia recondita of local wheat landraces
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 94, no. 3, pp. 287-293

---

(51)
ACCN:001847008 CTLN:4107012
ABSJ:G (Genetics Abstracts)
AUTH:Goldringer, I.;Brabant, P.;Gallais, A.
AFFN:Station de Genetique Vegetale, Ferme du Moulon, 91190 Gif sur Yvette, France
TITL:Estimation of additive and epistatic genetic variances for agronomic traits in a population of doubled-haploid lines of wheat
HTIL:HEREDITY
HSSN:0018-067X
HYER:19970700
HCOL:vol. 79, no. pt. 1, pp. 60-71

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(52)
ACCN:001847055 CTLN:4107059
ABSJ:G (Genetics Abstracts)
AUTH:Doerffling, K.;Doerffling, H.;Lesselich, G.;Luck, E.;Zimmermann, C.; Melz, G.;Juergens, H.U.
AFFN:Institute of General Botany, University of Hamburg, D-22609 Hamburg, Germany
TITL:Heritable improvement of frost tolerance in winter wheat by in vitro- selection of hydroxyproline-resistant proline overproducing mutants
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 93, no. 1, pp. 1-10

---

(53)
ACCN:001849086 CTLN:4109421
ABSJ:G (Genetics Abstracts)
AUTH:Segal, G.;Liu, B.;Vega, J.M.;Abbo, S.;Rodova, M.;Feldman, M.
AFFN:Dep. Plant Genet., Weizmann Inst. Sci., Rehovot 76100, Israel
TITL:Identification of a chromosome-specific probe that maps within the Ph1 deletions in common and durum wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970600
HCOL:vol. 94, no. 8, pp. 968-970

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(54)
ACCN:001851318 CTLN:4110107
ABSJ:G (Genetics Abstracts)
AUTH:Kim, H.S.;Ward, R.W.
AFFN:Dep. Crop and Soil Sci., Michigan State Univ., East Lansing, MI 48824, USA
TITL:Genetic diversity in Eastern U.S. soft winter wheat (Triticum aestivum L. em. Thell.) based on RFLPs and coefficients of parentage
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970300
HCOL:vol. 94, no. 3-4, pp. 472-479

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(55)
ACCN:001851321 CTLN:4110110
ABSJ:G (Genetics Abstracts)
AUTH:Castagna, R.;Gnocchi, S.;Perenzin, M.;Heun, M.
AFFN:Istituto Sperimentale per la Cerealicoltura, Via Mulino 3, 20079 S. Angelo Lodigiano (LO), Italy
TITL:Genetic variability of the wild diploid wheat Triticum urartu revealed by RFLP and RAPD markers
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970300
HCOL:vol. 94, no. 3-4, pp. 424-430

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(56)
ACCN:001851323 CTLN:4110112
ABSJ:G (Genetics Abstracts)
AUTH:Dweikat, I.;Ohm, H.;Patterson, F.;Cambron,

S.
AFFN:Agron. Dep., 1150 Lilly Hall, Purdue Univ., West Lafayette, IN 47907, USA
TITL:Identification of RAPD markers for 11 Hessian fly resistance genes in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970300
HCOL:vol. 94, no. 3-4, pp. 419-423

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(57)
ACCN:001851328 CTLN:4110117
ABSJ:G (Genetics Abstracts)
AUTH:Cuadrado, A.;Vitellozzi, F.;Jouve, N.;Ceoloni, C.
AFFN:Dep. Cell Biol. and Genet., Univ. Alcala de Henares, 28871 Alcala de Henares, Madrid, Spain
TITL:Fluorescence in situ hybridization with multiple repeated DNA probes applied to the analysis of wheat-rye chromosome pairing
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970300
HCOL:vol. 94, no. 3-4, pp. 347-355

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(58)
ACCN:001851332 CTLN:4110121
ABSJ:G (Genetics Abstracts)
AUTH:Ziegler, P.;Loos, K.;Wagner, G.
AFFN:Lehrstuhl Pflanzenphysiologie, Univ. Bayreuth, 95440 Bayreuth, Germany
TITL:Posttranslational origin of wheat leaf beta - amylase polymorphism
HTIL:J. PLANT PHYSIOL.
HSSN:0176-1617
HYER:19970400
HCOL:vol. 150, no. 5, pp. 537-545

