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Research article

Effect of seed size on the tissue culture response of callus from mature embryos of wheat species

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Summary

Effect of seed size on the culture response of callus from mature embryos of different genotypes of diploid (*T. monococcum* L. and *T. boeoticum* L.), tetraploid (*T. durum* Desf. 'Kunduru-1149') and hexaploid (*T. aestivum* L. 'Bezostaja-1') wheat was investigated using recently developed endosperm-supported mature embryo culture technique. After the separation of seeds among each genotype as being large and small, they are imbibed and wounded by moving the embryos from the seed without excision completely. Following their incubation in 8mg/l 2,4-dichlorophenoxyacetic acid (2,4-D) solution for callus induction, they are transferred onto auxin-free Murashige-Skoog (MS) medium for regeneration. Callus induction frequency, fresh weight of callus, regeneration capacity of callus and culture efficiency were found significantly higher in large seeds compare to small seeds in all genotypes. There were also significant correlation between seed weight and callus weight (r=0.86**) as well as callus weight and regenerative callus number (r=0.85**). These results suggested that efficient regenerative callus induction from endosperm-supported mature embryo culture of wheat could be obtained by using large seeds. Therefore, this technique provides an alternative use of wheat mature embryos as an explant which unlike immature embryos, are available at every periods of each year in unlimited quantities.

Key words: *Triticum* spp., Tissue culture, Embryo culture, Callus induction, Plant regeneration.

Introduction

The achievement of biotechnological methods used for improving some agricultural properties of

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plants, like resistance and quality, depends on development of the most suitable callus and regeneration system for each genotype. As for other plants, callus can be formed from cereals by using different explants and thus regenerative plants can be obtained. Similarly for somatic callus culture of wheat, several explants such as immature embryo (Sears and Deckard 1982; Felfoldi and Purnhauser 1992; Bohorova et al. 1995), immature inflorescence (Ozias-Akins and Vasil 1982; Maddock et al. 1983; Sharma et al. 1995), mature embryo (Ozias-Akins and Vasil 1983; Heyser et al. 1985; Kato et al. 1991), mesocotyl (Yurkova et al. 1982), seed (Gosch-Wackerle et al. 1979), apical meristem (McHugen 1983) and young leaves (Zamora and Scott 1983) were used. Immature embryos usually are the most successfully used explants (Maddock et al. 1983; and Redway et al. 1990). However, these embryos are available only for limited periods each year thus makes their usage difficult.

Conversely, mature embryos are available without limit at any time, but are the least frequently used as an explant source because of the low frequency of callus induction. However, recently developed techniques (Bartok and Sagi 1990; Ahmed et al. 1992; Özgen et al. 1996) such as endosperm-supported mature embryo methods have been approved to induce callus quicker and with higher regeneration capacity depending on the genotypes (Özgen et al.1996, 1998). As a known fact, callus induction and regeneration is influenced by the genotype (Sears and Deckard 1982; Mathias and Simpson 1986; Chowdhury et al. 1991), source of explant (Ozias-Akins and Vasil 1982; Redway et al.1990) and culture media (Mathias and Simpson 1986; Fennel et al. 1996). Besides, in endosperm-supported mature embryo culture, the size of the seed and consequently the size of the endosperm may additionally influence the callus induction and plant regeneration, since calli use the metabolites of the endosperm.

The objective of this study was to reveal the correlation between the different seed sizes and responses of mature embryo culture, in different wheat (*Triticum* spp.) genotypes using endosperm-supported mature embryo culture method.

Materials and methods

Four species of three ploidy groups of wheat; diploid (*T. monococcum* L. and *T. boeoticum* L.), tetraploid (*T. durum* Desf. 'Kunduru-1149') and hexaploid (*T. aestivum* L. 'Bezostaja-1') were used as sources of mature embryos. For each genotype, seed samples were grouped as large and small after they were sieved.

Seeds were surface sterilized for 5 min in 70% (v/v) ethanol, rinsed two times with sterile distilled water and followed by 25 min incubation in a commercial sodium hypochlorite solution containing a few drops of Tween 20. Finally, they were rinsed thoroughly at least 7 times with sterile distilled water. The seeds were then imbibed in sterile water for 11 h at 26°C. For hulled wheats, surface sterilization and imbibition procedures were applied after the hulls are removed.

For callus induction, mature embryos were aseptically moved slightly with a scalpel but not excised and were placed furrow downwards in sterile 10 cm petri dishes containing 8 mg/l 2,4-D, pH 5.8 solution which was autoclaved at 121°C for 15 minutes. Afterwards, they were left for incubation at 26°C in the dark for 11 days. At the end of the incubation period, the number of calli and their fresh weights were calculated.

The calli were transferred into hormone-free MS medium (Murashige and Skoog 1962) containing (2mg/l) glycine, (20g/l) sucrose and (7g/l) agar at pH 5.8. The transferred callus

cultures were incubated at 26°C in the dark for 3 weeks and grown further at 26°C 16 h light and 8 h dark period in a fresh medium prepared in the same way for regeneration. Photoperiod was obtained by using 40W tungsram (1500 lux) fluorescence lights.

A completely randomized design with three replications per seed group for each genotype was used. Petri dishes containing 20 seeds were considered the units of replication (total 120 seeds per genotype). The effect of species on culture responses was determined by analysis of variance and least significant difference (LSD) tests. Correlation coefficients were calculated for relationships between different characters. Differences between large and small seeds were evaluated with the chi-square test for independence (Steele and Torrie 1960).

Results and discussion

Beginning from the third day, an apparent callus formation is observed at the mature embryo of different genotypes according to their sizes. As a known fact, in methods where other explants are used, the callus inductions were observed to change between 10 to 21 days depending on the tissue (Sears and Deckard 1982; Lazar et al. 1983; Mathias and Simpson 1986). The reasons of faster calli formation, can be the result of wounding of the embryo due to its slight movement from the seed and as a response start of meristematic activity within the tissue as well as the use of natural sources of the endosperm without the requirement of adaptation as seen in the artificial media (Bartok and Sagi 1990). As a result of calculation of calli number and weight at the 11th day of the culture, when maximum weight and size are reached, there observed a significant difference within each genotype with respect to their seed size.

During the formation of callus besides of genotypic factors, the effects of nutritional supplements of the culture media are well known (Mathias and Simpson 1986; Kato et al. 1991). Also, correlation between seed size and several physiological events such as germination of the seed and development of the plantlet are also known to be significantly important (Kalakanavar et al. 1989; Ries and Everson 1973). Since in the endosperm-supported mature embryo culture method, nutritive materials of the endosperm are used during the formation of the calli, the amount of these materials with respect to seed size becomes another significant factor. Therefore, as shown in Table 1, for the cultured embryos of two different seed sizes for each genotype, while the response of callus induction of large seed changes between 90% to 100%, this value was observed to be between 76.6% to 88.3% for small size seeds. In the species, the variation of the callus induction ability with respect to seed size was also found to be statistically significant.

Such significant difference between calli fresh weight and seed size was also observed when compared both interspecifically and intraspecifically. In contrast, while genotypically higher 1000-kernel weight containing hexaploid (*T. aestivum*, 48.2±0.33g) and tetraploid (*T. durum*, 58.2±0.86g) wheats reached to highest average callus fresh weight (1462.0g and 1442.3g, respectively) at their large seed group, smaller 1000-kernel weight containing diploid wheats (*T. boeoticum*, 24.5±0.39g and *T. monococcum*, 23.8±0.49g) reached to much lower average callus fresh weight (1170.7g and 1051.0g, respectively) at their large seed group. When each species was examined within itself, mean weight of callus of large seed group was also found to be significantly higher than the small seed group. Seed size was observed to have obviously significant effect ($P<0.05$) on the weight of callus, especially when the results from the large seeds both genotypically and specially selected ones among the species, were compared with the small seeds.

As stated by Vasil (1987), embryonic calli with high regeneration capacity consist of low intercellular space containing compact tissue. Thus, such tissues of calli are expected to be heavier and as a consequence, callus fresh weight may be used as a good indicator of regeneration capacity. Besides, when the regeneration capacity of calli for each species were examined, calli with higher weight from large seeds had also higher regeneration capacity ($P<0.01$) than calli with lower weight from small seeds. This has also reflected on the culture efficiency of large seeds, which changed between 88.3%–93.3% whereas in small seeds of each species such change occurred with significant decrease ($P<0.01$) between 60%–65% (Table 1).

In conclusion, the results suggested that seed size have profound effect not only on the calli formation, but also on the fresh weight dependent increase in the regeneration capacity of those calli. It was also possible to support these results when the correlation values between seed size

Table 1. Embryo culture responses of large and small seeds in wheat species

Species and seed sizes	1000-seed weight (g)	Callus induction (%)	Total weight of callus (g)	Mean weight of callus (g)	Regeneration capacity of callus (%)[1]	Culture efficiency (%)[2]
T. aestivum						
large	48.2±0.33 b	100.0	4386	1462.0 a	90.0	90.0
small	21.1±0.62 e	88.3	2627	875.7 d	67.9	60.0
χ^2		12.5**			14.7**	22.4**
T. durum						
large	58.2±0.86 a	98.3	4327	1442.3 a	91.5	90.0
small	31.9±0.28 c	90.0	2880	960.0 d	72.2	65.0
χ^2		6.3*			12.6**	17.2**
T. boeoticum						
large	24.5±0.39 d	100.0	3512	1170.7 b	93.3	93.3
small	13.6±0.28 g	78.3	2147	715.7 e	80.8	63.3
χ^2		24.4**			7.0**	24.7**
T. monococcum						
large	23.8±0.49 d	90.0	3153	1051.0 c	98.1	88.3
small	15.3±0.32 f	76.6	2054	684.7 e	82.6	63.3
χ^2		6.5*			13.8**	15.7**

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

a–g: Means followed by the same letter are not significantly different at 0.05 probability level

1) No. of regenerable calli / No. of calli induced x 100

2) No. of regenerable calli / No. of embryos cultured x 100

(Regenerable callus = Nodular callus with green spots)

and total callus weight (r=0.86**) as well as between total callus weight and regenerative callus amount (r=0.85**) were examined. Significant positive correlation between callus induction and number of plants regenerated have been reported previously (Özgen et al. 1996). Finally, it is possible to conciliate that when the endosperm-supported mature embryo culture method is applied on genotypes with selectively larger seed size, callus induction and its regeneration can be increased significantly and mature embryos can be used as an effective explant source in wheat tissue culture.

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Research article

Characterization of dwarf trait in the tetraptoid wheat landrace, Aiganfanmai

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Summary

Aiganfanmai is a dwarfing tetraploid wheat (*Triticum turgidum* L.) landrace native to China. Genetic analysis on the dwarf trait of Aiganfanmai was carried out by crossing with the tall tetraploid wheat landrace Fenzhilanmai. χ^2 analysis revealed that F_2 population from the cross between Aiganfanmai and Fenzhilanmai segregated into a ratio of 1 (dwarf) : 3 (tall), which means that the dwarf trait of Aiganfanmai was controlled by a single recessive *Rht* (reduced height) gene. This conclusion was confirmed by the backcross test that showed 1 : 1 segregation in BC_1 progeny (F_1 x Aiganfanmai). The dwarf subpopulation in F_2 was significantly different from Aiganfanmai in the mean and variance of modified plant height, indicating that some modifiers for dwarfism existed. In addition, the reaction of seedlings of Aiganfanmai to the hormone gibberellic acid (GA) was investigated by using the GA-insensitive variety, Tom Thumb as check material. The measures of coleoptile and the first leaf of seedlings after GA-treatment indicated that the dwarf trait of Aiganfanmai was GA-sensitive. Based on these results, the usage of Aiganfanmai in lodging resistance breeding was discussed

Key words: Dwarf, Landrace, *Rht* gene, Tetraploid wheat, *Triticum turgidum*

Introduction

The development of short-straw high-yielding varieties to avoid lodging has been an important objective of breeding programs in wheat (*Triticum aestivum* L.) (Lupton 1987). This is partly because short-straw wheats allow further increases of yield to be obtained by their ability to utilize higher level of artificial fertilizer. The use of dwarf germplasm in breeding have contributed very much to the 'Green Revolution' of improved wheat production in the world. Nevertheless, the creation of and research on new dwarf germplasm is still very interesting to present wheat breeders.

Some changes in chromosome number could cause short-straw wheat (Law et al. 1987; Xue

et al. 1991). However, they were of little use in high-yield breeding programs because of their poor agronomic performance. Contrarily, the dwarf germplasm that carried some major reducing height (*Rht*) genes were important in agriculture. Up to now, 26 *Rht* genes were found and studied in dwarf wheat (McIntosh et al. 1998). But none of them intrinsically belonged to tetraploid wheat (*T. turgidum*) species. Breeders were compelled to use hexaploid wheat dwarf materials in tetraploid wheat lodging-resistance breeding by interspecies crossing, which needs many times of artificial backcrossing with tetraploid wheat to eliminate the genetic constitution of hexaploid wheat other than the *Rht* gene and thus is ineffective. So dwarf germplasm have been ardently desired at the tetraploid level. Gale et al. (1981) reported the semi-dwarfism in tetraploid wheat which *Rht* genes were introduced from hexaploid wheat Norin 10. Borner et a1 (1987) identified GA insensitive tetraploid wheats carrying *Rht* gene(s) from hexaploid wheat. On the other hand it should be emphasized that there exists dwarf tetraploid landrace native to Chian, Aiganfanmai.

Aiganfanmai is a dwarfing tetraploid wheat landrace that possessed normal chromosome number and normal chromosome constitution (Peng 1998). This paper describes experiments designed to investigate the inheritance of dwarf trait in Aiganfanmai, and the reaction to the hormone gibberellic acid (GA).

Materials and methods

In addition to the dwarfing tetraploid wheat landrace Aiganfanmai, native to Shaaxi, China, the tall tetraploid wheat landrace Fenzhilanmai native to Sichuan, China and the hexaploid wheat variety, Tom Thumb were used as the check materials in the investigation of reaction to GA, respectively. All the materials were obtained from Triticeae Research Institute, Sichuan Agricultural University, China. Aiganfanmai was crossed with Fenzhilanmai. Some F_1 hybrids were selfed to obtain F_2 seeds, the others were crossed with Aiganfanmai to obtain BC_1 seeds in the 1996-1997 cultivated season. The seeds of the two parents, the F_1 and the F_2 were sowed in the experiment field at the same day. Plants were kept 10 cm apart. All the seeds of each population were randomly planted with aids of label for identification. The backcross test was carried out in the 1997-1998 cultivated season by sowing the BC_1 (F_1 x Aiganfanmai) seeds in the field. Every internode length of the main stem was investigated at harvest. The length of all the internodes but the first one was recorded as the modified plant height.

The GA reaction test of seedlings was carried out on 45 unselected seeds from Aiganfanmai and Tom Thumb. Seeds were placed in petri dishes, moistened with running water for 1 day at 18-20 °C, then grown for 2 days at 2 °C to ensure even germination. Half the germinated seeds were treated with 0.15 mM GA, and the other half were continuously grown in running water. After a further 6 days at 18-20 °C with 12 hour light-12 hour dark period, the length of coleoptile and the first leaf were measured.

Results

Like other wheat plants, Aiganfanmai possessed seven internodes. Measurements indicate that all the internodes of Aiganfanmai were statistically shorter than those of the tall landrace, Fenzhilanmai except the first one (Table 1). The length of the first internode was mainly determined by the deepness of the seeds in soil. To some extent, the deeper the seeds were in soil,

Table 1. The internode length (cm) of main stem of Aiganfanmai and Fenzhilanmai (1997)

Internode	1	2	3	4	5	6	7	2+3....7
Aiganfanmai	3.2±0.42	6.4±0.09	8.1±0.05	9.4±0.11	12.1±0.18	15.3±0.21	36.3±1.13	87.6±0.81
Fenzhilanmai	3.1±0.31	7.3±0.32	10.7±0.34	13.7±0.29	16.3±0.40	20.2±0.38	48.2±1.01	116.7±1.46
Difference	0.1	0.9	2.6	4.3	4.2	4.9	11.9	29.1
P	0.927	0.006	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001

the longer the first internodes of stem were. This contributed to the non-correlation between the plant heights and the length of the first internode in 1996-1997 season ($r=0.203$, $p=0.059$). In addition, spike length of Aiganfanmai was 9.2±0.5 cm, which was obviously shorter than that of Fenzhilanmai (14.4±0.08 cm, $p < 0.001$). According to the previous report (Goud and Sridevi 1988), the spike length has its own genetic basis other than the *Rht* genes. So, the term plant height in this paper was designated to represent the total length of internodes from the second to the seventh, which was different from the term final plant height that included the length of both stem and spike in previous literature.

Aiganfanmai has been planted in our experiment field since 1993. The mean of plant height of Aiganfanmai varied considerably depending on the supply of water and artificial fertilizers in different cultivated seasons. However, the dwarf landrace Aiganfanmai was always very much shorter than the tall landrace Fenzhilanmai in the same season (Table 2). So, the dwarf trait of Aiganfanmai should have its genetic basis.

The mean plant height of the F_1 progeny (Aiganfanmai X Fenzhilanmai) is much higher than that of Aiganfanmai, and more close to that of Fenzhilanmai (Fig. 1). This result indicates that the dwarf trait of Aiganfanmai is recessive. The F_2 population segregated into dwarf and tall plants (Fig. 1). According to the plant height distributions we can arbitrate that the plants shorter than 106 cm are dwarf and those higher than 110cm are tall in F_2 population. Thus, the F_2 population comprised 85 dwarf plants (about 22.6 %) and 292 tall plants (about 77.4%). χ^2 analysis showed that the segregation of dwarf and tall plants in F_2 population fitted to the ratio of 1 : 3 very well ($\chi_c^2=1.083$, $p=0.298$). To confirm monohybrid segregation further, backcross test was carried out in 1997-1998 season. BC_1 (F_1 X Aiganfanmai) population segregated into 84

Table 2. The plant height (cm) of Aiganfanmai and Fenzhilanmai in different cultivated seasons

Cultivated season	1993–94	1994–95	1995–96	1996–97	1997–98
Aiganfanmai	85.3±0.94	97.8±1.06	81.2±0.77	87.6±0.81	90.8±0.96
Fenzhilanmai	111.4±0.92	132.5±1.25	105.6±0.98	116.7±1.46	127.5±1.74
Difference	26.3	34.7	24.4	29.1	36.7
P	<0.001	<0.001	<0.001	<0.001	<0.001

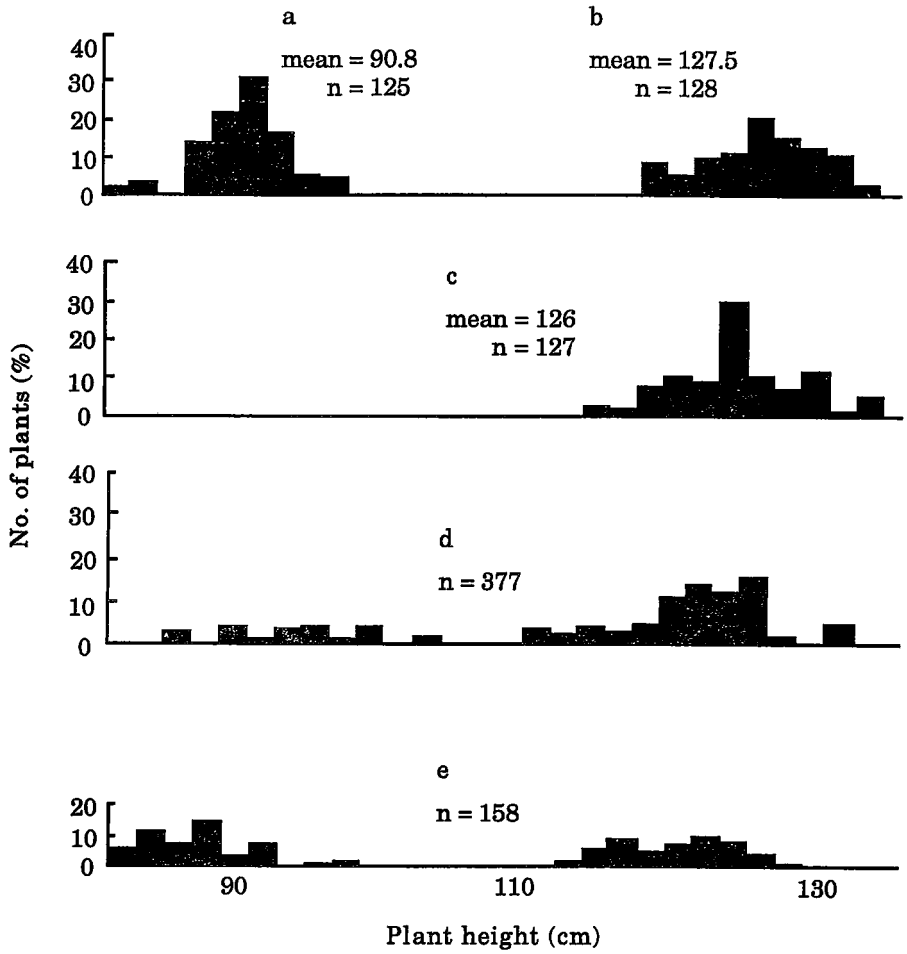

Fig. 1 The means and distributions for plant height of Aiganfanmai (a), Fenzhilanmai (b), F_1 (c), F_2 (d) and BC_1 (e) progenies (n = plant number investigated)

dwarfs (shorter than 100cm) and 74 talls (higher than 112cm). The segregation ratio fitted to the expected 1 : 1 very well (χ_c^2=0.513, p=0.481). Thus, it is evident that the dwarf trait of Aiganfanmai is conditioned by one gene.

Aiganfanmai showed short seedlings, as well as short straw. The seedlings of Aiganfanmai are regularly vigor. A distinct phenotype, thin stems with elongated leaf was observed in Aiganfanmai seedlings treated with gibberellic acid (GA) after germination. Compared with the check (CK), the GA treated seedlings of Aiganfanmai were 6.5 cm longer in the first leaf, and 1.8 cm longer in coleoptile (Table 3). Whereas seedlings of the hexaploid wheat variety, Tom Thumb did not show notable variation in the length of the first leaf and coleoptile after GA treatment (Table 3). Obviously, Aiganfanmai is GA sensitive, in contrast to Tom Thumb which is carrying *Rht3* gene and considered as GA insensitive (Gale et al. 1975; Morris et al. 1972).

Table 3. GA-response of Aiganfanmai and Tom Thumb

Cultivar	Leaf length (cm)			coleoptile length (cm)		
	GA*	CK*	GA−CK	GA	CK	GA−CK
Aiganfanmai	14.7±0.15	8.2±0.20	6.5	4.8±0.06	3.0±0.10	1.8
Tom Thumb	6.9±0.16	6.8±0.14	0.1	2.2±0.05	2.1±0.08	0.1

*GA and CK represent seedlings with and without gibberellic acid treatment, respectively

Discussion

Many environmental and genetic factors that regulate development, morphology or vigor, will have effects on plant height of wheat, which give the plant height quantitative nature of variation. Among them were the genes for spike length and the deepness of seeds in soil in this experiment, so the effects of these two factors were lessen by defining the term plant height as excluding the length of spike and the first internode. Nevertheless, quantitative nature of plant height was observed in Aiganfanmai, Fenzhilanmai and their descendant generations. This revealed the environmental effect and the complexity of the genetic basis of plant height.

The segregation ratio of 1 (dwarf) : 3 (tall) in F_2 population means that a single *Rht* gene caused the difference of plant height between Aiganfanmai and Fenzhilanmai. If the dwarf trait of Aiganfanmai was resulted only from a single *Rht* gene, the dwarf subpopulation in F_2 population should show similar mean value of plant height to Aiganfanmai. However, the mean plant height of dwarf subpopulation was 94.2cm, which is significantly higher than that of Aiganfanmai ($t=5.904$, $p=0.001$). Furthermore, F-test indicated that variation value of dwarf subpopulation in F_2 population was significantly higher than that of Aiganfanmai ($F=2.361$, $p < 0.01$). This difference could not be attributed to the effect of environmental factors, because of the random distribution of seeds that belonged to different populations. The best explanation should be that there existed more than one gene for dwarf trait. Considering that the dwarf subpopulation in F_2 population is just only slightly higher than Aiganfanmai, the gene(s) for plant height other than *Rht* was minor genes. In another word, the dwarf trait in tetraploid wheat landrace Aiganfanmai was controlled by a major *Rht* gene and some modifiers, which is similar to the situation of hexaploid wheat.

The fact that the mainly genetic base for the dwarf trait of Aiganfanmai was a single *Rht* gene indicated that it is very useful in lodging resistance breeding program. Although the recessiveness determined that the major *Rht* gene of Aiganfanmai could not express in F_1 progeny of crossing with high-straw recipient variety, tetraploid wheat breeders can successfully pick out dwarfing materials in segregating generations, which is far more effective than interspecies crossing with hexaploid wheat.

Besides the dwarf trait, Aiganfanmai showed high crossability with cultivated rye (Peng et al. 1998). Breeders have used Aiganfanmai to develop hexaploid Triticale. However, synthetic amphiploid (Aiganfanmai x rye) expressed only a little shorter than that of crossing ordinary tetraploid wheat with rye in our laboratory (data unpublished). This may be because of the existence of inhibitor of *Rht* in the R genome of rye, and indicating that the usage of *Rht* gene in

Aiganfanmai was limited in Triticale lodging-resistance breeding program.

The coleoptile and first leaf length were associated with mature plant height (Allan and Vogel 1964). In addition, Gale et al. (1975) successfully used seedlings to test the reaction of wheat to GA. Following their method, we revealed that short seedlings of Aiganfanmai was attributable to GA-sensitivity. Thus the dwarf trait of Aiganfanmai should be considered to be GA-sensitivity. However, the relationship between the *Rht* gene of Aiganfanmai and its response to GA may not be decisive only on the result of this study, because contradictory conclusions were reported in hexaploid wheat; the dwarf trait and the reaction to GA were under separate control by linked genes *Gai* and *Rht* (Hu 1974), and on the other hand, reaction to GA was pleiotropic effect of *Rht* gene (Gale and Law 1973; Gale et al. 1975). To determine whether the *Rht* of Aiganfanmai has this pleiotropic effect or not, a further study has initiated in our laboratory.

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Research article

Development of near-isogenic sets of derivatives with T1BL.1RS or 1B chromosome substitutions in bread wheat.

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Summary

Seventeen bread wheat (*Triticum aestivum* L.) cultivars homozygous for chromosome 1B or T1BL. 1RS were pollinated by diverse bread wheat cultivars to produce chromosome 1B,T1BL.1RS F_1 heterozygotes. Each F_1 combination was then pollinated by its respective bread wheat parent (maternal) to yield the first backcross (BC_1) derivatives. Heterozygous 1B,T1BL.1RS plants were identified by a combination of electrophoresis and Giemsa C-banding. These BC_1F_1 heterozygotes were backcrossed further to their respective maternal bread wheat parents to yield BC_2 derivatives, which were similarly advanced to BC_7 and then self-pollinated. From the selfed progeny, plants homozygous for chromosome 1B and T1BL.1RS were identified biochemically and cytologically. We discuss here the utility of these germplasms and their uniqueness.

Key words: Bread wheat, T1BL.1RS translocation, Isogenic lines

Introduction

Bread wheats (*Triticum aestivum* L.) with the T1BL.1RS translocation have been of interest over the past two decades, and are globally utilized in bread wheat breeding programs (Lukaszewski 1990). The 1RS chromosome arm possesses four race-specific biotic stress resistant genes (McIntosh 1983), contributing to the crops wide adaptation and yield potential (Rajaram et al. 1983; Villareal et al. 1994). Approximately 55 percent of our bread wheat germplasm possesses the T1BL.1RS translocation, and global cultivation of such wheats exceeds five million hectares.

The superior agronomic performance of T1BL.1RS wheats in comparison with 1B wheats has been an active study area, and has utilized various germplasm groups for experimentation. One such group comprised of several lines with the T1BL.1RS translocation or instead, with chromosome 1B. This set of germplasms developed by Mujeeb-Kazi et al. (1996) facilitated a stringent testing of the rye contribution in a near-isogenic cv. Seri M82 (Villareal et al. 1998). The need to evaluate the 1RS effect across several bread wheat genotypes led to our producing

the presently reported near-isogenic germplasms for seventeen bread wheat cultivars in which chromosomes 1B or T1BL.1RS were replaced by T1BL.1RS or 1B respectively by a series of backcrosses.

Materials and methods

Seventeen bread wheat cultivars homozygous for chromosome 1B or T1BL.1RS, the germplasms utilized in this study:

a) Parental wheats homozygous for chromosome 1B

Ten cultivars (Yecora, Agatha/6*Yecora, Yaco, Ciano T79, Mrl/Buc, Pfau, Opata, Ocoroni, Esmeralda, Buc//Maya/Mon) were crossed with either Glennson M81 or Seri M82 (T1BL.1RS homozygous) to generate 1B,T1BL.1RS heterozygote F_1 hybrids (Table 1). Each F_1 was backcrossed by its 1B parental cultivar to obtain 1B/1B or 1B, T1BL.1RS seed progeny. Endosperm halves of BC_1 of each cross were subjected to A-Page analysis and 1B homozygous progeny was discarded since they lacked the rye secalin bands which were present only in the 1B,T1BL.1RS heterozygotes. BC_1 heterozygote seeds were germinated and cytologically tested for the presence of one T1BL.1RS chromosome. Two seedlings were advanced/combination and used to generate the BC_2 generation as done for BC_1 production. The A-Page and cytological diagnostic protocols (Bushuk and Zillman 1978; Mujeeb-Kazi et al. 1996) were followed up to BC_7. Selfing the BC_7 heterozygote plants yielded a mixture of seed that were: (i) homozygous 1B and called "extracted", (ii) homozygous T1BL.1RS and (iii) the 1B,T1BL.1RS heterozygote, which were all identified by biochemical procedures. Endosperm halves from the BC_7 selfed seed were subjected to glucose phosphate

Table 1. Development of some bread wheat cultivars homozygous for chromosome 1B or T1BL.1RS and their near-isogenic BC_7 selfed derivatives possessing T1BL.1RS or 1B respectively. The donor cultivars of the T1BL.1RS or 1B chromosome in the 17 F_1 combinations are identified.

Recurrent bread wheat cultivars	Parental chromosome status	Cultivar used to produce F_1	BC_7 selfed status	
			Homozygous near-isolines	Homozygous "Extracted"
Yecora F70, Agatha/6*Yecora, Mrl/Buc, Pfau, Buc//Maya/Mon	1B	Seri M82	T1BL.1RS	1B
Yaco, Ciano T79, Opata M85, Ocoroni F86, Esmeralda M86	1B	Glennson M81	T1BL.1RS	1B
Glennson M81, Bagula, Bobwhite	T1BL.1RS	Ciano T79	1B	T1BL.1RS
Spinebill, Fink, Kauz, Veery 10	T1BL.1RS	Pavon 76	1B	T1BL.1RS

isomerase (GPI) analyses (Chojecki and Gale 1982) which separated the T1BL.1RS homozygotes. The remaining endosperm halves after the GPI assay were subjected to A-Page analyses which separated the 1B homozygotes (were saved), and 1B,T1BL.1RS heterozygotes that were discarded. Embryo portions corresponding to endosperm data for T1BL.1RS or 1B homozygotes were germinated and served for increasing seed of each combination.

b) Parental cultivars homozygous for chromosome T1BL.1RS.
Seven cultivars (Glennson M81, Spinebill, Bagula, Fink, Kauz, Bobwhite, Veery 10) were crossed with either Ciano T79 or Pavon 76 (1B homozygous) to produce heterozygote T1BL.1RS,1B F_1's. The protocols for the advance up to BC_7, selfing, identifying T1BL.1RS homozygotes (extracted), 1B homozygotes, and T1BL.1RS,1B heterozygotes to be discarded were similar to those described for the germplasm in (a).

After the seed increase, one plant per combination was analyzed by fluorescent *in situ* hybridization (Islam-Faridi and Mujeeb-Kazi 1995), seed increased if validated and serve as the cultivars genetic stock. For each of the seventeen cultivars, three groups of germplasm form a tester set. Each cultivar set will comprise of:
1) The original breeders line,
2) The line selected after BC_7 selfing possessing the same chromosomal 1B or T1BL.1RS composition as present in the breeders line and designated as "extracted" (Table 1), and
3) The line resembling the original breeders line but differing in having that cultivars 1B or T1BL.1RS chromosome replaced (substituted) by T1BL.1RS or 1B.

