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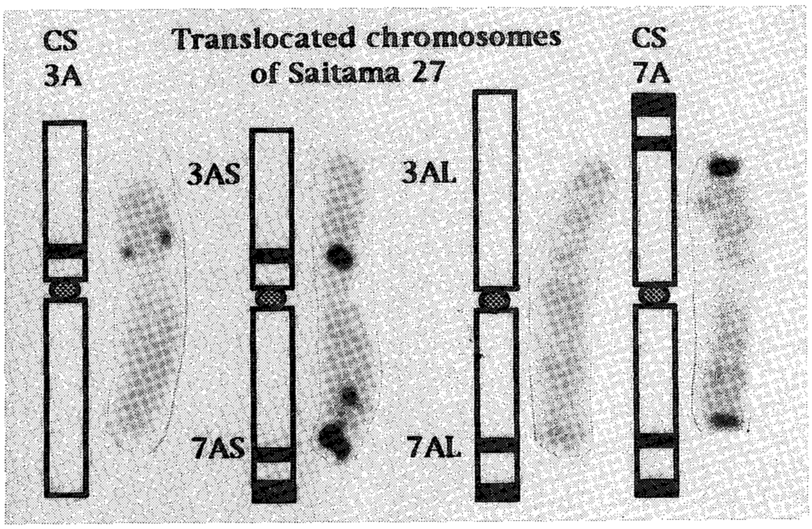
ISSN 0510-3517



No.79

December, 1994

Kihara Memorial

Yokohama Foundation for

the Advancement of Life Sciences

Yokohama, Japan

WHEAT INFORMATION SERVICE

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3. Research articles should include Title, Author's name(s) and address, Summary (300 words or less), Introduction, Materials and Methods, Results, Discussion, and References.
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Wheat Information Service
December 79: 1 – 17 (1994)

I. Review

Genetic resources and breeding of wheat and barley in Japan

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1. Agricultural Research Stations breeding wheat and barley

a) Breeding stations for wheat

At present, breeding of wheat is carried out at five National Agricultural Experiment Stations, i.e., Hokkaido (location: Sapporo City), Tohoku (Morioka), National Agriculture Research Center (Tsukuba), Chugoku (Fukuyama) and Kyushu (Chikugo), and at two Prefectural Agricultural Experiment Stations as part of a national project, i.e., Kitami and Nagano, and at the Gunma and Aichi Prefectural Agricultural Experiment Stations. In Japan, wheat cultivars have been developed only in national and prefectural agricultural experiment stations, and not in universities or private companies (Fig. 1).

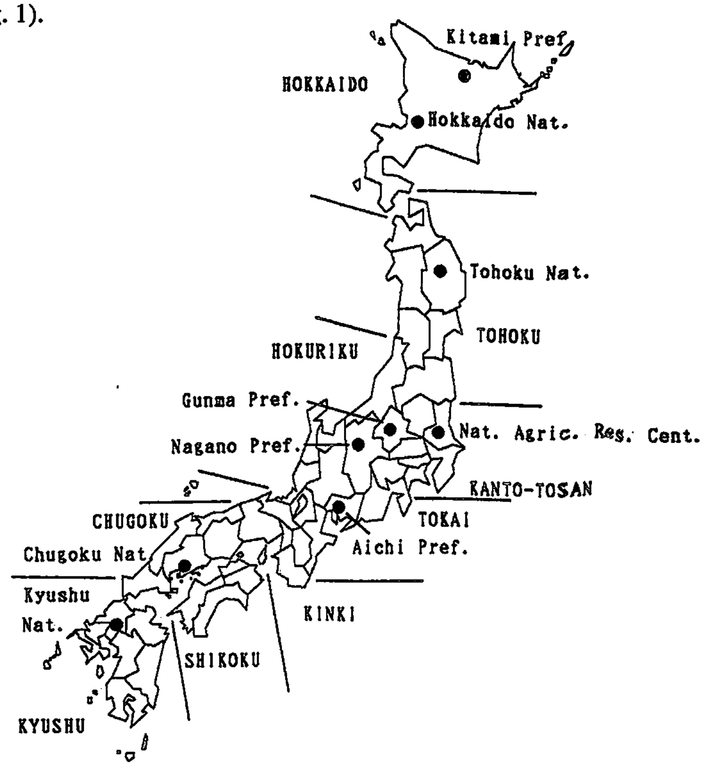

Fig. 1. Districts of Japan and location of the wheat breeding stations.

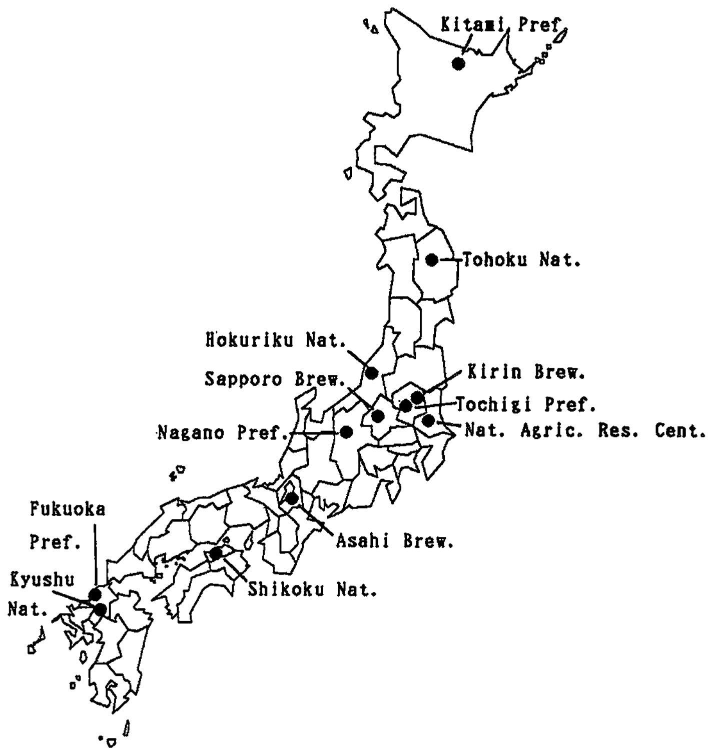

Fig. 2. Breeding stations for barley in Japan.

b) Breeding stations for barley

At present, breeding of hulled barley is carried out at four National Agricultural Experiment Stations, i.e., Tohoku, Hokuriku (Ojiya), National Agriculture Research Center and Kyushu, and at the Nagano Prefectural Agricultural Experiment Station. Breeding of naked barley is carried out at the Shikoku National Agricultural Experiment Station. Breeding of two-rowed malting barley is carried out by three brewing companies, namely Kirin, Sapporo and Asahi as well as at the Prefectural Agricultural Experiment Stations of Tochigi and Fukuoka as part of a national project, and at the Kitami Prefectural Agricultural Experiment Station (Fig. 2).

2. Objectives and results of common wheat (*Triticum aestivum* L.) breeding

In Japan, only common wheat cultivars among *Triticum* ssp. are commercially cultivated in farmer's fields and generally these cultivars are sown in autumn except in a small area in Hokkaido. Therefore, breeding efforts have concentrated on the improvements of common winter wheats.

The main objectives of wheat breeding in Japan are as follows: early maturity, cold resistance including tolerance to deep snow, short strong culm, high-yielding ability, disease resistance (leaf rust, scab, yellow mosaic, powdery mildew, etc.), resistance to preharvest sprouting and high grain quality.

1) Breeding for early maturity, cold resistance, short strong culm and high-yielding ability: These characters have consistently been the major objectives of wheat breeding in Japan and many superior cultivars have been developed.

Breeding cultivars with a short and strong culm has been achieved by introducing the *Rht1* and *Rht2* genes derived from Japanese landraces into improved lines. It was reported that more than 70% of 133 Norin varieties tested carried either the *Rht1* or *Rht2* gene (Yamada 1990). They have made it possible to use large amounts of fertilizer and to practice drill seeding and broadcasting at high seed rates. As a result, national average yields have reached over 3 t/ha since 1981.

Although the maturity time has been advanced by about one week during the past 60 years, wheat cultivars with earlier maturity are still required for the implementation of double cropping and for avoiding rain damage at ripening time. In order to achieve this objective, some difficult problems need to be solved. First, wheat cultivars in Japan, especially those cultivated in the warm regions west of the Kanto district, belong to the earliest maturing group in the world, and therefore the introduction of genes conferring earlier maturity is very difficult. Accordingly, attempts to induce new genes for earliness by mutation breeding have been made (Yamagata et al. 1989). Secondly, there is a highly negative correlation between the time to maturity and yielding ability. Recently, it has been shown at the Kyushu National Agricultural Experiment Station that yield decreases by about 3 percent a day with the advancement of the maturity date (Taya 1993). In order to develop cultivars with early maturity and high yielding ability, it will be necessary to find a strategy to overcome this negative correlation. Thirdly, in cultivars with early maturity internode elongation occurs earlier, and hence the cultivars are prone to suffer from cold or frost damage. Therefore, breeding of early maturing cultivars with photosensitivity or a slight winter habit is now being attempted. Such characters are expected to be effective in delaying the onset of internode elongation and hence avoiding cold or frost damage.

2) Breeding for resistance to leaf rust: Leaf rust disease of wheat caused by *Puccinia recondita* Roberge ex Desmazieres causes considerable damage especially in the cold regions of Japan, i.e., Tohoku and Hokkaido. There is no type of immunity to leaf rust among Norin varieties. Extensive efforts to breed resistant cultivars have been made, mainly at the Tohoku National Agricultural Experiment Station, by interspecific and intergeneric crossing, and four parental lines have been developed (Table 1).

Sabikei 40, a leaf rust resistant wheat parental line, was developed at the Tohoku National Agricultural Experiment Station from a cross between a F_3 line derived from {(Shimofusakomugi × RW-12) × Nanbukomugi} and a B_1F_3 line derived from {(Miyaginokomugi × AR-1) × Miyaginokomugi} (Mukade et al. 1986). This cross was made in 1970 with the objective of accumulating two different leaf rust resistance genes, one from RW-12, a line which has a single dominant gene derived from *Triticum turgidum* ssp. *dicoccoides* on chromosome 6B, and the other from AR-1, a line which has a single incompletely dominant gene derived from *Triticum timopheevi* on chromosome 1A. Sabikei 40 shows seedling resistance to the leaf rust races 6A, 37B and 21B which are predominant in the northern part of Japan and to the naturally occurring races in the field

Table 1. Wheat parental lines resistant to leaf rust (WPL No. 1, 2, 3 and 6) and resistant to scab (WPL No. 4)

Registered Name (Former Name)	Donor (Gene Source)
Wheat Parental Line No. 1 (Sabikei 40)	RW-12 (*Triticum turgidum* ssp. *dicoccoides*), AR-1 (*Triticum timopheevi*)
Wheat Parental Line No. 2 (Sabikei 43)	Petkus
Wheat Parental Line No. 3 (Sabikei 50)	WA-3 (*Elytrigia intermedia*), Hope x Timstein II 39-44 (*Triticum turgidum* ssp. *dicoccoides* or *T. turgidum* ssp. *durum*)
Wheat Parental Line No. 4 (Akakabikei 2)	Nobeokabouzukomugi Sobaku 3
Wheat Parental Line No. 6 (AS-5)	Agrus (*Elytrigia pontica*)

of the Tohoku National Agricultural Experiment Station. A high level of resistance has been observed in adult plants in the field where leaf rust prevails each year the variety has been tested. No selection was made from F_1 to F_4 bulk populations and the F_5 generation was screened for leaf rust resistance. The derived lines were selected for agronomic characters in succeeding generations. One promising line was obtained and named Sabikei 40 in the F_{12} generation in 1982. "Sabikei" means "leaf rust resistant line". It was registered by the Ministry of Agriculture, Forestry and Fisheries (MAFF) as a wheat parental line no. 1 in 1984 (Table 1).

Sabikei 43 is also a leaf rust resistant wheat parental line developed at the Tohoku National Agricultural Experiment Station (Mukade et al. 1986). It was selected from a cross between a 8x-Triticale line derived from the cross Norin 40 × Petkus and a wheat cultivar, Hachimankomugi. This cross was made in 1976 and attempts to transfer the leaf rust resistance from rye to wheat by spontaneous intergeneric translocation were made. After selfing the F_1 plants, the generation advancement from F_2 to F_4 bulk populations was accelerated in the greenhouse. In the F_5 generation, 546 plants were tested for leaf rust resistance and 18 plants resistant to the disease were cytologically examined. Out of these 18 plants, 11 carrying the translocated chromosome(s) were selected. Selection for agronomic characters was made in subsequent generations in the field. One promising line was obtained and named Sabikei 43 in the F_9 generation in 1983. Sabikei 43 was registered by the MAFF as a wheat parental line no. 2 in 1984. Sabikei 43 also shows seedling resistance to the leaf rust races 6A, 37B and 21B, and to the naturally occurring races collected in the field of the Tohoku National Agricultural Experiment Station. High adult plant resistance has been observed in the field where leaf rust prevails each year the variety has been tested. The resistance of Sabikei 43 to the race 21B is controlled by a single incompletely dominant gene (Table 1).

Sabikei 50 is also a leaf rust resistant wheat parental line developed at the Tohoku National Agricultural Experiment Station (Mukade et al. 1987). It was selected from a triple cross, Sabikei 25/Sabikei 23//Hanagasakomugi. This cross was made in 1976 with the view of accumulating three different leaf rust resistance genes, the first from Sabikei 25 whose complete resistance gene is inherited from RW-12 (see Sabikei 40), the second from Sabikei 23, a line which shows adult plant resistance probably derived from *Elytrigia intermedia* through WA-3, and the third from Hanagasakomugi, a cultivar which shows slow-rusting resistance probably derived from *Triticum turgidum* ssp. *dicoccoides* or *T. turgidum* ssp. *durum* through Hope-Timstein II 39-44. However, Sabikei 50 did not inherit the complete resistance gene from Sabikei 25. Sabikei 50 shows susceptible or mixed reaction to the leaf rust races 6A, 37B and 21B at the seedling stage, while the degree of resistance gradually increases as the plant grows (adult plant resistance). In the field, Sabikei 50 is resistant in the early period of ripening but becomes slightly infected towards maturity. However, the progress of leaf rust lesions is very slow (slow-rusting resistance) and hardly affects the photosynthetic ability of the plant. Sabikei 50 was registered by the MAFF as a wheat parental line no. 3 in 1986 (Table 1).