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(59)
ACCN:001851353 CTLN:4110142
ABSJ:G (Genetics Abstracts)
AUTH:Nagoka, T.;Ogihara, Y.
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., Maioka-cho 641-12, Yokohama 244, Japan
TITL:Applicability of inter-simple sequence repeat polymorphisms in wheat for use as DNA markers in comparison to RFLP and RAPD markers
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970400
HCOL:vol. 94, no. 5, pp. 597-602

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(60)
ACCN:001851355 CTLN:4110144
ABSJ:G (Genetics Abstracts)
AUTH:Bryan, G.J.;Collins, A.J.;Stephenson, P.;Orry, A.;Smith, J.B.;Gale, M. D.
AFFN:John Innes Cent., Norwich Research Park, Colney, Norwich NR4 7UJ, UK
TITL:Isolation and characterisation of microsatellites from hexaploid bread wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970400
HCOL:vol. 94, no. 5, pp. 557-563

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(61)
ACCN:001851361 CTLN:4110150
ABSJ:G (Genetics Abstracts)
AUTH:Gregova, E.;Tisova, V.;Kraic, J.*
AFFN:Res. Inst. Plant Prod., Bratislavska Cesta 122, 92168 Piest'any, Slovak Rep.
TITL:Genetic variability at the Glu-1 loci in old and modern wheats (Triticum aestivum L.) cultivated in Slovakia
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:19970800
HCOL:vol. 44, no. 4, pp. 301-306

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(62)
ACCN:001851363 CTLN:4110152
ABSJ:G (Genetics Abstracts)
AUTH:Filatenko, A.;Hammer, K.
AFFN:N.I. Vavilov Inst. for Plant Ind., St. Petersburg, Russia
TITL:New descriptions of hulled wheats on the infraspecific level
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:19970800
HCOL:vol. 44, no. 4, pp. 285-288

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(63)
ACCN:001851376 CTLN:4110165
ABSJ:G (Genetics Abstracts)
AUTH:Pedersen, C.;Zimny, J.;Becker, D.;Jaehne-Gaertner, A.;Loerz, H.
AFFN:Environ. Sci. and Technol. Dep., Plant Genet., Risoe Natl. Lab., P.O. Box 49, DK-4000 Roskilde, Denmark
TITL:Localization of introduced genes on the chromosomes of transgenic barley, wheat and triticale by fluorescence in situ hybridization
HTIL:THEOR. APPL. GENET.

HSSN:0040-5752
HYER:19970500
HCOL:vol. 94, no. 6-7, pp. 749-757

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(64)
ACCN:001851397 CTLN:4110186
ABSJ:G (Genetics Abstracts)
AUTH:Peil, A.;Schubert, V.;Schumann, E.;Weber, W.E.
AFFN:Inst. Plant Breeding and Plant Prot., Martin-Luther-Univ. Halle- Wittenberg, D-06188 Hohenthurm, Germany
TITL:RAPDs as molecular markers for the detection of Aegilops markgrafii chromatin in addition and euploid introgression lines of hexaploid wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970500
HCOL:vol. 94, no. 6-7, pp. 934-940

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(65)
ACCN:001851401 CTLN:4110190
ABSJ:G (Genetics Abstracts)
AUTH:Hu, X.Y.;Ohm, H.W.;Dweikat, I.
AFFN:Dep. Agron., 1150 Lilly Hall, Purdue Univ., West Lafayette, IN 47907- 1150, USA
TITL:Identification of RAPD markers linked to the gene PM1 for resistance to powdery mildew in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970500
HCOL:vol. 94, no. 6-7, pp. 832-840