Results and discussion

For each of the 17 bread wheats chromosome 1B in 10 cultivars (Yecora, Agatha/6*Yecora, Yaco, Ciano T79, Mrl/Buc, Pfau, Opata, Ocoroni, Esmeralda, Buc//Mayo/Mon) was substituted by T1BL.1RS, and chromosome T1BL.1RS in seven cultivars (Glennson M81, Spinebill, Bagula, Fink, Kauz, Bobwhite, Veery 10) was substituted by 1B (Table 1). The seven bread wheat cultivars involved allowed the end products of each cultivar to yield near-isogenic lines. For each cultivar three sets have been formulated to stringently evaluate the 1RS contributions in this diverse set of wheat cultivars. To exemplify further, in the three sets of each cultivar the first entry is the breeders original cultivar. If this cultivar was T1BL.1RS (e.g. Glennson M81, Table 1) then the second entry would be a near-isogenic Glennson M81 with the lB chromosome substitution. The third entry would be a T1BL.1RS line selected after selfing of the backcross 7 heterozygotes. This entry is called "extracted". Though it is a T1BL.1RS type phenotypically like the parent cultivar (Glennson M81), genetically it may differ from it due to several allelic variations on 40 chromosomes, and the 1BL arms, but not for the 1RS arm. These variations occur due to the recombination event that may happen when Glennson M81 is crossed by Ciano T79 to generate the F_1 heterozygote (T1BL.1RS,1B). Subsequent backcrosses to Glennson M81 give a Glennson M81 phenotype. Genetic differences however, will exist since 20 chromosomes of Glennson M81 and 20 of Ciano T79 are involved in recombination after the F_1 is produced and advanced up to BC_7. Only the 1RS arm remains similar, since it does not associate at meiosis remaining as the unpaired arm of the T1BL.1RS/1B rod bivalent.

Each of the cultivars which are T1BL.1RS homozygotes possess biotic stress resistance genes

Lr26, *Sr31*, *Yr9*, and *Pm8* located on the rye chromosome arm 1RS (McIntosh 1983). Agronomic differences amongst wheat cultivars have been attributed to the presence of the T1BL.1RS chromosome. These translocation genotypes give superior grain yield, aerial biomass, kernel weight, and spikelet fertility (Moreno-Sevilla et al. 1995; Carver and Rayburn 1994; Schlegel and Meinel 1994). Plant height reduction and delayed heading was observed by McKendry et al. (1996). T1BL.1RS associated positive effects for above-ground biomass at maturity, spikes m^{-2}, 1000-kernel weight, and test weight, were reported by Villareal et al. (1991, 1994) when diverse spring wheat cultivars were evaluated. Villareal et al. (1995) further reported a performance advantage of T1BL.1RS derivatives from random F_2-derived F_6 lines of the Nacozari (1B)/Seri M82 (T1BL.1RS) cross for higher grain yield, above-ground biomass, kernels $spike^{-1}$, 1000-kernel weight, and test weight. Considering these contributions from the above investigation we feel that the presently reported germplasm using the backcross protocol and having the "extracted" entry inclusion will be an asset to further evaluate the T1BL.1RS contributions more stringently.

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Research article

Isolation of a gene coding for a putative sterol C-24 methyltransferase in wheat

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Summary

A cDNA (p*WMT*) comprising the complete coding region of a wheat mRNA that encodes a putative sterol C-24 methyltransferase has been cloned. The nucleotide sequence of p*WMT* consists of 1392 base pairs (bp) and codes for a 363-amino acid (aa) polypeptide that has significant homology with the Smt 1 class of sterol C-24 methyltransferases present in plants. Using p*WMT* as a probe, we have also isolated two genomic fragments which together encompass the complete open reading frame containing 11 exons and 10 introns. By aneuploid analysis, *TA-MT* has been localized on the distal portion of the long arm of group 4 chromosomes.

Key words: Reverse transcription, Library screening, Chromosome localization

Introduction

Vascular plants produce a large array of sterols. Among them, 24-methyl cholesterol, sitosterol and stigmasterol account for 70% of the total sterols (Benveniste 1986). The feature that makes the plant and fungal sterols to differ from the animal sterols is the presence of an extra alkyl group at C-24 (Benveniste 1986). The 24-alkyl sterols are the precursors for the biosynthesis of the brassinosteroid group of plant hormones (Ikekawa 1991). A putative scheme for the biosynthesis of sterols in plants has been proposed (Benveniste 1986). A key step in the formation of 24-alkyl sterols is the transmethylation that converts cycloartenol to 24-alkyl sterols catalyzed

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The nucleotide sequences of p*WMT* and *TA-MT* reported in this paper have been submitted to GenBank under the accession numbers U60754 and U60755.

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by the enzyme, S-adenosyl-L-methionine: Δ^{24}-sterol-C-methyltransferase (SMT). Therefore, studies on the structure and function of SMT, as well as the characterization of the expression of its gene are essential to understand how the biosynthesis of 24-alkyl sterols is regulated.

Recently the cDNAs of SMTs have been isolated from *Arabidopsis* (Husselstein et al. 1996), soybean (Shi et al. 1996), maize (Grebenok et al. 1997), rice and tobacco (Bouvier-Nave et al. 1997, 1998). Here we report the isolation, for the first time, of a genomic clone encoding SMT in wheat. We have also isolated the corresponding full-length cDNA clone.

Materials and methods

Wheat (*Triticum aestivum* L. cv. Oasis) seedlings were grown on commercial potting soil (Hoffman, Landisville, PA) in a growth chamber under 14 h photoperiod at 23°C (night temperature, 19°C) with a minimum relative humidity of 70% for 7 days. Primary leaves were cut above the coleoptile and immediately frozen in liquid nitrogen. Total RNA was isolated by the guanidine thiocyanate/ CsCl centrifugation method and poly $(A)^+$ RNA was purified by 2 cycles of oligo-dT cellulose chromatography by following the standard protocols (Sambrook et al. 1989). The RT-PCR amplification using the degenerate oligonucleotides which are synthesized based on the yeast *ERG6* Amino acids sequence, GARTCNATHAARCGNCAYGARCAYTTYCT and CCADATNACYTCRAANCCNGCYTGYTT (where N=A,C,G or T; H=A,T or C; D=G,A or T; R= A or G; Y=T or C; K=A or T; S=G or C), was carried out as described previously (Subramaniam et al. 1996).

Double-stranded cDNA was synthesized by Gubler and Hoffman method using a commercially available kit (Promega, Madison, WI), ligated to λ ZAP Express vector (Stratagene, La Jolla, CA) using an *Eco*RI adapter and in vitro packaged in Gigapack II Gold packaging extract (Stratagene) by following the manufacturer's protocols. This library, which contained about 2×10^6 pfu, was screened using the RT-PCR product as described earlier (Subramaniam et al. 1996).

Chromosomal location of *TA-MT* was determined by aneuploid analysis using the ditelosomic (DT) and nullisomic-tetrasomic (NT) lines of the standard wheat cultivar Chinese Spring (CS) (Sharp et al. 1989). This method essentially involves the hybridization of the probe (radio-labeled p*WMT*) to a Southern blot containing the genomic DNA extracted from the euploid CS plants and its aneuploids that were digested by an enzyme that yields the characteristic '3-band' pattern (in this case *Hin*dIII). The hybridization conditions were as described earlier (Subramaniam et al. 1996).

The isolation of wheat genomic DNA, Southern hybridization, genomic library construction, library screening and DNA sequencing were carried out as described in detail earlier (Subramaniam et al. 1996).

Results and discussion

Cloning of a sterol C-24 methyltransferase cDNA from wheat.

Degenerate oligonucleotide primers were synthesized based on the amino acid sequence of the yeast sterol methyltransferase *ERG6* (Hardwick and Pelham 1994; Welihinda et al. 1994), and used in RT-PCR reactions with wheat cDNA as template. The nucleotide sequence of one of the DNA fragments (500 bp) obtained by RT-PCR, when compared with the GenBank database, showed

high similarity to that of the yeast *ERG6* gene which codes for sterol C-24 methyltransferase (Hardwick and Pelham 1994; Welihinda et al. 1994). A wheat cDNA library was screened using the RT-PCR product as probe and a full-length cDNA clone (p*WMT*; 1392 bp) was obtained. The nucleotide sequence of both the strands of the p*WMT* clone was determined.

Sequence comparison with other sterol C-24 methyltransferases.

The plant SMTs were classified into two families, smtl and smt2 (Grebenok et al. 1997; Bouvier-Nave et al. 1998). Sixteen other plant and yeast SMT genes that have high homology with *TA-MT* were retrieved from the GenBank and analyzed. The amino acid sequence alignment and the phylogenetic analysis clearly show that there are three distinct groups among these SMTs (Fig. 1). Two maize SMTs that belong to the Smt 1 class have the highest percentage (88.1%) similarity with *TA-MT*. An alignment of these SMT genes is shown in Fig. 2. There are three conserved motifs among these plant and yeast SMTs.

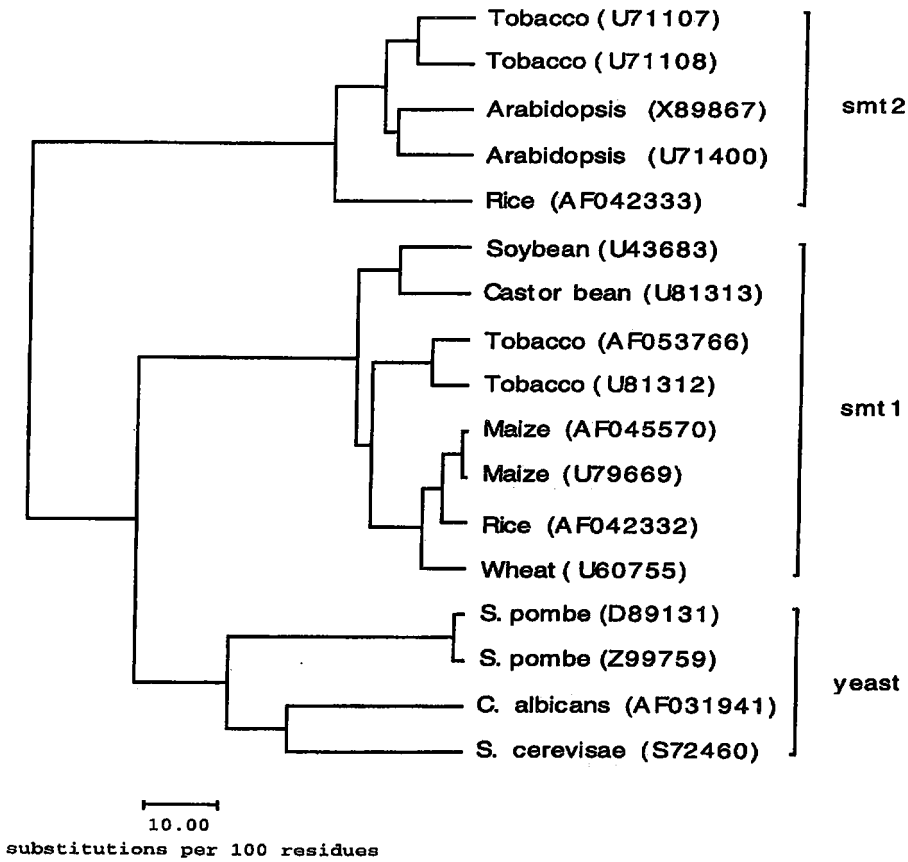

Fig. 1. Phylogenetic tree for the plant and yeast sterol methyltransferases. The deduced amino acids sequences of these sterol methyltransferase genes were retrieved from the GenBank with the accession numbers indicated. The tree was built using the Growtree program of the GCG Wisconsin package.

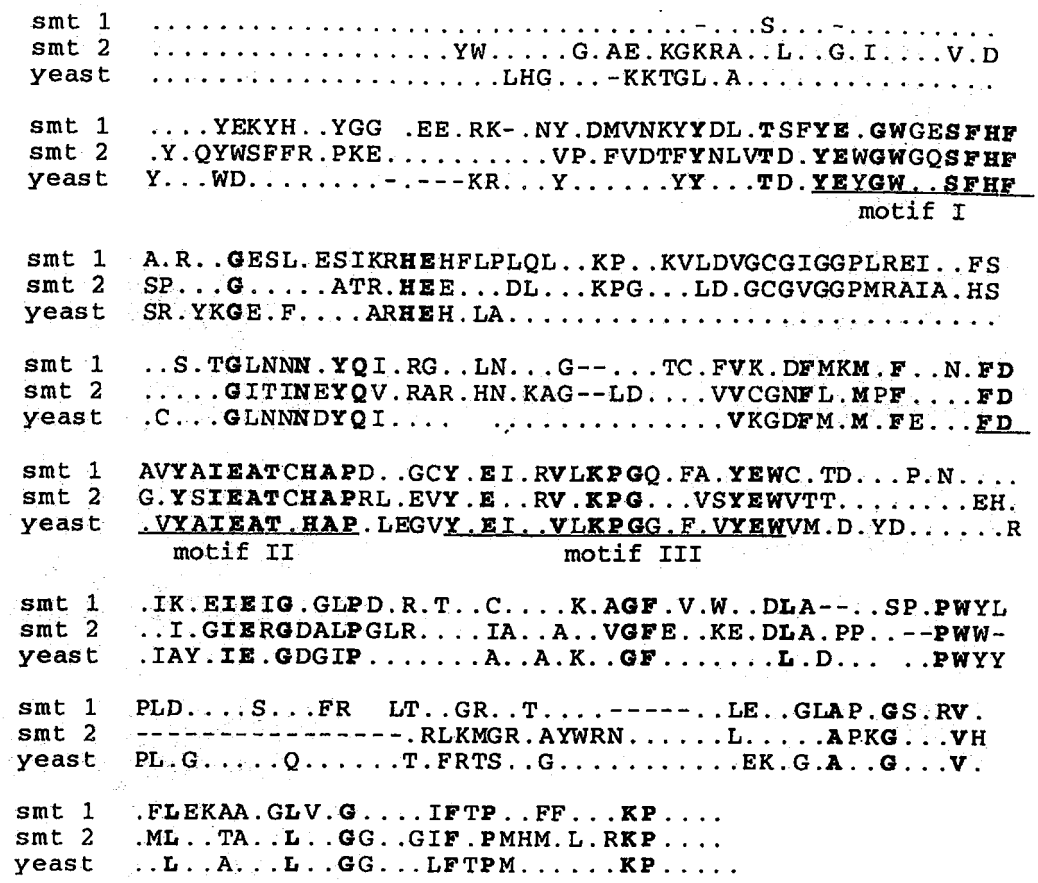

Fig. 2. Comparison of the deduced amino acid sequences of the plant and yeast SMTs. The letters represent the conserved residues in each group. The three conserved motifs (I, II, III) are underlined.

Cloning of the wheat sterol C-24 methyltransferase gene.

In Southern blot analyses of wheat genomic DNA digested with different restriction enzymes, the ^{32}P-labelled insert of p*WMT* hybridized to two *Bam*HI (15.0 and 7.0 kb), a single *Eco*RI (3.5 kb), and three each of *Hin*dIII (15.0, 9.0 and 4.0 kb) and *Sac*I (10.0, 7.0 and 5.1 kb) fragments (Fig. 3). Based on the Southern blot results, a sub-genomic library was constructed using the 5.0-3.0 kb fraction of the *Eco*RI-digest. This library was screened using p*WMT* insert as the probe. The genomic sequence of *TA-MT*, when compared with the p*WMT* cDNA clone, revealed the presence of 11 exons and 10 introns within the coding region.

Chromosomal localization of *TA-MT*.

We used the mapping system developed for wheat (Sharp et al. 1989) to assign the chromosomal location of *TA-MT* gene. Southern hybridization of the insert of p*WMT* to *Hin*dIII-digested DNA from 20 nullisomic-tetrasomic and 2 ditelocentric lines showed that the *TA-MT* gene is located on

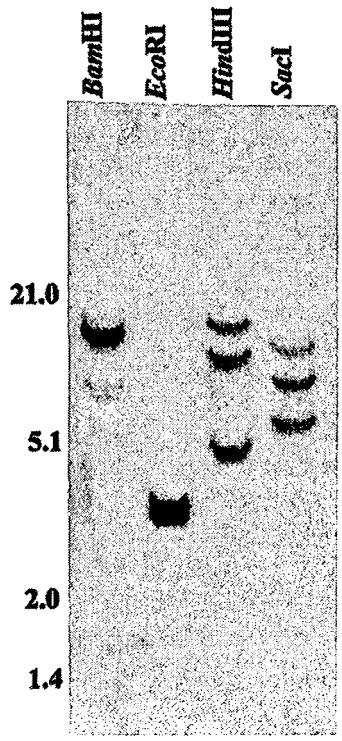

Fig. 3. Southern blot analysis. Genomic DNA (7 μg) isolated from 8-day old etiolated wheat seedlings was digested with restriction enzymes as indicated on the top of each lane, resolved on a 0.6% agarose gel, transferred onto nylon membrane and hybridized to p*WMT* probe. Molecular weight markers (in kb) are shown on the left.

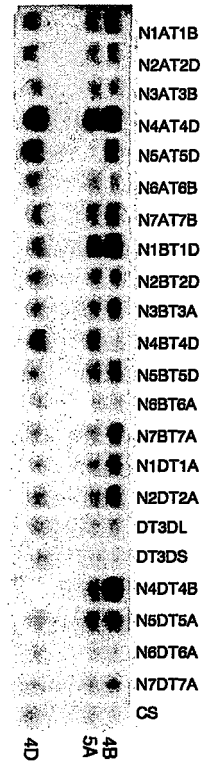

Fig. 4. Hybridization of *Hin*dIII-digested DNA from the ditelocentric (DT) and nullisomic-tetrasomic (NT) lines of Chinese Spring wheat to the insert of p*WMT* cDNA clone.

chromosomes 5A, 4B and 4D (Fig. 4). The localization on the 5A chromosome could be explained by the fact that, during the course of evolution of modern-day chromosome 4A, there had been a translocation event involving the distal regions of the long arm of chromosomes 4A and 5A (Devos et al. 1995). This implicates a relatively distal location on the long arm of group 4 chromosomes for *TA-MT* gene.

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Research article

Further evidences on the usefulness of *Lr34/Yr18* gene in developing adult plant rust resistant wheat genotypes

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Summary

During 1995-97 twenty one *aestivum* wheat genotypes were evaluated for AUDPC (area under disease progress curve) for *Puccinia striiformis tritici*. The genotypes fell in three categories representing strong vertical resistance (AUDPC below 1% of susceptible check), higher (AUDPC below 20% of susceptible check) and lower levels (AUDPC between 21-50% of susceptible check) of slow rusting. Parental lineage of these genotypes was examined by using a software package GRIPI developed by CIMMYT, Mexico. It revealed that slow rusting of higher level occurred in those genotypes which essentially involved Yaktana 54 in their parentage. Yaktana 54 could not be traced in the pedigree of those genotypes which had lower level of slow rusting. The slow rusting of higher level may be attributed to the presence of adult plant resistance (APR) gene *Yr18*. This APR gene against yellow rust seems to have descended into Yaktana 54 from one of its parent cultivar Frontana, which is a designated source of *Lr34* (an APR gene for brown rust) having tight linkage with *Yr18*.

Key words: Wheat, Yellow rust, Adult plant resistance, *Yr18*

Introduction

Yellow rust of wheat caused by *Puccinia striiformis* West. inflicts heavy yield losses in northern parts of India, if cool and humid weather persists between December to March. Use of genetic host resistance is the most effective, economic and ecofriendly approach for disease control. A number of genes are known to confer resistance to yellow rust (McIntosh et al. 1995). In general, major seedling genes such as *Yr2* (Sonalika), *Yr2* (Kalyansona) and *Yr9* have been widely used by Indian breeders for developing yellow rust resistant cultivars (Nayar et al. 1994). But, effectiveness of these race specific genes have reduced since matching pathotypes emerged from time to time

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(Kumar et al. 1989, 1990, 1991, 1994; Prashar et al. 1997). The introduction of resistance from proven durable resistance sources carrying genes other than major genes, may provide durable resistance (APR) to yellow rust. Several workers have demonstrated that adult plant resistance remains durable and appears to involve slow rusting mechanism (Allan et al. 1966; Johnson 1980; Krupinsky and Sharp 1979; Milus and Line 1986a,b; Pope 1968; Qayoum and Line 1985; Sharp 1968; Sharp et al. 1976; Singh and Rajaram 1994). Durability of field resistance in cultivars can be achieved by using partial adult plant resistance expressed as slow rusting as they are known to sustain longer in the field (Parlevliet 1988).

Materials and methods

The twenty one bread wheat lines were selected for the present study (Table 1) and these lines were subjected to multilocational evaluation for yield, disease resistance and quality traits before they were promoted as final year entries (prospective cultivars) in advanced varietal trials under All India Coordinated Wheat Improvement Project (AICWIP, ICAR) during 1995 (Initial Varietal Trial), 1996 (Advance Varietal Trial 1st Year) and 1997 (Advance Varietal Trial, Final Year) (Jag Shoran et al. 1997). Field response of genotypes to yellow rust was evaluated at Directorate of Wheat Research, Karnal, Haryana during normal crop seasons of 1996 and 1997. Seeds of each genotype were sown in a 2 meter row with a space of 20 cm between the rows. Three spreader rows (row to row gap of 15 cm) of mixture of five susceptible cultivars (Agra Local, Kathia Local, NP4, Lal Bahadur and C306) were planted on four sides of the plot on 3 different dates with interval of 15 days. The crop was fertilized at the rate of 120 Kg N/ha (split equally at seedling and stem elongation), 60 Kg P/ha and 40 Kg K/ha. Irrigation was provided at crown root initiation, stem elongation, flowering and grain formation stages of crop growth.

The yellow rust epidemic was initiated by inoculating 4 week old plants of spreader rows with the uredosporic dust having equal proportions of three pathotypes, N(46S102), P(46S103) and K(47S102). Inoculations were done following the syringe and spray techniques described by Joshi et al. (1988). Using the modified scale (Peterson et al. 1948), average disease severity on upper three leaves was first recorded at 40 days after inoculation when the susceptible control variety, Agra Local had reached 40% disease severity. The infection types (TR, R, TMS, MS, TS and S) were recorded by following McNeal et al. (1971) and defined as TR: necrotic/chlorotic flecks in traces without sporulation, R: necrotic/chlorotic stripes without sporulation, TMS: light sporulation, necrotic/chlorotic stripes in traces, MS: intermediate sporulation, necrotic/chlorotic stripes, TS: abundant sporulation, necrotic/chlorotic stripes in traces and S: abundant sporulation without chlorosis/necrosis. In all five readings of rust intensity were taken at weekly intervals. Area under disease progress curve (AUDPC) was calculated using a computer package developed at CIMMYT, Mexico (CIMMYT 1988). The relative AUDPC (percent) for each cultivar was calculated by dividing its actual AUDPC by susceptible cultivar Agra Local's AUDPC. The values of AUDPC were interpreted as below:

Group 1. Less than 1% AUDPC of susceptible check
Variety remained rust free and represented the strong vertical resistance, which may not impart a durable protection and likely to be lost through pathogenic adaptations. In some cases, disease initiated as necrotic/chlorotic flecks without sporulation (TR-infection type) on leaf surface and attained a final disease rating not more than 10R. This type of reaction was also considered to

represent the strong vertical resistance again.

Group 2. 1 to 20% AUDPC of susceptible check
Rust initiated as abundantly sporulating but chlorotic stripes (MS-infection type). Subsequently, the progress of rust development remained slower and was restricted to 1-20% of the susceptible check. These genotypes were interpreted to express a high degree of slow rusting.

Table 1. Rust severity and AUDPC measurements of 21 bread wheat genotypes at DWR, Karnal India

Genotype	Rust severity		AUDPC[3]			
	IDR[1]	FDR[2]	1996	1997	Mean	% of check
Group 1: Nearly immune/immune						
VL772	TR	5R	8.3	9.1	8.7	0.50
VL773	TR	5R	5.4	7.8	6.6	0.37
HS345	TR	5R	5.7	6.7	6.2	0.35
VL768	TR	10R	7.3	5.2	6.2	0.35
HS369	R	R	0	0	0	0
Group 2: High degree slow rusters						
HS 295	TMS	20MS	177	193	185	10.64
GW 275	TMS	20MS	182	177	179.5	10.32
K 9423	TMS	20MS	146	181	163.5	9.40
HUW 468	TMS	10MS	153	168	160.5	9.23
HP1731	TMS	20MS	169	136	152.5	8.77
PBW414	TMS	20MS	188	116	152	8.74
HS364	TMS	10MS	168	115	141.5	8.14
HUW482	TMS	10MS	133	149	141	8.11
Group 3: Low degree slow rusters						
RAJ3765	10S	40S	872	719	795.5	45.77
K8962	10S	40S	813	713	763	43.90
RL10-22	10S	40S	795	616	705.5	40.59
GW273	10S	40S	626	756	691	39.75
NW1014	TS	10S	520	629	574.5	33.0
HUW467	5S	20S	319	716	517.5	29.77
HS277	5S	20S	423	573	498	28.65
K9408	5S	20S	473	524	498.5	28.68
Susceptible check:						
Agra Local	40S	100S	1780	1695	1738	100

1) initial disease rating at 40th day of inoculation
2) final disease rating at 68th day of inoculation
3) area under disease progress curve

Group 3. 21-50% AUDPC of susceptible check

The incipient rust intensity was represented by abundantly sporulating non-chlorotic/necrotic stripes on the entire surface of leaf. But, further development was restricted to 21-50% of the susceptible check. These genotypes were supposed to represent a lower degree of slow rusting character.

Results and discussion

The initial disease rating (IDR) on 40th day of inoculation, the final disease rating (FDR) on 68th day of inoculation and AUDPC values recorded on the test genotypes are given in Table 1. Based on the AUDPC values, the genotypes were categorized into three distinct groups. The group 1 included those genotypes which either remained complete free of disease (immune) or exhibited TR-infection type at IDR and 5-10R at FDR. The AUDPC values on these genotypes were measured below 1% of the susceptible check variety Agra Local (AUDPC :1738). The genotypes of this group represented a strong vertical resistance (major genes), which may not impart a durable protection.

The genotypes exhibiting AUDPC values in the range of 1-20% of the check were placed in group 2, and between 21-50% of the check in group 3. Genotypes belonging to groups 2 and 3 did

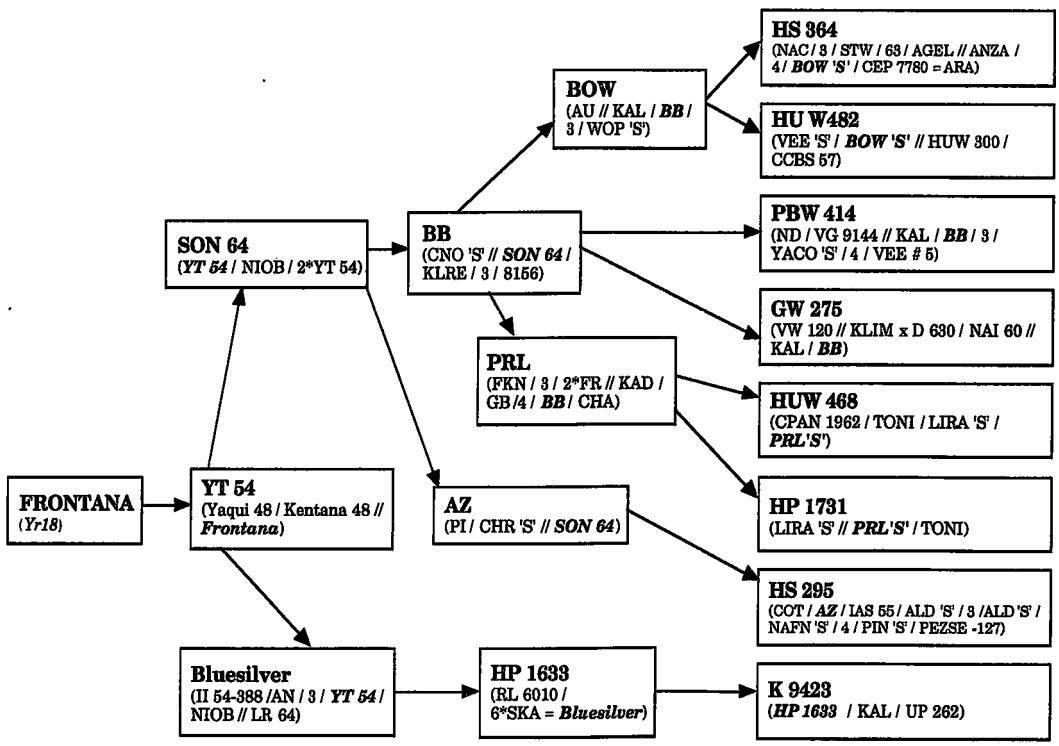

Fig. 1. Lineage of Frontana, the source of APR gene *Yr*18, in group 2 bread wheat genotypes possessing high degreece of slow rusting to yellow rust

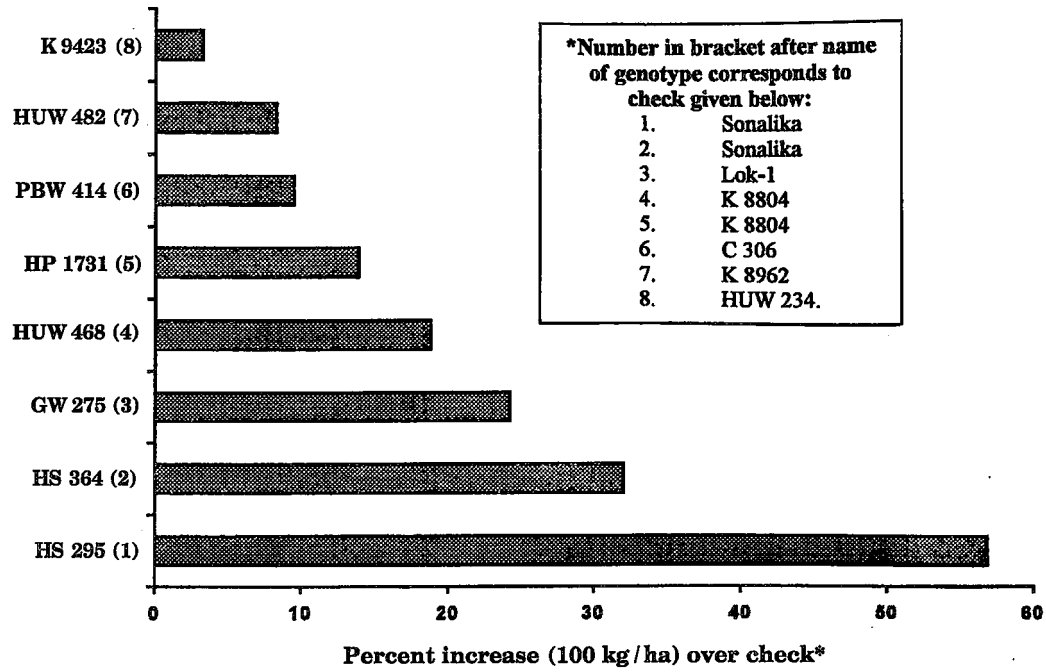

Fig. 2. Yield superiority of high degree yellow rust slow rusting genotypes of bread wheat (Based on data from Jag Shoran et al. 1997)

develop yellow rust but terminal severity was always low.

The genotypes of group 2 and 3 are characterized to be partially resistant since they developed epiphytotic of very low potential as indicated by their AUDPC values despite the ultimate expression of high infection type. Genotypes with these traits are designated as possessing genes that accord partial resistance (Parlevliet 1975, 1979, 1988). These genotypes exhibited AUDPC values ranging between 153-872, which is less than 50% of value of Agra Local, the check (AUDPC: 1780). Group 2 and 3 genotypes are further distinguished as the first cluster with better slow rusting (AUDPC below 20% of the check), while those in the latter group represented lower level of slow rusting (AUDPC between 20-50% of the check).