AS-5 is also a leaf rust resistant wheat parental line developed at the Tohoku National Agricultural Experiment Station (Yamaguchi et al. 1993). AS-5 carries the gene *Lr19* conferring resistance to the leaf rust races 6A, 37B and 21B for all the growing periods of wheat. The gene *Lr19* of AS-5 derived from *Elytrigia pontica* through a chromosome substitution line, Agrus. The endosperm of AS-5 is rich in lutein which is a carotenoid pigment and hence produces a flour with a yellowish color. This character is considered to be controlled by a gene(s) closely linked to *Lr19*. AS-5 was registered by the MAFF as a wheat parental line no. 6 in 1991 (Table 1).

3) Breeding for resistance to scab: In the south-western Japan, especially in Kyushu, scab disease caused by *Gibberella zeae* (Schw.) Petch, *Fusarium graminearum* Schw., etc. causes considerable damage and has become one of the most important problems in wheat production. No gene for complete resistance or immunity to scab has been identified yet. Extensive efforts to breed more resistant cultivars have been made by the accumulation of polygenes for resistance or by the induction of mutations mainly at the Kyushu National Agricultural Experiment Station and one parental line has been developed (Table 1).

Akakabikei 2 (synonym: Akakabi-kei 2), a scab resistant wheat parental line, was developed at the Kyushu National Agricultural Experiment Station from a cross between Nobeokabozukomugi (synonym: Nobeokabozu-komugi) and Sobaku 3 (synonym: Sumai 3) (Gocho et al. 1992). Both parents showed a higher resistance to scab than the other wheat varieties. However, Nobeokabozukomugi and Sobaku 3 cannot be commercially used due to their poor agronomic characteristics such as long culm and late maturity. The resistance of these varieties was conferred by polygenes. The cross between Nobeokabozukomugi and Sobaku 3 was made in 1977 with the view of accumulating these polygenes for resistance. No selection was made from F_1 to F_4 bulk populations and the F_5 generation was screened for lodging resistance. The derived lines were screened for scab resistance and other agronomic characters in succeeding generations. One promising line was obtained and named Akakabikei 2 in the F_{10} generation in 1984. "Akakabikei" means "scab resistant line". It was registered by the MAFF as a wheat parental line no. 4 in 1986 (Table 1).

The possibility of using *Elytrigia* and *Elymus* as sources of resistance to scab is now being investigated at the Kyushu National Agricultural Experiment Station.

4) Breeding for resistance to yellow mosaic virus and powdery mildew: These two severe diseases are often epidemic in the warm regions west of the Kanto district. Some cultivars highly resistant to these diseases have been developed, such as Horoshirikomugi (Norin 114), Takunekomugi (Norin 115), which are resistant to wheat yellow mosaic virus, and Ushiokomugi which is resistant to powdery mildew caused by *Erysiphe graminis* de Candolle f. sp. *tritici* Em. Marchal.

5) Breeding for resistance to preharvest sprouting: In Japan, the prevention of preharvest sprouting damage is an important problem in wheat production because harvesting time, early June to late July, coincides with the rainy season. Japanese wheat cultivars, Igachikugo Oregon and Zenkojikomugi (Norin 109), are mainly used as gene sources to prevent preharvest sprouting.

6) Breeding for improved grain quality: Japanese wheat is mainly used for making noodles. Superior cultivars suitable for noodle-making are characterized by an excellent milling score, creamy-white flour, low amylose content, etc. as well as low deterioration caused by rain. The amylose content of flour shows a highly negative correlation with the eating quality. Among the Japanese wheat cultivars, the breeding line Kanto 107 and its parent Kanto 79 were found to show a lower apparent amylose content (21.5% and 22.0%, respectively) than typical wheat cultivars (28~29%) (Kuroda et al. 1989), and the wheat mutants with a much lower apparent amylose content (14.0~16.7%) were induced by ethylmethanesulphonate (EMS) treatment (Oda et al. 1992).

7) Breeding high-yielding wheat varieties using F_1 hybrids: Initially, the male sterility from the *Triticum timopheevi* cytoplasm and the fertility-restorer gene *Rf3* from *Triticum aestivum* ssp. *spelta* var. *duhamelianum* were used for F_1 hybrids (Zeven 1967; Wilson 1968; Tahir 1970; Tahir and Tsunewaki 1971; Araki 1990). However, the F_1 hybrids could not be used commercially because they were susceptible to scab due to the *T. timopheevi* cytoplasm. In addition, the *Rf3* gene had incomplete restoring ability and thus low production of F_1 seeds. Recently, extensive efforts to breed F_1 hybrids have been made using the S^v type cytoplasm from *Aegilops kotschyi* and a wheat-rye translocation line with the 1BL-1RS chromosome constitution (Toriyama et al. 1993; Nonaka et al. 1993). The fertility-restorer gene *Rfv1* for the S^v type cytoplasm is carried on the short arm of chromosome 1B of wheat. The translocation line with a 1BL-1RS chromosome constitution and normal type cytoplasm (e.g., 911-B-8-11 in Fig. 3) is used as a female parent, and an "A" variety is backcrossed "n" times to the translocation line to develop the maintainer "A". In this process of backcrossing, plants having the 1BL-1RS chromosome constitution can be easily selected by using the leaf rust resistance gene *Lr26* as a marker because it is carried on the 1RS chromosome from rye.

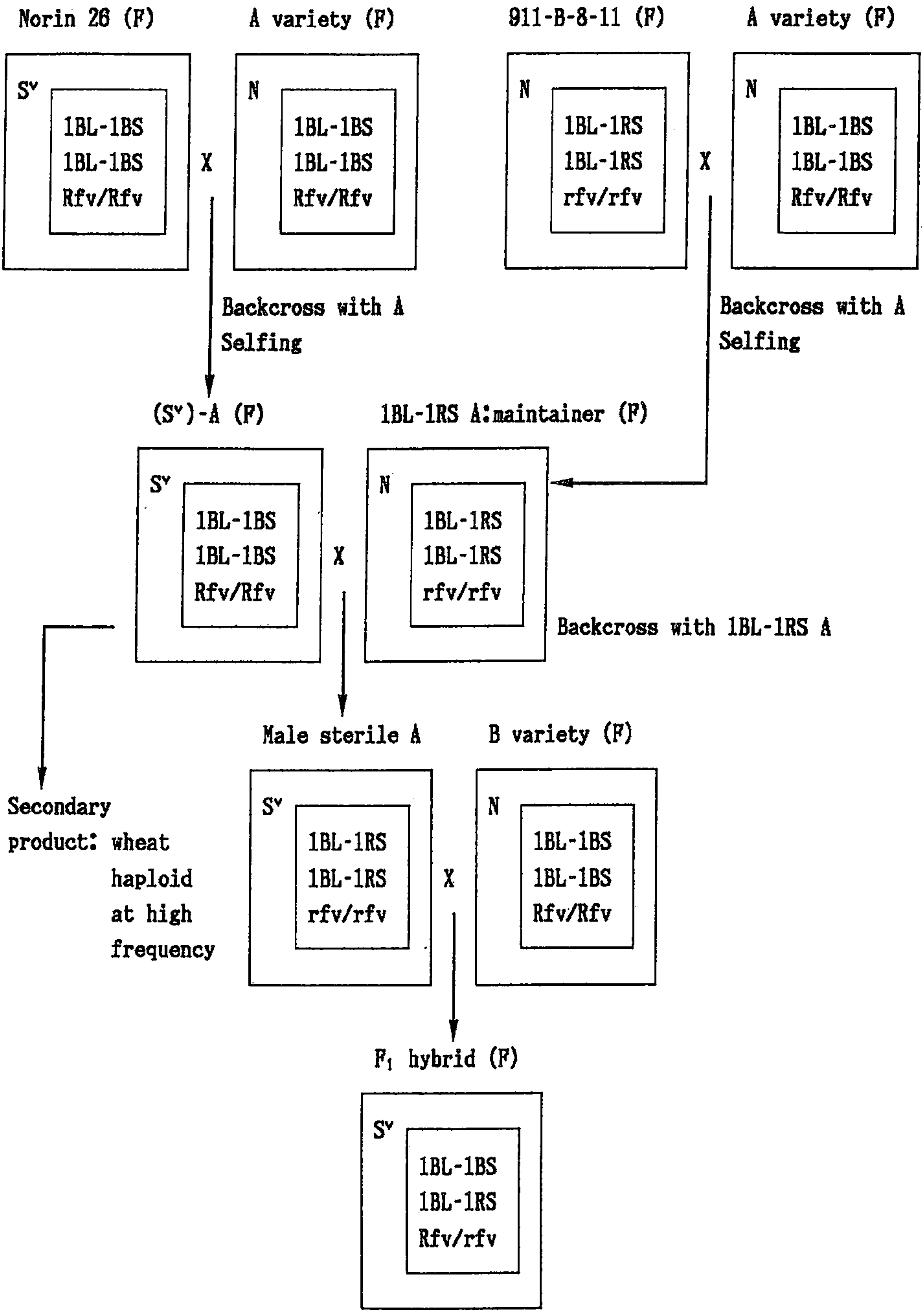

Fig. 3. Breeding F_1 hybrid wheat using an alien cytoplasm and translocation line.
(F): male fertile.
Rfv = *Rfv1*, rfv = *rfv1*.

Male sterile "A" line can be developed by crossing between the maintainer "A" and "A" line having the S^v type cytoplasm also developed by backcrossing (e.g., (S^v)-Norin 26 × "A" variety in Fig. 3). Almost all the wheat cultivars have a *Rfv1* genotype because the *Rfv1* gene is carried on the 1BS chromosome of wheat. Therefore, this breeding system does not require the development of any specific restorer (Fig. 3).

3. Objectives and results of barley (*Hordeum vulgare* L.) breeding

The main objectives of barley breeding in Japan are as follows: early maturity, cold resistance including tolerance to deep snow, short strong culm, high-yielding ability, disease resistance (barley yellow mosaic, barley yellow dwarf, powdery mildew, scab, etc.) and improved grain quality.

1) Breeding for early maturity, cold resistance, short strong culm and high-yielding ability: In Japan barley is sown in autumn, except in Hokkaido. Barley is the second crop in a rotation with rice or summer upland crops. Consequently, the interval between the harvesting of barley and the transplanting or sowing of the succeeding crops is very short. Double cropping is not possible in the northern part of Japan. To prevent maturity falling in the rainy season, early June to late July, it is essential to breed cultivars that mature as early as possible.

In the case of 6-rowed hulled barley, tall and late maturing, normal types of barley used to be grown, especially in Kanto district. However, due to the increased application of chemical fertilizers, improvement in lodging resistance of barley cultivars has become necessary. In order to breed cultivars resistant to lodging, there are two breeding strategies: 1) reduction of culm length, and 2) increase of culm stiffness. In the first strategy, the *uz* gene has been used for reducing the culm length. Tall and late maturing, normal types have been replaced by the semi-dwarf "uzu" type of cultivars which are early maturing and short, but retain a high yielding potential. In the second strategy, the cultivar Haganemugi has been used as a gene source for increasing culm stiffness. Haganemugi has stronger culm as a result of a thicker culm wall and a larger culm diameter (Oda et al. 1966). This results in a higher resistance to culm breaking when compared with a representative "uzu" type, Sekitorisai 1 (Table 2). Several cultivars have been developed from crosses involving Haganemugi.

2) Breeding for resistance to barley yellow mosaic virus (BaYMV): Barley yellow mosaic caused by BaYMV previously inflicted serious damage especially on two-rowed malting barley. Gene sources and virus strains have been identified, and effective resistant cultivars have been developed (Table 3).

In Japan, three virus strains, I, II and III, have been identified (Usugi et al. 1985; Kashiwazaki et al. 1989). Strain I shows the widest distribution in the country followed by strain II, and strain III now occurs in a limited small area in Ibaraki Prefecture (Usugi et al. 1985; Kashiwazaki et al. 1989).

Table 2. Comparison of characters relating to lodging resistance in barley (Oda *et al.*, 1966)

Cultivar	Dry wt. per unit culm length mg/mm	Thickness of culm wall mm	Culm diameter mm	Bending moment of culm at breaking g/cm
Haganemugi	18	1.10	5.60	1110
Sekitorisai 1	13	0.86	4.54	431

Table 3. Barley cultivars and their reaction to barley yellow mosaic virus strains

Cultivar		Donor		Virus Strain		
Name	Gene	Name	Gene	I	II	III
Misato Golden etc.	*Ym5*(t)	Mokusekko 3	*Ym, Ym5*(t)	R	R	S
		Mihorihadaka 3	*Ym2*	R	S	R
Masakadomugi	*ym3*	Ea52	*ym3*	R	R	R
Ishukushirazu etc.	*ym3*	Haganemugi	*ym3*	R	R	R
		Tokushima-mochihadaka	*ym3, ym4*	R	R	R
		Shimakei 1	*ym4*	R	R	?

R: resistant.
S: susceptible.
?: resistance not tested.

Five resistance genes, *Ym*, *Ym2*, *ym3*, *ym4* and *Ym5*(t), have been identified in Japan (Table 3). The variety Mokusekko 3 has two resistant genes *Ym* and *Ym5*(t) (Makino, personal communication). *Ym* is an incompletely dominant gene and linked to the gene *K* conferring hooded lemma with a recombination value of 29.4% on chromosome 4 (Takahashi et al. 1970). The resistance reaction of *Ym* to BaYMV strains I, II and III is probably S (susceptible), R (resistant) and R, respectively(Makino, personal communication). *Ym5*(t) is also incompletely dominant gene and linked to the complex loci (*Est1-Est2-Est4*) for the esterase isozymes with the recombination values ranging from 1.26 to 5.01% on chromosome 3 (Konishi et al. 1989). The resistance reaction of *Ym5*(t) to BaYMV strains I, II and III is R, R and S, respectively (Makino, personal communication).