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(66)
ACCN:001851402 CTLN:4110191
ABSJ:G (Genetics Abstracts)
AUTH:Metakovsky, E.V.;Branlard, G.;Chernakov, V.M.;Upelniek, V.P.;Redaelli, R.;Pogna, N.E.
AFFN:Istituto Sperimentale per la Cerealicoltura, Via Mulino, 3, 20079 S. Angelo Lodigiano (Milano), Italy
TITL:Recombination mapping of some chromosome 1A-, 1B-, 1D- and 6B- controlled gliadins and low-molecular-weight glutenin subunits in common wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970500
HCOL:vol. 94, no. 6-7, pp. 788-795

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(67)
ACCN:001852260 CTLN:4111123
ABSJ:G (Genetics Abstracts)
AUTH:Niwa, K.;Horiuchi, G.;Hirai, Y.
AFFN:Laboratory of Plant Breeding, Faculty of Agriculture, Tokyo University of Agriculture, Tokyo 156, Japan
TITL:Production and characterization of common wheat with B chromosomes of rye from Korea
HTIL:HEREDITAS
HSSN:0018-0661
HYER:19970000
HCOL:vol. 126, no. 2, pp. 139-146

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(68)
ACCN:001852668 CTLN:4111531
ABSJ:G (Genetics Abstracts)
AUTH:Ben Amer, I.M.;Korzun, V.;Worland, A.J.;Boerner, A.
AFFN:Institut fuer Pflanzengenetik und Kulturpflanzenforschung (IPK), Correnssstrasse 3, D-06466 Gatersleben, Germany
TITL:Genetic mapping of QTL controlling tissue-culture response on chromosome 2B of wheat (Triticum aestivum L.) in relation to major genes and RFLP markers
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970600
HCOL:vol. 94, no. 8, pp. 1047-1052

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(69)
ACCN:001853364 CTLN:4112227
ABSJ:G (Genetics Abstracts)
AUTH:Hanusova, R.;Bartos, P.;Zeller, F.J.
AFFN:Res. Inst. Crop Prod., Drnovska 507, CZ-161 06 Praha 6-Ruzyne, Czech Rep.
TITL:Characterization of the suppressor gene of powdery mildew resistance gene Pm8 in common wheat (Triticum aestivum L.) cv. Regina
HTIL:J. APPL. GENET.
HSSN:1234-1983
HYER:19970000
HCOL:vol. 38, no. 1, pp. 11-17

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(70)
ACCN:001853741 CTLN:4112647
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Gana, J.A.;Sutton, F.*;Kenefick, D.G.
AFFN:Plant Sci. Dep., Box 2108, South Dakota State Univ., Brookings, SD 57007, USA
TITL:cDNA structure and expression patterns of a low-temperature-specific wheat gene tacr7

HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:19970700
HCOL:vol. 34, no. 4, pp. 643-650

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(71)
ACCN:001853904 CTLN:4112810
ABSJ:G (Genetics Abstracts)
AUTH:Ortiz, J.P.A.;Ravizzini, R.A.;Morata, M.M.;Vallejos, R.H.
AFFN:Inst. Grassland and Environ. Res., Plas Gogerddan, Aberystwyth, Dyfed SY23 3EB, UK
TITL:A rapid system for studying foreign gene expression in wheat (Triticum aestivum L.)
HTIL:J. APPL. GENET.
HSSN:1234-1983
HYER:19970000
HCOL:vol. 38, no. 2, pp. 123-130

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(72)
ACCN:001859238 CTLN:4200964
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Barro, F.;Rooke, L.;Bekes, F.;Gras, P.;Tatham, A.S.;Fido, R.;Lazzeri, P.A.;Shewry, P.R.;Barcelo, P.*
AFFN:IACR-Rothamsted, Harpenden, Herts AL5 2JQ, UK
TITL:Transformation of wheat with high molecular weight subunit genes results in improved functional properties
HTIL:NAT. BIOTECHNOL.
HSSN:1087-0156
HYER:19971100
HCOL:vol. 15, no. 12, pp. 1295-1299

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(73)
ACCN:001859257 CTLN:4200984
ABSJ:G (Genetics Abstracts)
AUTH:Jaradat, A.A.
AFFN:Intl. Plant Genetic Resour. Inst., West Asia and North Africa Regional Office, P.O. Box 5466, Aleppo, Syria
TITL:Wild emmer wheat in Jordan: III. A core collection
HTIL:ISR. J. PLANT SCI.
HSSN:0792-9978
HYER:19970000
HCOL:vol. 45, no. 1, pp. 45-51