Parental lineages of group 2 and 3 genotypes were examined through a computer package named GRIPI developed by CIMMYT, Mexico (Skovmond et al. 1995). The pedigree analysis revealed that slow rusting lines of group 2 essentially had Yaktana 54 in their parental lineage (Fig. 1). Yaktana 54 could not be traced in the pedigrees of genotypes of group 3 which had less apparent slow rusting and higher terminal disease severity. The adult plant resistance expressed as slow rusting of higher level in genotypes of group 2 may be attributed to the presence of adult plant resistance gene *Yr18*. This APR gene for yellow rust resistance might have descended into Yaktana 54 from one of its parent cultivar Frontana, which is the designated source of *Lr34* (an APR gene for brown rust resistance) having tight linkage with *Yr18* (Singh 1992). The gene *Yr18* has been found to interact and produce enhanced level of resistance (Singh 1992; Johnson 1988; Milus and Line 1986 a,b). Therefore adding partially effective additive genes to genotypes already

carrying *Yr18* can lead to development of wheat lines with higher levels of resistance.

The partial resistance has been advocated to be more durable (Singh et al. 1991). Lines with acceptable levels of slow rusting invariably carry a combination of *Lr / Yr* genes and this restricts the evolution of pathogen since the changes of multiple point mutations are extremely rare (Schafer and Roelfs 1985). Stability of the pathogen population, and the avirulence / virulence structure would result in greater durability of cultivar resistance. Gene *Yr18*, if incorporated in varietal background has the potential to impart durable resistance to yellow rust as evident from its performance in several bread wheat cultivars (Singh 1992). As shown in Fig. 2, genotypes of group 2 possessing *Yr18* were able to combine both good yield and wide adaptation. Therefore, these genotypes may be considered as important genetic stocks having dual advantage of resistance to yellow rust as well as potential of higher yield.

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Research information

Transient expression of β-glucuronidase (GUS) gene in mature embryos of winter durum wheat via microprojectile bombardment

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Key words: Particle bombardment, Transformation, Transient expression, *Triticum durum*, Wheat

In durum wheat (*Triticum turgidum* L.), a biolistic transformation method has been developed, for the first time, by using scutella isolated from immature embryos (Bommineni et al. 1997; Takumi and Shimada 1997). Immature embryos are commonly used as targets for particle bombardment because the highest frequencies of callus induction and plant regeneration have been obtained from the immature embryos in both common and durum wheat. However, another explant is required because it is usually difficult to get immature embryos throughout the year and their suitable stage for bombardment is also strictly limited. Mature embryos are easily available without limit any time, but they are not used as targets for bombardment because of the low frequency of callus induction. However, some new techniques have successfully been developed in callus induction and plant regeneration from mature embryos of common and durum wheat (Ahmed et al. 1992; Özgen et al. 1996, 1998).

In this study, the winter durum wheat (*Triticum durum* Desf. cv. 'Berkmen 469') was used in transformation because of its high frequency of regeneration from mature embryo culture to fertile plants (Özgen et al. 1996). The objective of the present study was to investigate distance between stopping plate and target tissue, and rupture disk pressure affecting transient expression of β-glucuronidase (GUS) gene in winter durum wheat mature embryos introduced by the particle delivery system.

Mature seeds were sterilized and imbibed according to Özgen et al. (1998). For bombardment, mature embryos were aseptically excised with a scalpel from the imbibed seeds and placed with the scutellum upwards on a solid agar medium in the centre of sterile petri plates. The GUS gene

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was used as a reporter gene in order to calibrate and optimize physical conditions of the bombardment. All bombardments were carried out with the Bio-Rad Biolistic® PDS 1000/He particle delivery system according to the manufacturer's protocol. Bombardment was performed under partial vacuum (25" Hg). Tungsten particles, 0.7 μm mean diameter, were coated with 0.6 μg per shoot of pBI221.23 DNA which has the GUS gene and the *hpt* gene (Lonsdale et al. 1990) as described in manufacturer's protocol. Both genes are under the control of the cauliflower mosaic virus (CaMV) '35 S' promoter. Four different distances (6, 9, 12 and 15 cm) from stopping plate to the target mature embryos and three strengths (1100, 1550 and 1800 psi) of rupture disk were examined as physical parameters. Each plate, containing 60 mature embryos, was bombarded once. The mature embryos were subjected to histochemical GUS assay according to Lonsdale et al. (1990).

The GUS activity was observed as blue-coloured spots at 48 h after bombardment. The control explants were bombarded with tungsten particles lacking DNA and blue spots were not observed. The number of blue spots per embryo varied between 0.9±0.3 and 4.2±1.0 (Table 1). All spots were dark blue-coloured, which indicate a strong GUS positive response (Fig. 1). Increasing the distance to 15 cm from 6 cm and to 15 cm from 12 cm resulted in a slight increase of mean number of blue spots per embryo for 1550-psi and 1800-psi pressure, respectively. But changing the target distance between 6 cm and 9 cm does not have effect on transformation efficiency at 1100-psi pressure. At 1800 psi, the greatest pressure tested, there was a significant reduction in the number of blue spots. This could be due to the higher degree of aggregation of the particles when rupture disk pressure is high. The highest number of blue spots was observed when the targets were 15 cm away from the stopping plate under the pressure

Fig. 1. Mature embryos exhibited GUS-positive black spots (blue in color), assayed 48 h following particle bombardment

Table 1. The effect of different bombardment distances and pressures on transient expression of GUS gene in mature embryos of winter durum wheat

Distance-pressure	Number of blue spots			No. embryos bombarded
	Total	Mean/embryo	Range/embryo	
6-1100	193	3.2 ± 0.8	0–26	60
9-1100	190	3.2 ± 0.7	0–23	60
6-1550	227	3.8 ± 1.4	0–60	60
15-1550	254	4.2 ± 1.0	0–35	60
12-1800	51	0.9 ± 0.3	0–11	60
15-1800	64	1.1 ± 0.1	0–15	60

of 1550 psi.

The data showed that plasmid DNA was efficiently introduced into the mature embryos of winter durum wheat 'Berkmen 469' and the embryos are suitable recipients of foreign DNA introduced via particle bombardment. Therefore, mature embryos can be used as an effective explant source in direct gene transfer studies of durum wheat. Recently, mature embryos of oat (Torbert et al. 1998) and rice (Valdez et al. 1998) have successfully been used as an alternative source of totipotent target cells for microprojectile bombardment-mediated transformation. This study is the first demonstration of the transient GUS expression in mature embryos of winter durum wheat. Several factors might affect the efficiency of foreign gene delivery by particle bombardment. In this study, the effect of distance and pressure combination was evaluated. Further optimization of the other factors that may influence the efficiency of gene delivery, such as DNA concentration and the confirmation of plasmid DNA, is required.

In conclusion, mature embryos might become a useful target tissue in the transient transformation of durum wheat, when all bombardment parmeters are optimized further and a reliable selection technique of bombarded tissue is developed. Stable transformant was not obtained but this transient assay could be used to optimize some conditions for stable transformation of durum wheat. The next step of this study is to establish a stable transformation system of durum wheat.

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Wheat Information Service
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Genetic stocks

Aegilops species collected in California and Oregon, USA

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Aegilops species are not native to North America; however, *Ae. triuncialis*, *Ae. cylindrica* and *Ae. ovata* survive as adventitious species in the United States. *Ae. triuncialis* is the most widely spread *Aegilops* species in the world. This species has become a troublesome weed on the rangelands of California and Pennsylvania (van Slageren 1994). However, there is little or no awareness about its existence in Pennsylvania (Hartwig N: pers commun). *Ae. cylindrica* is also troublesome in fields and pastures. Its growth on the edges and within wheat fields is also troublesome. Gene transfer between wheat (*Triticum aestivum*) and *Ae. cylindrica* in the field may pose a potential problem since *Ae. cylindrica* may receive traits, such as herbicide resistance, from transgenic wheat cultivars through natural introgressive hybridization (Seefeldt et al. 1998; Zemetra et al. 1998). The geographical distribution of *Ae. cylindrica* was surveyed in 1993 by USDA-ARS (http:// www.janr.unl.edu/jgg/maps/). *Ae. cylindrica* is a serious weed in Northern Oregon, but not so much problematic in California. The distribution of *Ae. triuncialis* in North America is not well documented. However, information from herbarium specimen indicates a wide distribution area in the central regions of California. We had an opportunity to collect 17 populations of *Aegilops* species in California and Oregon from 28 June to 6 July, 1999, which is described in this report.

The collection sites and areas covered are presented in Table 1 and Fig. 1.

Aegilops triuncialis (1-6)

In the ranges of south of Milton and San Andreas, California, *Ae triuncialis* was found in massive stands. At Winters, however, it was found in dry and open ground between a dismantled railroad track and forage-road. *Ae. triuncialis* is widely distributed at altitude ranges of 300 m to 1000 m at the Experimental Station, University of California at Hopland. *Ae. triuncialis* is troublesome weed because of its narrow leaves and barbed spikes, which are not preferred by sheep for grazing. Burning is applied to reduce population size of *Ae. triuncialis* at the Experimental Station. We also found *Ae. triuncialis* on a southwest facing road-cut and a slope above the road-cut located three miles northeast of Nevada City. We did not find *Ae. triuncialis* in Oregon.

Table 1. Collection sites of *Aegilops triuncialis*, *Ae. cylindrica* and *Ae. ovata*.

No.	Collection site
Aegilops triuncialis (UUCC)	
1	Pasture, South of Milton, Caraveras County, CA
2	Pasture, San Andreas, Caraveras County, CA
3	Roadside, Winters, Solano County, CA
4	Pasture, Hopland, Lake County, CA (Elevation:300m)
5	Pasture, Hopland, Lake County, CA (Elevation:600m)
6	Roadside, NE of Nevada City, CA
Aegilops cylindrica (CCDD)	
7	Roadside, Water Dr./Fern Wood Dr., Crestline, CA
8	Old pasture, Ellwood Dr., Santa Barbara, CA
9	Edge of grassland, Oberlin Rd./Montague-Grenada Rd.(E of Yreka), Siskiyou County, CA
10	Pasture, East of Montague, Siskiyou County, CA
11	Wheat field (Brewer Ranch), Wasco County, OR
12	Barley field (Brewer Ranch), Wasco County, OR
13	Feed lot (Smith Ranch), NE of Antelop, Wasco County, OR
14	Dump site and wheat field, Condon, Gillian County, OR
15	Wheat field, Ella Rd./Rietmann Ln. (N of Ione), Morrow County, OR
16	Wheat field, Immigration Ln. /Dave Rietman Rd., Morrow County, OR
Aegilops ovata (UUM^{o}M^{o})	
17	Roadside, W of Willits, Mendocino County, CA

Aegilops cylindrica (7-16)

California was not widely infested with *Ae. cylindrica*. In Crestline, we found *Ae. cylindrica* growing together with wheat plants at the roadside. At Santa Barbara, *Ae. cylindrica* survives at the edge of an old pasture that used to be a cattle-feeding lot and now abandoned as grassland. It is thought that *Ae. cylindrica* might have spread as a contaminant of cattle feed. There is herbarium specimen collected in the Santa Cruz Island, near Santa Barbara (van Slageren 1994). *Ae. cylindrica* was found at roadsides and edges of grasslands from Yreka to Montague in the Siskiyou county. At the east of Montague, it was found in massive stands in a grassland leading to pastures. There is a report that *Ae. cylindrica* was found at Tulelake (Waines JG: pers commun), but we were unable to find it. In California, the distribution of *Ae. cylindrica* was restricted to the roadsides and edge of pastures.

Wasco, Gillian and Morrow are known to be the most infested Counties of *Ae. cylindrica* in Northern Oregon. As summarized in Table 1, *Ae. cylindrica* was found at the edges of wheat and barley fields and feed lots. At the edge of wheat field of Condon, we could easily find hybrid plants between wheat and *Ae. cylindrica* (Fig. 2). Hybrid plants were vigorous and their spikelets were sterile. Hybrid plants were also found in a wheat field at the corner of Ella Road and Rietmann Lane of Ione, Morrow County. In Northern Oregon, *Ae. cylindrica* survives at the edge of wheat field and invades into wheat field where natural hybrids are formed. It means that *Triticum* and *Aegilops* are in the process of evolution.

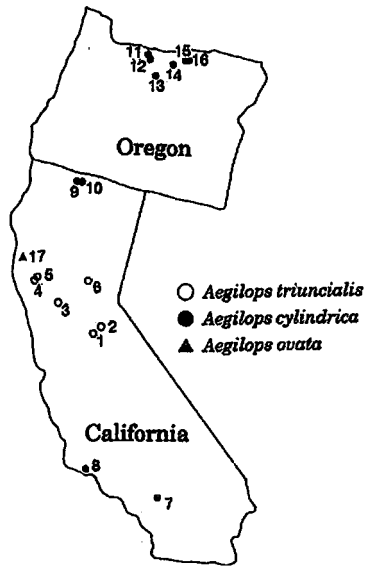

Fig. 1. Collection sites of *Aegilops triuncialis*, *Ae. cylindrica* and *Ae. ovata* in California and Oregon.
Note: Numbers are corresponded with those of collection sites in Table 1.

Fig. 2. The spikes of *Aegilops cylindrica*, a natural hybrid between wheat and *Aegilops cylindrica* and adjacent wheat plant. They were collected at Condon. Left to right: an adjacent wheat plant, a hybrid and *Ae. cylindrica*.

Aegilops ovata (17)

Ae. ovata was found in the roadside five miles west of Willits, California. It grows at the edge of the site and the plants are smaller in size than the surrounding other grass species. This is because *Ae. ovata* is less competitive than tall grass species. The population size was not so large. It is considered that *Ae. ovata* has also spread as a contaminant of cattle feed.

The *Ae. cylindrica* accessions described in this report will be added to the list given in Watanabe (1997), and will be used to assess genetic differentiation in this adventitious *Aegilops* species. *Ae. triuncialis* has a diphyletic origin from the reciprocal hybrids between *Ae. caudata* and Ae. *umbellulata*. (Ogihara and Tsunewaki 1982). It has three chloroplast genotypes (Murai and Tsunewaki 1986). However, it is not clear which cytoplasm type is predominant in the specific ecological niches. Unfortunately, there is no historical record on the introduction of *Ae. triuncialis* to California. Since the Spanish people first colonized California, one approach to trace back the route of introduction would be comparison of allelic and genotypic compositions between Spanish and Californian populations.

Acknowledgments

We are grateful to Dr. J.G. Waines, University of California, Riverside and Dr. L. Morrison, Oregon State University, Corvallis for their kind advises to collect the spikes of *Aegilops* species.

We are also grateful to Dr. G. Belay for his helpful comments on the manuscript. Our collection was partially supported by the grant to NW from Ministry of Education, Science and Culture, Japan (No. 09NP0901).

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Wheat Information Service
Number 89: 37-85 (1999)
Gene symbol

Catalogue of gene symbols for wheat: 1999 Supplement

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The most recent edition of the Catalogue appeared in the Proceedings of the 9th International Wheat Genetics Symposium Vol. 5 (A.E. Slinkard ed., University Extension Press, University of Saskatchewan, Saskatoon, Canada). A modified version is displayed on the Graingenes Website: grains@greengenes.cit.cornell.edu.

The present Supplement has been offered to the editors of Annual Wheat Newsletter and Wheat Information Service for inclusion in the respective journals. Researchers and readers are encouraged to advise the curators of updatings and errors as this will make the Catalogue more useful to others.

Significant Revisions for the 1998 Catalogue

Introduction

P1. Rule 6(ii) - change "homoeologous" to "orthologous" in both positions.

DNA Markers

P19. Immediately below the table insert: 'Markers are listed in alphabetical/numerical order within each group with the exception of markers whose symbol does not include a laboratory designation; these are listed at the beginning of each group.'

P23. *Xcmwg701-1A.1,.2* should be moved one line below its present position.

P26. *Xzens1(Adpg4)-1A.* Add reference {757} to synonymn *XAga7* and add probe: 'WE:aga7 {774}.'.

P31. *Xfba209.* Delete second entry. Modify first entry to:

Xfba209-2A, B.1, .2 [{154}], *2D.1, .2* {1160}. [*Xfba209b-2A, Xfba209a-2B, Xfba209c-2B* {154}]. FBA209. (5D).

P57. *XksuF43.* Delete second entry. Modify first entry to:

XksuF43-5D.1, .2 [{448}]. [*XksuF43(A), (B)-5D* {448}]. pTtksuF43. (1B,D, 2D, 4D, 6D).

P61. *XksuE3.* Should be listed after *XksuD27.*

1999 Supplement

Laboratory Designators for DNA markers

Add:

abg (Barley genomic* clones)
Kleinhofs, A. (see *abc*)

bg (Barley genomic* clones)
Lapitan, N.
Department of Soil and Crop Sciences
Colorado State University
Fort Collins, CO 80526
USA

cmwg (Barley cDNA* clones)

Graner, A. (see *mwg*)

cs Appels, R. (see *csb*)

fra Bernard, Michel
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234, Avenue du Brezet
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gbx Jacquemin, J.M.
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Japan

Morphological, Physiological, Molecular and DNA Traits

Gross Morphology: Spike characteristics

1. Squarehead/spelt

q. **ma:** *Q* - 9.3cM - *Xpsr370-5A* {9903}.

4. Branched spike

bh. 2AS add: {9907}. Add: 'A chromosome 2B gene of minor effect was identified {9907} and an inhibitor was associated with chromosome 2D {9907}.'

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

5. Elongated glume

In the existing preamble change *'P'* to *'P1 [P]'* and add: 'A second gene is present in chromosome 7B {9990}.'

P1. [*P* {911}; *Eg* {922}].

P2 {9990}. 7BL{9990}. **ti:** LD222*7/*T. ispahanicum* {9990}. **tv:** *T. ispahanicum* {9990}.

Anthocyanin Pigmentation

1. Purple anthers.

Add at end of section:

'***Pan2.*** 7AS {9959}. **tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}. **ma:** *Pan2* - 9.2 cM - *Rc1* - 12.2 cM - *Xutv1267-7A* (proximal) {9959}.'

3. Red/purple coleoptiles.

Rc1. Add at end of section: '**tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}. **ma:** *Pan2* - 9.2 cM - *Rc1* - 12.2 cM - *Xutv1267-7A* (proximal) {9959}.'

Brittle Rachis

Br1 {9970}. 3DS {9970}. A single dominant gene controlling brittle rachis in *T. aestivum* var. *tibetanum* was reported {9970}.

Dormancy (seed)

Phs. 7D {9960}. Semi-dominant {9960}. **v:** Soleil {9960}. **ma:** Weakly associated with *Xpsp3003-7D* {9960}.

DNA Markers

Group 1S

Amendments:

Xcdo388-1B,D. Add '3D', '4D', and '6D' in the last column.

Xcdo1188-1A,B,D. Change to '*Xcdo1188-1A.1* [{280}]^{3,5}, *1B.1* [{1529}]^{1}, *1D* {445}^{1}.' and add '(1AL,BL).' in the last column.

Xglk558-1D. Remove {822}, add '1B,DL', '3D', '6D', and '7D' in the last column, and remove 'Note: The arm location of *Xglk558-1D* in *T. tauschii* was not reported in {822}.'.

Xgwm30-1A. Add '3A' in the third column.

Xgwm33-1A. Revise to '*Xgwm33-1A* {1226}, *1B,D* {9929}.'.

XksuD14-1A.1. Change to '*XksuD14-1A.1,.2.*'.

Add:

XgbxG746-1B {9958}.		gbxG746.	
XgbxR507-1A {9958}.		gbxR507.	
XgbxR698-1A,B,D [{9958}].	[*XgbxR698c-1A*, *XgbxR698b-1B*, *XgbxR698a-1D* {9958}]. gbxR698.		
Xgwm18-1B {9929}.		WMS F18/WMS R18.	
Xgwm136-1A {9929}.		WMS F136/WMS R136.	
Xgwm273-1B {9929}.		WMS F273/WMS R273.	
Xgwm337-1D {9929}.		WMS F337/WMS R337.	
Xgwm550-1B {9929}.		WMS F550/WMS R550.	
Xgwm582-1B {9929}.		WMS F582/WMS R582.	
Xmgb40-1A,B {9959}^{2}.		MGB40.	
Xmwg67-1A {1529}.		MWG67 {467}.	(6A).
Xutv111-1B {9959}^{2}.		UTV111.	(3B).
Xutv786-1A,B {9959}^{2}		UTV786.	
Xutv1181-1A,B {9959}^{2}.		UTV1181.	
Xutv1334-1B {9959}^{2}.		UTV1334.	
Xutv1391-1A {9959}^{2}.		UTV1391.	(1A).
Xutv1518-1A,B {9959}^{2}.		UTV1518.	(7A).
Xycu1198-1A {9935}^{3}.		YCU1198.	

Group 1L

Amendments:

Xabg387-1A.1,.2, 1B,D. Add '6A,B' in the last column.

Xabg464-1A. Add '(2D).' in the last column.

Xbcd454-1A. Add '(5A).' in last column.

Xbg542-1D. Add '(3D).' in the last column.

Xcdo393-1A {1529}^{1}, {280}^{3}, *1B* {981050}. Change reference {981050} to '{154}^{1}'.

Xcdo1312-1B . Add '5D' in the last column.

Xcmwg706-1A. Add ', *1D.1,.2* {9926}[4]' in the 1st column.'

Xcmwg758-1A,B. Add '(1D).' in the 4th column.

Xglk427-1B {822}. Add '(1D, 3D).' in the 4th column.

Xglk558-1B,D. Delete ', *1D* {822}' from the 1st column and add '1DS,D', '3D', '6D' and '7D' in the last column.

Xgwm33-1B. Delete (moved to 1S).

XksuG55-1D.1,.2. Add '(2D).' in the last column.

XksuM114-1B,D. Add '(4D).' in the last column.

XpsrX-1A,B,D {905}. Delete this entry (the clone that detected the locus is unknown).

Xpsr946-1D. Add '6D' in the last column.

Add:

Xcdo1188-1A.2,B.2 [{9957}].	[*Xcdo1188-1A,B* {9957}].	CDO1188 {545}.	(1AS,BS,DS).
Xgbx3147-1B {9958}.		gbx3147.	
Xgbx3581-1B [{9958}].	[*Xgbx3581a-1B* {9958}].	gbx3581.	(4B).
XgbxG80-1B [{9958}].	[*XgbxG080-1B* {9958}].	gbxG080.	
XgbxG97-1A,D [{9958}].	[*XgbxG097a-1A, XgbxG097b-1D* {9958}]. gbxG097.		
XgbxG160-1B {9958}.		gbxG160.	
XgbxG177-1D {9958}.		gbxG177.	
XgbxG178-1B {[9958}].	[*XgbxG178a-1B* {9958}].	gbxG178.	
XgbxG259-1A,B.1,.2,D.1,.2 [{9958}]. [*XgbxG259c-1A, XgbxG259b,e-1B, XgbxG259a,d-1D* {9958}]. gbxG259.			
XgbxG557-1A {9958}.		gbxG557.	
XgbxG624-1D {9958}.		gbxG624.	
XgbxGx90-1B {9958}.		gbxGx90.	
XgbxR59-1B {9958}.		gbxR059.	
Xgwm99-1A {9929}.		WMS F99/WMS R99.	
Xgwm124-1B {9929}.		WMS F124/WMS R124.	
Xgwm131-1B {9929}.		WMS F131/WMS R131.	(3B).
Xgwm135-1A {9929}.		WMS F135/WMS R135.	
Xgwm136-1A {9929}.		WMS F136/WMS R136.	
Xgwm140-1B {9929}.		WMS F140/WMS R140.	
Xgwm153-1B {9929}.		WMS F153/WMS R153.	
Xgwm164-1A {9929}.		WMS F164/WMS R164.	
Xgwm259-1B {9929}.		WMS F259/WMS R259.	
Xgwm268-1B {9929}.		WMS F268/WMS R268.	
Xgwm274-1B {9929}.		WMS F274/WMS R274.	(7B).
Xgwm357-1A {9929}.		WMS F357/WMS R357.	
Xgwm403-1B {9929}.		WMS F403/WMS R403.	
Xgwm458-1D {9929}.		WMS F458/WMS R458.	
Xgwm497-1A {9929}.		WMS F497/WMS R497.	(2A, 3D).
Xgwm498-1B {9929}.		WMS F498/WMS R498.	
Xgwm642-1D {9929}.		WMS F642/WMS R642.	
Xgwm666-1A {9929}.		WMS F666/WMS R666.	(3A, 5A, 7A).
Xlogtp1(Pur-1)-1A {9976}.		P1A5/PCO3	
Xlogtp2(Pur-1)-1B {9976}.		P1B5/P1B3.	

Xlogtp3(Pur-1)-1D {9976}.		P1D5/PCO3.	
Xmgb2-1A,B {9959}[2].		MGB2.	
Xmgb44-1A {9959}[2].		MGB44.	
Xubp24-1A {9959}[2].		UBP24.	
Xutv618-1A,B {9959}[2].		UTV618.	
Xutv704-1B {9959}[2].		UTV704.	
Xutv765-1A {9959}[2].		UTV765.	
Xutv780-1A,B {9959}[2].		UTV780.	
Xutv1356-1A,B {9959}[2].		UTV1356.	
Xutv1425-1B {9959}[2].		UTV1425.	
Xutv1460-1A {9959}[2].		UTV1460.	

Group 1

Amendments:

Xcdo675-1D. Add '(2D, 7D).' in the last column.
Xglk652-1D. Add '3D' in the last column.
Xglk732-1A. Add '(2D).' in the last column.
Xglk764-1B. Add '(7D).' in the last column.
XksuD16-1D. Change last column to '(5A,B,D).'.
Xwg908-1A. Change last column to '(5A,B,D).'.

Add:

Xabc155-1D {9926}[4].		ABC155.	
Xabg458-1D {9926}[4].		ABG458.	(6A,B,D).
Xabg460-1D {9926}[4].		ABG460.	(3A, 4A).
Xabg702-1D {9926}[4].		ABG702.	
Xbg175-1D {9926}[4].		BG175.	
Xbg552-1D {9926}[4].		BG552.	
XcsSR3(Gsp)-1D [{9926}][4].	[*Xgsp-1D* {9926}].	pGsp.	(5A,B,D, 7D).
Xcmwg758-1D [{9926}][4].	[*Xmwg758-1D* {9926}].	cMWG758.	(1AL,BL).
Xgbx3076-1A {9958}.		gbx3076.	
XgbxGx74-1A {9958}.		gbxGx74.	
Xglk259-1D {9926}[4].		pTag259.	(6A).
Xglk427-1D {9926}[4].		pTag427.	(1B, 3D).
Xglk558-1D {822}.		pTag558.	(1BL,DS,D, 2B,D, 3D, 6D, 7D).
Xglk754-1D {9926}[4].		pTag754.	(5B).
Xgwm413-1B {9929}.		WMS F413/WMS R413.	
XksuB7-1D.1,.2,.3,.4 {9926}[4].		pTtksuB7.	(3D, 5D, 7D).
XksuE15-1D {9926}[4].		pTtksuE15.	
Xmwg584-1D.1,.2 {9926}[4].		MWG584.	(3A, 4A, 5D).

Xmwg660-1D {9926}[4].		MWG660.	
Xpsr547-1D {9926}[4].		PSR547.	(3B, 7A,B,D).
Xwg645-1D {9926}[4].		WG645.	(2A,B,D).
Xwg789-1D {9926}[4].		WG789.	(4D).

Group 2S

Amendments:

Xabg378-2A. Add '6A,D' in the last column.

Xbcd1709-2B. Change to '*Xbcd1709-2A* {9959}[2], *2B* {1060}[1].'.

Xcdo64-2A,B,D. Add '(3D, 4D).' in the last column.

Xgwm129-2B. Add '(5A).' in the last column.

Xgwm515-2D. Add '(2A)'. in the last column.

XksuD18-2B. Add superscript '1' to '{154}'.

XksuF11-2B. Add '2D' in the last column.

XksuF19-2A,B,D. Add 'The arm location of *XksuF19-2D* in *T. tauschii* was not reported in {448}.'.

Xpsr131-2A,B,D. Add '(5D).' in the last column.

Xpsr933-2A,D. Change to '*Xpsr933-2A* {256}[1], *2B* {9959}[2], *2D* {256}[1].'.

Xpsr946-2D. Add '1D' and '6D' in the last column.

Add:

XHak2-2A [{9932}][3], *2B,D* [{9932}][1].

[*XHvHAK2-2A* {9932}].	HvHAK2 {9932}.		
Xgbx3793-2B {9958}.		gbx3793.	
Xgbx3818-2A {9958}.		gbx3818.	
Xgbx3832-2A [{9958}].	[*Xgbx3832c-2A* {9958}].	gbx3832.	(2DL, 4A).
XgbxG35-2B [{9958}].	[*XgbxG035c-2B* {9958}].	gbxG035.	(4A, 7B).
XgbxG36-2A [{9958}].	[*XgbxG036a-2A* {9958}].	gbxG036.	(6A).
XgbxG218-2D [{9958}].	[*XgbxG218b-2D* {9958}].	gbxG218.	(7A,B).
XgbxG281-2A {9958}.		gbxG281.	
XgbxG536-2D {9958}.		gbxG536.	
XgbxG747-2A,D [{9958}].	[*XgbxG747b-2A, XgbxG747a-2D* {9958}]. gbxG747.		
XgbxGx71-2B {9958}.		gbxGx71.	
XgbxR618-2D {9958}.		gbxR618.	
XgbxR739-2B {9958}.		gbxR739.	
Xgwm71-2A.1 [{9929}].	[*Xgwm71.1-2A* {9929}].	WMS F71/WMS R71.	(2A, 3D).
Xgwm264-2B {9929}.		WMS F264/WMS R264.	(3B).
Xgwm359-2A {9929}.		WMS F359/WMS R359.	
Xgwm429-2B {9929}.		WMS F429/WMS R429.	
Xgwm455-2D {9929}.		WMS F455/WMS R455.	
Xgwm497-2A {9929}.		WMS F497/WMS R497.	(1A, 3D).
Xgwm614-2A {9929}.		WMS F614/WMS R614.	
Xgwm630-2B {9929}.		WMS F630/WMS R630.	
Xmgb225-2A {9959}[2].		MGB225.	
Xmgb243-2B {9959}[2].		MGB243.	

Xrsq805(Embp)-2B [{9959}]^{2}.	[*Xrsq805-2B* {9959}^{2}].	pGC19 {471}.	(3B, 5A,B,D, 6AL, 6BS, 7D).
Xucg1(ACCp)-2A,2B,2D {459}.		ucg1 {459}.	
Xutv1074-2B {9959}^{2}.		UTV1074.	
Xutv1340-2B.1 {9959}^{2}.		UTV1340.	(2AL, 2BL).
Xutv1343-2A {9959}^{2}.		UTV1343.	(4A, 5B).
Xutv1441-2A {9959}^{2}.		UTV1441.	(6B).
Xycu1137-2A {9935}^{3}.		YCU1137.	

Group 2L

Amendments:

Xabc451-2A. Add '(6D).' in the last column.

Xabg496-2A. Add '(5A).' in the last column.

Xbcd410-2A,D. Add '(7D).' in the last column.

Xbg123-2A. Add ', *2D* {9926}^{4}.' in the first column.

Xcdo388-2B . Add superscript '1' to '{1060}' and ', *2D* {9926}^{4}' and add '3D', '4D', and '6D' in the last column.

Xcmwg720-2A. Add ', *2D* {9926}^{4}' in the first column.

Xgwm16-2B. Add '(5D, 7D).' in the last column.

Xgwm30-2D. Add '3A' in the last column.

Xgwm47-2B. Change to '*Xgwm47-2A.1,.2* [{9929}], *2B* {1226,1225}.' and add '[*Xgwm47.1-2A, Xgwm47.2-2A* {9929}].' in the second column.

Xgwm55-2B. Change to '*Xgwm55-2B.1* [{1225}],{9929}.', add '[*Xgwm55-2B* {1225}].' in the second column, and add '(6D).' in the last column.

Xgwm191-2B. Add '(5B, 6B).' in the last column.

Xgwm382-2A,D. Change to '*Xgwm382-2A* {1225}, *2B* {9929}, *2D* {1225}.'.

Xgwm608-2D. Add '(4D).' in the last column.

XksuF1-2A,B. In the last column, delete '2B,D' and change '5A' to '5A,B,D'.

XksuF11-2A,B. Add '2D' in the last column.