The variety Mihorihadaka has the resistant gene *Ym2* which is incompletely dominant and linked to the gene *n* conferring naked caryopsis with a recombination value of 31.4% on chromosome 1 (Takahashi et al. 1970). The resistance reaction of *Ym2* to BaYMV strains I, II and III is R, S and R, respectively (Iida et al. 1992).

The gene *ym3* which is found in both Ea52 and Haganemugi is recessive and shows resistance to all Japanese strains of BaYMV (Iida et al. 1992). It was first found in a mutant line Ea52 (Ukai and Yamashita 1980). The chromosomal location of *ym3* has not been identified yet.

The gene *ym4* found in Tokushimamochihadaka, which carries also *ym3*, is recessive and is linked to the gene *n* on chromosome 1 (Fukuoka et al. 1991). A breeding line "Shimakei 1" which carries only *ym4* has been developed from a cross involving Tokushimamochihadaka. This line has resistance to BaYMV strains I and II (Makino, personal communication). The resistance reaction of *ym4* to strain III has not been tested yet.

The first source of resistance Mokusekko 3 was crossed with lines having a high malting quality at the Tochigi Prefectural Agricultural Experiment Station. As a result, two resistant malting barley cultivars Misato Golden (Seko et al. 1986) and Mikamo Golden (Yoshida et al. 1988) were released in 1985 and 1987, respectively. Another resistant cultivar Nishino Gold developed from a cross involving Mokusekko 3 was released from the Fukuoka Prefectural Agricultural Experiment Station in 1986 (Itoh et al. 1987). The resistance reaction of Misato Golden and Nishino Gold to BaYMV strains I, II and III is R, R and S, respectively (Iida et al. 1992, 1993). They probably inherited only *Ym5*(t) from Mokusekko 3 (Table 3). As malting barley breeders made extensive use of the Mokusekko 3 gene(s), most of the current promising lines are resistant to BaYMV.

In the six-rowed barley breeding program, the mutant line Ea52 has been used and promising lines have been developed. Ea52 was induced from the variety Chikurin Ibaraki 1 by treatment with gamma rays (Ukai and Yamashita 1980). Chikurin Ibaraki 1 is a six-rowed hulled barley with a winter habit. The mutant, Ea52, was originally selected as an early heading mutant in the M_3 generation after irradiation. Irradiation involved application of 250 R of gamma rays to plants at the vegetative stage. In a field severely infected with BaYMV, all the early heading mutants except Ea52 showed varying degrees of leaf yellowing. Ea52 is a rare example of an artificially induced mutant resistant to a virus disease. A new six-rowed hulled barley cultivar Masakadomugi whose resistance gene to BaYMV was inherited from Ea52 was released from the National Agriculture Research Center in 1989 (Table 3) (Makino et al. 1994).

Haganemugi, described above as a gene source for straw stiffness, has been also used as a gene source for improving resistance to BaYMV. An allelism test proved that the resistance gene of Haganemugi was identical with the gene *ym3* of Ea52 (Makino, personal communication). Kyushu National Agricultural Experiment Station released the first BaYMV resistant two-rowed non-malting barley cultivar Ishukushirazu from a cross involving Haganemugi in 1981 (Tsuru et al. 1983). Ishukushirazu inherited the gene *ym3* from Haganemugi (Kawada 1988) and shows the resistance to all Japanese strains of BaYMV (Table 3).

No cultivar has been developed from a cross involving Mihorihadaka having *Ym2* or Tokushimamochihadaka having *ym3* and *ym4* (Table 3).

3) Breeding for resistance to barley yellow dwarf virus (BaYDV): Barley yellow dwarf was first reported in Japan in 1983 (Kojima et al. 1983). The virus which is carried by aphids also attacks rice (Kojima et al. 1983). Consequently where double cropping of barley and rice is adopted, the occurrence of this disease may increase. Breeding for resistance to BaYDV was just started using the barley cultivars Atlas 68 and CM 67 as gene sources at the Shikoku National Agricultural Experiment Station. These two cultivars carry a resistance gene *Yd2* which is probably linked on chromosome 3 with the *lnt* gene which confers a small number of tillers (Schaller et al. 1964; Sϕgaard and Wettstein-Knowles 1987). The gene *lnt* may be a useful marker for the selection of resistance to BaYDV.

4) Breeding for improved grain quality: The nutritional quality of naked barley has been improved using an Ethiopian local variety Hiproly with a gene *lys* conferring a high lysine content as a gene source. The gene *lys* is linked to the gene *s* conferring short rachilla hairs with a recombination value of 8.4% on chromosome 7 (Munck et al. 1970; Karlsson 1972). In grains with a high protein content, hardness generally increases. Nanpuhadaka was used as the recurrent parent to incorporate the high protein quality from Hiproly into Japanese cultivars. In the early hybrid generations, the *s* gene and grain hardness were used as markers for selection. Naked barley parental line no. 1 (former name: Yonkei 8422) was developed at the Shikoku National Agricultural Experiment Station in 1984 (Kato et al. 1987). This line is comparable to Nanpuhadaka in agronomic characters such as earliness, plant height and yielding performance, and contains 16 percent more crude protein and 27 percent more essential amino acids than Nanpuhadaka. A new naked barley cultivar Sansyuu into which the high protein quality of Hiproly has been incorporated was also released from the Shikoku National Agricultural Experiment Station in 1989 (Ito et al. 1992).

5) Breeding high-yielding barley varieties using F_1 hybrids: In order to breed F_1 hybrids, attempts to use the male sterile gene *msg6* are being made at the National Agriculture Research Center. The male sterile plants with a genotype *o-msg6-sex1a-Uc2/o-msg6-sex1a-Uc2* can be efficiently selected from the selfed progenies of a maintainer with a genotype *o-Msg6-Sex1a-uc2/o-msg6-sex1a-Uc2* because the *o*, *msg6*, *sex1a* and *uc2* loci are closely linked with each other on chromosome 6, and the genes *sex1a* conferring shrunken endosperm and *uc2* conferring uniculm are useful marker genes for the selection of male sterile plants (Falk et al. 1981). On the other hand, a character to induce chasmogamy is indispensable for the production of F_1 seeds. Almost all the Japanese barley cultivars except for Satsuki Nijo showed cleistogamy. The chasmogamy of Satsuki Nijo is controlled by a single recessive gene (Kurauchi et al. 1993). Incorporation of the recessive gene conferring chasmogamy into other Japanese barley genotypes is also being carried out at the National Agriculture Research Center.

4. Production of wheat and barley haploid plants through intergeneric and interspecific crossing

The "bulbosum method" of haploid breeding using *Hordeum bulbosum* L. has recently been used by breeders of both wheat and barley. Tetraploid and diploid clones of *H. bulbosum* are used as pollen parents for obtaining the haploid immature embryos of wheat and barley (Kasha and Kao 1970; Barclay 1975). The "maize method" using the pollen of maize (*Zea mays* L.) or teosinte (*Zea mays* ssp. *mexicana* L.) has also been used to obtain haploid immature embryos of wheat (Laurie and Bennett 1986, 1987, 1988; Ushiyama et al. 1991). The application of the bulbosum method for wheat haploid production is restricted due to the presence of the cross-incompatibility genes, *Kr1* and/or *Kr2*, located on chromosomes 5B and 5A, respectively (Snape et al. 1979; Falk and Kasha 1981, 1983; Sitch et al. 1985). These cross-incompatibility genes are frequently found in wheat genotypes other than Japanese and Chinese ones (Snape et al. 1979; Falk and Kasha 1981; Inagaki and Snape 1982; Li and Hu 1986). Alternatively, the production of wheat haploid plants using maize pollen is successful even for the wheat genotypes which are cross-incompatible with *H. bulbosum* (Laurie and Bennett 1986, 1987, 1988). Haploid production of wheat from crosses between wheat × sorghum (*Sorghum bicolor*) and barley haploid production from crosses between barley × maize and barley × Italian ryegrass (*Lolium multiflorum* Lam.) has been also reported (Furusho et al. 1991; Ohkawa et al. 1992). An average of 20~30% of wheat and barley florets formed immature embryos when pollinated with *H. bulbosum* or maize (Inagaki 1986b; Suenaga and Nakajima 1989; Furusho et al. 1990; Inagaki and Tahir 1990). The injection of 2,4-dichlorophenoxyacetic acid (2,4-D) after pollination is necessary for the formation of haploid immature embryos of wheat and barley in the maize method (Suenaga and Nakajima 1989; Inagaki and Tahir 1990; Furusho et al. 1991).

A successful culture technique for haploid immature embryos of wheat and barley is essential for the development of haploid plants. There are two strategies for the development of haploid plants (Fig. 4). In the first strategy, haploid plants can be grown directly from haploid immature embryos on an agar medium without 2,4-D (Inagaki 1985a). This method is advantageous because the breeding period can be shortened. The other strategy involves culturing haploid immature embryos on an agar medium supplemented with 2,4-D for the formation of calli. Thereafter, haploid plants can be regenerated from the calli on an agar medium without 2,4-D (Inagaki 1986a). In this system, natural and artificial mutations can be expected during callus formation (Fig. 4).

A successful chromosome doubling technique for haploid plants of wheat and barley is essential for producing the doubled haploid plants which are homozygous and set fertile seeds (Fig. 4). Factors influencing chromosome doubling of wheat and barley haploid plants have been investigated and some treatment methods using colchicine solution have proved highly successful for chromosome doubling (Jensen 1974, 1976; Thiebaut et al. 1979; Inagaki 1985b).

Table 4. Number of accessions of wheat, barley, oats, rye, triticale and their relatives preserved in the Center Bank of National Institute of Agrobiological Resources of Japan (March 31, 1993)

Species	No. of accessions	
	Base collection	Active collection
Triticum aestivum (L.) Thell.	18274	13433
Triticum compactum Host.	48	48
Triticum dicoccoides Koern.	1	1
Triticum dicoccum (Schrank.) Schubl.	6	6
Triticum durum Desf.	4781	272
Triticum monococcum L.	1	1
Triticum polonicum L.	1	1
Triticum spp.	998	0
Triticum spelta L.	13	13
Triticum turgidum L.	5	5
Hordeum agriocrithon E. Aberg	2	2
Hordeum leiorrhynchum Koern.	1	1
Hordeum spontaneum C. Koch	31	31
Hordeum vulgare L.	10364	6292
Hordeum vulgare L. var. *distichon*	1838	1831
Aegilops aucheri Boiss.	56	56
Avena abyssinica Hochst	1	1
Avena barbata Pott	2	2
Avena brevis Roth	1	1
Avena byzantina C. Koch	3	3
Avena fatua L.	9	9
Avena hirtula Lag.	1	1
Avena longiglumis Dur.	1	1
Avena magna Murphy et Terrell	2	2
Avena murphyi Ladizinsky	1	1
Avena nuda L.	1	1
Avena orientalis Schreb.	1	1
Avena sativa L.	1086	1086
Avena sp.	15	15
Avena sterilis L.	4	4
Avena wiestii Schreb.	2	2
Secale cereale L.	44	44
Triticum sp. × *Secale* sp.	52	52

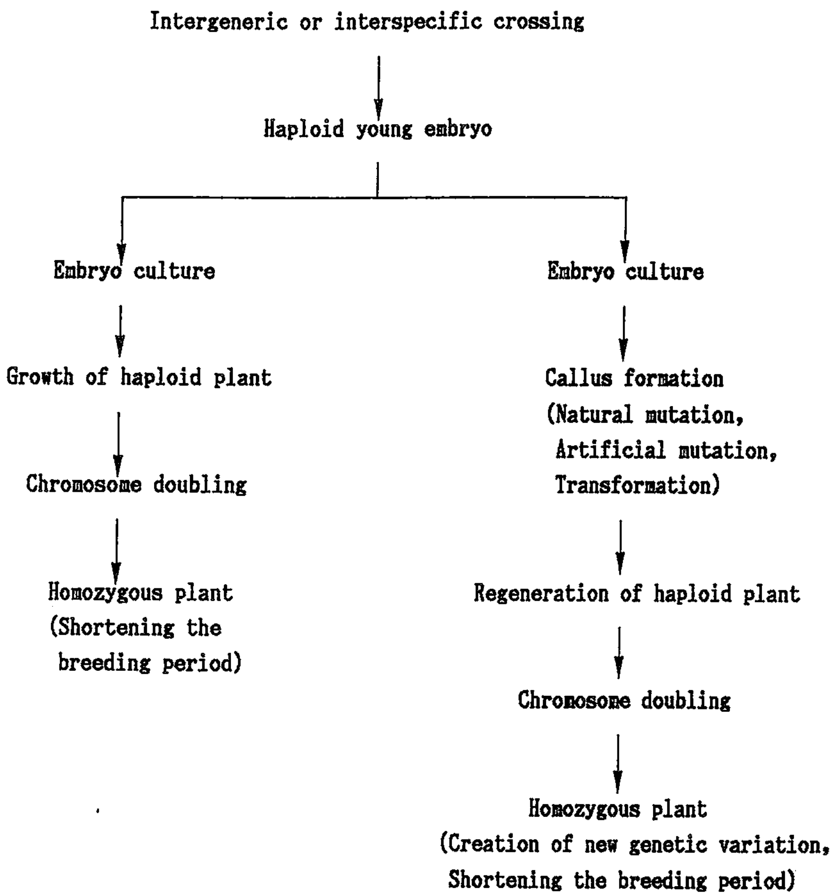

Fig. 4. Two strategies of doubled-haploid production in wheat and barley.