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(74)
ACCN:001859258 CTLN:4200985
ABSJ:G (Genetics Abstracts)
AUTH:Jaradat, A.A.
AFFN:Jordan Univ. Sci. & Technol., P.O. Box 3030, Irbid, Jordan
TITL:Wild emmer wheat in Jordan: II. Genetic distances between and within populations
HTIL:ISR. J. PLANT SCI.
HSSN:0792-9978
HYER:19970000
HCOL:vol. 45, no. 1, pp. 39-44

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(75)
ACCN:001859868 CTLN:4201622
ABSJ:G (Genetics Abstracts)
AUTH:Mehta, B.;Sharma, S.K.;Luthra, O.P.
AFFN:Dep. Genet., CCS Haryana Agric. Univ., Hisar-125 004, India
TITL:Genetic architecture of harvest index and yield component characters in wheat
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:19970600
HCOL:vol. 13, no. 1, pp. 37-40

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(76)
ACCN:001859891 CTLN:4201645
ABSJ:G (Genetics Abstracts)
AUTH:Lima-Brito, J.;Guedes-Pinto, H.;Harrison, G.E.;Heslop-Harrison, J.S.
AFFN:Dep. Genet. and Biotechnol., Univ. Tras-os-Montes and Alto Douro, 5000 Vila Real, Portugal and Karyobiology Group, John Innes Cent., Colney Lane, NR4 7UH Norwich, England
TITL:Molecular cytogenetic analysis of durum wheat x tritordeum hybrids
HTIL:GENOME
HSSN:0831-2796
HYER:19970600
HCOL:vol. 40, no. 3, pp. 362-369

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(77)
ACCN:001863494 CTLN:4205632
ABSJ:G (Genetics Abstracts)
AUTH:Matzk, F.;Meyer, H.-M.;Horstmann, C.;Balzer, H.-J.;Baeumlein, H.; Schubert, I.
AFFN:Institut fuer Pflanzengenetik und Kulturpflanzenforschung, Correnssstrasse 3, D-06466 Gatersleben, Germany
TITL:A specific alpha -tubulin is associated with the initiation of parthenogenesis in 'Salmon' wheat lines
HTIL:HEREDITAS
HSSN:0018-0661
HYER:19970000

HCOL:vol. 126, no. 3, pp. 219-224

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(78)
ACCN:001863614 CTLN:4205752
ABSJ:G (Genetics Abstracts)
AUTH:Mori, N.;Miyashita, N.T.;Terachi, T.;Nakamura, C.
AFFN:Laboratory of Plant Genetics, Faculty of Agriculture, Kobe University, 1 Rokkodai-cho, Nada-ku, Kobe 657, Japan
TITL:Variation in coxII intron in the wild ancestral species of wheat
HTIL:HEREDITAS
HSSN:0018-0661
HYER:19970000
HCOL:vol. 126, no. 3, pp. 281-288

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(79)
ACCN:001863695 CTLN:4205834
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Lalonde, S.;Morse, D.;Saini, H.S.*
AFFN:Institut de recherche en biologie vegetale, Universite de Montreal, 4101 rue Sherbrooke est, Montreal, Canada H1X 2B2
TITL:Expression of a wheat ADP-glucose pyrophosphorylase gene during development of normal and water-stress-affected anthers
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:19970600
HCOL:vol. 34, no. 3, pp. 445-453

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(80)
ACCN:001864859 CTLN:4207107
ABSJ:G (Genetics Abstracts)
AUTH:Anderson, O.D.;Litts, J.C.;Greene, F.C.
AFFN:USDA, ARS, Western Regional Res. Cent., 800 Buchanan St., Albany, CA 94710, USA
TITL:The alpha -gliadin gene family. I. Characterization of ten new wheat alpha -gliadin genomic clones, evidence for limited sequence conservation of flanking DNA, and Southern analysis of the gene family
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970700
HCOL:vol. 95, no. 1-2, pp. 50-58