Xmwg546-2B . Change 1st column to '*Xmwg546-2B* {1060}^{1}, *2D* {9926}^{4}.'.

Xpsr101(psk-1)-2A,B,D. Capitalize *'Psk'*.

Xwg184-2D. Add '3D' in the last column.

Xwg645-2A,B,D. Add '(1D).' in the last column.

Xwsu2(Pk)-2B. Change the clone entry from 'pKABAg1' to 'TaPK3 {1536} [PKABAg1 {1536}].'.

Add:

XHak1-2A,D [{9932}].	[*XHvHAK1-2A,D* {9932}].	HvHAK1 {9932}.	(3A,D, 4A,B,D, 6A,B,D).
Xcdo1417-2B {9959}^{2}.		CDO1417 {545}.	
Xgbx3832-2D [{9958}].	[*Xgbx3832a-2D* {9958}].	gbx3832.	(2AS, 4A).
XgbxG87-2B [{9958}].	[*XgbxG087-2B* {9958}].	gbxG087.	
XgbxG142-2B {9958}.		gbxG142.	
XgbxG145-2D {9958}.		gbxG145.	
XgbxG214-2A {9958}.		gbxG214.	
XgbxG303-2A {9958}.		gbxG303.	
XgbxG329-2B {9958}.		gbxG329.	

XgbxG575-2D [{9958}].	[*XgbxG575b-2D* {9958}].	gbxG575.	(7A).
XgbxR452-2B {9958}.		gbxR452.	
Xgwm311-2A,D {9929}.		WMS F311/WMS R311.	
Xgwm320-2D {9929}.		WMS F320/WMS R320.	
Xmgb5-2A {9959}^{2}.		MGB5.	
Xmgb57-2A,B {9959}^{2}.		MGB57.	
Xmgb236-2A,B {9959}^{2}.		MGB236.	
Xmgb342-2B {9959}^{2}.		MGB342.	
Xutv861-2B {9959}^{2}.		UTV861.	
Xutv1340-2A {9959}^{2}.		UTV1340.	(2BS, 2BL).
Xutv1340-2B.2,.3 {9959}^{2}.		UTV1340.	(2AL, 2BS).
Xutv1427-2A,B {9959}^{2}.		UTV1427.	

Group 2

Amendments:

Xglk222-2D. Add '5D' in the last column.

Xglk554-2A,B. Change to '*Xglk554-2A* {822,154}^{1}, *2B* {822}^{1}, *2D* {9926}^{4}.'.

Xgwm55-2B. Change to '*Xgwm55-2B.2* [{1225}],{9929}', add '[*Xgwm55-2B* {1225}].' in the second column, and add '(6D).' in the last column.

Xgwm210-2D {1225}. Change to '*Xgwm210-2B* {9929}, *2D* {1225}.'.

Xgwm249-2D. Change to '*Xgwm249-2A* {9929}, *2D* {1225}'.

Xgwm410-2B. Add '(5A).' in the last column.

XksuD8-2D. Move the superscript '1,3' from the marker symbol to the reference.

XksuF19-2D. Delete the entry (moved to Group 2S).

XksuF36-2D. Add '7D' in the last column.

XksuG49-2D.1,.2,.3,.4. Add '7D' in the last column.

XksuD18-2D(1) [{448}]. Change to

'*XksuD18-2D.1,.2* [{448}]. [*XksuD18(A)-2D, XksuD18(B)-2D* {448}]. pTtksuD18.'.

XksuD18-2D(2) [{448}]. Delete.

Xucg1(ACCp)2A,2B,2D. Delete (moved to 2S).

Add:

Xabg356-2D {9926}^{4}.	ABG356.	
Xabg464-2D {9926}^{4}.	ABG464.	(1A).
Xbcd828-2D {9926}^{4}.	BCD828.	(3A).
Xbg508-2D {9926}^{4}.	BG508.	
Xcdo675-2D {9926}^{4}.	CDO275.	(1D, 7D).
Xglk163-2D {9926}^{4}.	pTag163.	(1D, 4D).
Xglk197-2B {9926}^{4}.	pTag197.	(7B).
Xglk278-2D {9926}^{4}.	pTag278.	(4D, 5A,B).
Xglk301-2D {9926}^{4}.	pTag701.	(3D, 5D, 7A).
Xglk732-2D {9926}^{4}.	pTag732.	

Xglk757-2D {9926}[4].		pTag757.	(3B, 5A,D, 6A).
Xgbx4986-2A {9958}.		gbx4986.	
XgbxG212-2D {9958}.		gbxG212.	
XgbxG520-2B {9958}.		gbxG520.	
XgbxG542-2A [{9958}].	[*XgbxG542a-2A* {9958}].	gbxG542.	(3D).
XgbxG553-2B {9958}.		gbxG553.	
XgbxR635-2D {9958}.		gbxR635.	
Xgwm71-2A.1 [{9929}].	[*Xgwm71.1-2A* {9929}].	WMS F71/WMS R71.	(2AS, 3D).
Xgwm122-2A {9929}.		WMS F122/WMS R122.	
Xgwm275-2A {9929}.		WMS F275/WMS R275.	
Xgwm448-2A {9929}.		WMS F448/WMS R448.	
Xgwm473-2A {9929}.		WMS F473/WMS R473.	
Xgwm515-2A {9929}.		WMS F515/WMS R515.	(2DS).
XksuD38-2D {9926}[4].		pTtksuD38.	
XksuF11-2D {9926}[4].		pTtksuF11.	(2AL,BS,BL).
XksuG55-2D {9926}[4].		pTtksuG55.	(1D, 4D, 7A).
XksuH8-2D.1,.2 {9926}[4].		pTtksuH8.	(4A[m], 3D, 5A,B, 7AS,AL,BS,DL).
Xmwg520-2D {9926}[4].		MWG520.	
Xmwg820-2D {9926}[4].		MWG820.	(5A, 6A,B).
Xmwg557-2D {9926}[4].		MWG557.	
Xpsr680-2D {9926}[4].		PSR680.	(7A,B,D).
Xutv109-2B {9959}[2].		UTV109.	
Xwg405-2D {9926}[4].		WG405.	

Group 3S

Amendments:

Xabg460-3A. Add '1D' in the last column.

Xgwm2-3A. Change to '*Xgwm2-3A* {1226}, *3D* {9929}.'.

Xmwg584-3A. Add '1D' and '5D' in the last column.

Xpsr547-3B. Add '(1D).' in the last column.

Xpsr946-3A. Add '6D' in the last column.

Xtam12-3A,B,D. Add '[*Xth12-3D* {9929}].' in the second column.

Xtam55-3A,D. Add '[*Xth55-3D* {9929}].' in the second column.

Add:

XgbxG265-3D {9958}.		gbxG265.	
XgbxG392-3B {9958}.		gbxG392.	
XgbxG406-3A {9958}.		gbxG406.	
XgbxR80-3B [{9958}].	[*XgbxR080-3B* {9958}].	gbxR080.	
Xgwm71-3D {9929}.		WMS F71/WMS R71.	(2A).
Xgwm72-3B {9929}.		WMS F72/WMS R72.	
Xgwm77-3B {9929}.		WMS F77/WMS R77.	
Xgwm114-3D {9929}.		WMS F114/WMS R114.	(3BL).

Xgwm183-3D {9929}.		WMS F183/WMS R183.	
Xgwm264-3B {9929}.		WMS F264/WMS R264.	(1B).
Xgwm285-3B {9929}.		WMS F285/WMS R285.	
Xgwm369-3A {9929}.		WMS F369/WMS R369.	
Xgwm389-3B {9929}.		WMS F389/WMS R389.	
Xgwm376-3B {9929}.		WMS F376/WMS R376.	
Xgwm493-3B {9929}.		WMS F493/WMS R493.	
Xgwm533-3B.1,.2 [{9929}].	[*Xgwm533.1,.2-3B* {9929}].	WMS F533/WMS R533.	
Xmgb77-3A {9959}^{2}.		MGB77.	
Xmgb228-3A {9959}^{2}.		MGB228.	
Xutv103-3A,B {9959}^{2}.		UTV3.	

Group 3L

Amendments:

Xabc174-3B,D. Change to '*Xabc174-3A* {9961}, *B,D* {1061}.'.

Xabg377-3A. Add '(6D).' in the last column.

Xabg387-3A. Add '6A,B' in the last column.

Xbcd828-3A. Add '(2D).' in the last column.

Xbg131-3B. Add superscript '1' to '{1061}' and ', *3D* {9926}^{4}' in the first column.

XksuG62-3A,B,D. Delete 'The arm location of *XksuG62-3D* in *T. tauschii* was not reported in {448}.' and add the comment 'Eight *XksuG62-3D* loci were reported in {9926}.'.

Xmwg802-3A. Add superscript '1' to '{1061}' and ', *3D* {9926}^{4}' in the first column.

Xpsr156(L13)-3A,B,D. Change references to {1329,1392}

Xpsr1203-3A. Add superscript '1' to '{247}' and ', *3D* {9926}^{4}' in the first column.

Xrsq805(Embp)-3B. Add '(2B).' to last column.

Xtam33-3A,B,D. Change first column to '*Xtam33-3A,B* {245}, *3D* {245,9929}.', add '[*Xth33-3D* {9929}].' in the second column, and add the comment 'The arm locations of *Xtam33-3A,B,D* were not determined in {245}.'.

Xwg177-3A. Add superscript '1' to '{1061}' and ', *3D* {9926}^{4}' to the first column and remove '4A' from the last column.

Xwia483(Cxp1)-3A,B,D. Add '(6D).' in the last column.

Add:

XHak1-3A,D [{9932}].	[*XHvHAK1-3A,D* {9932}].	HvHAK2 {9932}.	(2A,D, 4A,B,D, 6,B,D).
Xabg389-3A {9961}.		ABG389 {664}.	
Xgbx3864-3D [{9958}].	[*Xgbx3864a-3D* {9958}].	gbx3864.	(6A).
XgbxG34-3A [{9958}].	[*XgbxG034-3A* {9958}].	gbxG034.	
XgbxG37-3B [{9958}].	[*XgbxG037b-3B* {9958}].	gbxG037.	(5D, 7B).
XgbxG65-3B [{9958}].	[*XgbxG065-3B* {9958}].	gbxG065.	
XgbxG111-3B [{9958}].	[*XgbxG111a-3B* {9958}].	gbxG111.	
XgbxG199-3B {9958}.		gbxG199.	
XgbxG242-3A {9958}.		gbxG242.	
XgbxG305-3D {9958}.		gbxG305.	
XgbxG469-3B {9958}.		gbxG469.	
XgbxG499-3A {9958}.		gbxG499.	
XgbxG542-3D [{9958}].	[*XgbxG542b-3D* {9958}].	gbxG542.	(2A).

XgbxG773-3B {9958}.		gbxG773.	
XgbxR187-3D {9958}.		gbxR187.	
Xgwm112-3B {9929}.		WMS F112/WMS R112.	(7B).
Xgwm114-3B {9929}.		WMS F114/WMS R114.	(3DS).
Xgwm131-3B {9929}.		WMS F131/WMS R131.	(1B).
Xgwm155-3A {9929}.		WMS F155/WMS R155.	
Xgwm162-3A {9929}.		WMS F162/WMS R162.	
Xgwm181-3B {9929}.		WMS F181/WMS R181.	
Xgwm247-3B {9929}.		WMS F247/WMS R247.	
Xgwm299-3B {9929}.		WMS F299/WMS R299.	
Xgwm314-3D {9929}.		WMS F314/WMS R314.	
Xgwm383-3D {9929}.		WMS F383/WMS R383.	
Xgwm391-3A {9929}.		WMS F391/WMS R391.	
Xgwm480-3A {9929}.		WMS F480/WMS R480.	
Xgwm547-3B {9929}.		WMS F547/WMS R547.	
Xgwm645-3D {9929}.		WMS F645/WMS R645.	
Xgwm664-3D {9929}.		WMS F664/WMS R664.	
Xgwm666-3A.2 [{9929}].	[*Xgwm666.2-3A* {9929}].	WMS F666/WMS R666.	(1A, 3A, 5A, 7A).
Xlars10(taVp1)-3A,B,D {9961}.		taVP1.	
Xtam32-3A,B,D {245}.	[*Xth32-3D* {9929}].	TAM32.	
Xutv111-3B {9959}[2].		UTV111.	(1B).
Xutv416-3A {9959}[2].		UTV416.	
Xutv560-3A {9959}[2].		UTV560.	
Xutv1055-3A {9959}[2].		UTV1055.	
Xutv1302-3A {9959}[2].		UTV1302.	
Xutv1532-3A {9959}[2].		UTV1532.	

Group 3

Amendments:

Xcdo395-3A. Add a superscript '1' to '{1061}' and add ', *3D* {9926}[4]' in the first column.

Xglk652-3B. Add a superscript '1' to '{822}' and add ', *3D* {9926}[4]' in the first column.

Xglk756-3B. Add '2D' and '5D' in the last column.

Xtam32-3A,B,D. Delete (moved to 3L).

Add:

Xabg380-3D {9926}[4].	ABG380.	
Xbg542-3D {9926}[4].	BG542.	(1D).
Xbg933-3D.1,.2 {9926}[4].	BG933.	
Xcdo64-3D {9926}[4].	CDO64.	(2A,B,D, 4D).
Xcdo388-3D.1,.2 {9926}[4].	CDO388.	(1B,D, 2B, 4A,D, 5A,B, 6A,D).
Xglk301-3D {9926}[4].	pTag301.	(2D, 5D, 7A).
Xglk317-3D {9926}[4].	pTag317.	(4D, 5A, 6A).

Xglk334-3D {9926}[4].		pTag334.	(6A,B).
Xglk427-3D {9926}[4].		pTag427.	(1D).
Xglk558-3D {9926}[4].		pTag558.	(1BL,DS,D, 2B,D, 6D, 7D).
Xgwm30-3A {9929}.		WMS F30/WMS R30.	(1A, 2D).
Xgwm32-3A {9929}.		WMS F32/WMS R32.	
Xgwm284-3B {9929}.		WMS F284/WMS R284.	
Xgwm341-3D {9929}.		WMS F341/WMS R341.	
Xgwm456-3D {9929}.		WMS F456/WMS R456.	
Xgwm497-3D {9929}.		WMS F497/WMS R497.	(1A, 2A).
Xgwm566-3B {9929}.		WMS F566/WMS R566.	
Xgwm666-3A.1 [{9929}].	[*Xgwm666.1-3A* {9929}].	WMS F666/WMS R666.	(1A, 3AL, 5A, 7A).
Xgwm674-3A {9929}.		WMS F674/WMS R674.	
Xksu1-32-4-3D [{9926}][4].	[*Xksu32-4-3D* {9926}].	pTtksu1-32-4.	(6D, 7D).
XksuB7-3D {9926}[4].		pTtksuB7.	(1D, 5D, 7D).
XksuG53-3D {9926}[4].		pTtksuG53.	
XksuG419-3D {9926}[4].		pTtksuG419.	(4D, 5D).
XksuH8-3D [{9926}][4].	[*XksuH8-3D.3* {9926}].	pTtksuH8.	(2D, 4A^{m}, 5A,B, 7AS,AL,BS,DL).
XksuM117-3D 9926}[4].		pTtksuM117.	
XksuI19-3D.1,.2 {9926}[4].		pTtksuI19.	
Xmgb58-3A {9959}[2].		MGB58.	
Xmwg526-3D {9926}[4].		MWG526.	
Xwg178-3D {9926}[4].		WG178.	
Xwg184-2D {9926}[4].		WG184	(2D, 4D).

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

Amendments:

Xcdo669-4A,B,D. Add '7D' in the last column.

Xgwm165-4B. Delete (moved to 4AS:4BL:4DL).

XksuG12-4A. Add '7D' in the last column.

Xmwg634-4B,D. Add '(4A,B, 7D).' in the last column.

Xwg184-4D. Add '(2D, 3D).' in the last column.

Xwg909-4B. Add '(5A,B,D, 7B).' in last column.

Add:

Xmgb7-4A {9959}[2].	MGB7.
Xutv1386-4B {9959}[2].	UTV1386.
Xwg876-4A {9959}[2].	WG876 {028}.

4A^{m}S.

Amendments:

Xabg387-4A. Change last column to '(1A,B,D, 3A, 5A, 6A,B).'.

Xabg460-4A.1. Add '1D' in the last column.
Xcdo669-4A. Add '7D' in the last column.
Xmwg584-4A.1. Add '1D' and '5D' in the last column.

Group 4L (4AS:4BL:4DL)
Amendments:
Xabg484-4A,B. Add '(4A^{m}L, 6D).' in the last column.
Xcdo1312-5A,4B,D. Add '5D' in the last column.
Xcdo1337-4A,B. Add superscript '1' to '{1008}' and ', *4D* {9926}^{4}' in the 1st column.
Xfbb58-4B. Delete (moved to 5AL:4BL:4DL).
Xgwm165-4D. Change to '*Xgwm165-4A,B* {9929}, *4D* {117}.' and add the comment 'A 4BS *Xgwm165-4B* was reported in {724}.'.
Add:

XHak1-4B,D [{9932}].	[*XHvHAK1-4B,D* {9932}].	HvHAK1 {9932}.	(2A,D, 3A,D, 4A, 6A,B,D).
XgbxG81-4D [{9958}].	[*XgbxG081-4D* {9958}].	gbxG081.	
XgbxG129-4D {9958}.		gbxG129.	
XgbxG147-4B {9958}.		gbxG147.	
XgbxG152-4D {9958}.		gbxG152.	
XgbxG192-4A,B,D [{9958}].	[*XgbxG192a-4A, XgbxG192c-4B, XgbxG192b-4D* {9958}].	gbxG192.	
XgbxG260-4B {9958}.		gbxG260.	
XgbxR247-4A {9958}.		gbxR247.	
XgbxR866-4A {9958}.		gbxR866.	
Xmgb299-4A {9959}^{2}.		MGB299.	
Xgwm4-4A {9929}.		WMS F4/WMS R4.	
Xgwm194-4D {9929}.		WMS F194/WMS R194.	
Xgwm251-4B {9929}.		WMS F251/WMS R251.	
Xgwm368-4B {9929}.		WMS F368/WMS R368.	
Xgwm538-4B {9929}.		WMS F538/WMS R538.	
Xgwm601-4A {9929}.		WMS F601/WMS R601.	
Xgwm609-4D {9929}.		WMS F609/WMS R609.	
Xgwm624-4D {9929}.		WMS F624/WMS R624.	

4A^{m}L.
Amendments:
Xabg460-4A.2. Add '1D' in the last column.
Xabg463-4A. Add '(4D, 5D).' in the last column.
Xabg484-4A. Add '6D' in the last column.
Xmwg584-4A.2. Add '1D' and '5D' in the last column.

4AL:4BL:4DL
Add:

Xgwm610-4A {9929}**.	WMS F610/WMS R610.

Whether *Xgwm610-4A* belongs to the 4AL:4BL:4DL arm group or the 4AL:5BL:5DL arm group is uncertain.

5AL:4BL:4DL

Amendments:

Xgwm410-5A. Add '(2B).' in the last column.

XksuH11-5A, 4B,D. Add '6A' in the last column.

Add:

Xbcd1312-5A {9933}[1,3].		BCD1312.	
Xfbb58-4B {1059,9966}.		FBB058.	
Xgbx3581-4B [{9958}].	[*Xgbx3581b-4B* {9958}].	gbx3581.	(1B).
XgbxG276-4B {9958}.		gbxG276.	
XgbxG367-4D [{9958}].	[*XgbxG367a-4D* {9958}].	gbxG367.	(7A).
XgbxG623-4B {9958}.		gbxG623.	
Xglk335-4B {822,9966}.		pTag335.	

The arm location of *Xglk335-4B* was not reported in {822}.

Xgwm126-5A {9929}.		WMS F126/WMS R126.	
Xgwm595-5A {9929}.		WMS F595/WMS R595.	

Group 4

Amendments:

Xfba211-4A {1059}. Change to '*Xfba211-4A* {1059}, *4D* {9957}.'.

Xglk335-4B {822}. Delete (moved to 5AL:4BL:4DL).

Xglk578-4A,B {822}. Change to '*Xglk578-4A,B* {822}, *4D* {9966}.'.

XksuB5-4D. Add '(5D).' in the last column.

XksuG55-4D. Add '2D' in the last column.

Xmwg634-4A,B. Add '(4BS,DS, 7D).' in the last column.

Add:

XHak1-4A [{9932}].	[*XhvHAK1-4A* {9932}].	HvHAK1 {9932}.	(2A,D, 3A,D, 4BL,DL, 6A,B,D).
Xabg383-4D {9926}[4].		ABG383.	
Xabg397-4D {9926}[4].		ABG397.	
Xabg463-4D [{9926}][4].	[*Xabg463-4D.2* {9926}].	ABG463.	(4A^{m}, 5D).
Xbg969-4D {9926}[4].		BG930.	
Xbg930-4D {9926}[4].		BG969.	
Xbg1021-4D {9926}[4].		BG1021.	
Xcdo64-4D {9926}[4].		CDO64.	(2A,B,D, 3D).
Xcdo388-4D.1,.2 {9926}[4].		CDO388.	(1B,D, 2B, 3D, 4A^{m}, 5A,D, 6A,D).
Xcmwg652-4D {9926}[4].		cMWG652.	(6A,B,D).
Xglk163-4D {9926}[4].		pTag163.	(1D, 2D).
Xglk278-4D {9926}[4].		pTag278.	(2D, 5A,B).
Xglk317-4D {9926}[4].		pTag317.	(3D, 5A, 6A).
XgbxG57-4B [{9958}].	[*XgbxG057-4B* {9958}]	gbxG057.	
XgbxR657-4B {9958}.		gbxR657.	

Xgwm66-4B {9929}.	WMS F66/WMS R66.	(5B).
Xgwm107-4B {9929}.	WMS F107/WMS R107.	
Xgwm113-4B {9929}.	WMS F113/WMS R113.	
Xgwm495-4B {9929}.	WMS F495/WMS R495.	
Xgwm513-4B {9929}.	WMS F513/WMS R513.	
Xgwm608-4D {9929}.	WMS F608/WMS R608.	(2D).
Xksu3-4D {9926}[4].	pZmksu3 {9928}.	
XksuG419-4D {9926}[4].	pTtksuG419.	(3D, 5D).
XksuM147-4D {9926}[4].	pTtksuM147.	
XksuM91-4D {9926}[4].	pTtksuM91.	
XksuM92-4D {9926}[4].	pTtksuM92.	
XksuM114-4D {9926}[4].	pTtksuM114.	(1B,D).
Xmwg542-4D {9926}[4].	MWG542.	
Xpsr157-4D {9926}[4].	PSR157.	
Xwg516-4D.1,.2 {9926}[4].	WG516.	(5D).
Xwg789-4D {9926}[4].	WG789.	(1D).

4A^m

Amendments:

Xcdo388-4A. Change last column to '(1B,D, 2B, 3D, 4D, 5A,D, 6A,D).'.

XksuH8-4A. Change probe symbol to 'pTtksuH8' and add '2D' and '3D' in the last column.

Xcdo669-4A. Add '7D' in the last column.

Xmwg584-4A.1. Add '1D' and '5D' in the last column.

Group 5S

Amendments:

XcsSR3(Gsp)-5A. Delete the entire entry and substitute

'*XcsSR3(Gsp)-5A,B,D* [{446}][1], *5A* {282}[3].
[*Xgsp-5A,B,D* {446}]. pGsp {1185}. (1D, 7D).'.

Xglk317-5A.1,.2, 5A. Add '3D' and '4D' in the last column.

Xglk424-5A. Add '(5D).' in the last column

Xgsp-5A,B,D. Delete the entire entry.

Xgwm129-5A. Add '(2B).' in the last column.

XksuH8-5A,B. Add '2D' and '3D' in the last column.

Xpsr946-5D. Add '6D' in the last column.

Xwg341-5A. Add ', *5D* {9926}[4]' in the first column.

Add:

XgbxG37-5D [{9958}].	[*XgbxG037a-5D* {9958}].	gbxG037.	(3B, 7B).
XgbxG625-5A {9958}.		gbxG625.	
Xgwm16-5D {9929}.		WMS F16/WMS R16.	(2B, 7B).
Xgwm66-5B {9929}.		WMS F66/WMS R66.	(4B).
Xgwm154-5A {9929}.		WMS F154/WMS R154.	
Xgwm159-5B {9929}.		WMS F159/WMS R159.	

Xgwm190-5D {9929}.	WMS F190/WMS R190.
Xgwm191-5B {9929}.	WMS F191/WMS R191. (2B, 6B).
Xgwm192-5D {9929}.	WMS F192/WMS R192.
Xgwm205-5A,D {9929}.	WMS F205/WMS R205.
Xgwm293-5A {9929}.	WMS F293/WMS R293.
Xgwm304-5A {9929}.	WMS F304/WMS R304.
Xgwm358-5D {9929}.	WMS F358/WMS R358.
Xgwm443-5B {9929}.	WMS F443/WMS R443.
Xgwm540-5B {9929}.	WMS F540/WMS R540.
Xgwm544-5B {9929}.	WMS F544/WMS R544.
Xmgb191-5A {9959}[2].	MGB191.
Xmgb341-5A {9959}[2].	MGB341.
Xubp3-5A {9959}[2].	UBP3.

Group 5L

Amendments:

Xabg387-5A. Add '6A,B' in the last column.

Xabg391-5A. Add superscript '1' to '{1059}' and add ', *5D* {9926}[4]' in the first column.

Xabg473-5B. Change to '*Xabg473-5A* {9933}[1,3], *5B* {1059}[1].'.

Xbcd9-5A,B. Add '(6D).' in the last column.

Xcdo348-5A,B. Add ', *5D* {9926}[4]' in the first column.

Xcdo388-5A,D. Add '(1B,D, 2B,D, 3D, 4A,D, 6A,D).' in the last column.

Xcdo786-5A,D. Add '7D' in the last column.

Xcdo1168-5A. Add ', *5D.1,.2* {9926}[4]' in the first column.

Xcdo1312-5B. Add superscript '1' to '{446}' and ', *5D.1,.2* {9926}[4]' in the first column, and add '(1B, 5A,4B,D)' in the 4th column.

Xglk222-5B. Revise the first column to '*Xglk222-5B* [{446}][1], *5D* {9926}[4].'.

Xglk651-5B,D. Add '6D' in the last column.

Xglk754-5B. Add '(1D).' in the last column.

XksuD42-5A,B,D. Add '(6D).' in the last column.

XksuF1-5A,B,D. Change the last column to '(2A,B).'

XksuG12-5D. Add '7D' in the last column.

Xmwg522-5A {1059}, *pTamwg522-5B* {446}. Change the first column to '*Xmwg522-5A* {1059}[1], *5B* {446}[1], *5D* {9926}[4].'.

Xmwg820-5A. Add '2D' and '6B' in the last column.

Xrsq805(Embp)-5A,B,D. Add '(2B).' to last column.

Xttu1937(Wsip16)-5A.1,.2. Delete the entire entry and substitute the following:

'*Xttu1937(Wsip16)-5A.1,.2* [{281}][3], *5D* {9926}[4].

[*XDhn2-5A.1,.2* {278}, *Xttu1937(Wsip16)[XDhn3]-5D* {9926}].

pTaWSP16 {662}. (6A).

The arm location of *Xttu1937(Wsip16)-5D'* in *T. tauschii* was not reported in {9926}.'.

Add:

Xabc717-5A {9933}[1,3].		ABC717.	
Xabg314-5A {9933}[1,3].		ABG314.	
Xabg496-5A {9933}[1,3].		ABG496.	
Xbcd21-6A {9933}.		BCD21.	(6A,B,D).
Xbcd454-5A {9969}.		BCD454 {545}.	(1A).
Xbcd603-5A {9933}[1,3].		BCD603.	
Xcdo548-5A {9933}[1,3].		CDO548.	
Xcdo590-5A {9969}.		CDO590 {545}.	
Xcdo735-5A {9933}[1,3].		CDO735.	
XgbxG60-5B [{9958}].	[*XgbxG060-5B* {9958}].	gbxG060.	
XgbxG70-5D [{9958}].	[*XgbxG070-5D* {9958}].	gbxG070.	
XgbxG134-5D {9958}.		gbxG134.	
XgbxG198-5B {9958}.		gbxG198.	
XgbxG333-5B,D [{9958}].	[*XgbxG333b-5B, XgbxG333a-5D* {9958}].	gbxG333.	
XgbxG521-5B {9958}**.		gbxG521.	

Whether *XgbxG521-5B* belongs to the 5L or 4AL:5BL:5DL arm group is uncertain.

XgbxG541-5B {9958}.		gbxG541.	
XgbxG722-5A,B,D [{9958}].	[*XgbxG722b-5A, XgbxG722a-5B,XgbxG722c-5D* {9958}].	gbxG722.	
XgbxG723-5B {9958}.		gbxG723.	
XgbxG739-5B {9958}.		gbxG739.	
XgbxR33-5A {[9958}].	[*XgbxR033-5A* {9958}].	gbxR033.	
XgbxR570-5B {9958}**.		gbxR570.	

Whether *XgbxR570-5B* belongs to the 5L or 4AL:5BL:5DL arm group is uncertain.

XgbxR678-5D {9958}.		gbxR678.	
XgbxR697-5D {9958}.		gbxR697.	
Xgwm67-5B {9929}.		WMS F67/WMS R67.	
Xgwm68-5B {9929}.		WMS F68/WMS R68.	(7B).
Xgwm121-5D {9929}		WMS F121/WMS R121.	(7D).
Xgwm156-5A {9929}.		WMS F156/WMS R156.	
Xgwm182-5D {9929}.		WMS F182/WMS R182.	
Xgwm212-5D {9929}.		WMS F212/WMS R212.	
Xgwm269-5D {9929}.		WMS F269/WMS R269.	
Xgwm271-5D {9929}.		WMS F271/WMS R271.	
Xgwm292-5D {9929}.		WMS F292/WMS R292.	
Xgwm371-5B {9929}.		WMS F371/WMS R371.	
Xgwm408-5B {9929}.		WMS F408/WMS R408.	
Xgwm499-5B {9929}.		WMS F499/WMS R499.	
Xgwm554-5B {9929}.		WMS F554/WMS R554.	
Xgwm565-5D {9929}.		WMS F565/WMS R565.	
Xgwm583-5D {9929}.		WMS F583/WMS R583.	
Xgwm604-5B {9929}.		WMS F604/WMS R604.	

Xgwm617-5A {9929}.	WMS F617/WMS R617.	(6A).
Xgwm654-5D {9929}.	WMS F654/WMS R654.	
Xgwm639-5A,B,D {9929}.	WMS F639/WMS R639.	
Xgwm666-5A {9929}.	WMS F666/WMS R666.	(1A, 3A, 7A).
Xmgb63-5A {9959}[2].	MGB63.	
Xpsp2120-5B [{9965}].	PSP2120F/PSP2120R [PC3-9 {9965}].	
Xpsr167(Hpr)-5B [{1329,9959[2]}]. [*Xpsr167-5B* {1329,9959}[2]].	PSR167 {1329}.	(6A,B,D).

The arm location of *Xpsr167(Hrp)-5B* was not reported in {1329}.

Xrc472-5A {9933}[1,3].	RC473.	
Xrg1112-5A {9933}[1,3].	RG1112.	
Xrgc711-5A {9969}.	RGC711 {740}.	
Xrgr2311-5A {9969}.	RGR2311 {740}.	
Xrgr2404-5A {9969}.	RGR2404 {740}.	
Xrgr2443-5A {9969}.	RGR2443 {740}.	
Xrgr3226-5A {9969}.	RGR3226 {740}.	
Xrz474-5A {9969}.	RZ474 {170}.	
Xrz630-5A {9969}.	RZ630 {170}.	
Xrz698-5A {9969}.	RZ698 {170}.	
Xutv1015-5B {9959}[2]**.	UTV1015.	

Whether *Xutv1015-5B* belongs to the 5L or 4AL:5BL:5DL arm group is uncertain.

Xutv1378-5B {9959}[2]**.	UTV1378.	(7A).

Whether *Xutv1378-5B* belongs to the 5L or 4AL:5BL:5DL arm group is uncertain.

4AL:5BL:5DL

Add:

XgbxR221-4A {9958}.	gbxR221.	
Xgwm397-4A {9929}**.	WMS F397/WMS R397.	