5. Conservation of wheat and barley genetic resources in MAFF

The current number of germplasm of wheat, barley, oats, rye, triticale and their relatives preserved in the Center Bank of the National Institute of Agrobiological Resources, Tsukuba, is shown in Table 4. A part of them is also preserved in the Sub-Banks of the National Agricultural Experiment Stations including the National Agriculture Research Center. Some dozens of *Elytrigia* and *Elymus* clones are preserved in the Sub-Bank of the Kyushu National Agricultural Experiment Station. Almost two hundred clones of *Hordeum bulbosum* L. are preserved in the Sub-Banks of National Agriculture Research Center, Shikoku National Agricultural Experiment Station, National Center for Seeds and Seedlings, etc. They have been collected mainly by collecting missions and international exchange.

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Wheat Information Service
December 79: 18 – 23 (1994)

II. Articles

Combining ability analysis for yield and its components in bread wheat over environments

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Summary

Combining ability analysis was undertaken in 10×10 half parental diallel progenies (F_1 & F_2) for grain yield and its component traits pooled over three environments. The gca and sca components of variance were significant for most of the yield components. However, gca component of variance was predominant. Both the gca and sca effects were highly influenced by the environments. The parents Raj 1432 and HD 2204 were the best general combiners for grain yield and also high to average combiners for most of the important traits. The best specific crosses for grain yeild were Kharchia 65 × Chiroca, WL 711 × Chiroca, Brochis × Kharchia 65, Brochis × Rai 821 and Brochis × D 65 which involved Indian × Mexican combinations. These crosses could be utilized extensively in future breeding programmes. To ensure further increase in the grain yield combination of desirable yield components is advocated. Further, biparental mating and/or diallel selective mating systems under favourable environments are suggested for a more tangible advance.

Introduction

Wheat today occupies a unique position among cereals in India. Recent breakthrough in wheat production is not sufficient to the rapidly growing population of the country which is estimated to cross one billion by the end of this century. This necessitates the acceleration of improvement in this crop. For this combining ability studies are frequently used by plant breeders to evaluate newly developed cultures for their parental usefulness and to assess the gene action involved in various characters, so as to design an efficient breeding plan for further genetic upgrading of the existing material. However, the combining ability studies in a single environment may not provide precise information as environmental effects play an important rôle and greatly influence the combining ability estimates. Such information on combining ability analysis of wheat over environments is scanty. It is, therefore, necessary to assess combining ability, components of variance and combining ability × environment interaction for yield and its components to ensure better prediction and gain under selection. Present study deals with such endeavours.

Materials and Methods

Ten varieties of bread wheat [*Triticum aestivum* (L.) Thell], namely, Moncho, Pavon, Brochis, Chiroca, HD 2204, Raj 1482, WL 711, Raj 821, D 65 and Kharchia 65, were corssed in all possible combinations excluding reciprocals. The resulting 45 F_1's were grown to get F_2's seeds. Parents along with their 45 F_1's and F_2's were grown in a randomised block design with three replications under early, normal and late sown conditions (environments). Each plot consisted of single 5m row length of parent and F_1 and 10 rows of F_2 with the spacing of 30 cm between rows and 15 cm between plants. Ten competitive plants in parents and F_1's and twenty plants in F_2 progenies were selected randomly for recording observations (Table 1) under each environment separately.

The mean of each plot was used for statistical analysis. The data were first subjected to the usual analysis followed for a randomised block design for pooled over environments. The combining ability analysis was done following Method 2, Model 1 of Griffing (1956).

Results and Discussion。

Pooled analysis of variance over the environments revealed highly significant differences amongst them. So was true for genotype × environment interactions.

Table 1. Analysis of variance for combining ability for grain yield and its component traits pooled over environments

Source of variation	Generation	d.f.	Days to heading	Days to maturity	Plant height (cm)	Tiller nmber	Spike length (cm)	Number of spikelets per spike	No. of grains per spike	Grain weight per spike (g)	1000 grain weight (g)	Grain yield (g)
Environment	F_1	2	306.84**	7998.20**	3808.36**	873.00**	3.93**	3.89**	86.69**	1.06**	183.58**	2971.46**
	F_2	2	115.47**	7964.15**	3364.15**	736.85**	6.33**	9.11**	13.65*	0.70**	110.64**	2108.22**
gca	F_1	9	442.37**	40.52**	2050.38**	26.09	14.33**	23.12**	405.69**	0.64*	240.67**	24.23
	F_2	9	305.99**	32.10**	1562.13**	28.58	13.03**	24.57**	494.84**	0.67**	107.27**	57.77*
sca	F_1	45	4.93	7.35*	42.66**	5.20	0.34*	0.63	47.59**	0.24**	31.86**	59.84**
	F_2	45	14.33**	11.02**	41.71**	4.41	0.78*	1.03**	25.21	0.16**	10.63**	36.10**
gca ×	F_1	18	55.59**	5.94**	105.15**	12.02**	0.78**	2.89**	68.69**	0.22**	19.34**	13.41**
Environment	F_2	18	42.04**	5.39**	97.65**	13.30**	1.01**	3.37**	49.65**	0.10**	16.04**	18.05*
sca ×	F_1	90	3.47**	4.29**	15.75**	4.90**	0.22**	0.51**	24.65**	0.10**	7.08**	15.50**
Environment	F_2	90	5.46**	4.60**	11.68**	3.40**	0.49**	0.47**	21.00**	0.08**	4.61**	18.61**
Error	F_1	324	0.40	0.62	3.89	0.90	0.05	0.17	3.72	0.02	1.77	1.46
	F_2	324	0.52	0.68	3.74	0.95	0.06	0.16	3.15	0.02	2.40	11.86

*P=0.05, **P=0.01

The analysis of variance for combining ability for the data pooled over three environments (Table 1) showed that mean squares due to general combining ability (gca) and specific combining ability (sca) were significant for all the traits studied in both F_1 and F_2 generations except tiller number and variance due to gca for grain yield, sca for days to heading, number of spikelets per spike in F_1 generation, sca for number of grains per spike in F_2 generation, signifying the importance of both additive and non-additive gene effects in controlling the inheritance of yield and its component traits.

However, the gca variance was found higher than sca variance in both the generations, indicating the preponderance of additive gene effects for yield components but for grain yield sca variance was predominant. The findings of Jaimini and Mathur (1980), Shrivastava et al. (1981), Sharma and Singh (1983), Sharma et al. (1986), Rajora (1992), Singh et al. (1993) and Solanki et al. (1993) are in agreement with the present results. Results further revealed that tiller number, days to heading, number of spikelets per spike and number of grains per spike were highly influenced by the genotype environmental interaction. This is corroborated by the estimates of heterosis as heterosis for these traits was non-significant.

Both the gca and sca exhibited highly significant interaction with the environments for yield and its components in both the generations, indicating the role of environment in influencing the gene effects. Other studies (Jatasara and Paroda 1981; Sharma and Singh 1982; Kumar et al. 1983; Singh et al. 1986; Dasgupta and Mondal 1988) substantiate this point. However, gca x environment interaction variances were higher than sca x environment variances for all the traits except grain yield in both the generations, further signifying the importance of additive genetic variance for yield components.

Thus, it may be concluded that the variance due to gca is by and large more important in a crop like wheat. However, both gca and sca variances were highly influenced by their interaction with environments. The sca variance was more pronounced for grain yield than the other yield components. Most of the sca was retained in the successive generations. This is encouraging because it indicates the fixable nature of non-additive gene effects. In a crop like wheat, this is important because commercial hybrid production is not the objective. But the genic interactions that would be fixable would lead to transgressive segregation wherein some segregants would exceed the limits of their parents.

A perusal of the general combining ability (gca) estimates (Table 2) showed the transcendency of the parents HD 2204 and Raj 1482 for grain yield as good general combiners (on the basis of F_2 analysis) while Brochis was a consistently low combiner for grain yield. The two high combiners for grain yield also showed superior high combining ability for some of the component traits. Parent HD 2204 was also a high combiner for earliness, dwarfness, number of grains per spike, grain weight per spike and 1000 grain weight. Similar results were shown by parent Raj 1482 but it was not a high combiner for 1000 grain weight. It was an average combiner for grain weight per spike and a low combiner for 1000 grain weight.

Apparently, therefore, there is still further scope for improving upon the combining ability for component traits as none of the high combiners for grain yield was a high combiner or at least an

Table 2. Estimates of general combining ability effects for yield and its component traits pooled over environments.

Estimates	Generation	Days to heading	Days to maturity	Plant height (cm)	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	Grain weight per spike (g)	1000 grain weight (g)	Grain yield (g)
Moncho	F_1	4.69L	0.21	-0.17	0.79H	0.71H	3.60H	0.05	-0.89	-
	F_2	3.75L	0.99	0.02	0.48H	0.68H	3.23H	0.10	-0.89	-1.15
Pavon	F_1	4.01L	0.52	-4.49D	0.73H	0.57H	2.23	0.08	-3.76L	-
	F_2	2.88L	-0.56	-2.45	0.74H	0.73H	2.33	-0.01	-2.35L	-1.54L
Brochis	F_1	3.53L	1.36L	-4.18D	-0.15	0.20	0.75	0.15	-2.25L	-
	F_2	3.77L	1.23L	-3.35D	0.04	0.32	1.32	-0.10	-1.97	-1.85L
WL711	F_1	0.42	0.45	-2.40	0.67H	0.41	1.94	0.16	0.88	-
	F_2	0.22	0.77	-2.19	0.80H	0.43	1.57	0.11	0.63	1.29
D 65	F_1	-1.47	-0.83	11.67T	-0.99L	-0.56L	-4.84L	-0.04	3.16H	-
	F_2	-1.02	-0.77	9.12T	-1.093L	-0.29	-3.40L	-0.13	1.72H	1.08
Kharchia 65	F_1	0.44	0.07	15.78T	-0.77L	-0.98L	-4.73L	-0.19L	2.70H	-
	F_2	0.41	0.57	14.15T	-0.77L	-1.03L	-5.94L	-0.23L	1.49	0.11
Chiroca	F_1	-0.17	1.19L	-2.23	-0.14	0.79H	3.80H	0.15	-1.47	-
	F_2	-0.20	0.57	-1.30	0.08	0.78H	4.45H	0.17H	-1.26	-0.92
HD2204	F_1	-4.97E	-0.16	-7.56D	0.24	0.68H	1.74	0.14	0.88	-
	F_2	-4.29E	-0.39	-7.55D	0.16	0.56	2.93	0.17H	0.70	1.23
RaJ 1482	F_1	-0.81	-0.57	-4.39D	-0.52L	-0.42	-0.72	0.15	-2.71L	-
	F_2	-1.20	-1.10E	-4.86D	0.35L	-0.63L	-1.38	-1.08	-0.09	1.38H
RaJ 821	F_1	-5.67E	-2.23E	-2.08	0.15	-1.46L	-3.85L	-0.05	3.45H	-
	F_2	-4.33E	-1.31E	-1.60	-0.16	-1.55L	-5.13L	0.01	2.76H	-
S.Em.(+)	F_1	1.18	0.39	1.62	0.14	0.27	1.31	0.09	0.70	-
	F_2	1.05	0.37	1.56	0.16	0.29	1.11	0.05	0.63	0.38
C.D	F_1	3.44	1.13	4.73	0.41	0.79	3.83	0.22	2.03	-
	F_2	3.00	1.07	4.57	0.46	0.85	3.26	0.15	1.85	1.96

*P=0.05, **P=0.01

average combiner for all the desirable traits. As compared to this, the lowest combiner Brochis was average to low combiner for all the component traits. Almost similar situation was shown by other low combiners, namely, Pavon and Kharchia 65. Other parent Moncho was high combiner only for spike length, number of spikelets per spike, number of grains per spike; WL 711 for spike length; D65 for 1000 grain weight; Raj 821 for earliness, 1000 grain weight and parent Chiroca for number of spikelets per spike, number of grains per spike and grain weight per spike.

It seems feasible, therefore, that the gca rank for grain yield is related to the gca for the useful yield components. It is, therefore, recommended that breeders should breed for superior combining ability for the component traits with an ultimate objective to improve the overall gca for grain yield in wheat. The parents HD 2204 and Raj 1482 could be utilized extensively in hybridization programme to accelerate the pace of genetic improvement of grain yield in bread wheat.

The analysis of specific combining ability (sca) effects revealed that nine crosses showed high sca on the basis of F_1 analysis but in the F_2 only three crosses seemed to show high sca for grain yield. However, cross WL 711 × Chiroca showed the highest sca effects for grain yield in both F_1 and F_2 generations. This cross also exhibited maximum heterosis of 89 per cent for grain yield. Apart from this cross, however, there seems to be no correlation between the rank for sca and the rank for heterosis. This could be expected, because heterosis estimates are worked out from the mean values whereas the sca estimates are related to the gca of parents. The most consistent cross for high sca effects was Kharchia 65 × Chiroca which showed high sca under all situations. Other best crosses for grain yield was Brochis × Kharchia 65, Brochis × Raj 821 and Brochia × D 65. All the best crosses for grain yield also showed average to high sca for most of the yield components. It is, therefore, recommended that new materials are used in future breeding programmes for recombining the desirable traits in the envisaged elite genotypes.

It is noteworthy that all the crosses showing high sca effect for grain yield in F_1 and F_2 generations were combinations of Indian × exotic types (Indigenous × extraneous germplasm). This emphasises the need for combining two diverse germplasma to create maximum genetic variability which is the prime requirement and this would alone help in raising the limits of envisaged progress through selection in any successful breeding programme. The best cross combinations for grain yield further showed very interesting results of depicting the genetic diversity of parents and there were clear cut divergences between these crosses with regards to sca for component traits.

The present study revealed the existence of both additive and non-additive type of gene effects for yield component traits. Therefore, biparental mating and/or diallel selective mating which may allow intermating of the selects in the different cycles could hold promise for genetic improvement of the traits of bread wheat.

Acknowledgement

The authors are thankful to the Director of Research, Rajasthan Agricultural University, for providing necessary facilities during the course of investigation.