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(81)
ACCN:001864865 CTLN:4207113
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Liu, B.;Segal, G.;Vega, J.M.;Feldman, M.*;Abbo, S.
AFFN:Dep. Plant Genet., Weizmann Inst. Sci., Rehovot 76100, Israel
TITL:Isolation and characterization of chromosome-specific DNA sequences from a chromosome arm genomic library of common wheat
HTIL:PLANT J.
HSSN:0960-7412
HYER:19970500
HCOL:vol. 11, no. 5, pp. 959-965

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(82)
ACCN:001864888 CTLN:4207136
ABSJ:G (Genetics Abstracts)
AUTH:Galiba, G.;Kerepesi, I.;Snape, J.W.;Sutka, J.
AFFN:Agric. Res. Inst. Hungarian Acad. Sci., H-2462 Martonvasar, Hungary
TITL:Location of a gene regulating cold-induced carbohydrate production on chromosome 5A of wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970700
HCOL:vol. 95, no. 1-2, pp. 265-270

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(83)
ACCN:001864906 CTLN:4207154
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:De Block, M.;Debrouwer, D.;Moens, T.
AFFN:Plant Genetic Systems N.V., Jozef Plateaustraat 22, 9000 Gent, Belgium
TITL:The development of a nuclear male sterility system in wheat. Expression of the barnase gene under the control of tapetum specific promoters
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970700
HCOL:vol. 95, no. 1-2, pp. 125-131

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(84)
ACCN:001864926 CTLN:4207174
ABSJ:G (Genetics Abstracts)
AUTH:Bebeli, P.J.;Zhou, Z.;Somers, D.J.;Gustafson, J.P.
AFFN:Dep. Plant Breeding and Biometry, Athens Agric. Univ., Athens 11855, Greece
TITL:PCR primed with minisatellite core sequences yields DNA fingerprinting probes in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970700

HCOL:vol. 95, no. 1-2, pp. 276-283

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(85)
ACCN:001869451 CTLN:4214149
ABSJ:G (Genetics Abstracts)
AUTH:Heun, M.;Schaefer-Pregl, R.;Klawan, D.;Castagna, R.;Accerbi, M.;Borghi, B.;Salamini, F.*
AFFN:Max-Planck-Inst. Zuechtungsforschung, Carl-von-Linne-Weg 10, D-50829 Koeln, Germany
TITL:Site on einkorn wheat domestication identified by DNA fingerprinting
HTIL:SCIENCE (WASH.)
HSSN:0036-8075
HYER:19971100
HCOL:vol. 278, no. 5341, pp. 1312-1314

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(86)
ACCN:001875505 CTLN:4219245
ABSJ:G (Genetics Abstracts)
AUTH:Foote, T.;Roberts, M.;Kurata, N.;Sasaki, T.;Moore, G.*
AFFN:John Innes Cent., Norwich Res. Park, Colney, Norwich, NR4 7UH, UK
TITL:Detailed comparative mapping of cereal chromosome regions corresponding to the Ph1 locus in wheat
HTIL:GENETICS
HSSN:0016-6731
HYER:19971000
HCOL:vol. 147, no. 2, pp. 801-807

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(87)
ACCN:001876666 CTLN:4220674
ABSJ:G (Genetics Abstracts); D (Ecology Abstracts)
AUTH:Jaradat, A.A.
AFFN:Jordan Univ. Sci. & Technol., P.O. Box 3030, Irbid, Jordan
TITL:Wild emmer wheat in Jordan: I. Ecotypes and phenotypic variation
HTIL:ISR. J. PLANT SCI.
HSSN:0792-9978
HYER:19970000
HCOL:vol. 45, no. 1, pp. 31-37

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(88)
ACCN:001878391 CTLN:4223098
ABSJ:G (Genetics Abstracts)
AUTH:Taylor, G.J.;Basu, A.;Basu, U.;Slaski, J.J.;Zhang, Guichang;Good, A.
AFFN:Dep. Biol. Sci., Univ. Alberta, Edmonton, Alberta T6G 2E9, Canada
TITL:Al-induced, 51-kilodalton, membrane-bound proteins are associated with resistance to Al in a segregating population of wheat
HTIL:PLANT PHYSIOL.
HSSN:0032-0889
HYER:19970500
HCOL:vol. 114, no. 1, pp. 363-372