Whether *Xgwm397-4A* belongs to the 4AL:5BL:5DL arm group or the 4AL:4BL:4DL arm group is uncertain.

Xgwm637-4A {9929}**.	WMS F637/WMS R637.	

Whether *Xgwm637-4A* belongs to the 4AL:5BL:5DL arm group or the 7AS:4AL:7DS arm group is uncertain.

Xmgb12-4A {9959}[2].	MGB12.	
Xutv434-4A.1 {9959}[2].	UTV434.	(4AL).

The other 4AL locus belongs to the 7AS:4AL:7DS arm group.

Xutv1343-4A.1,.2,5B {9959}[2].	UTV1343.	(2A).

Group 5

Amendments:

Xglk278-5A,B. Add '(2D, 4D).' in the last column.

Xglk554-5B. Change last column to '(2A,B,D).'.

Xglk612-5A. Add superscript '1' to '{822}' and ', *5D* {9926}[4]' in the first column.

Xglk756-5A. Add superscript '1' to '{822}' and ', *5D*'{9926}[4]' in the first column and add '2D' in the last column.

Xpsr167(Hpr)-5B. Delete (moved to 5L arm group).

Xwg908-5B. Change last column to '(1A, 5AL,BL,DL).'.

Add:

Xabg463-5D.1,.2 {9926}[4].	ABG463.	(4A,D).
Xbg823-5D {9926}[4].	BG823.	
Xcdo1312-5D.1,.2 {9926}[4].	CDO1312.	
Xglk301-5D {9926}[4].	pTag701.	(2D, 3D, 7A).
Xglk424-5D {9926}[4].	pTag424.	(5A).
XgbxR958-5D {9958}.	gbxR958.	
Xgwm213-5B {9929}.	WMS F213/WMS R213.	
Xgwm335-5B {9929}.	WMS F335/WMS R335.	
XksuB5-5D {9926}[4].	pTtksuB5.	(4D).
XksuB7-5D {9926}[4].	pTtksuB7.	(1D, 3D, 7D).
XksuG419-5D.1,.2 {9926}[4].	pTtksuG419.	(3D, 4D).
XksuG465-5D {9926}[4].	pTtksuG465.	
XksuM9S-5D {9926}[4].	pTtksuM9S.	
XksuM159-5D {9926}[4].	pTtksuM159.	
Xmwg584-5D {9926}[4].	MWG584.	(1D, 3A, 4A).
Xpsr131-5D {9926}[4].	PSR231.	(2A,B,D).
Xwg420-5D.1,.2 {9926}[4].	WG420.	(7A,D).
Xwg516-5D {9926}[4].	WG516.	(4D).

Group 6S

Amendments:

Xabc173-6D. Change to '*Xabc173-6A* {9927}[2], *6D* {900}[1].'.

Xabg458-6A. Delete and substitute

'*Xabg458-6A* {282}[3], *6B* {9927}[2], *6D.1,.2* {9926}[4].	ABG458.	(1D).

The arm locations of *Xabg458-6D.1* and *Xabg458-6D.1* in *T. tauschii* were not reported in {9926}.'.

Xbcd21-6A,B,D. Add '(5A).' in the last column.

Xcmwg652-6A. Delete and substitute

'*Xcmwg652-6A* {900}[1], *6B* {9927}[2], *6D* {9926}[4].	cMWG652.	(4D).'.

Xcmwg684-6B. Change to '*Xcmwg684-6B.1*', add '[*Xcmwg684-6B* {1272}].' in the second column, and add '(6AL,BL).' in the last column.

Xglk547-6D. Add '(5BL).' in the last column.

XksuG48-6A,B,D . Revise the first column to '*XksuG48-6A,B* {187}[2], *6D* {448}[4],{444,862}[1].', add '[DG G48 {862}].' in the third column, and add '3B' in the last column.

XksuG48-6A,D. Delete the entire entry.

XksuG48-6D. Delete the entire entry.

XksuH11-6A. Add '(5A, 4B,D, 6D).' in the last column.

XksuM9S-6D. Add superscript '4' to '{448}' and add '[*XksuM9-6D* {9926}].' in the second column.

Xmwg67-6A. Add '(1A).' to last column.

Xmwg573-6A.2. Change to '*Xmwg573-6A.2* {282}[3], *6B* {9922}[2], *6D* {9926}[4]', and add '(7D).' in the last column.

Xmwg820-6A. Add '2D' and '6B' in the last column.

Xmwg916-6D. Change to '*Xmwg916-6A* {9927}[2], *6D* {900}[1].'.

Xpsr106(Cyc)-6A,B,D. Change *'Cyc'* to *'Cyp'*.

Xpsr141(Pgk2)-6A,B,D. Add '(7D).' in the last column.

Xpsr167(Hpr)-6A,B,D. Add *'Xpsr167(Hr)-6D* {9926}' in the second column.

Xrsq805(Embp)-6B. Add '(2B).' in the last column.

Xtam68-6D. Delete (incorrect entry).

Add:

XHak1-6A [{9932}][3], *6D* [{9932}][1].	[*XhvHAK1-6A,D* {9932}].	HvHAK1 {9932}.	(2A,D, 3A,D, 4A,B,D, 6B).
Xabg378-6A {9927}[2], *6D* {9926}[4].ABG378.		(2A, 7A).	
Xabg387-6A,B {9927}[2].		ABG387.	(1A,B,D, 3A, 4A, 5A).
Xcdo497-6B {9927}[2].		CDO497	(6A).
Xcdo534-6B {860}[1], {9927}[2].		CDO534.	(1B, 6D, 7A).
The arm location of *Xcdo534-6B* in *T. aestivum* was not reported in {860}.			
Xcdo1158-6A {9927}[2], *6B* {860}[1]. CDO1158.			
The arm location of *Xcdo1158-6A* in *T. aestivum* was not reported in {860}.			
Xcdo1380-6B {9927}[2].		CDO1380.	
A 6BS *Xcdo1380-6B* was mapped in in {9921}.			
Xcmwg653-6A {9927}[2].		cMWG653.	
Xcmwg679-6A.1,.2, 6B.1,.2 {9927}[2].		cMWG679.	
Xcmwg690-6A,B {9927}[2].		cMWG690.	
XksuM90-6D {9926}[4].		pTtksuM90.	
The arm location of *XksuM90-6D* in *T. tauschii* was not reported in {9926}.			
Xglk537-6A {822}[1], {9927}[2].		pTag537.	
The arm location of *Xglk537-6A* in *T. aestivum* was not reported in {822}.			
Xglk562-6A {822}[1], *6B* {9927}[2].		pTag562.	
The arm location of *Xglk562-6A* in *T. aestivum* was not reported in {822}.			
Xglk582-6B {822}[1], {9927}[2].		pTag562.	
Xgbx3165-6B,D [{9958}].	[*Xgbx3165a-6B, Xgbx3165b-6D* {9958}]. gbx3165.		
Xgbx3327-6B {9958}.		gbx3327.	
XgbxG36-6A [{9958}].	[*XgbxG036b-6A* {9958}].	gbxG036.	(2A).
XgbxG83-6B [{9958}].	[*XgbxG083-6B* {9958}].	gbxG083.	
XgbxG84-6B [{9958}].	[*XgbxG084-6B* {9958}].	gbxG084.	
XgbxG138-6B {9958}.		gbxG138.	
XgbxR593-6A {9958}.		gbxR593.	
Xgwm70-6B {9929}.		WMS F70/WMS R70.	
Xgwm88-6B {9929}.		WMS F88/WMS R88.	
Xgwm132-6B {9929}.		WMS F132/WMS R132.	
Xgwm133-6B {9929}.		WMS F133/WMS R133.	
Xgwm191-6B {9929}.		WMS F191/WMS R191.	(2B, 6B).
Xgwm361-6B {9929}.		WMS F361/WMS R361.	
Xgwm459-6A {9929}.		WMS F459/WMS R459.	

Xgwm469-6D {9929}.	WMS F469/WMS R469.	
Xgwm508-6B {9929}.	WMS F508/WMS R508.	
Xgwm518-6B {9929}.	WMS F518/WMS R518.	
Xgwm613-6B {9929}.	WMS F613/WMS R613.	
Xgwm644-6B {9929}.	WMS F644/WMS R644.	(7B).
Xmwg59-6A,B {9926}^{4}.	MWG59.	
Xmwg79-6B {9927}^{2}.	MWG79.	
Xmwg620-6A {9927}^{2}.	MWG620.	
Xmwg887-6A.1 {9927}^{2}.	MWG887.	(6AL).
Xmwg966-6A {9927}^{2}.	MWG966.	
Xpsr546-6A {9927}^{2}.	PSR546.	(6BL,DL).
Xutv707-6A {9959}^{2}.	UTV707.	
Xutv1034-6A {9959}^{2}.	UTV1034.	
Xutv1035-6A {9959}^{2}.	UTV1035.	
Xutv1280-6B {9959}^{2}.	UTV1280.	
Xutv1391-6A {9959}^{2}.	UTV1391.	(1A).
Xutv1471-6A {9959}^{2}.	UTV1471.	
Xwsuj1(Gst)-6A,B,D {9972}.	GST TSI-1 {9973}.	
Xycu1194-6A {9935}^{3}.	YCU1194.	

Group 6L

Delete:

'XksuG48-6A {900}, *6D* [{862}],{900}.

[*XksuG48(A)*{862}]. pTtksuG48 {448}.
[DG G48 {862}].'

Amendments:

Xabc175-6D. Change to '*Xabc175-6A* {9927}^{2}, *6D* {900}^{1}.'.

Xabg473-6B. Add '5A' in the last column.

Xcdo388-6A. Change to '*Xcdo388-6A* {900}^{1}, *6D* {9926}^{4}.' and revise last column to '(1B,D, 2B, 3D, 4A,D, 5A,D).'.

Xcdo507-6B. Change to '*Xcdo507-6A* {9927}^{2}, *6B* {900}^{1}.'.

Xcdo772-6A. Change to '*Xcdo772-6A* {900}, *6B* {9921}.'.

Xcmwg669-6D. Change to '*Xcmwg669-6A,B* {9927}^{2}, *6B* {900}^{1}' and add '(7D).' in the last column.

XksuF19. Add ', *6D* {9926}^{4}' in the first column and add '(2A,B,D).' in the last column.

XksuF36-6D, XksuG12-6B and *XksuG49-6A.* Add '7D' in the last column.

Xmwg74-6B. Change to '*Xmwg74-6A* {9927}^{2}, *6B* {900}^{1}.'.

Xmwg573-6A.1. Revise last column to '(6AS,BS,DS, 7D).'.

Xmwg798-6A. Change to '*Xmwg798-6A* {282}^{3}, *6B* {9927}^{2}.'.

Xpsr546-6B,D. Add '(6AS).' in the last column.

Xrsq805(Embp)-6A. Add '(2B).' to last column.

Xwg223-4A,B,D. Change to *'Xwg223-6A,B,D'.*

Xwg286-4A,B,D. Change to *'Xwg286-6A,B,D'.*

Xwg341-6B.1,.2. Add '5D' in the last column.

Add:

Xabg474-6A {9927}[2].		ABG474.	
Xbcd880-6A,B {9927}[2].		BCD880.	
Xbcd1426-6B {865,9921}.		BCD1426.	
The arm location of *Xbcd1426-6B* was not reported in {865}.			
Xcdo516-6A,B {9927}[2].		CDO516.	
Xcdo1091-6A {9927}[2], *6B* {860}[1].		CDO1091.	
Xcdo1380-6B {9921}.		CDO1380.	
A 6BS *Xcdo1380-6B* was mapped in {9927}.			
Xcmwg674-6A {9927}[2].		cMWG674.	
Xcmwg684-6A,B.2 [{9927}][2].	[*Xcmwg684-6B* {9927}].	cMWG684.	(6BS).
Xgbx3213-6B {9958}.		gbx3213.	
Xgbx3317-6D {9958}.		gbx3317.	
Xgbx3864-6A [{9958}].	[*Xgbx3864b-6A* {9958}].	gbx3864.	(3D).
Xgbx4071-6A {9958}.		gbx4071.	
XgbxG176-6B {9958}.		gbxG176.	
Xglk334-6A,B {822}[1],{9927}[2].		pTag334.	(3D).
The arm location of *Xglk334-6A* and *Xglk334-6B* in *T. aestivum* was not reported in {822}.			
Xglk495-6B {9927}[2], *6D* {822}[1].		pTag495.	
Xglk520-6B [{822}][1],{9927}[2].	[*Xglk520d* {822}].	pTag520.	(1B, 2A, 3B, 5A).
Xglk547-6A {9927}[2].		pTag547.	(6DS).
Xglk680-6A,B {822}[1],{9927}[2].		pTag680.	
Xglk705-6A {9927}[2], *6B* {822}[1].		pTag705.	
Xglk762-6A {822}[1], {9927}[2].		pTag762.	
Xgwm219-6B {9929}.		WMS F219/WMS R219.	
Xgwm427-6A {9929}.		WMS F427/WMS R427.	
Xgwm570-6A {9929}.		WMS F570/WMS R570.	
Xgwm617-6A {9929}.		WMS F617/WMS R617.	(5A).
Xgwm626-6B {9929}.		WMS F626/WMS R626.	
Xmgb339-6A {9959}[2].		MGB339.	
Xmwg19-6A {9927}[2].		MWG19.	
Xmwg21-6A {9927}[2].		MWG21.	
Xmwg820-6B {9927}[2].		MWG820.	(2D, 5A, 6A).
Xmwg887-6A.2 {9927}[2].		MWG887.	(6AS).
Xmwg897-6B {9927}[2], *6D* {9926}[4].		MWG897.	
Xmwg987-6A {9927}[2].		MWG897.	
Xmwg2029-6A,B {9927}[2].		MWG2029.	
Xmwg2053-6A,B {9927}[2].		MWG2053.	
Xmwg2061-6A {9927}[2].		MWG2061.	

Xrg1085-5A {9933}[1,3].		RG1085.	
Xutv1441-6B {9959}[2].		UTV1441.	(2A).
Xutv1469-6A,B {9959}[2].		UTV1469.	

Group 6

Amendments:

Xα-Amy-6D(1),(2),(3). Change to '*Xα-Amy-6D.1,.2,.3* [{448}][4].'.

Xbcd1426-6B. Delete (moved to 6L).

Xcdo534-6B, Xcdo1158-6B, and *Xcdo1091-6B.* Delete (moved to either 6S or 6L).

Xcdo1380-6B {860}. Add 'A *Xcdo1380-6B* was mapped in 6BS in {9927} and in 6BL in {9921}.'.

Xcsb112(Dhn5)-6D. Add '[*Xcsp112(Dhn5)-6D* {9926}[4]].' in the second colunmn.

Xglk317-6A. Add '3D' and '4D' in the last column.

Xglk259-6A. Add '(1D).' in the last column.

Xglk334-6A. Delete (moved to 6L).

Xglk479-6A, Xglk736-6B, Xglk705-6B, and *Xglk762-6A.* Add a superscript '1' to '{822}' and add ', *6D* {9926}[4]' in the first column.

Xglk495-6D, Xglk520-6B, Xglk537-6A, Xglk562-6A, Xglk582-6B and *Xglk680-6B.* Delete (moved to either 6S or 6L).

Xglk756-6A. Add '2D' and '5D' in the last column.

Xglk762-6A. Delete (moved to 6L).

Xksu1-32-4. Change to '*Xksu1-32-4-6D*' and add '(3D, 7D).' in the last column.

XksuH11-6D. Add '6A' in the last column.

Add:

XHak1-6B [{9932}].	[*XhvHAK1-6B* {9932}].	HvHAK1 {9932}.	(2A,D, 3A,D, 4A,B,D, 6AS,DS).
Xabc451-6D {9926}[4].		ABC451.	(2A).
Xabg377-6D {9926}[4].		ABG377.	(3A).
Xabg379-6D {9926}[4].		ABG379.	
Xabg484-6D {9926}[4].		ABG484.	(4AS,BL, $4A^{m}L$).
Xabg476-6D {9926}[4].		ABG476.	
Xbcd9-6D {9926}[4].		BCD9.	(5A,B).
Xbcd269-6D {9926}[4].		BCD269.	
Xbg544-6D {9926}[4].		BG544.	
Xbg547-6D {9926}[4].		BG547.	
Xcdo388-6D.1,.2 {9926}[4].		CDO388.	(1B,D, 2B, 3D, 4A, 5A,D, 6AL).
Xcdo497-6A {9927}[2].		CDO497	(6BS).
Xcmwg664-6A {9927}[2].		cMWG664.	
Xgbx3321-6A,B [{9958}].	[*Xgbx3321a-6A, Xgbx3321b-6B* {9958}].	gbx3321.	
XgbxG549-6A {9958}.		gbxG549.	
XgbxG728-6A {9958}.		gbxG728.	
XgbxR4-6A [{9958}].	[*XgbxR004-6A* {9958}].	gbxR004.	

Xglk558-6D {9926}[4].		pTag558.	(1BL,DS,D, 2B,D, 3D, 7D).
Xglk573-6D.1,.2 {9926}[4].		pTag573.	(7D).
Xglk651-6D {9926}[4].		pTag651.	(5B,D, 7A).
Xgwm55-6D {9929}.		WMS F55/WMS R55.	(2B).
Xgwm494-6A {9929}.		WMS F494/WMS R494.	
XksuD42-6D {9926}[4].		pTtksuD42.	(5A,B,D).
XksuF48-6D {9926}[4].		pTtksuF48.	(7D).
XksuG43-6D {9926}[4].		pTtksuG43.	
Xmwg573-6D {9926}[4].		MWG573.	(6AS,AL,BS, 7D).
Xpsr946-6D {9926}[4].		PSR946	(1D, 2D, 3A, 5D, 7AS,DS,DL).
Xwg223-6D.1,.2 {9926}[4].		WG223.	(4A,B,D).
Xwia483(Cxp1)-7D [{9926}][4].	[*Xcxp1* {9926}].	pc.3.	(3A,B,D).

Group 7S

Amendments:

Xabc465-7A. Add ', *7D* {9926}[4]' in the first column.
Xglk61-7A. Change last column to '(7BL,DL).'.
Xglk301-7A. Add '(2D, 3D, 5D).' in the last column.
Xglk651-7A. Add '6D' in the last column.
Xgwm68-7B. Add '(5B).' in the last column.
XksuH8-7A,B. Add '2D' and '3D' in the last column.
Xwg909-7B. Add '4B' in last column.

Add:

Xgbx3110-7B {9958}.		gbx3110.	
Xgbx3336-7B {9958}.		gbx3336.	
XgbxG277-7B {9958}.		gbxG277.	
XgbxG367-7A [{9958}].	[*XgbxG367b-7A* {9958}].	gbxG367.	(4D).
XgbxG597-7B {9958}.		gbxG597.	
XgbxGx46-7B {9958}.		gbxGx46.	
Xgwm16-7B {9929}.		WMS F16/WMS R16.	(2B, 5D).
Xgwm130-7A {9929}.		WMS F130/WMS R130.	
Xgwm233-7A {9929}.		WMS F233/WMS R233.	
Xgwm350-7A,D {9929}.		WMS F350/WMS R350.	
Xgwm400-7B {9929}**.		WMS F400/WMS R400.	

Whether *Xgwm400-7B* belongs to the 7S arm group or the 7BS:5BL:5DL arm group is uncertain.

Xgwm471-7A {9929}.		WMS F471/WMS R471.	
Xgwm537-7B {9929}**.		WMS F537/WMS R537.	

Whether *Xgwm537-7B* belongs to the 7S arm group or the 7BS:5BL:5DL arm group is uncertain.

Xgwm569-7B {9929}**.		WMS F459/WMS R569.	

Whether *Xgwm569-7B* belongs to the 7S arm group or the 7BS:5BL:5DL arm group is uncertain.

Xgwm573-7A,B {9929}.		WMS F573/WMS R573.	

Xgwm635-7A,D {9929}.		WMS F635/WMS R635.	
Xgwm666-7A {9929}.		WMS F666/WMS R666.	(1A, 3A, 5A).
Xmgb39-7A {9959}^{2}**.		MGB39.	

Whether *Xmgb39-7A* belongs to the 7S or 7AS:4AL:7DS arm group is uncertain.

Xutv913-7B {9959}^{2}.		UTV913.	
Xutv1110-7A {9959}^{2}.		UTV1110.	
Xutv1267-7A {9959}^{2}.		UTV1267.	
Xutv1268-7B {9959}^{2}.		UTV1268.	
Xutv1557-7B {9959}^{2}.		UTV1557.	
Xutv1378-7A {9959}^{2}.		UTV1378.	(5B).

7AS:4AL:7DS

Amendment:

Xabg378-7A. Add '(2A, 6A,D). in the last column.

XksuF36-4A. Add '7D' in the last column.

XksuF48-7D. Add '(6D).' in the last column.

XksuG49-4A. Add '7D' in the last column.

Xpsr946-7A.1,.2,D.1,.2. Add '6D' in the 4th column.

Add:

Xgbx3480-4A,7D [{9958}].	[*Xgbx3480a-4A, Xgbx3480b-7D* {9958}].	gbx3480.	
Xgbx3832-4A [{9958}].	[*Xgbx3832b-4A* {9958}].	gbx3832.	(2A,D).
XgbxG35-4A [{9958}]**.	[*XgbxG035b-4A* {9958}].	gbxG035.	(2B, 7B).

Whether *XgbxG35-4A* belongs to the 7AS:4AL:7DS or 4AL:5BL:5DL arm group is uncertain.

XgbxG141-4A {9958}.		gbxG141.	
XgbxG564-7D [{9958}].	[*XgbxG564a-7D* {9958}].	gbxG564.	
XgbxR522-4A {9958}.		gbxR522.	
XgbxR799-7A,4A [{9958}].	[*XgbxR799b-7A, XgbxR799a-4A* {9958}].	gbxR799.	
Xgwm160-4A {9929}.		WMS F160/WMS R160.	
Xmgb9-7A,4A {9959}^{2}.		MGB9.	
Xutv434-4A.2 {9959}^{2}.		UTV434.	(4AL).

The other 4AL locus belongs to the 4AL:5BL:5DL arm group.

Xutv1025-4A {9959}^{2}.		UTV1025.	
Xutv1071-4A {9959}^{2}.		UTV1071.	
Xutv1371-7A,4A {9959}^{2}.		UTV1371.	
Xwyep835(Wx)-4A [{9975}].		pCSS22F/pCSS22R [{9975}].	

Group 7L

Amendments:

Xglk61-7B. Add superscript '1' to '{553}' and ', *7D.1,.2* {9926}^{4}' in the first column.

Xglk197-7B. Add '(2D).' in the last column.

Xglk301-7A. Add '(2D, 3D, 5D).' in the last column.

Xglk642-7A. Add '(3D).' in the last column.

XksuB7-7B,D. Change the first column to '*XksuB7-7B,D* {553}[1], *7D* {448}[4].', add '(1D, 3D, 5D).' in the last column, and add 'The arm location of *XksuB7-7D* in *T. tauschii* was not reported in {448}.'.

XksuG12-7A. Add superscript '1' to '{553,154}' and ', *7D* {9926}[4]' in the first column and add the comment 'The arm location of *XksuG12-7D* in *T. tauschii* was not reported in {9926}.'.

XksuH8-7A,D. Add '2D' and '3D' in the last column.

Xpsr547-7A,B,D. Add '(1D).' in the last column.

Xpsr680-7A,B,D. Add '(2D).' in the last column.

Xpsr946-7D.2. Change the first-column entry to *'Xpsr946-7D.3.'*.

Xrsq805(Embp)-7D. Add '(2B).' in last column.

Xwg341-7A,B,D. Add '5D' in the last column.

Xwg420-7A,D. Add '(5D).' in the last column.

Add:

Xgbx3241-7B {9958}.		gbx3241.	
Xgbx4046-7B {9958}.		gbx4046.	
XgbxG35-7B [{9958}].	[*XgbxG035a-7B* {9958}].	gbxG035.	(2B, 4A).
XgbxG37-7B [{9958}].	[*XgbxG037d-7B*{9958}].	gbxG037.	(3B, 5D).
XgbxG46-7B [{9958}].	[*XgbxG046-7B* {9958}].	gbxG046.	
XgbxG218-7A,B [{9958}].	[*XgbxG218c-7A, XgbxG218a-7B* {9958}].		
		gbxG218.	(2D).
XgbxG411-7A,B,D.1,D.2 [{9958}].			
[*XgbxG411b-7A, XgbxG411a-7B, XgbxG411c,d-7D*{9958}].			
		gbxG411.	
XgbxG451-7D {9958}.		gbxG451.	
XgbxG575-7A [{9958}].	[*XgbxG575a-7A* {9958}].	gbxG575.	(2D).
XgbxR35-7A [{9958}].	[*XgbxR035b-7A* {9958}].	gbxR035.	
XgbxR138-7A {9958}.		gbxR138.	
XgbxR595-7B {9958}.		gbxR595.	
Xgwm63-7A {9929}.		WMS F63/WMS R63.	
Xgwm111-7D {9929}.		WMS F111/WMS R111.	
Xgwm112-7B {9929}.		WMS F112/WMS R112.	(3B).
Xgwm114-3B {9929}.		WMS F114/WMS R114.	
Xgwm121-7D {9929}.		WMS F121/WMS R121.	(5D).
Xgwm146-7B {9929}.		WMS F146/WMS R146.	
Xgwm274-7B {9929}.		WMS F274/WMS R274.	(1B).
Xgwm276-7A {9929}.		WMS F276/WMS R276.	
Xgwm282-7A {9929}.		WMS F282/WMS R282.	
Xgwm295-7D {9929}.		WMS F295/WMS R295.	
Xgwm302-7B {9929}.		WMS F302/WMS R302.	
Xgwm332-7A {9929}.		WMS F332/WMS R332.	
Xgwm344-7B {9929}.		WMS F344/WMS R344.	
Xgwm428-7D {9929}.		WMS F428/WMS R428.	
Xgwm437-7D {9929}.		WMS F437/WMS R437.	
Xgwm577-7B {9929}.		WMS F577/WMS R577.	
Xgwm611-7B {9929}.		WMS F611/WMS R611.	

Xubp18-7B {9959}[2].		UBP18.	
Xutv147-7B {9959}[2].		UTV147.	
Xutv809-7A {9959}[2].		UTV809.	
Xutv914-7A {9959}[2].		UTV914.	
Xutv934-7A,B {9959}[2].		UTV934.	
Xutv1199-7A {9959}[2].		UTV1199.	
Xutv1518-7A {9959}[2].		UTV1518.	(1A,B).
Xutv1531-7A {9959}[2].		UTV1531.	

Group 7

Amendments:

Xglk356-7B. Add ', *7D* {9926}[4]' in the first column.

Xglk642-7A. Add '(3D).' in the last column.

XksuB7-7D. Delete (moved to 7L).

XksuG55-7A. Add '(1D, 2D, 4D, 7A).' in the last column.

Xgsp-7D. Delete the entire entry and substitute

'*XcsSR3(Gsp)-7D* [{757}][4].	[*Xgsp-7D* {757}].	pGsp {757}.	(1D, 5A,B,D).'.

Add:

Xbcd410-7D {9926}[4].		BCD410.	(2A,D).
Xcdo669-7A {9926}[4].		CDO669.	(4A,B,D).
Xcdo675-7D {9926}[4].		CDO275.	(1D, 2D).
Xcdo786-7D {9926}[4].		CDO786.	(5A,D).
Xcmwg669-7D {9926}[4].		cMWG669.	(6A,B,D).
Xcmwg703-7D.1,.2,.3 {9926}[4].		cMWG703.	
Xgbx4899-7A {9958}.		gbx4899.	
XgbxG161-7D {9958}.		gbxG161.	
XgbxG732-7A {9958}.		gbxG732.	
XgbxGx228-7A {9958}.		gbxGx228.	
Xgwm333-7B {9929}.		WMS F333/WMS R333.	
Xgwm644-7B {9929}.		WMS F644/WMS R644.	(6B).
Xksu7-7D {9926}[4].		pHvksu7 {9928}.	
XksuF36-7D {9926}[4].		pTtksuF36.	(2D, 4A, 6D).
XksuG1-7D {9926}[4].		pTtksuG1.	
XksuG49-7D.1,.2,.3 {9926}[4].		pTtksuG49.	(2D, 4A, 6A).
Xglk558-7D {9926}[4].		pTag558.	(1BL,DS,D, 2B,D, 3D, 6D).
Xglk573-7D {9926}[4].		pTag573.	(6D).
Xglk764-7D {9926}[4].		pTag764.	(1B).
Xksu1-32-4-7D [{9926}][4].	[*Xksu32-4-7D* {9926}].	pTtksu1-32-4.	(3D, 6D).
Xmwg539-7D {9926}[4].		MWG539.	

Xmwg634-7D {9926}[4].		MWG634.	(4A,B,D).
Xmwg573-7D.1,.2 [{9926}][4].	[*Xmwg537-7D.1* {9926}].	MWG573.	(6A,B,D).
Xmwg704-7D {9926}[4].		MWG704.	
Xpsr141-7D {9926}[4].		PSR141.	(6A,B,D).
Xwg687-7D {9926}[4].		WG687.	
Xwg710-7D {9926}[4].		WG710.	

Flour Colour

Loci controlling flour colour were identified and mapped in a recombinant inbred population derived from hexaploid wheat cultivars Schomburgk and Yarralinka {9936}. Regions in 3A and 7A accounted for 13% and 60% of the genetic variation, respectively, and *Xbcd828-3A, Xcdo347-7A* and *Xwg232-7A.1* were significantly associated with flour colour. The association was highly significant in all three replicates only for the 7A QTL, however. Symbols were not assigned to the flour colour loci.

Gibberellic Acid Response (insensitivity)

Gai1.

Add at end of *Gai1* section :

'A 4B gene conferring gibbberellic acid insensitivity was mapped in a cross between durum wheat cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343. **ma:** *Xpsr622-4B* (distal) - 1.9 cM - *Gai1* - 8.3 cM - *Xbcd110-4B* (proximal) {9959}.'

Glume Colour

1. Red (brown/bronze).

Rg1. Add: **v:** Diamant I {9906}; *T. petrapavlovskyi* {9906}. Milturum 321 *Rg3* {9906}; Milturum 553 *Rg3* {see 9906}; Strela *Rg3* {9906}.

Add at end of section:

'A 1B gene controlling red glume colour was mapped in a cross between durum wheat cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343. **ma:** *Xutv1518-1B* (distal) - 7.7 cM - *Rg1* - 0.8 cM - *Gli-B1* (proximal) {9959}.'

Rg2. Add: **i:** Saratovskaya 29*5//T. *timopheevii/T. tauschii* {9906}.

Rg3. 1AS {add: see 9906}. Add: **v:** CS/Strela Seln {9906}; Iskra {9906}; Zhnitstra {9906}. Milturum 553 *Rg1* {see 9906}; Milturum 321 *Rg1* {9906}; Strela *Rg1* {9906}.

2. Black.

Add at end of section:

'A 1A gene controlling black glume colour was mapped in a cross between durum wheat cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343. **ma:** *Xutv1391-1A* (distal) - 3 cM - *Bg* - 1.6 cM - *Hg* - 2.4 cM - *Gli-A1* (proximal) {9959}.'

Hairy Glume

Add at end of section:

'A 1A gene controlling hairy glumes was mapped in a cross between durum wheat cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343. **ma:** *Xutv1391-1A* (distal) - 3 cM - *Bg* - 1.6 cM - *Hg* - 2.4 cM - *Gli-A1* (proximal) {9959}.'

Height

Reduced height: Ga-insensitive

Rht-D1.

Add at end of first sentence:

'; *Rht-D1* - 2.8 cM - *Xglk578-4D* {9966}.'

Reduced height: GA-sensitive

Rht8.

Add at end of section:

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

Rht8a. Associated with a 165-bp fragment of WMS 261 {9962}. **v:** Autonomia {9962}; Bobwhite {9962}; Brevor {9962}; Chaimite {9962}; Ciano 67 {9962}; Chris {9962}; Dugoklasa {9964}; Federation {9962}; Frontana {9962}; Glennson 81 {9962}; Jupateco 73 {9962}; Kenya {9962}; Klein 32 {9962}; Lerma Rojo {9962}; Lusitano {9962}; Maringa {9962}; Mentana {9962}; Nainari 60 {9962}; Newthatch {9962}; Opata 85 {9962}; Othello {9962}; Penjamo 62 {9962}; Quaderna {9962}; Rex {9962}; Riete {9962}; Saitama 27 {9962}; Spica {9962}; Veery S {9962}; Victo {9962}.