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Wheat Information Service
December 79: 24–27 (1994)

Intermeiocyte connections and cytomixis in intergeneric hybrids III: *Roegneria tsukushiensis* × *Psathyrostachys huashanica*

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Summary

The F_1 intergeneric hybrid of *Roegneria tsukushiensi* (Honda) B.R.Lu et J.L. Yang with *Psathyrostachys huashanica* Keng was made and studied cytologically. Conjugation openings were observed. Intercellular migration of chromatin material led to the formation of coenocytism and variation in cell size. These events could lead to spontaneous variation in chromosome numbers. As a possible consequence of migration of chromatin materials, polyploid and aneuploid PMCs appeared. It may combine two different gene pools. There is possibility for transferring drought resistance character from *P. huashanica* into *R. tsukushiensis* by chromatin migration among cells. The observed result in this hybrid supports further that N^h genome of *P. huashanica* has a genetic system for controlling this process.

Key words: Cytomixis; Conjugation opening; Aneuploid; Polyploid; Variation in chromosome number, *Roegneria tsukushiensis*, *Psathyrostachys huashanica*

Introduction

Roegneria tsukushiensis is one of a few good forage grass in Triticeae in South Subtropic region of Far East, but it lacks resistance to drought. *Psathyrostachys huashanica* Keng is a diploid perennial species. It is restricted to a narrow region in the Huashan Mountain of central China where it occurs on mountain slopes, but is a hardened and drought resistant plant. The intergeneric cross of the *R. tsukushiensis* with *P. huashanica*, was made. The intergeneric F_1 hybrid was studied cytologically.

We had previously studied the intermeiocyte connections and cytomixis in intergeneric hybrids of *Roegneria ciliaris* (Trin.) Nevski, *Aegilops tauschii* Cosson and *Triticum aestivum* L. with *P. huashanica* (Sun et al. 1992, 1993b; Yen et al. 1993). It was found that chromatin was transferred through conjugation opening or tube before, during and after meiosis in these hybrids. Consequently, unusual nuclear behavior frequently occurred, such as coenocytism, high level chromosome multiplication, multipolar division, variation in size of pollen grain, aneuploid formation, non-synchronous, and delayed chromatin condensation

According to our observation, chromatin material migration among cells had been found in all the intergeneric hybrids derived from *P. huashanica*. We suggested that the N^h genome has a gene system for controlling this process. In order to prove this suggestion, we studied the microsporogensis of *R. tsukushiensis* × *P. huashanica* F_1 hybrid. The transfer of nucleate materials through conjugation opening was also found. The results of observation are described and discussed in the present paper.

Materials and Methods

Three accessions of *Roegneria tsukushiensis* (Honda) B.R. Lu et J.L. Yang (2n=42, SSHHYY) used in this study were collected from Yaan and Yibin, Sichuan Province respectively. Two accessions of *Psathyrostachys huashanica* Keng (2n=14, N^hN^h) were collected from Mt. Huashan, Shaanxi Province, China. All these accessions were cultivated at Triticeae Research Institute, Sichuan Agricultural University in 1990.

Hybridization was made by pollinating hand-emasculated spikes of *R. tsukushiensis* with pollen of *P. huashanica*. Three F_1 seeds were germinated in petri-dish, then transplanted into pots.

For cytological study, young spikes of the three F_1 hybrids derived from three different accessions of *R. tsukushiensis* crossed with one accession of *P. huashanica* and their parents were fixed in Carnoy's fluid for 24 hours. They were transferred to 70% ethanol and stored at 4°C. Microsporogensis was studied on slides prepared by standard acetocarmine squashing.

Results and Dicussion

The intergeneric F_1 hybrid of *R. tsukushiensis* with *P. huashanica* is theoretically expected to have 28 chromosomes. Chromosome numbers counted at metaphase I of the pollen mother cells (PMCs) met the expectation (Fig. 1-1). The meiotic data indicated that *R. tsukushiensis* shared no common genome with *P. huashanica* (Sun et al. 1993a).

Abnormal microspore formation was observed in microsporogenesis of this intergeneric hybrid. Chromatin materials were transferred through conjugation opening among neighbouring cells from the time before meiosis until the young pollen grains stage (Fig. 1-2~7). The amount of chromatin materials transferred varied among cells. The process of chromatin migration among cells causes coenocytes, multiplication and diminution of chromosomes greatly, and variation in cell size. Fig. 1-2 shows PMC a and PMC b in contact with each other and forming a fused big opening. The numbers of anaphase chromosomes in these two cells are unequal. Anaphase chromosomes also show non-synchronous separation. In cell a, there are 9 anaphase chromosomes and 7 chromatids; in cell b there are 2 anaphase chromosomes and 3 chromatids. In Fig. 1-3, two PMCs at chromonema stage contacted each other, chromonemata migration takes place through the conjugation opening. In Fig. 1-4, cell a has two separate synchronous nuclei at chromonema stage; cell b with small cell size has only one chromosome and two chromatids. The chromosome diminution might be caused by uneven distribution of chromosomes before cytokinesis of two conjugated PMCs as shown in Fig. 1-2. After cytokinesis, this kind of small size PMC has occurred as a result a diminished number of chromosomes. In cell c, two chromonema stage nuclei are mixed together. A nucleus has twice as many chromosomes as the usual one. Polyploidy or aneuploidy will occur. A bud-like structure has a micronucleus (Fig. 1-4). The young pollen grains are shown

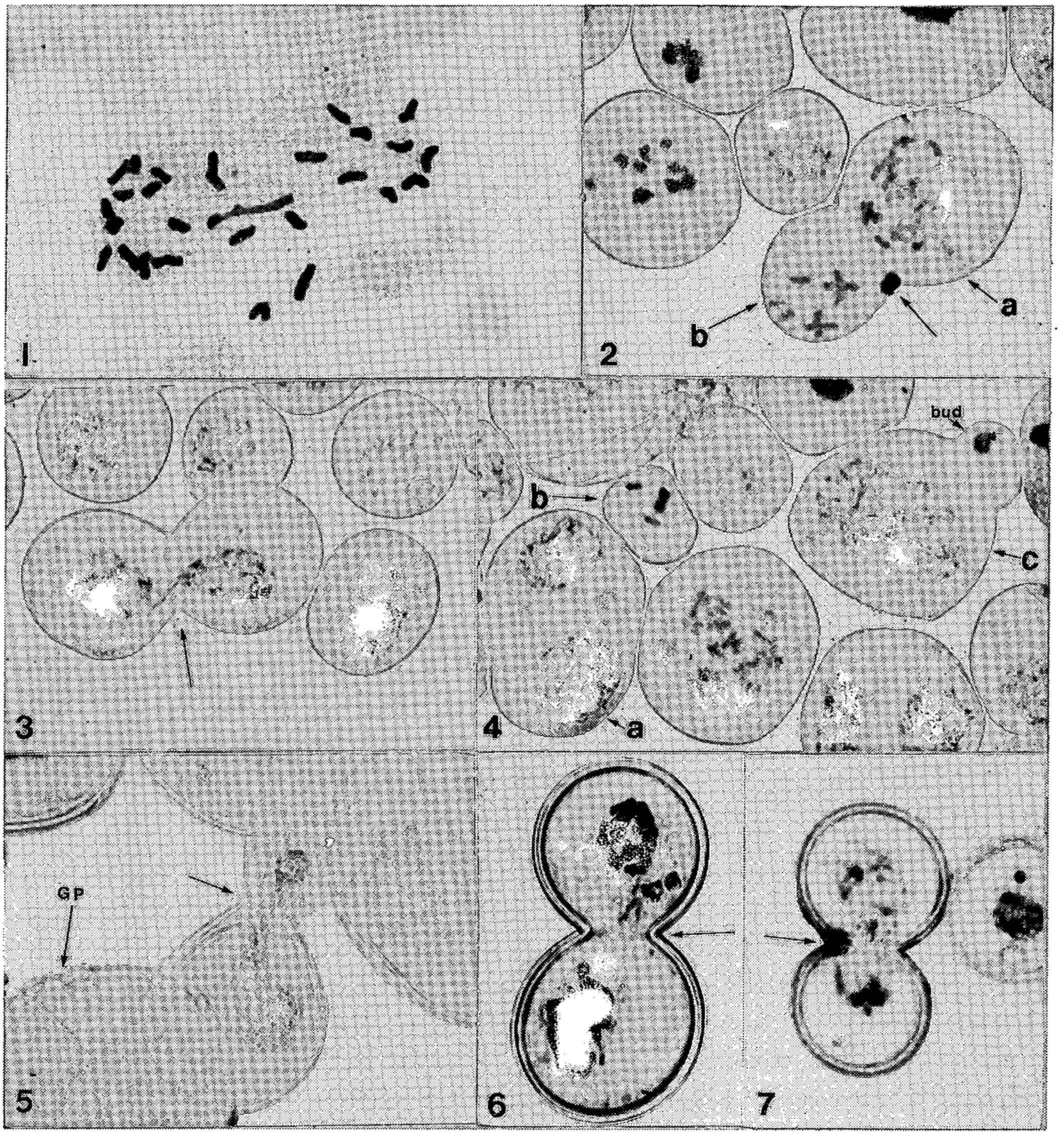

Fig. 1. PMC's and young pollen grains showing intermeiocyte connections and cytomixis

1. A normal PMC of *R. tsukushiensis* × *P. huashanica* hybrird has 28 chromosomes.
2. PMC a and PMC b contacting each other and forming a big opening or being somewhat fused. The number of anaphase chromosomes distributed in these two cells is unequal. Anaphase chromosomes also show non-synchronous separation. In cell a, there are 9 anaphase chromosomes with 7 chromatids; in cell b, there are 2 anaphase chromosomes with 3 chromatids.
3. Two chromonema stage PMCs contacting each other, and chromonemata migration just taking place through conjugation opening.

in Figures 1-5~7. We can see that the resting stage nuclei are just migrating through the conjugation opening between two young pollen grains. They have germ pore on their thick walls. In Figure 1-6, the focus section of the conjugated pollen grains shows the structure of opening very clearly. Figure 1-7 shows the same conjugation opening as in Figure 1-6, but the chromonema is just migrating through the conjugation opening. It is suggested that a gene system of *P. huashanica* also controls conjugation opening formation in this hybrid as well as in those previously reported hybrids of *R. ciliaris* × *P. huashanica* (Yen et al. 1993), *T. aestivum* × *P. huashanica* (Sun et al. 1993b) and *Ae. tauschii* × *P. huashanica* (Sun et al. 1992). The result indicates that the N^h genome of *P. huashanica* has a gene system for controlling this process, because this kind of behavior appears in all the hybrids which are derived from *P. huashanica*.

The chromatin mirgation may cause coenocytes. If a coenocyte has synchronized nuclei, the chromosome number could be doubled or redoubled by nuclei fusion and a unified high level polyploid nucleus could be formed, although in some cases nuclei may not remain fused in coenocytes. This might be a way in which spontaneous chromosome doubling occurs. It is one way of natural polyploid formation, especially high level alloautopolyploid. If the transfer of a nucleus into a neighboring cell is not complete, aneuploid PMCs will appear. A loss or gain of one or more chromosomes has two obvious possibilities: firstly extremely deficient gametes will not survive and they will be eliminated; and secondly, those gametes which contain chromosome numbers different from the normal and are able to survive. In hybrid descendants of *R. tsukushiensis* with *P. huashanica*, polyploids and aneuploids which contain two different gene pools of *R. tsukushiensis* and *P. huashanica* may be obtained. Thus, it is possible to transfer drought resistance from *P. huashanica* into *R. tsukushiensis* by backcrossing F_1 hybrid with *R. tsukushiensis*.

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4. Cell a has two separate synchronous nuclei at chromonema stage; cell b with small cell size has only one chromosome and two chromatids; cell c, two chromosonema stage nuclei mixed together. A nucleus has twice as many chromosomes as the usual one; a bud-like structure has a micronucleus.

5. The resting stage nuclei are just migrating through conjugation opening (arrow) between two young pollen grains, and they have germ pore on their thick walls.

6. The focus section of the conjugated pollen grains shows the structure of opening (arrow) very clearly.

7. Chromonemata is just migrating through conjugation opening(arrow) at young pollen grain stage.

Wheat Information Service
December 79: 28 – 32 (1994)

The ineffectiveness of the *ph1b* gene on chromosome association in the F1 hybrid, *Triticum aestivum* × *Psathyrostachys huashanica*

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Summary

An intergeneric cross was made between Chinese Spring *ph1b* mutant and perennial *Psathyrostachys huashanica* Keng. The meiotic chromosome pairing in the hybrid was 27.14 univalents and 0.43 bivalents. The result indicated that the *ph1b* gene did not induce homoeologous chromosome pairing between common wheat and *P. huashanica*, as well as among the common wheat chromosomes. Therefore, the presence of a *Ph1* or *Ph1*-like gene in *P. huashanica* was suggested.

Introduction

The evolutionary success of many polyploid species is largely due to their diploid-like cytological behavior, which is expressed by the virtually exclusive formation of bivalents, rather than multivalents, at the first metaphase of meiosis. Common wheat, *Triticum aestivum* L., contains several unlinked diploidizing gene systems (Sears 1976). The *ph1b* gene mutant was obtained by Sears (1977). This mutant allows homoeologous pairing in common wheat and in its hybrids.

The transfer of alien genetic material to common wheat through homoeologous recombination is an importment step in the efforts to increase the genetic variation. The previous studies indicated that the *ph1b* gene has strong effect on inducing homoeologous pairing in the hybrids between bread wheat and *Aegilops variabilis*, *Ae. triuncialis*, *Ae. turcomenica*, *Ae. triaristata*, *Ae. cylindrica*, *Ae. colmnaris*, and *Ae. ovata* (Kushnir et al. 1982; Sharma et al. 1986; Fan et al. 1992, 1993). However, the effectiveness of the *ph1b* gene inducing chromosome pairing in the hybrid between common wheat and *Psathyrostachys huashanica* has not been demonstrated yet.

This paper reports the first production of an intergeneric hybrid between Chinese Spring *ph1b* mutant and *P. huashanica*, and the meiotic analysis of the hybrid. The possible presence of a *Ph1*-like gene in *P. huashanica* is discussed in connection with the result of the meiotic analysis.