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(89)
ACCN:001880969 CTLN:4225999
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Vasil, I.K.;Anderson, O.D.
AFFN:Laboratory of Plant Cell and Molecular Biology, 1143 Fifield Hall, University of Florida, Gainesville, FL 32611-0690, USA
TITL:Genetic engineering of wheat gluten
HTIL:TRENDS PLANT SCI.
HSSN:1360-1385
HYER:19970800
HCOL:vol. 2, no. 8, pp. 292-297

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(90)
ACCN:001892563 CTLN:4238494
ABSJ:G (Genetics Abstracts)
AUTH:Takvorian, A.;Coville, J.L.;Haouazine-Takvorian, N.;Rode, A.;Hartmann, C.
AFFN:Inst. de Biotechnologie des Plantes, URA CNRS 1128, Batiment 630, Univ. de Paris Sud, F-91405 Orsay, France
TITL:The wheat mitochondrial rps13 gene: RNA editing and co-transcription with the atp6 gene
HTIL:CURR. GENET.
HSSN:0172-8083
HYER:19970000
HCOL:vol. 31, no. 6, pp. 497-502

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(91)
ACCN:001892822 CTLN:4238853
ABSJ:G (Genetics Abstracts)
AUTH:Rodriguez-Quijano, M.;Nieto-Taladriz, M.T.;Carrillo, J.M.
AFFN:Unidad de Genetica, E.T.S.I. Agronomos, Univ. Politecnica, 28040- Madrid, Spain
TITL:Variation in B-LMW glutenin subunits in Einkorn wheats
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:19971200
HCOL:vol. 44, no. 6, pp. 539-543

Wheat Information Service
Number 86: 101 (1998)

Editorial remarks

Time has come for the 9th International Wheat Genetics Symposium at Saskatoon, Canada. The symposium (Aug.2-7) involves 8 oral and 3 poster sessions with workshops and field trip. The detail information can be obtained through the internet (http://www.usask.ca/agriculture/cropsci/winter-wheat/9th-iwgs/acc.htm/), or the latest issue of WIS. WIS will open an information desk in the lobby during the symposium. Let's enjoy to communicate each other and learn research progress from wheat colleagues.

In the present issue, we are glad to have a good-timing report by Dr. D. R. Knott, co-chairperson of the 9th IWGS, reviewing production and research of wheat in Canada. Also, the efforts by Drs. McIntosh and others on the catalogue of gene symbol (1998 suppl.) should be thanked, which will guarantee, for sure, the success of 9th IWGS.

In the symposium, it is also timely and important to have a workshop on "Global wheat genetic resources networks and conservation of wheat experimental genetic stocks" in the evening of Aug. 3. Since genetic erosion of landraces and wild species has been serious in worldwide scale, and since the genetic stocks have become one of critical bases for the research especially under the modern advancement of molecular techniques, we should not compete but cooperate for conservation of these materials by overcoming narrow-sense nationalism. Issues to be discussed should be sent to Dr. T. Endo (organizer of the workshop) through e-mail; endo@kias.kyoto-u.ac.jp.

Recent volumes of WIS have published informal research information, research proposal, materials or methods as Research Information. The articles are not reviewed, but because of space limitation and for the journal qualification, we have to select among the contributions. The style format for Research Information is not fixed but follow the instructions in the front page (within two printed pages).

During last years, proportion of acceptance for the research articles (reviewed by members of editorial board) is about 60%. The most of rejected ones are because of regional reports of variety performance, but not for international-interest. For these cases, I would suggest to describe in your manuscript why your research or trial is important internationally to be published. Please keep in mind to contribute to international advancement of wheat genetics.

Thank you also for many describers for their financial contribution to WIS. The contributors will receive a beautiful card of receipt.

See you in midland of Canadian wheat in August.

T.S. (Secretary of WIS)

PS: A photo of the article by J. Schulz-Schaeffer in the previous issue No. 86 was not clear in print. Please substitute the attached sheet page 21-22 of No. 86.

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