Rht8b. Associated with a 174-bp fragment of WMS 261 {9962}. **v:** Balkan {9962}; Bunyip {9962}; Cappelle-Desprez {9962}; Eureka {9962}; Festival {9962}; Fronteira {9962}; Fultz {9962}; Gabo {9962}; Heine VII {9962}; Inallettabile 95 {9962}; Jena {9962}; Klein Rendidor {9962}; Leonardo {9962}; Lutescens 17 {9962}; Mironovskaya 808 {9962}; Norin 10 {9962}; Norin 10/Brevior 14 {9962}; Podunavka {9962}; Record {9962}; Red Coat {9962}; Soissons {9962}; Talent {9962}; Tevere {9962}; Timstein {9962}; Wilhelmina (9962}.

Rht8c. Associated with a 192-bp fragment of WMS 261 {9962}. **v:** Alfa {9962}; Aquila {9962}; Ardito {9962}; Argelato {9962}; Avrora {9962}; Banija {9964}; Baranjka {9964}; Beauchamps {9962}; Bezostaya {9962}; Biserka {9962}; Campodoro {9962}; Centauro {9962}; Chikushi-Komugi (Norin 121) {9962}; Damiano {9962}; Djerdanka {9964}; Dneprovskaya {9962}; Duga {9964}; Etoile-de-choisy {9962}; Etruria {9962}; Fakuho-Kumugi (Norin 124) {9962}; Farnese {9962}; Favorite {9962}; Fiorello {9962}; Fortunato {9962}; Funo {9962}; Gala {9962}; Haya Komugi {9962}; Impeto {9962}; Irnerio {9962}; Jarka {9964}; Jugoslavia {9962}; Kavkas {9962}; Kolubara {9964}; Kosava {9964}; Libellula {9962}; Lonja {9964}; Lovrin 32 {9962}; Macvanka-2 {9964}; Mara {9962}; Marzotto {9962}; Neretva {9962}; Nizija {9962}; N.S. Rana1 {9962}; N.S. Rana 2 {9962}; N.S. 649 {9962}; N.S. 3014 {9962}; Orlandi {9962}; Osjecanka {9964}; OSK 5 5/15 {9964}; OSK 4 57/8 {9964}; OSK 3 68/2; Partizanka {9962}; Partizanka Niska {9962}; Poljarka {9964}; Posavka 1 {9964}; Posavka 2 {9962}; Pomoravka {9962}; Produttore {9962}; Radusa {9962}; Salto {9962}; Sanja {9962}; San Pastore {9962}; Sava {9962}; Siette Cerros {9962}; Sinvaloche {9962}; Skopjanka {9962}; Skorospelka 3B {9962}; Slavonija {9964}; Somborka {9964}; Sremica {9964}; Superzlatna {9962; Tisa {9964}; Transilvania {9962}; Una {9962}; Villa Glori {9962}; Zagrebcanka {9964}; Zelengora {9964}; ZG 6103/84 {9964}; ZG 7865/83 {9964}; Zitarka {9964}; Zitnica {9962}; Zlatna Dolina {9964}; Zlatoklasa {9964}; Svezda {9962}.

Rht8d. Associated with a 201-bp fragment of WMS 261 {9962}. **v:** Pliska {9962}; Courtot {9962}.

Rht8e. Associated with a 210-bp fragment of WMS 261 {9962}. **v:** Chino {9962}; Klein Esterello {9962}; Klein 157 {9962}.

Rht8f. Associated with a 215-bp fragment of WMS 261 {9962}. **v:** Klein 49 {9962}.'

Add a new section at the bottom of the height section :

'**Reduced Height**

QTL loci mapped include:

QHt.fra-1A [{9957}]. **ma:** Linkage with *Xfba393-1A*.

QHt.fra-1B [{9957}]. **ma:** Linkage with *Xcdo1188-1B.2*.

QHt.fra-4B [{9957}]. **ma:** Linkage with *Xglk556-4B*.

QHt.fra-7A [{9957}]. **ma:** Linkage with *Xglk478-7A*.

QHt.fra-7B [{9957}]. **ma:** Linkage with *XksuD2-7B*.'

Proteins

2. Enzymes

2.6. Endopeptidase

Ep-A1d {894}. Isozyme 6. **v:** PI 294994 {894}.

Ep-D1e {894}. Isozyme 5. **v:** PI 294994 {894}.

2.20. Aromatic alcohol dehydrogenase

Aadh-A1.

Add at bottom of *Aadh-A1* section: '**ma:** *XksuG44-5A* (proximal) - 6.9 cM - *Aadh-A1* - 24.7 cM - *Xcdo412-5A* (distal) {9959}.'

2.29. Starch branching enzyme

SbeI1 {9937}.	1DL {9937}.	**v:** CS {9937}.
SbeI2 {9937}.	7BL {9937}.	**v:** CS {9937}.

3. Endosperm Storage Proteins

3.1. Glutenins

At the end of the *Glu-B1* section, delete

'Variation in the staining intensity of subunit 7 in different varieties has also been observed {1069}; possible low gene expression at *Glu-B1* has been noted for *Glu-B1w,* where subunits 6*+8* stain very faintly {1146}.'

and substitute

'Variation in the staining intensity of subunit 7 in different varieties has also been observed {1069}; a duplication of the gene encoding subunit 7 has probably occurred in cultivar 'Red River 68', as evidenced by increased intensity of the subunit in SDS-PAGE and by approximately doubled intensity of restriction fragments carrying the gene in Southern blotting {9989}. Possible low gene expression at *Glu-B1* has been noted for *Glu-B1w,* where subunits 6*+8* stain very faintly {1146}.'.

3.2. Gliadins

Revision of preamble:

Delete

'Variation at the *Gli-1* loci was described earlier {634,996,1126} and applied in mapping experiments {1243,1125,196,422,1120}. A rational system of naming the alleles was produced by E.V. Metakovsky, N.I. Vavilov Institute of General Genetics, Moscow {988}. This nomenclature is reproduced below. Where two cultivars are given as prototypes for an allele, the first named is from the USSR and the second from elsewhere.'

and substitute

'Variation at the *Gli-1* loci was described earlier {634,996,1126} and applied in mapping experiments {1243,1125,196,422,1120}. A rational system of naming the alleles has been produced by Dr. E.V. Metakovsky (Present Address: Unidad de Genética, Departamento de Biotecnologia, E.T.S.I. Agrónomos, Universidad Politecnica de Madrid, 28040 Madrid, Spain) {988}. This nomenclature is reproduced below. A considerable number of alleles have been added to the original list given in {988}, and referenced here accordingly. A few alleles have been deleted, because, following much detailed comparison, there is now doubt that they can be reliably distinguished from existing alleles {9981}; for the moment, however, the allelic letter in these cases has not been reused. To facilitate practical use of the list, the aim has been to give at least three standard cultivars from a range of countries for each allele {9981}. This has been achieved for the vast majority of entries and is a change from the original list compiled from {988}, where up to two standards were given. While the three or more standards described almost always include the original standards, some have been replaced for various reasons, such as international awareness of the cultivar, availability of seed, or the ease with which an allele can be identified in a particular genetic background {9981}. In the original list, where two cultivars were given as prototypes for an allele, the first named was from the USSR and the second from elsewhere; this is no longer the case, although pains have been taken to include a Russian cultivar where possible, to

maintain the base of germplasm in which the alleles are available to be as wide as possible, as well as to acknowledge the research groups in the country where much of the pioneering work was carried out.
For discussion of null alleles at the *Gli-1* and *Gli-2* loci, see {9984}.'.

Delete the following from the preamble:
'A number of novel gliadin alleles were reported in {991}; they will be included in the next supplement to the catalogue.'

At the end of the preamble, delete
'The *Gli-1* loci may be recognised by probes pcP387 {372} and pTag1436 {065}, and by specific microsatellite primers {252}.'

and substitute
'The *Gli-1* loci may be recognised by probes pcP387 {372} and pTag1436 {065}, and by specific microsatellite primers {252}. Furthermore, it has been shown that probe pTag1436 differentiates gliadin alleles rather well; using this probe, families of gliadin alleles and some of their relationships have been described {9988}.'.

Gli-A1

Delete the previous corresponding entries and substitute the following:

Gli-A1a {988}.	**v:** CS {988}; Castan {991}; Mentana {9986}; Mara {9986}.
Gli-A1b {988}.	**v:** Bezostaya 1{988}; Mercia {988}; Tracy {991}.
Gli-A1c {988}.	**v:** Ukrainka {988}; Gazul {9985}; Sava {994}.
Gli-A1d {988}.	**v:** Dankowska {988}; Cabezorro {9985}.
Gli-A1e {988}.	**v:** Open {991}; Touzelle {991}; Falchetto {988}.
Gli-A1f {988}.	**v:** Maris Freeman {988}; Mironovskaya 808 {988}; Arminda {991}.
Gli-A1g {988}.	**v:** Gabo {988}; Adalid {9985}.
Gli-A1h {988}.	**v:** Sadovo I {988}; Predela {9981}; Krajinka {9981}.
Gli-A1i {988}.	**v:** Saratovskaya 36 {988}.
Gli-A1j {988}.	**v:** Lutescens 62 {988}.
Gli-A1k {988}.	**v:** Courtot {991}; Soissons {991}; Spada {9986}; Skala (heterogeneous) {988}.
Gli-A1l {988}.	**v:** Lesostepka 75 {988}; David {9986}; Salmone {9986}; Mura {9981}.
Gli-A1m {988}.	**v:** Marquis {988}; Dneprovskaya 521 {988}; Carat {991}; Liocorno {9986}.
Gli-A1n {988}.	**v:** Intensivnaya {988}.
Gli-A1o {988}.	**v:** Cappelle-Desprez {991}; Capitole {991}; Oderzo {9986}; Odesskaya 16 (heterogeneous) {988}.
Gli-A1p {988}.	**v:** Pyrotrix 28 {988}; Zagore {9981}.
Gli-A1q {988}.	**v:** Akmolinka 1 {988}.
Gli-A1r {988}.	**v:** Ranniaya 73 {988}; Barbilla {9985}.

Omission:

Gli-A1s.

Gli-A1s, not previously listed in the catalogue but reported in {9986}, is omitted from the catalogue temporarily because its status is in need of further confirmation {9981}.

Add:

Gli-A1t {9985}. v: Jeja del País {9985}.

Gli-A1u {9985}. v: Candeal Alcala {9985}.

Gli-A1null {9984,9987}. v: Saratovskaya 29 (mutant) {9987}; E.Mottin {9981}.

Gli-B1

Delete the previous corresponding entries and substitute the following:

Gli-B1a {988}. v: CS {988}.

Gli-B1b {988}. v: Bezostaya 1 {988}; Marquis {988}; Soissons {991}; Carat {991}; Liocorno {9986}.

Gli-B1c {988}. v: Siete Cerros 66 {988}; Prinqual {991}; Loreto {9986}.

Gli-B1d {988}. v: Chopin {991}; Dneprovskaya 521 {988}; Petrel {991}; Tiberio {9986}; Yécora {9985}.

Gli-B1e {988}. v: Lutescens 62 {988}; Apexal {991}; Fournil {991}; Oderzo {9986}.

Gli-B1f {988}. v: Maris Freeman {988}; Dankowska {988}; Mercia {988}; Cappelle-Desprez {991}; Capitole {991}.

Gli-B1g {988}. v: Galahad {988}; Sadovo 1 {988}; Champtal {991}; Tracy {991}; Mara {9986}.

Gli-B1h {988}. v: Krasnodonka {988}; Pepital {991}; Rudi {991}; Cabezorro {9985}.

Gli-B1i {988}. v: Insignia {988}; Ghurka {988}.

Gli-B1j {988}. v: Cluj 650 {988}.

Gli-B1k {988}. v: Mentana {9986}; Kremena {988}; De Carolis {9986}; Crvenkapa {994}.

Gli-B1l {988}. v: Clement {991}; Damier {991}; Fiocco {9986}.

Gli-B1m {988}. v: Pyrotrix 28 {988}; Et.d'Choisy {991}; Costantino {9986}.

Gli-B1n {988}. v: Intensivnaya {988}.

Gli-B1o {988}. v: Pippo {9986}; Levent {988}; Aragón 03 {9985}; San Rafael {9985}.

Gli-B1p {988}. v: New Pusa 834 {988}; Inia 66 {9985}.

Gli-B1q {9986}. v: Goelent {991}; Goya {991}; Gallo {9986}.

Gli-B1r {995}. v: Gazul {9985}; Sevillano {9985}; Chinook {995}.

Add:

Gli-B1s {9986}. v: Salmone {9986}; Resistente {9986}; E.Mottin {9981}.

Omission:

Gli-B1t.

Gli-B1t, not previously listed in the catalogue but reported in {9986}, is omitted from the catalogue temporarily because its status is in need of further confirmation {9981}.

Add:

Gli-B1u {9985}. v: Negrillo {9985}.

Gli-B1v {9985}. v: Montjuich {9985}.

Gli-B1null {9984,9987,991}. v: Touzelle {991}; Florence Aurora {9985}.

Gli-D1

Delete the previous corresponding entries and substitute the following:

Gli-D1a {988}. v: CS {988}; Marquis {988}; Saratovskaya 36 {988}; Mentana {9986}; Prinqual {991}.

Gli-D1b {988}. v: Bezostaya 1 {988}; Galahad {988}; Cappelle-Desprez {991}; Et.d'Choisy {991}.

Gli-D1c {988}. v: Skorospelka Uluchshennaya (biotype) {988,9982}.

Gli-D1d {988}. v: De Carolis {9986}; Solo {988}.

Gli-D1e {988}. v: Gerek 79 {988}.

Gli-D1f {988}. v: Maris Freeman {988}; Gabo {988}; Carlos {991}; Orso {9986}.

Gli-D1g {988}. v: Ghurka {988}; Mironovskaya 808 {988}; Fournil {991}; Open {991}.

Gli-D1h {988}. v: Sadovo 1 {988}; Zlatostrui {9981}.

Gli-D1i {988}. v: Insignia {988}; Tselinogradka {988}; Napayo (biotype) {995}; San Rafael {9985}.

Gli-D1j {988}. v: Aubain {991}; Promin {988}; Petrel {991}; Inia 66 {9985}; Chinook {995}.

Gli-D1k {988}. v: Mara {9986}; Pippo {9986}; Kremena {988}; Cargimarec {991}.

Gli-D1l {988}. v: Longbow {988}; Artaban {991}; Corin {991}.

Add:

Gli-D1m {991}. v: Heurtebise {991}.

Gli-D1n {9981}. v: Blanquillo de Toledo {9985}.

Gli-D1null {9984,9987,991}. v: Darius {991}; Touzelle {991}; Saratovskaya 29 (mutant) {9987}.

Gli-A2

Delete the previous corresponding entries and substitute the following:

Gli-A2a {988}.	v: CS {988}; Insignia {988}; Rieti DIV {9986}; Cabezorro {9985}.
Gli-A2b {988}.	v: Bezostaya 1 {988}; Rivoli {991}; Tiberio {9986}; Aradi {9985}.
Gli-A2c {988}.	v: Siete Cerros 66 {988}; Prinqual {991}; Loreto {9986}; Escualo {9985}.
Gli-A2d {988}.	v: Dneprovskaya 521 {988}; Mocho Sobarriba {9985}.
Gli-A2e {988}.	v: Sadovo 1 {988}; Cobra {991}; Mentana {9986}; Resistente {9986}; Sevillano {9985}.
Gli-A2f {988}.	v: Maris Freeman {988}; Gala {991}; Sistar {9986}; Adalid {9985}.
Gli-A2g {988}.	v: Cappelle-Desprez {991}; Ducat {988}; Mara {9986}; Mahissa 1 {9985}.
Gli-A2h {988}.	v: Hereward {988}; Apollo {991}; N.Strampelli {9986}; Montjuich {9985}.
Gli-A2i {988}.	v: Lesostepka 75 {988}.
Gli-A2j {988}.	v: Recital {991}; Camp Remy {991}; Avalon {9981}; E.Mottin {9981}.
Gli-A2k {988}.	v: Pyrotrix 28 {988}; Akmolinka 1 {988}; Estica {991}; Renan {991}; Zena {9986}.
Gli-A2l {988}.	v: Longbow {988}; Champlein {991}; Chamorro {9985}.
Gli-A2m {988}.	v: Marquis {988}; Rex {991}.
Gli-A2n {988}.	v: Mironovskaya 808 {988}.
Gli-A2o {988}.	v: Castan {991}; Touzelle {991}; Lontra {9986}; Calatrava {9985}.
Gli-A2p {988}.	v: Capitole {991}; Pliska {988}; Clement {991}; S.Lorenzo {9986}; Cajeme 71 {9985}; Yecora {9985}.
Gli-A2q {988}.	v: Saratovskaya 39 {988}; Montcada {9985}; Candeal Alcalá {9985}.
Gli-A2r {988}.	v: Riband {988}; Open {991}; Genial {991}.
Gli-A2s {988}.	v: Saratovskaya 36 {988}.
Gli-A2t {988}.	v: Courtot {991}; Soissons {991}; Rinconada {9985}; Prostor {9981}.
Gli-A2u {988}.	v: Titien {991}; Aragon 03 {9985}; Kirgizskaya Yubileinaya {988}; Saunders {995}.
Gli-A2v {988}.	v: Kzul-Bas {988}.
Gli-A2w {988}.	v: Bezenchukskaya 98 (biotype) {988}.
Gli-A2x {988}.	v: Solo {988}.

Add:

Gli-A2y {9981}. v: Gentil Rosso 202 {9981}; PI 191245 {9981}.

Gli-A2z {9986}. v: Gallo {9986}; Giuliana {9986}.

Gli-A2aa {9985}. v: Navarro 122 {9985}.

Gli-A2ab {9985}. v: Navarro 150 {9985}.

Gli-A2null {9984,9987}. v: Saratovskaya 29 (mutant) {9987}.

Gli-B2

Delete the previous corresponding entries and substitute the following:

Gli-B2a {988}. v: CS {988}.

Gli-B2b {988}. v: Bezostaya 1 {988}; Cobra {991}; Sideral {991}; Gladio {9986}.

Gli-B2c {988}. v: Siete Cerros 66 {988}; Gabo {988}; Courtot {991}; Prinqual {991}; Loreto {9986}; Manital {9986}; Sinton {995}; Escualo {9985}; Yecora {9985}.

Gli-B2d {988}. v: Akmolinka 1 {988}; Tselinnaya 20 {988}; Friedland {991}.

Gli-B2e {9986}. v: Veronese {9986}; Arsenal {991}; Zlatna Dolina {994}.

Gli-B2f {988}. v: Maris Freeman {988}; Master {991}.

Gli-B2g {988}. v: Galahad {988}; Cappelle-Desprez {991}; Capitole {991}; Forlani {9986}.

Gli-B2h {988}. v: Mentana {9986}; Sadovo 1 {988}; Castan {991}; Sistar {9986}; Pane 247 {9985}; Partizanka {994}.

Gli-B2i {988}. v: Insignia {988}; Ghurka {988}.

Gli-B2j {988}. v: Farnese {9986}; Funo R250 {9986}; Novosadska Rana 1 {994}.

Gli-B2k {988}. v: Skala {988}.

Gli-B2l {988}. v: Longbow {988}; Tracy {991}; Clement {991}.

Gli-B2m {988}. v: Mironovskaya 808 {988}; Open {991}; Renan {991}.

Gli-B2n {988}. v: Solo {988}.

Gli-B2o {988}. v: Mara {9986}; Hardi {9981}; Rivoli {991}; Pippo {9986}; Slavianka {9981}; Odesskaya 16 {988}.

Gli-B2p {988}. v: Champtal {991}; Oderzo {9986}; Recital {991}; Gazul {9985}; Pliska {988}.

Gli-B2q {988}. v: Saratovskaya 39 {988}.

Gli-B2r {991}. v: Genial {991}; Arminda {991}; Jeja del País {9985}.

Gli-B2s {988}. v: Saratovskaya 36 {988}.

Gli-B2t {988}. v: Tselinogradka {988}.

Gli-B2u {988}. v: Kirgizskaya Yubileinaya {988}.

Gli-B2v {988}. v: Garant {991}; Libellula {9986}; Mahissa 1 {9985}; Poljarka {988}; Declic {991}.

Gli-B2w {995,9986}. v: Rieti DIV {9986}, Palata {9986}, Pembina {995}.

Add:

Gli-B2x {994}. v: Super Zlatna (biotype) {994}; Prostor {9981}; 251/83 {9981}.

Gli-B2y {9986}. v: Centauro {9986}; E.Morandi {9986}.

Gli-B2z {9985}. v: Maestro {9985}.

Gli-B2aa {9986}. v: Salmone {9986}; E.Mottin {9981}.

Omission:

Gli-B2ab.

Gli-B2ab, not previously listed in the catalogue but reported in {991}, is omitted from the catalogue because its status is in need of further confirmation {9981}.

Add:

Gli-B2ac {991}. v: Scipion {991}; Artaban {991}; Riol {991}; Lontra {9981}.

Gli-B2ad {991}. v: Champion {991}; Chopin {991}.

Gli-B2ae {991}. v: Priam {991}; Et.d'Choisy {991}; Campeador {9985}; Krajinka (biotype) {994}.

Gli-B2af {9985}. v: Montjuich {9985}; Mocho Sobarriba {9985}.

Gli-B2null {9984,9987}. v: Saratovskaya 29 {9987}.

Gli-D2

Delete the previous corresponding entries and substitute the following:

Gli-D2a {988}. v: CS {988}; Maris Freeman {988}; Tracy {991}; Sistar {9986}.

Gli-D2b {988}. v: Bezostaya 1 {988}; Cobra {991}; Farnese {9986}; Partizanka {994}.

Gli-D2c {988}. v: Siete Cerros 66 {988}; Eridano {9986}; Rieti DIV {9986}; Escualo {9985}.

Gli-D2d {988}. v: Dneprovskaya 521 {988}.

Gli-D2e {988}. v: Mironovskaya 808 {988}; Open {991}; Dollar {9985}; Lada {9981}.

Gli-D2f {988}. v: Rempart {991}; Créneau {991}; Kirgizskaya Yubileinaya {988}; Skorospelka Uluchshennaya {988}.

Gli-D2g {988}. v: Capelle-Desprez {991}; Futur {991}; Galahad {988}; Ghurka {988}; Mec {9986}.

Gli-D2h {988}. **v:** Capitole {991}; Garant {991}; Thatcher {995}; Chinook {995}; Sadovo 1 {988}.

Gli-D2i {988}. **v:** Insignia {988}; Lario {9986}.

Gli-D2j {988}. **v:** Mentana {9986}; Inia 66 {9985}; Gallo {9986}; Arcane {991}; Gazul {9985}.

Gli-D2k {988}. **v:** Skala {988}; Cabezorro {9985}; Crvencapa {994}.

Gli-D2l.

Gli-D2l is deleted from the catalogue because it has been shown not to demonstrate reliable differences compared with existing alleles {9981}.

Gli-D2m {988}. **v:** Marquis {988}; Rex {991}; Veronese {9986}; Yecora {9985}; Rinconada {9985}.

Gli-D2n {988}. **v:** Mercia {988}; Castan {991}; Pippo {9986}; Mahissa 1 {9985}; Champlein {991}.

Gli-D2o {988}. **v:** Omskaya 12 {988}.

Note: cultivars Salmone and Resistente, which carry *Gli-D2aa* {9981}, were erroneously given as standards for allele *Gli-D2o* in {9986}.

Gli-D2p {988}. **v:** New Pusa {988}.

Gli-D2q {988}. **v:** Soissons {991}; Fournil {991}; E.Mottin {9981}; Volshebnitsa (biotype) {988}.

Gli-D2r {988}. **v:** Mara {9986}; Montcada {9985}; Kremena {988}.

Gli-D2s {988}. **v:** Akmolinka1 {988}; Bezenchukskaya 98 {988}; Selkirk (biotype) {995}.

Add:

Gli-D2t {9986}. **v:** Golia {9986}; Gabo {9981}; Manital {9986}; Bokal {9981}.

Gli-D2u {9986}. **v:** Loreto {9986}; Martial {991}; Cibalka {9981}.

Gli-D2v {991}. **v:** Epiroux {991}; Arbon {991}.

Gli-D2w {9985}. **v:** Navarro 150 {9985}; Javelin {9981}; Hopps {9981}; Canaleja {9985}.

Gli-D2x {9985}. **v:** Montjuich {9985}; Blanquillo {9985}.

Gli-D2y {9985}. **v:** Candeal Alcalá {9985}.

Gli-D2z {9985}. **v:** Aragon 03 {9985}.

Gli-D2aa {9981}. **v:** Salmone {9981}; Resistente {9981}.

Gli-D2null {9984,9987}. **v:** Saratovskaya 29 (mutant) {9987}.

Gli-A3

Add:

Gli-A3a {9983}. **v:** CS, Prinqual, Courtot, Tselinogradka, Bezenchukskaya 98.

Gli-A3b {9983}. v: Bezostaya 1.
Gli-A3c {9983}. v: Anda.
Gli-A3d {9983}. v: Saratovskaya 210, Kharkovskaya 6, Richelle.

Each of the above *Gli-A3* alleles, apart from *Gli-A3d*, which is a null, controls one minor omega-gliadin with molecular mass about 41k that occurs in the middle of the omega-region of APAGE fractionation. Gliadins controlled by these alleles differ in their electrophoretic mobility in APAGE in that the fastest of three known *Gli-A3*-gliadins is controlled by *Gli-A3a* and the slowest by *Gli-A3c* {9983}.

In the paragraph that begins,

'It is not clear how *Gli-S^{l}4* and *Gli-S^{l}5* relate to ...',

delete

'It has yet to be established whether this is one of a series of orthologous loci.

Gli-A4 {1205}. 1AS {1205}. v: Perzivan biotype 2.

Dubcovsky *et al.* {277} did not find evidence for the simultaneous presence of both *Gli-A3* and *Gli-A4* in five 1A or 1A^{m} mapping populations and concluded that *Gli-A4* should be considered to be *Gli-A3* until conclusive evidence for the former is obtained.'

and substitute

'However, Metakovsky et al. {9983} have since shown that this locus and *Gli-A3* are, in fact, the same locus. Furthermore, Dubcovsky et al. {277} did not find evidence for the simultaneous presence of both *Gli-A3* and *Gli-A4* in five 1A or 1A^{m} mapping populations and concluded that *Gli-A4* should be considered to be *Gli-A3* until conclusive evidence for the former is obtained. For these reasons, the locus *Gli-A4* is deleted from the catalogue.'.

In the paragraph that begins,

'A locus designated *Gli-5* controlling omega-gliadins was mapped ....',

delete

'An estimate for the map distance between *Gli-A5* and *Gli-A1* was not reported, although evidence was provided that the linkage is of a similar order of magnitude to the *Gli-B5* - *Gli-B1* distance, Although no orthologous locus was reported for chromosome 1D, the authors cited studies {992,987} reporting a recombination distance of 1 % between two gliadin loci on chromosome 1D, which they considered may have been due to the presence of a locus on 1D orthologous to *Gli-B5*.'

and substitute

'An estimate for the map distance between *Gli-A5* and *Gli-A1* was not reported, although evidence was provided that the linkage is of a similar order of magnitude to the *Gli-B5* - *Gli-B1* distance, and, since then, *Gli-A5* has been shown to be tightly linked (0-2%) to *Gli-A1* {9983}. Although no orthologous locus was reported for chromosome 1D, the authors cited studies {992,987} reporting a recombination distance of 1 % between two gliadin loci on chromosome 1D, which they considered may have been due to the presence of a locus on 1D orthologous to *Gli-B5*.'.

Gli-A5

Add:

Gli-A5a {9983}. v: CS.
Gli-A5b {9983}. v: Marquis.

Gli-A5a is null. Allele *Gli-A5b* controls two slow-moving, easily-recognizable omega-gliadins. It is present in all common wheat cultivars having alleles *Gli-A1m* and *Gli-A1r* (and, probably, in those having *Gli-A1e*, *Gli-A1l* and *Gli-A1q*), because earlier (for example, in {988}) two minor omega-gliadina encoded by *Gli-A5b* were considered to be controlled by these *Gli-A1* alleles {9983}.

Gli-B5

Add:

Gli-B5a {1147}. **v:** CS.

Gli-B5b {1147}. **v:** Salmone.

The situation is fully analogous with *Gli-A5*: There are currently two alleles differing in the presence/absence of two minor omega-gliadins. *Gli-B5a* is null. In {988}, omega-gliadins controlled by *Gli-B5* (allele *Gli-B5b*) were attributed to alleles at the *Gli-B1* locus (alleles *Gli-B1c, i, k, m, n* and *o*).

Add:

Gli-A6 {9983,993}. 1AS {9983}.

Gli-A6a {9983}. **v:** CS, Bezostaya 1.

Gli-A6b {9983}. **v:** Bezenchukskaya 98.

Gli-A6c {9983}. **v:** Courtot, Anda, Mironovskaya 808.

Gli-A6 was first explicitly described in {9983}, but it is now known that it was first observed without designation in {993}. There is strong evidence that it is distinct from *Gli-A3* and *Gli-A5*, mapping distally to *Gli-A1*, with which it recombines at a frequency of 2-5%. Currently three alleles are known, of which *Gli-A6c* is particularly well-described in {9983}: the molecular mass of the omega-gliadin controlled by this allele is slightly lower than those of the omega-gliadins controlled by *Gli-A3* alleles. In {988}, the omega-gliadin controlled by *Gli-A6c* was attributed to *Gli-A1f*. *Gli-A6c* is rather frequent in common wheat and may relate to dough quality (preliminary data {9983}). *Gli-A6a* is null {9983}.

Delete from end of gliadin section:

'The *Gli-1* loci may be recognised by pcP387 {372}, pTag1436 {066} and by specific microsaellite primers {252}.'

5. Other proteins

5.1. Lipopurothionins

Pur-A1

Add at end of section: 'A PCR marker specific for *Pur-A1* was developed in {9976}.'

Pur-B1

Add at end of section: 'A PCR marker specific for *Pur-B1* was developed in {9976}.'

Pur-D1

Add at end of section: 'A PCR marker specific for *Pur-D1* was developed in {9976}.'

Pur-R1

Add at end of section: 'A PCR marker specific for *Pur-R1* was developed in {9976}.'

5.6. Waxy Proteins

Add: 'Lists of cultivars, lines and landraces of tetraploid and hexaploid wheats with different, mostly null, alleles at the *Wx* loci are given in {9910,9911,9912,1053,1054,9913,9915,9916,1650,9917}.'

Quality Parameters

1. Sedimentation Value

Qsev.mgb-6A {9920}. 6AL{9920}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population {9920}.
ma: Associated with *Xrsq805-6A* {9920}.

Qsev.mgb-7A {9920}. 7BS {9920}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population {9920}.
ma: Associated with *Xpsr103-7A* {9920}.

Response to Vernalization

Vrn-A1. **ma:** *Vrn-A1* - 0.8 cM - *Xbcd450-5A, rg395* - 4.2 cM - *Xpsr426-5A* {9903}.

Last paragraph: {add: 1173, 9902}.

Add final paragraph: 'New combinations of *vrn* alleles from Mironovskaya 808 with a high vernalization requirement and Bezostaya 1 with a lower requirement gave progenies with higher and lower vernalization requirements than the respective parents {9902}. The allelic variants were designated with subscripted letters $vrn1^B$, $vrn2^B$, $vrn3^B$ and

vrn1^{M}, *vrn2*^{M}, *vrn3*^{M}. Multiple alleles also were reported in {9930}, and the dominant allele of Novosibirskaya 67 and the weaker dominant allele of Pirotrix 28 were designated *Vrn1a* and *Vrn1b*, respectively.'

Restorers for Cytoplasmic Male Sterility

1. Restorers for *T. timopheevi* cytoplasm

Rf3. **ma:** Distal....*Xcdo388-1B* - 1.2 cM - *Rf1* - 2.6 cM - *Xabc156-1B*....Proximal {9934}.

Ribosomal RNA

5S rRNA genes

5S-Rrna-B1.