Materials and methods

The *ph1b* mutants of a common wheat cultivar Chinese Spring (abbreviated to CS *ph1b*) was kindly provided by the Cytogenetic Laboratory of Sichuan Agricultural University. Professor Z.L. Ren proved the authenticity of the mutant *ph* by cytogenetic method (personal communciation). The euploid Chinese Spring (CS) was kept at the Triticeae Research Institute, Sichuan Agricultural

University, *Psathyrostachys huashanica* Keng (2n=14, genomes NN) is an endemic species of Huashan mountain, Shaanxi Province, China. All materials were grown in the field at the Triticeae Research Institute.

The euploid Chinese Spring and *ph1b* mutant were used as female parents. Their spikes were emasculated, covered with cellulose bags, and few days later, artificially pollinated with *P. huashanica*. Well-developed 14 to 16 day-old embryos were excised, and cultured on N_6 basic medium. When the hybrid seedings had three leaves, they were transplanted into sand-pot and kept in an airconditioned room to survive the hot summer.

Young spikes of the hybrid were fixed in Carnoy's solution (95% ethanol:glacial acetic acid=3:1) for 24hr, transferred to 70% ethanol, and stored at 4°C in a refrigerator. The 1% aceto-orcein smear method was used for the cytological study.

The F_1 hybrid was backcrossed with the *Ph1b* mutant.

Results

1. Production of intergeneric hybrid: The result of the crosses is shown in Table 1. The cross CS *ph1b* × *P. huashanica* produced 5 embryos out of 286 pollinated florets. One well-developed seedling was obtained by means of embryo culture. No hybrid embryo was obtained from the cross between CS and *P. huashanica*. The previous studies (Chen et al. 1991; Sun et al. 1992) and the present result showed that the crossibility of *P. huashanica* with different common wheat cultivars varies 0 to 2.81% (Table 1).

Table 1. Results of crosses between common wheat and *P. huashanica*

Combination	Florets pollinated	Seed set		Reference
		No.	%	
CS × *P. huashanica*	560	0	0	Present study
Cs *ph1b* × *P. huashanica*	286	5	1.75	Present study
J-11 × *P. huashanica*	450	9	2.81	Sun et al. (1992)
CS × *P. huashanica*	320	0	0	Sun et al. (1992)
7182-0-11-1 × *P. huashanica*	166	2	1.20	Chen et al. (1991)
Common wheat × *P. huashanica*	1576	3	0.19	Chen et al. (1991)

2. Cytology: The chromosome pairing at metaphase I of the pollen mother cells (PMCs) of the hybrid CS *ph1b* × *P. huashanica* is shown in Table 2. The hybrid (2n=28) had 22 to 28 univalents, 27.14 on an average. Of 58 PMCs examined, 38 PMCs had 28 univalents (Fig. 1-1). Twenty PMCs contained 1 to 3 rod bivalents (Fig. 1-2). No ring bivalents and multivalents were observed. The average number of bivalents was 0.43 per cell. The chiasma frequency was 0.43 per cell. There were lagging chromosomes at anaphase I and II and micronuclei were found at the tetrad stage.

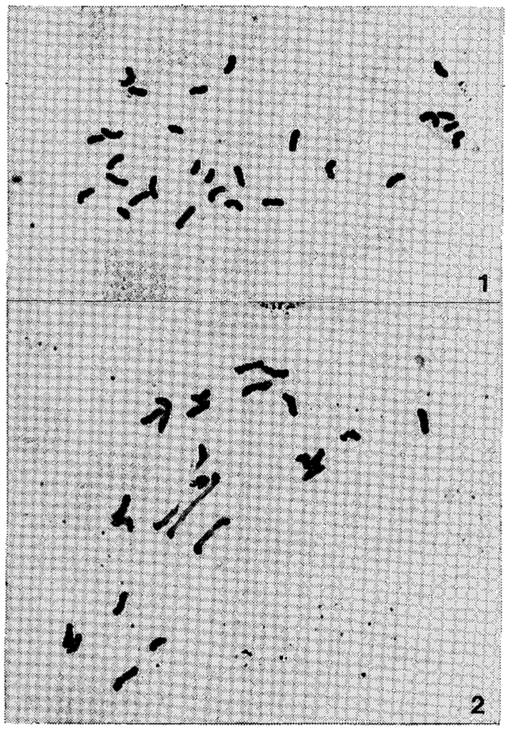

Fig. 1. Chromosome pairing of the CS *ph1b* × *P. huashanica* at meiotic metaphase-I
1. 28 univalents; 2. 22 univalents and 3 rod bivalents.

Table 2. Chromosome configurations of F_1 hybrids wheat × *P. huashanica*

Combinations	No. of cells examined	I	II			III	Chiasma frequency	Reference
			Total	rod	ring			
CS *ph1b* × *P. huashanica*	58	27.14 (22-28)	0.43 (0-3)	0.43 (0-3)	0	0	0.43	Present study
J-11 × *P. huashanica*	173	26.72 (17-28)	0.62 (0-4)	0.62 (0-4)	0	0.01 (0-1)	0.64	Sun et al. (1992)
H881	495	26.01 (22-28)	0.99 (0-3)	0.99	0	0	0.99	Chen et al. (1991)

3. Fertility of F_1 hybrid: The hybrid had yellowish white anthers, which did not dehisce. Staining of the pollen grains with Iodine-KI solution showed that the hybrid plant was completely male sterile. The F_1 hybrid plant was back crossed with CS *ph1b*, and three well-developed embryos were obtained from 210 pollinated florets.

Discussion

Fan et al. (1992) reported that PMCs of the hybrids between *ph1b* and *Aegilops ovata*, and between CS and *Ae. ovata* had 12.88 and 0.94 chiasmata at metaphase I, respectively. A similar result was reported with the hybrids of *Ae. umbellulata* with CS and *ph1b* (Fan et al. 1993). These show that the *ph1b* gene has a strong effect on inducing homoeologous pairing in the hybrids of *Ae. ovata*, *Ae. umbellulata* with common wheat (Fan et al. 1992, 1993). In the present study, only the F_1 hybrid between *ph1b* and *P. huashanica* was obtained. However, Chen et al. (1991) and Sun et al. (1992) reported successful hybridizations of common wheat cultivars 7182-09-11-1 and J-11 with *P. huashanica*, respectively (Table 2). The scarce chromosome pairings in the hybrids confirmed the non-homology between the genomes of *T. aestivun* (ABD) and *P. huashanica* (N). Miller and Chapman (1976), and McGuire and Dvorak (1982) reported 0.24 and 0.27 chiasmata per cell in CS haploid plants, respectively. The low chiasma frequency of the hybrid between *ph1b* and *P. huashanica* (0.43), which was lower than those of the hybrids of common wheat cultivars with *P. huashanica* (Table 2), indicated that *ph1b* gene did not induce homoeologous chromosome pairing in the hybrid.

Wang and Hsiao (1984) suggested that the existence of a diploidizing genetic system in *Leymus* (JN genomes), which is similar to the *Ph* gene system found in *T. aestivum*. Dovrak (1981) demonstrated that some species of *Thinopyron* (J genome) promoted heterogenetic pairing in hybrids involving *T. aestivum*. Our data implied that the N genome of *P. huashanica* had a *Ph*-like gene. If so, the high level of auto-alloploidy of *Leymus angustus* (2n=84, containing several N and J genomes), which forms bivalents, would be explained.

Acknowledgements

The authors thank Mrs. B.H. Wu for her technical assistance. This work was supported by the Sciences and Technology Council of Sichuan Province.

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Wheat Information Service
December 79: 33 – 36 (1994)

Telosomic mapping of wheat genes for resistance to inappropriate formae speciales of *Erysiphe graminis*

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Summary

Pm11 and *Pm15* are wheat genes for resistance to *Erysiphe graminis* f.sp. *agropyri*. Telosomic analyses suggested that genetically *Pm11* on chromosome 6B short was closely linked to the centromere but that *Pm15* on chromosome 7D short was very distant from the centromere.

Introduction

Erysiphe graminis is the causal agent of powdery mildews of gramineous plants, and widely distributed in the world. It comprises several formae speciales, e.g., f.sp. *tritici* parasitic on *Triticum*, f.sp. *secalis* parasitic on *Secale*, and f.sp. *agropyri* parasitic on *Agropyron*. In other words, *Triticum* spp., for example, are susceptible to only f.sp. *tritici* and resistant to f.sp. *agropyri*, f.sp. *secalis*, and so on. This type of host-parasite specificity has been called forma specialis - genus specificity (Tosa et al. 1987).

Tosa (1989) crossed f.sp. *agropyri*, Ak-1 with f.sp. *tritici*, Tk-1, and obtained 240 F_1 cultures between them. Using these hybrids, Tosa and his coworkers (Tosa et al. 1987, 1988; Tosa and Sakai 1990) identified several genes that controlled the resistance of wheat to f.sp. *agropyri*. The wheatgrass mildew fungus, Ak-1, was avirulent on both of common wheat cultivars, Norin 4 (N4) and Chinese Spring (CS), and the wheat mildew fungus, Tk-1, was highly virulent on both. However, Gw-180, an F_1 culture between Ak-1 and Tk-1, was avirulent on CS but highly virulent on N4. This culture revealed a phenotypic difference between the two cultivars, and made genetic analyses possible. When F_2 seedlings derived from the cross, CS × N4, were inoculated with Gw-180, resistant and susceptible seedlings segregated in a 3:1 ratio, indicating that the resistance of CS to Gw-180 was controlled by one major gene. This gene was designated as *Pm11* (Tosa et al. 1988). Subsequently, we found an F_1 culture, Gw-121, that was avirulent on both CS and N4, but highly virulent on another cultivar Red Egyptian (RE). When F_2 seedlings from CS × RE and N4 × RE were inoculated with Gw-121, resistant and susceptible seedlings segregated in a 3:1 ratio. A cross between CS and N4 yielded no susceptible F_2 seedlings. These results indicated that the resistance of CS and N4 to Gw-121 was controlled by the same major gene. This gene was designated as *Pm15* (Tosa and Sakai 1990). *Pm11* and *Pm15* were considered to be involved in the resistance of wheat to f.sp. *agropyri*.

Pm11 and *Pm15* are located on the short arms of chromosomes 6B and 7D, respectively (Tosa et al. 1988; Tosa and Sakai 1990). In this study we tried telosomic mapping of these genes.

Materials and methods

1. Fungal cultures: Fungal cultures used were Gw-180 and Gw-121, F_1 hybrids derived from the cross between *Erysiphe graminis* DC. f.sp. *agropyri* Em. Marchal, Ak-1, and f.sp. *tritici* Em. Marchal, Tk-1. They were maintained at 3 ±1°C on susceptible seedlings growing in 2 × 35cm glass test tubes with paper plugs.

2. Plant materials: Plant materials used were *Triticum aestivum* (L.) Thell. cv. Norin 4 (N4), cv. Red Egyptian (RE), and ditelocentrics of cv. Chinese Spring (CS). Infection types of N4, RE, and CS with Tk-1, Ak-1, Gw-180, and Gw-121 are shown in Table 1. *Pm10* is a gene for resistance to f.sp. *agropyri* identified with another F_1 culture, Gw-34 (Tosa et al. 1987), but does not operate against Gw-180 nor Gw-121.

Table 1. Wheat cultivars used, and their infection types with *Erysiphe graminis* f.sp. *tritici*, Tk-1, *E. graminis* f.sp. *agropyri*, Ak-1, and their F_1 hybrids, Gw-180 and Gw-121

Cultivar		Resistance genes	Infection type with:			
			Tk-1	Gw-180	Gw-121	Ak-1
Chinese Spring	(CS)	*Pm11*, *Pm15*	4	0(*Pm11*)	0(*Pm15*)	0(*Pm11*, *Pm15*)
Norin 4	(N4)	*Pm10*, *Pm15*	4	4	0(*Pm15*)	0(*Pm10*, *Pm15*)
Red Egyptian	(RE)	-	4	3	4	0

Infection types are as follows: 0, no mycelial growth or sporulation; 3, slightly reduced sporulation; 4, heavy sporulation. Genes controlling the resistance are given in parentheses.

3. Determination of infection types: Seeds of test plants were germinated on a wet filter paper in a petri dish for a few days. After root tips were removed for cytological examination, seeds with roots were sown in soil in 2 × 35 cm test tubes. Five to six days after sowing, primary leaves of the test plants were inoculated with conidia from 8-day-old colonies of Gw-180 or Gw-121 using writing brushes. The seedlings were grown in a controlled-environment room under fluorescent lighting (2000-4000 lux) before and after inoculation. The temperature in the room was 23 ±1°C during the light cycle (13 hr) and 20 ±1°C during the dark cycle (11 hr). Eight days after inoculation, infection was rated using 13 progressive grades from 0 to 4: 0, no mycelial growth or sporulation; 0+, mycelial growth without sporulation; 1-, conidiophore formation without visible powder-like conidia; 1,1+, scant sporulation; 2-,2,2+, reduced sporulation; 3-,3,3+, slightly reduced sporulation; 4-,4, heavy sporulation.

Results and Discussion

For mapping of *Pm11* (controlling the resistance to Gw-180) ditelo 6BS of CS (resistant to Gw-180) was pollinated with N4 (susceptible to Gw-180), and the resulting F_1 plants were backcrossed with N4. The B_1F_1 plants were examined cytologically and then inoculated with Gw-180 (Table 2).

Table 2. Frequencies of parental and recombinant chromosomes in telosomic mapping

Cross	Gene involved	Test culture	No. of B_1F_1 plants: without a telosome		with a telosome			Recombination value (%)
			Susceptible[a]	Resistant[b]	Susceptible[b]	Resistant[a]	Total	
(CSdt6BS × N4) × N4	*Pm11*	Gw-180	46	0	1	55	102	0.98
(CSdt7DS × RE) × RE	*Pm15*	Gw-121	14	10	14	10	48	50.0

[a] Parental [b] Recombinant

All of the seedlings that did not carry the telosome were susceptible (infection types 2+ to 4), and most of the seedlings carrying it were resistant (infection type 0). These results suggested that genetically *Pm11* on chromosome 6B short (Tosa et al. 1988) was closely linked to the centromere. The distance between the centromere and *Pm11* was calculated to be 0.98cM or 0.98 map unit. However, the gene may not be located in the chromosomal region near the centromere because crossing over is highly suppressed in the sat-chromosomes.

For mapping of *Pm15* (controlling the resistance to Gw-121) ditelo 7DS of CS (resistant to Gw-121) was pollinated with RE (susceptible to Gw-121), and the resulting F_1 plants were backcrossed with RE. The B_1F_1 plants were examined cytologically and then inoculated with Gw-121. Although the number of B_1F_1 seedlings tested were small, it was apparent that the telosome and the resistance to Gw-121 were segregated independently (Table 2). The recombination value was 50%. These results suggested that *Pm15* on chromosome 7D short (Tosa and Sakai 1990) was very distant from the centromere.

Acknowledgments

The authors thank Dr. U. Hiura, emeritus professor of Okayama University, Okayama, and Dr. K. Tsunewaki, emeritus professor of Kyoto University, Kyoto, for providing the common wheat cultivars.

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Wheat Information Service
December 79: 37 – 41 (1994)

Identification of translocated chromosomes in a Japanese common wheat variety Saitama 27

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Summary

The Japanese common wheat variety Saitama 27 contributes significantly to the wheat breeding in Europe through its distinctive semi-dwarfing gene. Two independent reciprocal translocations were identified in Saitama 27 by means of the pairing configurations in its monotelodisomic hybrids with Chinese Spring ditelosomics. One was centromeric translocation between 3A and 7A which was possibily originated by centric breakage-fusion of univalents at meiosis, giving rise to T3AS•7AS and T3AL•7AL. The other translocation was of small segments between 1A and one of the B genome chromosomes other than 1B, 2B and 5B. Thus, these translocations are not expected to be transmitted with the semi-dwarfing gene of Saitama 27 to the European wheat, unless they contain other breeding potentials.

Introduction

Saitama 27 carries a single gibberellic acid insensitive semi-dwarfing gene (Worland and Petrovic 1988, Yamada 1990). This gene is allelic to the *Rht1* and *Rht3* on chromosome 4B, and was named as *Rht1S* (Worland and Petrovic 1988). The *Rht1S* gene of Saitama 27 was introduced into the Italian variety Orlandi, and has spread into many Southern European varieties. This gene has a selective advantages in these regions due to its less sensitivity to heat stress (Worland 1986, Worland and Petrovic 1988).

We reported that Saitama 27 contains two independent reciprocal translocations (Ali et al. 1992). However, the co-transmission of these translocations with the semi-dwarfing gene into the European wheat is not determined. This paper describes the identification of the translocated chromosomes by using Chinese Spring ditelosomics.

Materials and Methods

The variety Saitama 27 was crossed with 22 ditelosomic (DT) lines of the variety Chinese Spring (CS). F_1 monotelodisomic plants were grown in the field. Spikes at appropriate growth stage were collected and fixed in Carnoy's solution. Pairing configurations involving the telosome at the first metaphase (MI) were observed to determine the translocated chromosomes by acetocarmine squash method.

The breakpoints of translocations were estimated by comparing the C-banding patterns of the translocated chromosomes with those of the critical chromosomes of CS.

Results and Discussion

Table 1 shows the frequencies of MI cells with different pairing configurations in 22 different monotelodisomic hybrids between Saitama 27 and CSDT lines.

Two multivalents plus one heteromorphic bivalent were observed in 1.6 and 1.4% cells of two hybrids involving CSDT 2DS and 5DL, respectively. This confirms that Saitama 27 had two independent reciprocal translocations relative to CS, and that one of them was of small segments.

Table 1. Frequencies of MI cells with different pairing configurations in F_1 plants from the crosses between Saitama 27 and Chinese Spring ditelosomics

		Number of cells having					
Arm tested	No. of cells	No multi-valents[1]	$2''''$ (or $1''''+1'''$) + $t1''$	$1''''$ (or $1'''$) + $t1''$	$t3''''$	$1''''+1'''$ + t'	$1'''+t'$
1AS	85	25 (29.4)[2]	0 (0.0)	57 (67.1)	0 (0.0)	2 (2.4)	1 (1.1)
1BL	70	24 (34.3)	0 (0.0)	46 (65.7)	0 (0.0)	0 (0.0)	0 (0.0)
1DL	65	14 (21.5)	0 (0.0)	51 (78.5)	0 (0.0)	0 (0.0)	0 (0.0)
2AS	70	19 (27.1)	0 (0.0)	51 (72.9)	0 (0.0)	0 (0.0)	0 (0.0)
2BL	76	25 (32.9)	0 (0.0)	51 (67.1)	0 (0.0)	0 (0.0)	0 (0.0)
2DS	64	10 (15.6)	1 (1.6)	53 (82.8)	0 (0.0)	0 (0.0)	0 (0.0)
3AS	154	56 (36.4)	2 (1.3)[3]	0 (0.0)	75 (48.7)	0 (0.0)	21 (13.6)
3AL	166	74 (44.6)	0 (0.0)	0 (0.0)	78 (47.0)	0 (0.0)	14 (8.4)
3BL	76	24 (31.6)	0 (0.0)	51 (67.1)	0 (0.0)	1 (1.3)[4]	0 (0.0)
3DS	72	16 (22.2)	0 (0.0)	56 (77.8)	0 (0.0)	0 (0.0)	0 (0.0)
4AL	85	26 (30.6)	0 (0.0)	59 (69.4)	0 (0.0)	0 (0.0)	0 (0.0)
4BS	82	16 (19.5)	0 (0.0)	66 (80.5)	0 (0.0)	0 (0.0)	0 (0.0)
4DS	50	12 (24.0)	0 (0.0)	38 (76.0)	0 (0.0)	0 (0.0)	0 (0.0)
5AL	70	14 (20.0)	0 (0.0)	56 (80.0)	0 (0.0)	0 (0.0)	0 (0.0)
5BL	65	15 (23.1)	0 (0.0)	50 (76.9)	0 (0.0)	0 (0.0)	0 (0.0)
5DL	70	17 (24.3)	1 (1.4)	52 (74.3)	0 (0.0)	0 (0.0)	0 (0.0)
6AL	81	28 (34.6)	0 (0.0)	53 (65.4)	0 (0.0)	0 (0.0)	0 (0.0)
6BS	60	17 (28.3)	0 (0.0)	43 (71.7)	0 (0.0)	0 (0.0)	0 (0.0)
6DS	70	21 (30.0)	0 (0.0)	49 (70.0)	0 (0.0)	0 (0.0)	0 (0.0)
7AL	90	31 (34.4)	0 (0.0)	0 (0.0)	48 (53.3)	0 (0.0)	11 (12.2)
7BS	67	18 (26.9)	0 (0.0)	49 (73.1)	0 (0.0)	0 (0.0)	0 (0.0)
7DS	65	17 (26.2)	0 (0.0)	48 (73.8)	0 (0.0)	0 (0.0)	0 (0.0)

1) Cells having bivalents and univalents. 2) ( ) Percentages. 3) These cells had $1''''+t3''''$.
4) This cell had a configuration of $1''''+1'''+16''+2'+t'$.

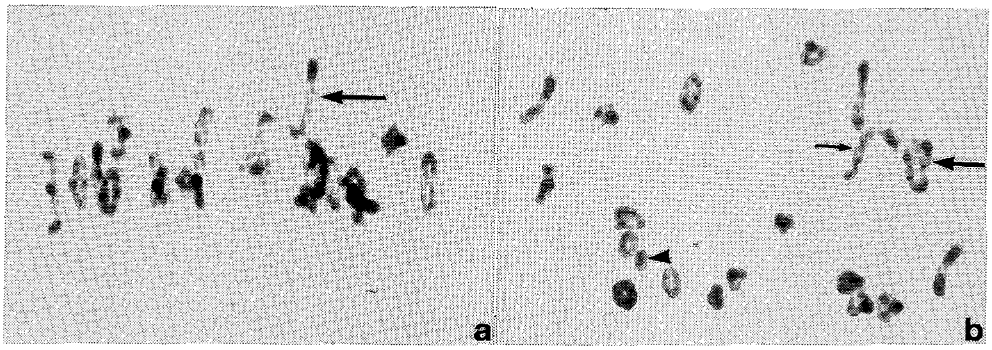

Fig. 1. Representative meiotic MI plates in the critical hybrids of Saitama 27 with; (a) CSTD 3AL showing one chain t3'''' (arrow), and (b) CSDT 1AS having ring 1'''' (large arrow), 1''' (small arrow) and t' (arrow head).

Among the 22 kinds of hybrid, only those involving CSDT 3AS, 3AL and 7AL had shown a quadrivalent with telosome (t3'''') in 48.7, 47.0 and 53.3% cells, respectively (Table 1, Fig. 1a). The remaining hybrids did not show t3'''' (Table 1). These indicate that chromosomes 3A and 7A were involved in one reciprocal translocation in Saitama 27.

In the hybrids of Saitama 27 with CSDT 3AS and 3AL, there were no significant differences in frequencies of MI cells with different configurations involving the telosome (x^2 = 5.97, df=4, 0.25>P>0.1) (Table 1). This suggests that the translocation between 3A and 7A involves large interchanged segments sufficient for chiasma formation. The C-banding patterns of the translocated chromosomes were compared with the standard ones in CS. Chromosome pairing and C-banding analysis suggest that the breakpoints in this translocation were within the centromeric regions. However, the arm combination of the translocated chromosomes could not be identified because 7AS and 7AL were not distinguished. Saitama 27 formed 1'''' in 26.0% of cells in the hybrid with Igachikugo Oregon having translocated chromosomes T3AS•7AL and 3AL•7AS (Ali et al. 1992, Nakata et al. 1993). This indicates that the reciprocal translocation between 3A and 7A in Saitama 27 differs in the interchanged arm combinations from that of Igachikugo Oregon. Thus, the translocated chromosomes in Saitama 27 are probably T3AS•7AS and T3AL•7AL (Fig.2).

In the hybrid involving CSDT 1AS, two cells having a configuration of 1'''' + 1''' + 17'' + t' were observed (Fig. 1b). This indicates that chromosome 1A was involved in translocation of small segments. Though the hybrid with CSDT 3BL showed a configuration of 1'''' + 1''' + 16'' + 2' + t' (Table 1), the involvement of 3B in this translocation is not certain due to the presence of two univalents. In this study, the counterpart in this translocation could not be identified because the size of the interchanged segment is too small to pair with its homologous telosome.

Saitama 27 formed hexavalent in the hybrid with Eshimashinriki (Ali et al. 1992). This implies that a common chromosome was involved in two different reciprocal translocations in both of the varieties. Chromosomes 3B, 4B, 6B and 7B were involved in two independent reciprocal transloca-

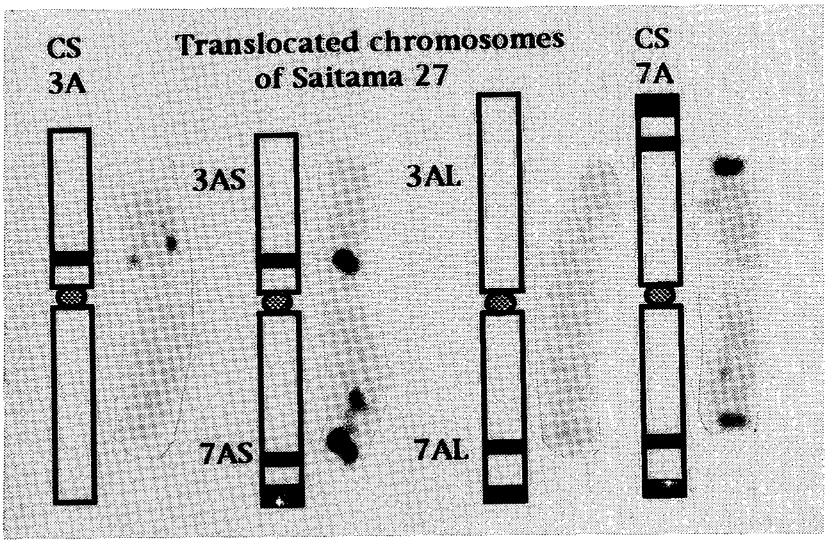

Fig. 2. Idiogram and C-banding comparison of chromosomes 3A and 7A of Chinese Spring (CS) and the translocated chromosomes of Saitama 27.

tions in Eshimashinriki (Ali et al. 1994b). Thus, one of these four chromosomes could be involved in the translocation of small segments present in Saitama 27.

Saitama 27 was developed from a cross of the F_1 hybrid between California and Soujukuakage with Hayakomugi (Fukunaga and Inagaki 1985). Soujukuakage had two translocations relative to CS, whereas Hayakomugi had not (Ali et al. 1994a). This suggests that Saitama 27 might have inherited these translocations from Soujukuakage.

Meiotic instabilities and the occurrence of aneuploids were occasionally reported in the course of wheat breeding (Riley and Kimber 1961, Watanabe 1962, Worland and Law 1985, Suarez et al. 1988). Watanabe (1962) reported that 37 of 207 Japanese varieties showed high frequencies (5-20%) of abnormal tetrad associated with the occurrence of high frequency of univalents at meiosis. The univalents of wheat chromosomes misdivide with high frequency. Sears (1954) showed that the frequencies of plants having telosome or isochromosome in the progenies of CS monosomics varied from 0.9% of 4D to 16.9% of 6A. Merker (1992) obtained 11 (1.98%) plants with T5B•5R in the selfed 575 progenies of monosomic 5B-5R substitution plants. These reports suggest that the centromeric translocation between 3A and 7A of Saitama 27 might be resulted from meiotic irregularities and centromeric misdivision-fusion of univalents.