Add at end of section: 'A PCR marker specific for *5S-Rrna-B1* was developed in {9974}.'

5S-Rrna-D1.

Add at end of section: 'A PCR marker specific for *5S-Rrna-D1* was developed in {9974}.'

5S-Rrna-R1.

Add at end of section : 'A PCR marker specific for *5S-Rrna-R1* was developed in {9974}.'

Segregation Distortion

QSd.ksu-1D {9931}. 1DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xcmwg706-1D* {9931}.

QSd.ksu-3D {9931}. 3DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc TA1704 {9925}. **ma:** Association with *Xwg177-3D* {9931}.

QSd.ksu-4D {9931}. 4DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *XksuF8-4D* {9931}.

QSd.ksu-5D.1 {9931}. 5D {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xcdo677-5D* {9931}.

QSd.ksu-5D.2 {9931}. 5DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xglk614-5D* (synonym *'Xtag614-5D'*) {9931}.

QSd.ksu-5D.3 {9931}. 5DL {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xwg1026-5D* {9931}.

QSd.ksu-7D {9931}. 7DS {9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704 {9925}. **ma:** Association with *Xglk439-7D* (synonym *'Xtag439-7D''*) {9931}.

Tiller Inhibition

tin1. [*Tin* {1212}].

tin2. [*Tin* {9909}]. Tiller-reducing affect of this allele was dominant {9909}. 2A {9909}. **v:** 88 F2 185 {9909}.

Pathogenic Disease/Pest Reaction

Reaction to *Diuraphis noxia*

Dn2.

Add at end. **ma:** 'Myburg et al. {9968} identified two SCAR markers that mapped 3.3 cM proximal to *Dn2.*'

Dn7 {9918}. 1B = 1BL.1RS {9918}, 1R {9918}. **v:** 93M45-14 {9918}.

Reaction to *Erysiphe graminis*

Pm25 {1343}. [*PmTmb* {1344}]. 1A {1343}. **v:** NC94-3778 {1344}. NC96BGTA5 = Saluda*3/PI 427662
Pm3a {1343}. **dv:** *T. monococcum* PI 427662 {1343}. **ma:** Linked with 3 RAPDs, the nearest,
950

OPAG04 , at 12.8± 4.0 cM {1343}.

Reaction to *Fusarium graminearum*

QFhs.ndsu.2A {9925}. 2AL {9925}. **v:** Sumai 3 {9925}. **ma:** Association with RFLP *XksuH16-2A* {9925}.

QFhs.ndsu.3B {9925}. 3BS {9925}. **v:** Stoa {9925}. **ma:** Association with AFLP *XEagcMcta.1* {9925}.

Reaction to *Heterodena avenae*

Replace current listing with:

Cre2 {238}. Derived from *Ae ventricosa* 10 {238,9990}. $6M^v$ {9990}. Although H93-8 is a double M^v(5A), $7M^v$ (7D) substitution line, *Cre2* was presumed to be located in a separate undetected translocated $6M^v$ segment {9991}.

Reaction to *Mayetiola destructor* (Say)

H21. **ma:** A RAPD amplified by primer OPE-13 was shown to co-segregate with *H21* {9938}.

Reaction to *Pseudocercosporella herpotrichoides* (Fron) Deighton

DV

Pch {618}. 4VL {618}. Change **s:** to **su:** and replace as 4VL(4D), Yangmai 5 {618}.

Add at end of section: '**ma:** Distally located: Cent....*Xcdo949-4V* - 16cM - *PchDv* - 17cM - *Xbcd588-4V* {618}.'

Reaction to *Puccinia graminis*

Sr39. Add: *Sr39* is closely linked with *Lr35* {651}. **ma:** A SCAR marker was developed {9923}.

Complex genotypes:

AC Taber: *Sr2, Sr9b, Sr11, Sr12* {9905}.

Pasqua: *Sr5, Sr6, Sr7a, Sr9b, Sr12.* Gene *Lr34* acted as an enhancer of APR {9905}.

Reaction to *Puccinia recondita*

Lr3. **ma:** Co-segregation with *Xmwg798-6B* {9921}.

Lr28. In the 'ma' entry, change 'OPJ-02' to 'OPJ-01'.

Lr35. Insert after gene symbol: derived from *Ae. speltoides* {651}. Adult plant resistance {651}. Add at end of section: **ma:** A. SCAR marker was developed {9923}.

Lr47 {9901}. Derived from *Aegilops speltoides* {9901}. 7AS = Ti7AS-7S#1S-7AS.7AL {9901}. **v:** Pavon derivative PI 603918 {9901}. **ma:** *Lr47* was located in the distal one-third of 7AS, 2-10cM from the centromere and within a 20-30cM segment {9901}. Complete linkage with several RFLP markers {9901}. 7A = T7AS-7S#1S.7S#1L {389}. **v:** CI 17882, CI 178884, CI 17885, KS 90H450 {9901}. 7AL = Ti7AS.7AL-7S#1L-7AL. **v:** Pavon derivative PI 603919 {9901}.

Reaction to *Puccinia striiformis*

Yr15. **ma:** *Xgwm33-1B* - 5cM - *Yr15* {9904}.

Reaction to *Pyrenophora tritici-repentis*

2. Resistance to chlorosis induction

QTsc.ndsu-1A {9924}. *Tsc1* {344}. **ma:** Delete last line of entry and insert: '**ma:** Association with *Gli-A1* {344}.'

Reaction to *Schizaphis graminum*

Gb5. Add: 7AL = Ti7AS.7AL-7S#1L-7AL {9901}.

Reaction to *Tilletia indica* Mitra

Add at bottom :

'QTL loci mapped include :

Qkb.cnl-3B [{9956}]. **ma:** Located in the interval *XATPase-3B - Xcdo1164-3B.*

Qkb.cnl-5A.1 [{9956}]. **ma:** Located in the interval *Xmwg2112-5A - Xcdo20-5A.*

Qkb.cnl-5A.2 [{9956}]. **ma:** Located in the interval *Xabg391-5A - Xfba351-5A.*

GENETIC LINKAGES

Chromosome 1A

	Pm3a	-	*Pm25*	21%	{1343}.

Chromosome 1B

1BS	*Glu-B3*	-	*Gli-B1*	2.8 ± 1.3 cM	{9922}.
	Glu-B3	-	*Gli-B5*	8.9 ± 2.2 cM	{9922}.
	Gli-B1	-	*Gli-B5*	3.5 ± 1.4 cM	{9922}.
	Gli-B1	-	*Rf3*	18.6 cM	{9934}.
	Nor-B1	-	*Rf3*	22.3 cM	{9934}.

Chromosome 1D

1DS	*Sr45*	-	Cent.	21 ± 3.4%.	{894}.
	Sr45	-	*Sr33*	9 ± 1.9 cM	{894}.

Most likely order: Cent - *Sr45* - *Sr33* - *Lr21* {894}.

Chromosome 1R

1RS	*Dn7*	-	*Lr26*	14.5 ± 3.9 cM	{894}.
	Telomere (C-band)	-	*SrR*	16.0 ± 48 cM	{9919}.
	Sec1	-	Cent	26.1 ± 43 cM	{9919}.
	Sr31/Lr26/Yr9	-	*Sec1*	5.4 ± 1.7 cM	{9919}.

Chromosome 5A

	Xpsr164-5A	-	*B1*	57 cM	{9903}.

Chromosome 6B

6BL	*Xcdo772*/cent	-	*Xbcd-6B*	41.2 cM	{9921}.
	Xbcd-6B	-	*Lr3/Xmwg798*	32.1 cM	{9921}.

Chromosome 7D

7BS	*Pc*	-	*P2*	29.6 ± 7.3cM	{9990}.
7BL	*P2*	-	*cn-B1b*	36.5 ± 5.6cM	{9990}.
7D	*Dn5*	-	*Ep-D1*	32 ± 4.97%	{894}.
7D	*Dn5*	-	*cn-D1*	37 ± 6.3%	{894}.

Additions to Summary Table 1

Aba	Abscisic acid
Acl1	Leaf acyl carrier protein (Acl1.1, Acl1.2 and Acl1.3 are leaf acyl carrier proteins I, II and III, respectively)
Adpg	ADPglucose pyrophosphorylase
Ald	Aldolase
ATPase	Adenosinetriphosphatase
ß-Atp	ß-Adenosinetriphosphatase
Br	Brittle rachis
Brz	Bronze
Caa	Carbonic anhydrase
Cab	Chlorophyll a/b binding protein
Chs	Chalcone synthase
CM16	CM16 protein
Cyp	Cyclophilin
Esi	Early-salt-induced mRNAs
Fbpa	Fructose bisphosphate aldolase
Fedr	Ferrodoxin-$NADP^+$ reductase
Gdd	Glycine decarboxylase
Ger	Germin
Glp	Germin-like protein
Glob	7S storage globulin
Gsp	Grain softness protein
Gst	Glutathione S-transferase
Hak	High affinity potassium transporter
Hpr	NAD^+ hydroxypyruvate reductase

Hsp	Heat shock protein
Hmgp	High mobility group protein
Ht	Height
Ica	Chymoptrypsin inhibitor
Lhcb	Chlorophyl a/b binding protein CP29 of photosystem II
Lrk	Receptor-like kinase associated with *Lr* locus
L13	Chloroplast ribosomal protein L13
Phs	Preharvest sprouting
PhyA	Phytochrome A
Pk	Protein kinase
Pki	Protein kinase inhibitor
Plc	Plastocyanin
Pp	P protein
Ppc	Phosphoenolpyruvate carboxylase
Psah	10.2 kDa photosystem I polypeptide
Psif	Protein synthesis initiation factor
Psk	Chloroplast photosystem I PSK-I subunit
Rbca	Rubisco activase
Rbp	Rubisco binding protein
Sam	S-adenosyl methionine decarboxylase
Sbe	Starch branching enzyme
Sdh	Succinate dehydrogenase
sev	Sedimentation value
Sus	Sucrose synthase
taVp1	Viviparous *(Triticum aestivum)*
Tel	Telomere
Tha	Thaumatin
VAtpB2	V-Adenosinetriphosphatase subunit B
Vdac	Voltage-dependent anion-channel protein
Wsip	Water-stress induced protein
60S	60S ribosomal protein
17D	17 kDa protein

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Amendments.

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Wheat Information Service
Number 89: 86-99 (1999)
Recent publications

Recent publications on wheat genetics

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1998

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(144)
ACCN:002058427 CTLN:4402897
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Gianoli, E.;Niemeyer, H.M.
AFFN:Departamento de Ciencias Ecologicas, Facultad de Ciencias, Universidad de Chile, Casilla, 653, Santiago, Chile
TITL:DIBOA in wild Poaceae: Sources of resistance to the Russian wheat aphid (Diuraphis noxia) and the greenbug (Schizaphis graminum)
HTIL:Euphytica [Euphytica]
HSSN:0014-2336
HYER:19980000
HCOL:vol. 102, no. 3, pp. 317-321

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(145)
ACCN:002058525 CTLN:4405316
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Myburg, A.A.;Cawood, M.;Wingfield, B.D.;Botha, A.-M.
AFFN:Department of Botany and Genetics, Faculty of Science, University of the Free State, PO Box 339, Bloemfontein, 9300, South Africa; E-mail: ambothao@scientia.up.ac.za
TITL:Development of RAPD and SCAR markers linked to the Russian wheat aphid resistance gene Dn2 in wheat
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19980600
HCOL:vol. 96, no. 8, pp. 1162-1169

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(146)
ACCN:002061068 CTLN:4437373
ABSJ:G (Genetics Abstracts)
AUTH:Begu, D.;Mercado, A.;Farre, J.-C.;Moenne, A.;Holuigue, L.;Araya, A.;Jordana, X.
AFFN:Laboratoire de Replication et Expression des Genes Eucaryotes et Retroviraux, EP-630, C.N.R.S.-Universite de Bordeaux II, 1, rue Camille Saint-Saens, F-33077 Bordeaux Cedex, France; E-mail: Alexandre. Araya@ibgc.u-bordeaux2.fr
TITL:Editing status of mat-r transcripts in mitochondria from two plant species: C-to-U changes occur in putative functional RT and maturase domains
HTIL:Current Genetics [Curr. Genet.]
HSSN:0172-8083
HYER:19980600
HCOL:vol. 33, no. 6, pp. 420-428

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(147)
ACCN:002061072 CTLN:4437400
ABSJ:G (Genetics Abstracts)
AUTH:Cheng, X.Y.;Gao, M.W.;Liang, Z.Q.;Liu, G.Z.
AFFN:Institute of Nuclear Agricultural Sciences, Zhejiang Agricultural University, Hangzhou, China
TITL:Somaclonal variation in winter wheat (Triticum aestivum L.): frequency, occurrence and inheritance
HTIL:Journal of Applied Genetics [J. Appl. Genet.]
HSSN:1234-1983
HYER:19980000
HCOL:vol. 39, no. 1, pp. 59-72

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(148)
ACCN:002061115 CTLN:4437581
ABSJ:G (Genetics Abstracts)
AUTH:Barrett, B.A.;Kidwell, K.K.
AFFN:Dep. of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA; E-mail: kidwell@mail.wsu.edu
TITL:AFLP-Based Genetic Diversity Assessment among Wheat Cultivars from the Pacific Northwest
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19981000
HCOL:vol. 38, no. 5, pp. 1261-1271

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(149)
ACCN:002061116 CTLN:4437582
ABSJ:G (Genetics Abstracts)
AUTH:Barrett, B.A.;Kidwell, K.K.;Fox, P.N.
AFFN:Dep. of Crop and Soil Sciences, Washington State Univ., Pullman, WA 99164-6420, USA; E-mail: kidwell@mail.wsu.edu
TITL:Comparison of AFLP and Pedigree-Based Genetic Diversity Assessment Methods Using Wheat Cultivars from the Pacific Northwest
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19981000
HCOL:vol. 38, no. 5, pp. 1271-1278

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(150)
ACCN:002061124 CTLN:4437629
ABSJ:G (Genetics Abstracts)
AUTH:Souza, E.;Fox, P.N.;Skovmand, B.
AFFN:Dep. of Plant, Soils, and Entomological Science, Univ. of Idaho, Aberdeen Research and Extension Center, P.O. Box AA, Aberdeen, ID 83210; E-mail: esouza@uidaho.edu
TITL:Parentage analysis of international spring wheat yield nurseries 17 to 27
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980400
HCOL:vol. 38, no. 2, pp. 337-341

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(151)
ACCN:002061130 CTLN:4437647
ABSJ:G (Genetics Abstracts)
AUTH:Storlie, E.W.;Allan, R.E.;Walker-Simmons, M.K.
AFFN:USDA-ARS, Wheat Genetics, Quality, Physiology and Disease Research Unit, 209 Johnson Hall, Washington State Univ., Pullman WA 99164-6420, USA; E-mail: ksimmons@wsu.edu
TITL:Effect of the Vrn1-Fr1 interval on cold hardiness levels in near- isogenic wheat lines
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980400
HCOL:vol. 38, no. 2, pp. 483-488

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(152)
ACCN:002066692 CTLN:4449656
ABSJ:G (Genetics Abstracts)
AUTH:Cao, Wenguang;Hucl, P.;Scoles, G.;Chibbar, R.N.
AFFN:Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Sask., S7N 5A8, Canada
TITL:Genetic diversity within spelta and macha wheats based on RAPD analysis
HTIL:Euphytica [Euphytica]
HSSN:0014-2336
HYER:19980000
HCOL:vol. 104, no. 3, pp. 181-189

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(153)
ACCN:002074104 CTLN:4437350
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Wu-Yun, Y.;Chi, Y.;Jun-Liang, Y.;You-Liang, Z.;Deng-Cai, L.
AFFN:Triticeae Research Institute, Sichuan Agricultural University, Dujianyan City, Sichuan 611830, P.R. China
TITL:Evaluation of Aegilops tauschii Coss for resistance to physiological strains CYR sub(30) and CYR sub(31) of wheat stripe rust in China
HTIL:Genetic Resources and Crop Evolution [Genet. Resour. Crop Evol.]
HSSN:0925-9864
HYER:19981000
HCOL:vol. 45, no. 5, pp. 395-398

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(154)
ACCN:002074123 CTLN:4437569
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Knox, R.E.;Fernandez, M.R.;Brule-Babel, A.L.;DePauw, R.M.
AFFN:SPARC, AAFC, Box 1030, Swift Current, SK S9H 3X2; and A.L Brule-Babel, Dep. of Plant Science, Univ. of Manitoba, Winnipeg, MB R3T 2N2, USA; E-mail: knoxr@em.agr.ca
TITL:Inheritance of Common Bunt Resistance in Androgenetically Derived Doubled Haploid and Random Inbred Populations of Wheat
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19981000
HCOL:vol. 38, no. 5, pp. 1119-1124

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(155)
ACCN:002077478 CTLN:4469790
ABSJ:G (Genetics Abstracts)
AUTH:Lima-Brito, J.;Guedes-Pinto, H.;Heslop-Harrison, J.S.;Jenkins, G.
AFFN:Department of Genetics and Biotechnology, University of Tras-os-Montes and Alto Douro, 5000 Vila Real, Portugal; E-mail: hgp@utad.pt
TITL:The activity of nucleolar organizing chromosomes in multigeneric F sub(1) hybrids involving wheat, triticale, and tritordeum
HTIL:Genome [Genome]
HSSN:0831-2796
HYER:19981200
HCOL:vol. 41, no. 6, pp. 763-768

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(156)
ACCN:002077480 CTLN:4469793
ABSJ:G (Genetics Abstracts)
AUTH:Spielmeyer, W.;Robertson, M.;Collins, N.;Leister, D.;Schulze-Lefert, P.;Seah, S.;Moullet, O.;Lagudah, E.S.;Moens, P.B.
AFFN:CSIRO Plant Industry, Canberra ACT 2601, Australia; E-mail: lagudah@pi. csiro.au
TITL:A superfamily of disease resistance gene analogs is located on all homoeologous chromosome groups of wheat (Triticum aestivum)
HTIL:Genome [Genome]
HSSN:0831-2796
HYER:19981200
HCOL:vol. 41, no. 6, pp. 782-788

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(157)
ACCN:002077485 CTLN:4469799
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Liu, J.Q.;Kolmer, J.A.;Griffiths, A.J.F.
AFFN:Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada; E-mail: JKOLMER@EM.AGR.CA
TITL:Molecular and virulence diversity and linkage disequilibria in asexual and sexual populations of the wheat leaf rust fungus, Puccinia recondita
HTIL:Genome [Genome]
HSSN:0831-2796
HYER:19981200
HCOL:vol. 41, no. 6, pp. 832-840

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(158)
ACCN:002077488 CTLN:4469803
ABSJ:G (Genetics Abstracts)
AUTH:Clarke, B.C.;Appels, R.;Scoles, G.J.
AFFN:C.S.I.R.O., Division of Plant Industry, G.P.O. Box 1600, A.C.T. 2601, Australia; E-mail: b.clarke@pi.csiro.au
TITL:A transient assay for evaluating promoters in wheat endosperm tissue
HTIL:Genome [Genome]
HSSN:0831-2796
HYER:19981200
HCOL:vol. 41, no. 6, pp. 865-871

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(159)
ACCN:002090389 CTLN:4486402
ABSJ:G (Genetics Abstracts)
AUTH:Enjalbert, J.;Goldringer, I.;David, J.;Brabant, P.
AFFN:Station de genetique vegetale, Institut national de recherche agronomique, Inapg, Ups, Ferme du Moulon, 91190 Gif-sur-Yvette, France
TITL:The relevance of outcrossing for the dynamic management of genetic resources in predominantly selfing Triticum aestivum L. (bread wheat)
HTIL:Genetics Selection Evolution [Genet. Sel. Evol.]
HSSN:0999-193X
HYER:19980000
HCOL:vol. 30, pp. S197-S211

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(160)
ACCN:002090455 CTLN:4487010
ABSJ:V (Virology & AIDS Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Anon.
TITL:Faster ID of Wheat Resistant to BYD Virus
HTIL:Agricultural Research [Agric. Res.]
HSSN:0002-161X
HYER:19980600
HCOL:vol. 46, no. 6, pp. 24-25

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(161)
ACCN:002090621 CTLN:4487736
ABSJ:G (Genetics Abstracts)
AUTH:Redha, A.;Schmid, J.E.;Bueter, B.;Stamp, P.;Attia, T.
AFFN:Department of Biological Sciences, Kuwait University, P.O. Box 5969, Safat, 13060, Kuwait; E-mail: SMTP%"Amina@.Kuc01.Kuniv.Edu.Kw"
TITL:Cytological Investigation of R sub(1) and R sub(2)-Generations of Spontaneously and Colchicine Induced Diploid Anther Derived Wheat Plants
HTIL:Cytologia
HSSN:0011-4545
HYER:19980900
HCOL:vol. 63, no. 3, pp. 267-278

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(162)
ACCN:002090633 CTLN:4487756
ABSJ:G (Genetics Abstracts)
AUTH:Fischer, R.A.;Rees, D.;Sayre, K.D.;Lu, Z.-M.;Condon, A.G.;Saavedra, A. L.
AFFN:ACIAR, GPO Box 1571, Canberra, ACT 2601, Australia; E-mail: fischer@aciar.gov.au
TITL:Wheat Yield Progress Associated with Higher Stomatal Conductance and Photosynthetic Rate, and Cooler Canopies
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19981200
HCOL:vol. 38, no. 6, pp. 1467-1475

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(163)
ACCN:002097437 CTLN:4425882
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); D (Ecology Abstracts)
AUTH:Owen, P.G.;Pei, Ming;Karp, A.;Royle,

D.J.;Edwards, K.J.
AFFN:IACR-Long Ashton Research Station, Department of Agricultural Sciences, University of Bristol, Long Ashton, Bristol, BS41 9AF, UK; E-mail: ming.pei@bbsrc.ac.uk
TITL:Isolation and characterization of microsatellite loci in the wheat pathogen Mycosphaerella graminicola
HTIL:Molecular Ecology [Mol. Ecol.]
HSSN:0962-1083
HYER:19981100
HCOL:vol. 7, no. 11, pp. 1611-1612

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(164)
ACCN:002105665 CTLN:4504098
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Pathania, N.;Basandarai, A.K.;Tyagi, P.D.
AFFN:Department of Plant Pathology, Himachal Pradesh Krishi Vishvavidyalaya, Palampur 176 062, Himachal Pradesh, India
TITL:Postulation of powdery mildew resistance genes in some wheat stocks
HTIL:Journal of Mycology and Plant Pathology [J. Mycol. Plant Pathol.]
HSSN:0971-9393
HYER:19980400
HCOL:vol. 28, no. 1, pp. 11-14

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(165)
ACCN:002117104 CTLN:4513322
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Stoger, E.;Williams, S.;Keen, D.;Christou, P.
AFFN:John Innes Centre, Norwich, NR4 7UH, UK; E-mail: Stoger@bbsrc.ac.uk
TITL:Molecular characteristics of transgenic wheat and the effect on transgene expression
HTIL:Transgenic Research [Transgenic Res.]
HSSN:0962-8819
HYER:19981100
HCOL:vol. 7, no. 6, pp. 463-471

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(166)
ACCN:002117229 CTLN:4513731
ABSJ:G (Genetics Abstracts)
AUTH:Vaishnavi, R.;Sethi, G.S.
AFFN:Department of Plant Breeding and Genetics, Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (H. P.), India
TITL:Relative drought tolerance of rye-introgressed bread wheat (Triticum aestivum L. em thell.) genotypes in osmoticum
HTIL:Annals of Biology [Ann. Biol.]
HSSN:0970-0153
HYER:19981200
HCOL:vol. 14, no. 2, pp. 169-173

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(167)
ACCN:002119035 CTLN:4525330
ABSJ:G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Sayre, K.D.;Singh, R.P.;Huerta-Espino, J.;Rajaram, S.
AFFN:International Maize and Wheat Improvement Center (CIMMYT), Lisboa 27, Apdo. Postal 6-641, 06600 Mexico, D.F; E-mail: RSINGH@CIMMYT.MX
TITL:Genetic progress in reducing losses to leaf rust in CIMMYT-derived Mexican spring wheat cultivars
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980600
HCOL:vol. 38, no. 3, pp. 654-659

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(168)
ACCN:002119038 CTLN:4525334
ABSJ:G (Genetics Abstracts)
AUTH:Vargas, M.;Crossa, J.;Sayre, K.;Reynolds, M.;Ramirez, M.E.;Talbot, M.
AFFN:Biometrics and Statistics Unit, CIMMYT, Lisboa 27, Apdo, Postal 6-641, 06600 Mexico, D.F., Mexico; E-mail: JCROSSA@ALPHAC.CIMMYT.MX
TITL:Interpreting genotype x environment interaction in wheat by partial least squares regression
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980600
HCOL:vol. 38, no. 3, pp. 679-689

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(169)
ACCN:002119055 CTLN:4525356
ABSJ:G (Genetics Abstracts)
AUTH:Fabrizius, M.A.;Busch, R.H.*;Khan, K.;Huckle, L.
AFFN:Plant Science Res. Unit, USDA-ARS, 411 Borlaug Hall, Univ. of Minnesota, St. Paul, MN 55108, USA; E-mail: busch005@maroon.tc.umn.edu
TITL:Genetic Diversity and Heterosis of Spring Wheat Crosses
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980800
HCOL:vol. 38, no. 4, pp. 1108-1112

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(170)
ACCN:002119058 CTLN:4525359
ABSJ:G (Genetics Abstracts)
AUTH:Almouslem, A.B.;Jauhar, P.P.*;Peterson, T.S.;Bommineni, V.R.;Rao, M.B.

AFFN:USDA-ARS, Northern Crop Science Lab., Fargo, ND 58105; E-mail: pjauhar@badlands.nodak.edu
TITL:Haploid Durum Wheat Production via Hybridization with Maize
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980800
HCOL:vol. 38, no. 4, pp. 1080-1087

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(171)
ACCN:002119059 CTLN:4525360
ABSJ:G (Genetics Abstracts)
AUTH:Wang, E.;Xing, H.;Wen, Y.;Zhou, W.;Wei, R.*;Han, H.
AFFN:State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics, Chinese Academy of Sciences, Beijing 100101; E-mail: rxwei@public.east.cn.net
TITL:Molecular and Biochemical Characterization of a Non-Robertsonian Wheat-Rye Chromosome Translocation Line
HTIL:Crop Science [Crop Sci.]
HSSN:1679-2020
HYER:19980800
HCOL:vol. 38, no. 4, pp. 1076-1080

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(172)
ACCN:002139062 CTLN:4547594
ABSJ:G (Genetics Abstracts)
AUTH:Yuan, W.-Y.;Tomita, M.;Sun, S.-C.;Yasumuro, Y.
AFFN:Laboratory of Plant Genetics and Breeding, Faculty of Agriculture, Tottori University, Tottori 680-8553, Japan
TITL:Introduction of multi-alien chromatins carrying different powdery mildew-resistant genes from rye and Haynaldia villosa into wheat genome
HTIL:Genes & Genetic Systems [Genes Genet. Syst.]
HSSN:1341-7568
HYER:19981200
HCOL:vol. 73, no. 6, pp. 377-384

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(173)
ACCN:002139883 CTLN:4556323
ABSJ:G (Genetics Abstracts)
AUTH:Gonzalez, M.;Osuna, L.;Echevarria, C.;Vidal, J.;Cejudo, F.J.
AFFN:Instituto De Bioquimica Vegetal y Fotosintesis, Centro De Investigaciones Cientificas "Isla De la Cartuja," Avda Americo Vespucio s/n, 41092-Sevilla, Spain; E-mail: fjcejudo@cica.es
TITL:Expression and Localization of Phosphoenolpyruvate Carboxylase in Developing and Germinating Wheat Grains
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19980400
HCOL:vol. 116, no. 4, pp. 1249-1258

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(174)
ACCN:002139922 CTLN:4556392
ABSJ:G (Genetics Abstracts)
AUTH:Schuppler, U.;He, P.;John, P.C.L.;Munns, R.
AFFN:Plant Cell Biology Group, Research School of Biological Sciences, Australian National University, G.P.O. Box 475, Canberra 2601, Australia; E-mail: rana.munns@pi.csiro.au
TITL:Effect of Water Stress on Cell Division and Cdc2-Like Cell Cycle Kinase Activity in Wheat Leaves
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19980600
HCOL:vol. 117, no. 2, pp. 667-678

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(175)
ACCN:002139978 CTLN:4556495
ABSJ:G (Genetics Abstracts)
AUTH:Nakamura, T.;Vrinten, P.;Hayakawa, K.;Ikeda, J.
AFFN:Tohoku National Agriculture Experimental Station, Akahira 4, Morioka 020-01, Japan; E-mail: tnaka@tnaes.affrc.go.jp
TITL:Characterization of a Granule-Bound Starch Synthase Isoform Found in the Pericarp of Wheat
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19981000
HCOL:vol. 118, no. 2, pp. 451-459

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(176)
ACCN:002139986 CTLN:4556511
ABSJ:G (Genetics Abstracts)
AUTH:Wang, T.;Gassmann, W.;Rubio, F.;Schroeder, J.I.;Glass, A.D.M.
AFFN:Department of Botany, University of British Columbia, Vancouver, Canada V6T 1Z4; E-mail: aglass@unixg.ubc.ca
TITL:Rapid Up-Regulation of HKT1, a High-Affinity Potassium Transporter Gene, in Roots of Barley and Wheat following Withdrawal of Potassium
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19981000
HCOL:vol. 118, no. 2, pp. 651-659

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(177)
ACCN:002140009 CTLN:4556556
ABSJ:G (Genetics Abstracts)
AUTH:Nakahira, Y.;Baba, K.;Yoneda, A.;Shiina, T.;Toyoshima, Y.
AFFN:Graduate School of Human and

Environmental Studies, Kyoto University, Yoshida-nihonmatu-cho, Sakyo-ku, Kyoto 606-8501, Japan; E-mail: toyoshima@soumu1.jinkan.kyoto-u.ac.jp
TITL:Circadian-Regulated Transcription of the psbD Light-Responsive Promoter in Wheat Chloroplasts
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19981100
HCOL:vol. 118, no. 3, pp. 1079-1088

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(178)
ACCN:002140016 CTLN:4556568
ABSJ:G (Genetics Abstracts)
AUTH:Masci, S.;D'Ovidio, R.;Lafiandra, D.;Kasarda, D.D.
AFFN:Dipartimento di Agrobiologia e Agrochimica, Universita' della Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy; E-mail: masci@unitus. it
TITL:Characterization of a Low-Molecular-Weight Glutenin Subunit Gene from Bread Wheat and the Corresponding Protein That Represents a Major Subunit of the Glutenin Polymer
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19981200
HCOL:vol. 118, no. 4, pp. 1147-1158

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(179)
ACCN:002142917 CTLN:4567226
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Grewal, A.S.;Nanda, G.S.;Randhawa, A.S.;Sharma, S.K.
AFFN:Department of Plant Breeding, Punjab Agricultural University, Ludhiana 141 004, India
TITL:Durable resistance to stripe and leaf rust with confirmed resistance to loose smut in wheat
HTIL:Crop Improvement [Crop Improv.]
HSSN:0256-0933
HYER:19980600
HCOL:vol. 25, no. 1, pp. 34-38

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(180)
ACCN:002142918 CTLN:4567227
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Saini, R.G.;Dhindsa, S.;Bansal, M.;Gupta, A.K.
AFFN:Department of Genetics, Punjab Agricultural University, Ludhiana - 141 004, India
TITL:Adult plant leaf rust resistance of wheat cultivar Tobari 66 and its inheritance against two variants of race 77
HTIL:Crop Improvement [Crop Improv.]
HSSN:0256-0933
HYER:19980600
HCOL:vol. 25, no. 1, pp. 39-42

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(181)
ACCN:002142930 CTLN:4567239
ABSJ:G (Genetics Abstracts)
AUTH:Yadav, R.;Tyagi, B.S.;Jagshoran
AFFN:Directorate of Wheat Research, P. Box 158, Karnal- 132001, India
TITL:AMMI analysis of wheat varietal yield trial
HTIL:Crop Improvement [Crop Improv.]
HSSN:0256-0933
HYER:19980600
HCOL:vol. 25, no. 1, pp. 105-110

1999

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(1)
ACCN:002063105 CTLN:4442817
ABSJ:G (Genetics Abstracts)
AUTH:Molina, A.;Goerlach, J.;Volrath, S.;Ryals, J.
AFFN:Biotechnology and Genomics Center, Novartis Crop Protection Inc., Research Triangle Park, NC 27709-2257, USA; E-mail: molina@bit.etsia.upm.es
TITL:Wheat Genes Encoding Two Types of PR-1 Proteins Are Pathogen Inducible, but Do Not Respond to Activators of Systemic Acquired Resistance
HTIL:Molecular Plant-Microbe Interactions [Mol. Plant-Microbe Interactions]
HSSN:0894-0282
HYER:19990100
HCOL:vol. 12, no. 1, pp. 53-58

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(2)
ACCN:002079783 CTLN:4481871
ABSJ:G (Genetics Abstracts); N (Biochemistry Abstracts 2: Nucleic Acids); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Delhaize, E.;Hebb, D.M.;Richards, K.D.;Lin, J.;Ryan, P.R.;Gardner, R.C.
AFFN:Plant Industry, Commonwealth Scientific Industrial and Research Organisation, GPO Box 1600, Canberra, Australian Capital Territory 2601, Australia
TITL:Cloning and Expression of a Wheat (Triticum aestivum L.) Phosphatidylserine Synthase cDNA: Overexpression in Plants Alters the Composition of Phospholipids
HTIL:Journal of Biological Chemistry [J. Biol.

Chem.]
HSSN:0021-9258
HYER:19990312
HCOL:vol. 274, no. 11, pp. 7082-7088

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(3)
ACCN:002091093 CTLN:4489221
ABSJ:G (Genetics Abstracts)
AUTH:Zantoko, L.;Shukle, R.H.*
AFFN:USDA-ARS, Purdue University, West Lafayette, IN 47907, USA
TITL:An STS Linked to a Hessian Fly Locus Controlling Virulence to Resistance Gene H13 in Wheat
HTIL:Journal of Heredity [J. Hered.]
HSSN:0022-1503
HYER:19990200
HCOL:vol. 90, no. 1, pp. 242-247

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(4)
ACCN:002101172 CTLN:4486539
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Stoger, E.;Williams, S.;Christou, P.;Down, R.E.;Gatehouse, J.A.*
AFFN:Crop Protection Group, Plant Molecular Biology Section, Department of Biological Sciences, University of Durham, South Road, Durham DH1 3LE, UK; E-mail: j.a.gatehouse@durham.ac.uk
TITL:Expression of the insecticidal lectin from snowdrop (Galanthus nivalis agglutinin; GNA) in transgenic wheat plants: effects on predation by the grain aphid Sitobion avenae
HTIL:Molecular Breeding [Mol. Breed.]
HSSN:1380-3743
HYER:19990000
HCOL:vol. 5, no. 1, pp. 65-73

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(5)
ACCN:002101477 CTLN:4487721
ABSJ:G (Genetics Abstracts)
AUTH:Wagoire, W.W.;Hill, J.;Stoelen, O.;Ortiz, R.
AFFN:Department of Agricultural Sciences, The Royal Veterinary and Agricultural University, 40 Thorvaldsensvej, DK-1871, Frederiksberg C, Copenhagen, Denmark
TITL:Impact of genotype-environment interactions on the inheritance of wheat yield in low-yielding environments
HTIL:Euphytica
HSSN:0014-2336
HYER:19990000
HCOL:vol. 105, no. 1, pp. 17-23

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(6)
ACCN:002103678 CTLN:4495737
ABSJ:G (Genetics Abstracts)
AUTH:Swire-Clark, G.A.;Marcotte, W.R.,Jr.*
AFFN:Department of Biological Sciences, Clemson University, 132 Long Hall, Clemson, SC 29634-1903, USA
TITL:The wheat LEA protein Em functions as an osmoprotective molecule in Saccharomyces cerevisiae
HTIL:Plant Molecular Biology [Plant Mol. Biol.]
HSSN:0167-4412
HYER:19990101
HCOL:vol. 39, no. 1, pp. 117-128

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(7)
ACCN:002104847 CTLN:4500248
ABSJ:G (Genetics Abstracts)
AUTH:Berna, A.;Bernier, F.*
AFFN:Institut de Biologie Moleculaire des Plantes, Institut de Botanique, 28 rue Goethe, 67083 Strasbourg Cedex, France
TITL:Regulation by biotic and abiotic stress of a wheat germin gene encoding oxalate oxidase, a H sub(2)O sub(2)-producing enzyme
HTIL:Plant Molecular Biology [Plant Mol. Biol.]
HSSN:0167-4412
HYER:19990200
HCOL:vol. 39, no. 3, pp. 539-549

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(8)
ACCN:002105386 CTLN:4502588
ABSJ:G (Genetics Abstracts)
AUTH:Vrinten, P.;Nakamura, T.;Yamamori, M.
AFFN:Tohoku National Agricultural Experiment Station, Akahira 4, Morioka, Iwate 020-0123, Japan; E-mail: tnaka@tnaes.affrc.go.jp
TITL:Molecular characterization of waxy mutations in wheat
PBSR:Springer-Verlag
HTIL:Molecular and General Genetics [Mol. Gen. Genet.]
HSSN:0026-8925
HYER:19990401
HCOL:vol. 261, no. 3, pp. 463-471

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(9)
ACCN:002105434 CTLN:4502753
ABSJ:G (Genetics Abstracts)
AUTH:Ciaffi, M.;Dominici, L.;Tanzarella, O.A.;Porceddu, E.
AFFN:Department of Agro-biology and Agro-chemistry, University of Tuscia, 01100 Viterbo, Italy
TITL:Chromosomal assignment of gene sequences coding for protein disulphide isomerase (PDI) in wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752

HYER:19990324
HCOL:vol. 98, no. 3/4, pp. 405-410

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(10)
ACCN:002105437 CTLN:4502756
ABSJ:G (Genetics Abstracts)
AUTH:Fahima, T.;Sun, G.L.;Beharav, A.;Krugman, T.;Beiles, A.;Nevo, E.
AFFN:Institute of Evolution, University of Haifa, Mount Carmel, Haifa 31905, Israel
TITL:RAPD polymorphism of wild emmer wheat populations, Triticum dicoccoides, in Israel
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990324
HCOL:vol. 98, no. 3/4, pp. 434-447

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(11)
ACCN:002105438 CTLN:4502758
ABSJ:G (Genetics Abstracts)
AUTH:D'Ovidio, R.;Marchitelli, C.;Ercoli Cardelli, L.;Porceddu, E.
AFFN:Dipartimento di Agrobiologia e Agrochimica, Universita della Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:Sequence similarity between allelic Glu-B3 genes related to quality properties of durum wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990324
HCOL:vol. 98, no. 3/4, pp. 455-461

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(12)
ACCN:002105441 CTLN:4502761
ABSJ:G (Genetics Abstracts)
AUTH:Kato, K.;Miura, H.;Sawada, S.
AFFN:Department of Crop Science, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, 080-8555, Japan
TITL:QTL mapping of genes controlling ear emergence time and plant height on chromosome 5A of wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990324
HCOL:vol. 98, no. 3/4, pp. 472-477

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(13)
ACCN:002106969 CTLN:4510158
ABSJ:G (Genetics Abstracts)
AUTH:Pinto-Carnide, O.;Guedes-Pinto, H.
AFFN:Genetics and Biotechnology Department, University of Tras-os-Montes and Alto Douro, Ap. 202, 5000 Vila Real, Portugal
TITL:Aluminum tolerance variability in rye and wheat Portuguese germplasm
HTIL:Genetic Resources and Crop Evolution [Genet. Resour. Crop Evol.]
HSSN:0925-9864
HYER:19990200
HCOL:vol. 46, no. 1, pp. 81-85

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(14)
ACCN:002107682 CTLN:4512286
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Anderson, J.A.;Effertz, R.J.;Faris, J.D.;Francl, L.J.;Meinhardt, S.W.; Gill, B.S.
AFFN:Department of Agronomy and Plant Genetics, 411 Borlaug Hall, University of Minnesota, St. Paul, MN 55108, USA
TITL:Genetic analysis of sensitivity to a Pyrenophora tritici-repentis necrosis-inducing toxin in durum and common wheat
HTIL:Phytopathology
HSSN:0331-949X
HYER:19990000
HCOL:vol. 89, no. 4, 293

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(15)
ACCN:002115667 CTLN:4502757
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Cenci, A.;D'Ovidio, R.;Tanzarella, O.A.;Ceoloni, C.;Porceddu, E.
AFFN:Dipartimento di Agrobiologia e Agrochimica, Universita della Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:Identification of molecular markers linked to Pm13, an Aegilops longissima gene conferring resistance to powdery mildew in wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990324
HCOL:vol. 98, no. 3/4, pp. 448-454

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(16)
ACCN:002115668 CTLN:4502787
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Nemoto, Y.;Kawakami, N.;Sasakuma, T.
AFFN:Kihara Institute for Biological Research and Graduate School of Integrated Science, Yokohama City University, Maioka 641-1Z, Totsuka-ku, Yokohama 244-0813, Japan
TITL:Isolation of novel early salt-responding genes

from wheat (Triticum aestivum L.) by differential display
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990423
HCOL:vol. 98, no. 5, pp. 673-678

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(17)
ACCN:002115669 CTLN:4502793
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Hernandez, P.;Hemmat, M.;Weeden, N.F.;Dorado, G.;Martin, A.
AFFN:Instituto de Agricultura Sostenible (CSIC), Apdo. 4084, 14080 Cordoba, Spain
TITL:Development and characterization of Hordeum chilense chromosome-specific STS markers suitable for wheat introgression and marker-assisted selection
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990423
HCOL:vol. 98, no. 5, pp. 721-727

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(18)
ACCN:002116083 CTLN:4505921
ABSJ:G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Robert, O.;Abelard, C.;Dedryver, F.*
AFFN:INRA, Station d'Amelioration des Plantes, Laboratoire Cereales, BP 29, 35653 Le Rheu Cedex, France; E-mail: person@rennes.inra.fr
TITL:Identification of molecular markers for the detection of the yellow rust resistance gene Yr17 in wheat
HTIL:Molecular Breeding [Mol. Breed.]
HSSN:1380-3743
HYER:19990000
HCOL:vol. 5, no. 2, pp. 167-175

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(19)
ACCN:002116674 CTLN:4510153
ABSJ:G (Genetics Abstracts)
AUTH:Hede, A.R.;Skovmand, B.;Reynolds, M.P.;Crossa, J.;Vilhelmsen, A.L.; Stoelen, O.
AFFN:The International Maize and Wheat Improvement Center (CIMMYT), Lisboa 27, Apdo. Postal 6-641, 06600, Mexico, D.F., Mexico
TITL:Evaluating genetic diversity for heat tolerance traits in Mexican wheat landraces
HTIL:Genetic Resources and Crop Evolution [Genet. Resour. Crop Evol.]
HSSN:0925-9864
HYER:19990200
HCOL:vol. 46, no. 1, pp. 37-45

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(20)
ACCN:002116905 CTLN:4512294
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Bai, G.;Kolb, F.L.;Shaner, G.;Domier, L.L.
AFFN:NCAUR-USDA-ARS, 1815 North University Street, Peoria, IL 61604, USA
TITL:Amplified fragment length polymorphism markers linked to a major quantitative trait locus controlling scab resistance in wheat
HTIL:Phytopathology
HSSN:0331-949X
HYER:19990000
HCOL:vol. 89, no. 4, 343

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(21)
ACCN:002117555 CTLN:4514665
ABSJ:V (Virology & AIDS Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Gooding, P.S.;Batty, N.P.;Goldsbrough, A.P.;Mullineaux, P.M.
AFFN:CSIRO Plant Industry, PO Box 350, Glen Osmond, South Australia 5064, Australia; E-mail: paul.gooding@pi.csiro.au
TITL:Plant cell-directed control of virion sense gene expression in wheat dwarf virus
HTIL:Nucleic Acids Research [Nucleic Acids Res.]
HSSN:0305-1048
HYER:19990401
HCOL:vol. 27, no. 7, pp. 1709-1718

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(22)
ACCN:002118367 CTLN:4519154
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Shan, X.;Blake, T.K.;Talbert, L.E.*
AFFN:Plant Sciences Department, Montana State University, Bozeman, MT 59717, USA; E-mail: usslt@montana.edu
TITL:Conversion of AFLP markers to sequence-specific PCR markers in barley and wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 1072-1078

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(23)
ACCN:002118368 CTLN:4519155
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Bliffeld, M.;Mundy, J.;Potrykus, I.;Fuetterer,

J.*
AFFN:Institute of Plant Sciences, ETH Zuerich, Universitaetstr. 2, CH 8092 Zuerich, Switzerland; E-mail: johannes.fuetterer@ipw.biol.ethz.ch
TITL:Genetic engineering of wheat for increased resistance to powdery mildew disease
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 1079-1086

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(24)
ACCN:002118375 CTLN:4519162
ABSJ:G (Genetics Abstracts)
AUTH:Mingeot, D.;Jacquemin, J.M.
AFFN:Centre de Recherches Agronomiques, Departement de Biotechnologie, 234 chaussee de CharPeroi, 5030 Gembloux, Belgium Fax: 32 81 61 04 59; E-mail: jacquemin@cragx.fgov.be
TITL:Mapping of RFLP probes characterized for their polymorphism on wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 1132-1137

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(25)
ACCN:002118383 CTLN:4519170
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Peng, J.H.;Fahima, T.;Roeder, M.S.;Li, Y.C.;Dahan, A.;Grama, A.;Ronin, Y.I.;Korol, A.B.;Nevo, E.*
AFFN:Institute of Evolution, University of Haifa, Mount Carmel, Haifa 31905, Israel Fax: +972-4-8246554; E-mail: nevo@research.haifa.ac.il
TITL:Microsatellite tagging of the stripe-rust resistance gene YrH52 derived from wild emmer wheat, Triticum dicoccoides, and suggestive negative crossover interference on chromosome 1B
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 862-872

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(26)
ACCN:002118384 CTLN:4519171
ABSJ:G (Genetics Abstracts)
AUTH:Li, Y.C.;Fahima, T.;Beiles, A.;Korol, A.B.;Nevo, E.*
AFFN:Institute of Evolution, University of Haifa, Haifa 31905, Israel Fax: 972-4-8246554; E-mail: nevo@research.haifa.ac.il
TITL:Microclimatic stress and adaptive DNA differentiation in wild emmer wheat, Triticum dicoccoides
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 873-883

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(27)
ACCN:002118392 CTLN:4519179
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Takumi, S.;Murai, K.;Mori, N.;Nakamura, C.
AFFN:Laboratory of Plant Genetics, Department of Biological and Environmental Science, Faculty of Agriculture, Kobe University, Nada-ku, Kobe 657-8501, Japan; E-mail: takumi@ans.ans.kobe-u.ac.jp
TITL:Trans-activation of a maize Ds transposable element in transgenic wheat plants expressing the Ac transposase gene
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 947-953

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(28)
ACCN:002118396 CTLN:4519183
ABSJ:G (Genetics Abstracts)
AUTH:Araki, E.;Miura, H.*;Sawada, S.
AFFN:Department of Crop Science, Obihiro University of Agriculture and Veterinary Medicine, Obihiro 080-8555, Japan; E-mail: miurahm@obihiro.ac.jp
TITL:Identification of genetic loci affecting amylose content and agronomic traits on chromosome 4A of wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990511
HCOL:vol. 98, no. 6/7, pp. 977-984

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(29)
ACCN:002119456 CTLN:4527538
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Hernandez, P.;Martin, A.;Dorado, G.
AFFN:Instituto de Agricultura Sostenible (CSIC), Apdo. 4084, 14080 Cordoba, Spain; E-mail:

gelhemop@uco.es
TITL:Development of SCARs by direct sequencing of RAPD products: a practical tool for the introgression and marker-assisted selection of wheat
HTIL:Molecular Breeding [Mol. Breed.]
HSSN:1380-3743
HYER:19990000
HCOL:vol. 5, no. 3, pp. 245-253

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(30)
ACCN:002119457 CTLN:4527539
ABSJ:G (Genetics Abstracts)
AUTH:Rasco-Gaunt, S.;Riley, A.;Lazzeri, P.;Barcelo, P.
AFFN:Biochemistry and Physiology Department, IACR-Rothamsted, Harpenden, Hertfordshire AL5 2JQ, UK; E-mail: Sonriza.Rasco-Gaunt@gbr.dupont.com
TITL:A facile method for screening for phosphinothricin (PPT)-resistant transgenic wheats
HTIL:Molecular Breeding [Mol. Breed.]
HSSN:1380-3743
HYER:19990000
HCOL:vol. 5, no. 3, pp. 255-262

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(31)
ACCN:002119592 CTLN:4532531
ABSJ:G (Genetics Abstracts); J (Microbiology Abstracts B: Bacteriology)
AUTH:Szymanski, C.M.;Yao, R.;Ewing, C.P.;Trust, T.J.;Guerry, P.*
AFFN:Enteric Dis. Program, Nav. Med. Res. Cent., Rockville, MD, USA; E-mail: guerryp@nmripo.nmri.nnmc.navy.mir
TITL:Evidence for a system of general protein glycosylation in Campylobacter jejuni
PBSR:Blackwell Science Ltd.
HTIL:Molecular Microbiology [Mol. Microbiol.]
HSSN:0950-382X
HYER:19990600
HCOL:vol. 32, no. 5, pp. 1022-1030

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(32)
ACCN:002124826 CTLN:4486538
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts); Z (Entomology Abstracts)
AUTH:Altpeter, F.;Diaz, I.;McAuslane, H.;Gaddour, K.;Carbonero, P.;Vasil, I. K.*
AFFN:Laboratory of Plant Cell and Molecular Biology, 1143 Fifield Hall, University of Florida, Gainesville, FL 32611-0690, USA; E-mail: ikv@gnv.ifas.ufl.edu
TITL:Increased insect resistance in transgenic wheat stably expressing trypsin inhibitor CMe
HTIL:Molecular Breeding [Mol. Breed.]
HSSN:1380-3743
HYER:19990000
HCOL:vol. 5, no. 1, pp. 53-63

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(33)
ACCN:002129938 CTLN:4542557
ABSJ:G (Genetics Abstracts)
AUTH:Kato, K.;Miura, H.;Sawada, S.
TITL:Comparative mapping of the wheat Vrn-AI region with the rice Hd-6 region
HTIL:Genome
HSSN:0831-2796
HYER:19990400
HCOL:vol. 42, no. 2, pp. 204-209

---

(34)
ACCN:002129946 CTLN:4542569
ABSJ:G (Genetics Abstracts)
AUTH:Allaby, R.G.;Banerjee, M.;Brown, T.A.
TITL:Evolution of the high molecular weight glutenin loci of the A, B, D, and G genomes of wheat
HTIL:Genome
HSSN:0831-2796
HYER:19990400
HCOL:vol. 42, no. 2, pp. 296-307

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(35)
ACCN:002129949 CTLN:4542572
ABSJ:G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Hartl, L.;Mohler, V.;Zeller, F.J.;Hsam, S.L.K.;Schweizer, G.
TITL:Identification of AFLP markers closely linked to the powdery mildew resistance genes Pm1c and Pm4a in common wheat (Triticum aestivum L.)
HTIL:Genome
HSSN:0831-2796
HYER:19990400
HCOL:vol. 42, no. 2, pp. 322-329

---

(36)
ACCN:002129951 CTLN:4542574
ABSJ:G (Genetics Abstracts)
AUTH:David, J.L.;Dusautoir, J.C.;Raynaud, C.;Roumet, P.
TITL:Heritable variation in the ability to produce haploid embryos via pollination with maize and embryo rescue in durum wheat
HTIL:Genome
HSSN:0831-2796
HYER:19990400
HCOL:vol. 42, no. 2, pp. 338-342

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(37)
ACCN:002129952 CTLN:4542576
ABSJ:G (Genetics Abstracts)

AUTH:Blake, N.K.;Lehfeldt, B.R.;Lavin, M.;Talbert, L.E.
TITL:Phylogenetic reconstruction based on low copy DNA sequence data in an allopolyploid: The B genome of wheat
HTIL:Genome
HSSN:0831-2796
HYER:19990400
HCOL:vol. 42, no. 2, pp. 351-360

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(38)
ACCN:002130431 CTLN:4548497
ABSJ:G (Genetics Abstracts)
AUTH:Grausgruber, H.;Lemmens, M.;Buerstmayr, H.;Ruckenbauer, P.
AFFN:University of Agricultural Sciences Vienna, Department of Plant Breeding, Gregor Mendel Strasse 33, A-1180 Vienna, Austria; E-mail: h330pj@edvl.boku.ac.at
TITL:Resistance of 'Chinese Spring' substitution lines carrying chromosomes from 'Cheyenne', 'Hope' and 'Lutescens 62' wheats to head blight caused by Fusarium culmorum
HTIL:Hereditas
HSSN:0018-0661
HYER:19990000
HCOL:vol. 130, no. 1

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(39)
ACCN:002130760 CTLN:4549529
ABSJ:G (Genetics Abstracts)
AUTH:Korzun, V.;Roeder, M.S.;Wendehake, K.;Pasqualone, A.;Lotti, C.;Ganal, M.W.;Blanco, A.
AFFN:Institut fuer Pflanzengenetik und Kulturpflanzenforschung, Corrensstrasse 3, D-06466, Gatersleben, Germany Fax: +49 39482 5137; E-mail: korzunv@idk-gatersleben.de
TITL:Integration of dinucleotide microsatellites from hexaploid bread wheat into a genetic linkage map of durum wheat
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990616
HCOL:vol. 98, no. 8, pp. 1202-1207

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(40)
ACCN:002130764 CTLN:4549534
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Gill, K.S.;Arumuganathan, K.;Lee, J.
AFFN:Department of Agronomy, P.O. Box 830915, University of Nebraska-Lincoln, Lincoln, NE 68583-0915, USA; E-mail: kgill@unl.edu
TITL:Isolating individual wheat (Triticum aestivum) chromosome arms by flow cytometric analysis of ditelosomic lines
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990616
HCOL:vol. 98, no. 8, pp. 1248-1252

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(41)
ACCN:002130988 CTLN:4553842
ABSJ:G (Genetics Abstracts)
AUTH:Simonetti, M.C.;Bellomo, M.P.;Laghetti, G.;Perrino, P.;Simeone, R.; Blanco, A.
AFFN:Institute of Plant Breeding, University of Bari, Via Amendola 1 65/A, 70126 Bari, Italy
TITL:Quantitative trait loci influencing free-threshing habit in tetraploid wheats
PBSR:Kluwer Academic Publisher
HTIL:Genetic Resources and Crop Evolution [Genet. Resour. Crop Evol.]
HSSN:0925-9864
HYER:19990600
HCOL:vol. 46, no. 3, pp. 267-271

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(42)
ACCN:002137414 CTLN:4510119
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Bouhssini, E.;Nsarellah, M.N.;Nachit, M.M.;Bentika, A.;Benlahbib, O.; Lhaloui, S.
AFFN:International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria
TITL:First source of resistance in durum wheat to Hessian fly (Diptera: Cecidomyiidae) in Morocco
HTIL:Genetic Resources and Crop Evolution [Genet. Resour. Crop Evol.]
HSSN:0925-9864
HYER:19990400
HCOL:vol. 46, no. 2, pp. 107-109

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(43)
ACCN:002139262 CTLN:4549530
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Li, Z.;Rahman, S.;Kosar-Hashemi, B.;Mouille, G.;Appels, R.;Morell, M.K.
AFFN:CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia; E-mail: m.morell@.pi.csiro.au
TITL:Cloning and characterization of a gene encoding wheat starch synthase I
PBSR:Springer-Verlag
HTIL:Theoretical and Applied Genetics [Theor. Appl. Genet.]
HSSN:0040-5752
HYER:19990616

HCOL:vol. 98, no. 8, pp. 1208-1216

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(44)
ACCN:002140054 CTLN:4556635
ABSJ:G (Genetics Abstracts)
AUTH:Dominguez, F.;Cejudo, F.J.
AFFN:Instituto de Bioquimica Vegetal y Fotosintesis, Centro de Investigaciones Cientificas "Isla de la Cartuja," Avda Americo Vespucio s/n, 41092 Sevilla, Spain; E-mail: fjcejudo@cica.es
TITL:Patterns of Starchy Endosperm Acidification and Protease Gene Expression in Wheat Grains following Germination
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19990100
HCOL:vol. 119, no. 1, pp. 81-88

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(45)
ACCN:002140074 CTLN:4556666
ABSJ:G (Genetics Abstracts)
AUTH:Kurek, I.;Aviezer, K.;Erel, N.;Herman, E.;Breiman, A.
AFFN:The George S. Wise Faculty of Life Sciences, Department of Plant Sciences, Tel Aviv University, Tel Aviv, Israel 69978; E-mail: adina@ccsg.tau.ac.il
TITL:The Wheat Peptidyl Prolyl cis-trans-Isomerase FKBP77 Is Heat Induced and Developmentally Regulated
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19990200
HCOL:vol. 119, no. 2, pp. 693-704

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(46)
ACCN:002140090 CTLN:4556705
ABSJ:G (Genetics Abstracts)
AUTH:Loggini, B.;Scartazza, A.;Brugnoli, E.;Navari-Izzo, F.
AFFN:Dipartimento di Chimica e Biotecnologie Agrarie, Universita degli Studi di Pisa, 56124 Pisa, Italy; E-mail: fnavari@agr.unipi.it
TITL:Antioxidative Defense System, Pigment Composition, and Photosynthetic Efficiency in Two Wheat Cultivars Subjected to Drought
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19990300
HCOL:vol. 119, no. 3, pp. 1091-1100

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(47)
ACCN:002140147 CTLN:4556807
ABSJ:G (Genetics Abstracts)
AUTH:Wu, G.;Wilen, R.W.;Robertson, A.J.;Gusta, L.V.
AFFN:Crop Development Centre, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N 5A8; E-mail: gusta@duke.usask.ca
TITL:Isolation, Chromosomal Localization, and Differential Expression of Mitochondrial Manganese Superoxide Dismutase and Chloroplastic Copper/ Zinc Superoxide Dismutase Genes in Wheat
HTIL:Plant Physiology [Plant Physiol.]
HSSN:0032-0889
HYER:19990600
HCOL:vol. 120, no. 2, pp. 513-520

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(48)
ACCN:002141233 CTLN:4559472
ABSJ:G (Genetics Abstracts)
AUTH:Shimosaka, E.;Sasanuma, T.;Handa, H.
AFFN:Laboratory of Plant Genecology, Hokkaido National Agricultural Experiment Station, Sapporo, 062-8555 Japan
TITL:A Wheat Cold-Regulated cDNA Encoding an Early Light-Inducible Protein (ELIP): Its Structure, Expression and Chromosomal Location
HTIL:Plant & Cell Physiology [Plant Cell Physiol.]
HSSN:0032-0781
HYER:19990300
HCOL:vol. 40, no. 3, pp. 319-325

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(49)
ACCN:002141614 CTLN:4560834
ABSJ:G (Genetics Abstracts)
AUTH:Clarke, F.R.;Baker, R.J.*;DePauw, R.M.
AFFN:Department of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8
TITL:Using height to adjust for interplot interference in spring wheat yield trials
HTIL:Canadian Journal of Plant Science/Revue Canadienne de Phytotechnie [Can. J. Plant Sci./ Rev. Can. Phytotech.]
HSSN:0008-4220
HYER:19990400
HCOL:vol. 79, no. 2, pp. 169-174

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(50)
ACCN:002141711 CTLN:4561213
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Kemp, G.;Botha, A.;Kloppers, F.J.;Pretorius, Z.A.
AFFN:Department of Botany and Genetics, Faculty of Science, University of the Orange Free State, Bloemfontein, South Africa
TITL:Disease development and beta -1,3-glucanase expression following leaf rust infection in

resistant and susceptible near-isogenic wheat seedlings
PBSR:Academic Press
HTIL:Physiological and Molecular Plant Pathology [Physiol. Mol. Plant Pathol.]
HSSN:0885-5765
HYER:19990700
HCOL:vol. 55, no. 1, pp. 45-52

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(51)
ACCN:002142900 CTLN:4567183
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts); N (Biochemistry Abstracts 2: Nucleic Acids)
AUTH:Digeon, J.-F.;Guiderdoni, E.;Alary, R.;Michaux-Ferriere, N.;Joudrier, P.;Gautier, M.-F.*
AFFN:Unite de Biochimie et Biologie Moleculaire des Cereales, INRA, 2 Place Viala, 34060 Montpellier cedex 01, France
TITL:Cloning of a wheat puroindoline gene promoter by IPCR and analysis of promoter regions required for tissue-specific expression in transgenic rice seeds
HTIL:Plant Molecular Biology [Plant Mol. Biol.]
HSSN:0167-4412
HYER:19990400
HCOL:vol. 39, no. 6, pp. 1101-1112

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(52)
ACCN:002143370 CTLN:4569443
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Murai, J.;Taira, T.;Ohta, D.
AFFN:Laboratory of Plant Genes and Physiology, College of Agriculture, Osaka Prefecture University, Sakai, Osaka 599-8531, Japan
TITL:Isolation and characterization of the three Waxy genes encoding the granule-bound starch synthase in hexaploid wheat
PBSR:Elsevier Science B.V.
HTIL:Gene
HSSN:0378-1119
HYER:19990624
HCOL:vol. 234, no. 1, pp. 71-79

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(53)
ACCN:002143878 CTLN:4571781
ABSJ:G (Genetics Abstracts)
AUTH:Enjalbert, J.;Goldringer, I.*;Paillard, S.;Brabant, P.
AFFN:Station de Genetique Vegetale, INRA/INA-PG UPS, Ferme du Moulon, F- 91190 Gif-sur-Yvette, France; E-mail: isa@moulon.inra.fr
TITL:Molecular markers to study genetic drift and selection in wheat populations
HTIL:Journal of Experimental Botany [J. Exp. Bot.]
HSSN:0022-0957
HYER:19990300
HCOL:vol. 50, no. 332, pp. 283-290

Editorial remarks

This is the final issue of Wheat Information Service dated on 1900's. In this volume, we are glad to have the new version of gene catalogue after 9th IWGS, which has been done with great effort by Drs. McIntosh, Hart, Devos, and Rogers.

Since spring of this year, we have been calling your attention for continuation of subscription of WIS, and have renewed the mailing list, which allowed us to save the cost. But, at the same time, we are afraid of missing some wheat researchers who need WIS or whom we should not miss from our community. Please notify him/her, if you know, who did not receive the present issue in despite of his/her willing. Also, we are always welcoming new comers to WIS community. WIS is a nonprofit international journal of mutual help and cooperation for wheat research, which is supported economically by subscriber's donation (2,000 Japanese Yen; ca. US$25 as a standard per year), and voluntary contributions of concerned people for editing. Wheat researcher who is interested in subscription or contribution, touch our business office through e-mail (yamabosi@yokohama-cu.ac.jp) or FAX (+81-45-825-3307).

Also, the editorial board is willing to print more articles for "Research information", which should be informative but not suitable for full paper; for instance, idea of the experiment, establishment of experimental lines, candidate gene isolated, proposal for cooperation, etc. Research should be effective and useful in the type of information journal like WIS.

There are several issues being discussed on international panels about the exchange of germplasm or genetic rescues. Since the international agreement at Rio de Janeiro in 1993, the introduction or exchange of genetic resources has become a political issue. Also, the recent advances of gene-manipulation techniques have brought further complexity of exchanging plant materials. We may discuss freely these subjects on WIS.

The editor of WIS

To colleagues:

The Kihara Memorial Foundation (KMF) was established in 1985 in memory of the late Dr. Hitoshi Kihara, a world famous geneticist and evolutionary scientist. The activities of the KMF are promotion of life science by supporting symposia, workshops, and technical courses for researchers, enlightenment of scientific information to citizens, awarding of 'KMF Prize' and 'Child Scientist Prize', and publication of journals such as 'Wheat Information Service'.

The coming 21st century will be one of life sciences. KMF intends to continue contribution for a better future of the earth to solve many problems facing us such about health, food, resources and environment.

The recent economic condition in Japan is limiting our support of these KMF activities. KMF is, therefore, taking up subscriptions from colleagues who approve of the activities of KMF. We would appreciate receiving from you inquiries about this matter, thank you.

Kihara Memorial Foundation

Business Office

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