The identified translocated chromosomes were not related to the semi-dwarfing gene of Saitama 27. Consequently, these translocations are not expected to exist in the European wheat, unless they contain other useful breeding factors. The obvious difference in the genetic background between the Japanese and European wheat would enable the exclusion of any undesirable genetic factors from the progenies of the initial intervarietal cross.

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Wheat Information Service
December 79: 42 – 46 (1994)

Two new sources of gametocidal genes from *Aegilops longissima* and *Ae. sharonensis*

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Summary

Two new gametocidal (*Gc*) genes were identified in the progenies of a cytoplasmic substitution line of common wheat with *Ae. longissima* cytoplasm and an amphidiploid between *T. dicoccum* and *Ae. sharonensis*. C-banding analyses indicated that one gene was located on either chromosome $5S^l$ of *Ae. longissima* or an arranged chromosome similar to $5S^l$, whereas the other was on $4S^l$ of *Ae. sharonensis*.

Introduction

Gametocidal (*Gc*) genes in wheat relatives, which were originally characterized as factors causing gamete abortion, have been revealed to cause chromosome breakage and other abnormal phenomena (Tsujimoto and Tsunewaki 1985, Endo 1988). These genes have been extensively applied for production of chromosome deletion lines in wheat for use in cytological mapping of genes and molecular markers (Tsujimoto and Noda 1990, Werner et al. 1992, Gill et al. 1993, Kota et al. 1993, Ogihara et al. 1994).

So far, several accessions of *Aegilops* species carrying the C, S or S^l genome have been reported to possess the *Gc* gene. In the present study two new *Gc* genes in *Ae. longissima* and *Ae. sharonensis* are reported and their characteristics are described.

Materials and methods

The original sources of the present gametocidal genes were the cytoplasmic substitution line of *Triticum aestivum* cv. Chinese Spring (CS) with the cytoplasm of *Aegilops longissima* strain TL05 (line C20, BC_4F_2 generation), and the amphidiploid between *T. dicoccum* cv. Vernal and *Ae. sharonensis* strain KU5-1 (F_{20} generation). These cytoplasmic substitution and amphidiploid lines were originally established by Drs. K. Tsunewaki and M. Sasaki, respectively. These lines were crossed with Chinese Spring, and the seed fertility (seed setting of the first and second florets) and chromosome constitutions of the progenies were observed. The C-banding method of Tsujimoto and Noda (1990) was used for the analysis.

Results

1. *Gc* gene from *Ae. longissima*: Chromosomes of the original alloplasmic line, C20, were observed. Three and six of the plants carried 43 and 44 meta or submetacentric chromosomes, respectively. A pair of extra chromosomes was included in all the plants, whose C-banding pattern was similar to that of chromosome $5S^l$ of *Ae. longissima* (Friebe 1993, Fig. 1a).

Both the plants with 43 and 44 chromosomes were self-pollinated or crossed as males to normal CS, and the karyotypes of the progenies were observed (Table 1). Most of the selfed progeny possessed 44 normal chromosomes, whereas many of the crossed progenies contained broken chromosomes, though the mode of the chromosome numbers was 43. The selfed and crossed progenies had respectively a pair of chromosomes and one chromosome similar to $5S^l$. This result indicates that this alien chromosome carried a *Gc* gene and, therefore, was preferentially transmitted to the next generation. The chromosome carrying *Gc* gene was heterobrachial as seen in root tip mitoses, and formed a univalent with a satellite in the backcrossed plants (Fig. 2a). Some

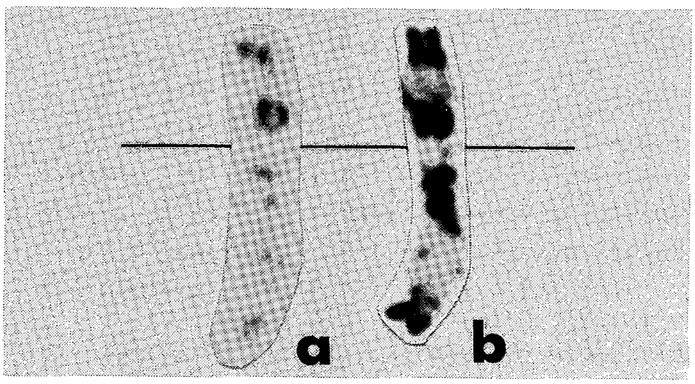

Fig. 1. Chromosomes of *Ae. longissima* (a) and *Ae. sharonensis* (b) carrying gametocidal genes

Table 1. Chromosome constitutions of the selfed and crossed progenies of line C20

Cross combination*		No. of plants						
		without breakage				with breakage		
	2n =	41	42	43	44	42	43	44
C20a self		0	0	0	8	0	0	2
C20b self		0	0	1	18	0	0	0
CS × C20a		1	0	13	0	1	2	0
CS × C20b		4	2	4	0	1	5	0

*) a: 2n = 43, b: 2n = 44.

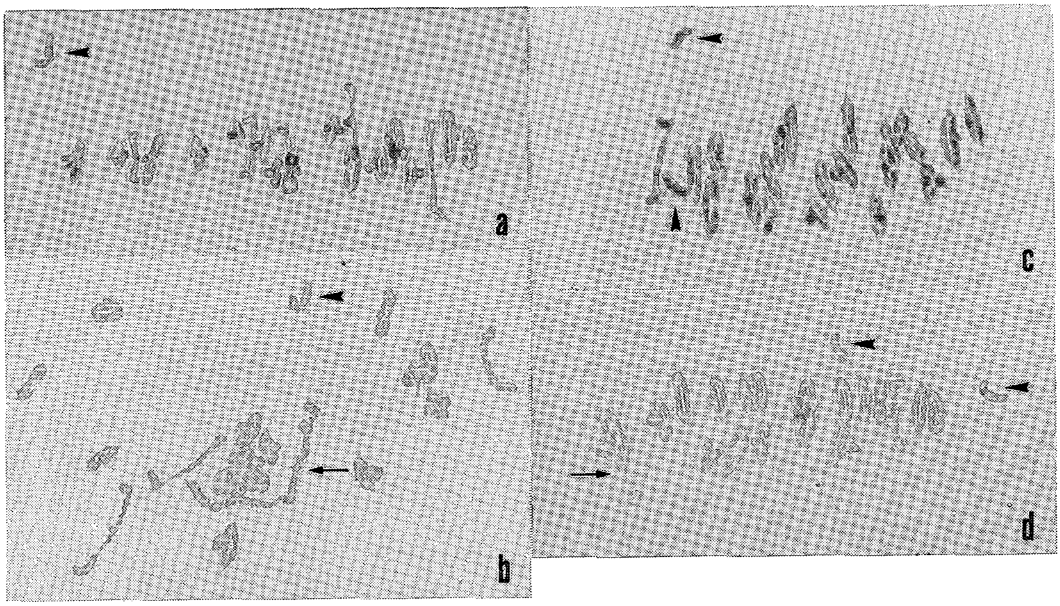

Fig. 2. Meiotic chromosome configuration of the back crossed offspring of the cytoplasmic substitution line with *Ae. longissima* cytoplasm (a and b) and of amphidiploid between *T. dicoccum* and *Ae. sharonensis* (c and d). Arrowheads and arrows indicate univalents and multivalents, respectively. Chromosome configuration: a=$1'+21''$, b=$1'+19''+1^{iv}$, c=$2'+20''$, and d=$2'+19''+1'^{o}$. $1'^{o}$ means a bivalent consisting of a normal chromosome and a ring chromosome.

of the plants carried one or two multivalents that must have been products of translocated chromosomes caused by this *Gc* gene (Fig. 2b). The seed fertility of the crossed plants was very low (10.3 % ± SE 1.3), indicating that the original cytoplasmic substitution line, C20, carried a pair of *Ae. longissima* chromosomes possessing a *Gc* gene.

2. *Gc* gene from *Ae. sharonensis*: The original amphidiploid between *T. dicoccum* and *Ae. sharonensis* (genome AABBS^{l}S^l) was crossed with CS. The F_1 was recurrently backcrossed with CS. In the BC_4F_1 generation, I noticed segregation of the stem color at three red and three white. Each plant with red or white stems was separately backcrossed with CS. In the next generation (BC_5F_1), all the progenies from BC_4F_1's with white stems (cross 1) had white stems, whereas progenies of plants with red stems (cross 2) segregated at three red and six white. Meiotic configuration of plants with red and white stems from these crosses indicated that all the plants from cross 1 carried one extra chromosome only (Fig. 2c), whereas all red and some white plants from cross 2 contained other alien or translocated chromosome(s) with an alien chromosome segment (Fig. 2d). The C-banding pattern of the alien chromosome that was transmitted preferentially, regardless of the stem color, was similar to that of chromosome 4S^l of *Ae. longissima* (Friebe et al. 1993, Fig. 1b). In plants with 41 or 42 chromosomes, this alien chromosome was substituted for

chromosome 4B of common wheat (instead of 4D). Therefore, this chromosome is $4S^l$ of *Ae. sharonensis*.

Discussion

There are two types of gametocidal chromosomes in *Ae. longissima* and *Ae. sharonensis* (Endo 1985). One belongs to homoeologous group 2 and another 4 of wheat. The *Gc* genes on group-4 chromosomes are epistatic to the ones on group-2 chromosomes (Endo 1982). There are no reports, so far, that any *Gc* gene is located on group-5 chromosomes. However, the C-banding pattern, heterobrachial shape, and satellite in the univalent of the present *Ae. longissima* chromosome are the characteristics of chromosome $5S^l$ (Friebe et al. 1993). There is no evidence, however, that this alien chromosome is substitutable for group-5 chromosomes of wheat or that it carries genetic markers for group-5 chromosomes. Thus, this chromosome is most probably chromosome $5S^l$, but it remains a possibility that it is a product of a complicated translocation involving the chromosome $2S^l$ or $4S^l$.

The *Gc* gene of the present *Ae. sharonensis* strain was located on chromosome $4S^l$. Maan (1975), Endo (1981), and Miller et al. (1982) also reported *Gc* genes on either chromosome $2S^l$ or $4S^l$ of this species. In the course of this study I found that the *Ae. sharonensis* strain KU5-1 used for the present amphidiploid ($AABBS^lS^l$) was the same as the strain for the alloplasmic line from which Endo (1981) had identified his *Gc* gene. However, Endo's chromosome was $2S^l$ though the present chromosome was $4S^l$. Obviously, the *Ae. sharonensis* strain KU5-1 carries at least two gametocidal genes, one on chromosome $2S^l$ and one on $4S^l$.

Acknowledgment

I thank Drs. K. Tsunewaki, Kyoto University, and M. Sasaki, Tottori University, for providing the original lines carrying the gametocidal chromosomes.

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Wheat Information Service
December 79: 47 – 56 (1994)

III. Gene Symbol

Catalogue of Gene Symbols for Wheat: 1994 Supplement

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The most recent edition of the Catalogue (9441) will appear in the Proceedings of the 8th International Wheat Genetics Symposium held in Beijing, China, 1993. This Supplement has been offered to the editors of Annual Wheat Newsletter and Wheat Information Service for inclusion in their respective journals.

Revision of the DNA-marker section of the 'Guidelines for Nomenclature of Biochemical/Molecular Loci in Wheat and Related Species' and addition to the document of nomenclature for quantitative trait loci (QTLs) was approved at the Eighth International Wheat Genetics Symposium. The revised DNA-marker section (section 5, now entitled 'Symbols for DNA markers and alleles') and a new section dealing with QTLs (section 6, entitled 'Symbols for loci and alleles controlling quantitative characters') may be found at the end of this supplement, following the references.

The 'Recommended Rules for Gene Symbolization in Wheat' and the 'Guidelines for Nomenclature for Biochemical/Molecular Loci for Wheat and Related Species' are located at the beginning of the Catalogue, and guidelines for nomenclature of genes controlling reaction to pathogenic diseases and pests are located within the body of the Catalogue, at the beginning of the pathogenic disease/pest reaction section. To give these latter guidelines greater prominence, they have been entitled 'Guidelines for Nomenclature of Genes for Reaction to Pathogenic Diseases and Pests' and are reproduced at the end of this supplement.

Additions to Symbols list:

Bls	Reaction to *Xanthomonas compestris* pv *undulosa*
Bza	Histone gene binding protein (ßZIP class) subfamily 1a
Bzb	Histone gene binding protein (ßZIP class) subfamily 1b
Eg	Elongated glume
Fe	Iron deficiency
Hst	Histone proteins

Anthocyanin pigmentation

1. <u>Purple Anthers</u>

Pan1 (9428). 7DS (9428). **v:** Ilyitchevka (9428); Mironovskaya 808 (9428); Novosibirskaya 67 (9428); Pyrothrix 28 (9428); Saratovskaya 210 (9428); Strela (9428); Ukrainka (9428).
tv: *T. polonicum* (9428).

4. <u>Purple/red culm/straw/stem</u>

Pc1. *Pc* (534).
Pc2 (9428). 7DS (9428). **v:** Ilyitchevka (9428); Mironovskaya 808 (9428); Novosibirskaya 67 (9428); Pyrothrix 28 (9428); Saratovskaya 210 (9428); Strela (9428); Ukrainka (9428).

5. Purple grain/pericarp

Complementary dominant genes

Pp1 (9430).	6A (9430).	**i:**	Saratovskaya 29*8/Purple (Australia) *Pp2* (9429).
Pp2 (9430).	7B (9430).	**tv:**	*T. durum* Desf. subsp. *abyssinicum* Vav. (9429).

Piech and Evans (808) located complementary genes on chromosomes 3A and 7B.

Awnedness

1. Dominant Inhibitors

Tipped 1

B1a (9430).	5AL.	**s:**	Saratovskaya 29*8/ Festiguay 5A (9430).
B1b (9430).		**s:**	Saratovskaya 29*8/Aurora 5A (9430).
B1c (9430).		**s:**	Saratovskaya 29*8/Mironskaya 808 5A (9430).

In a common genetic background carriers of *B1a* have the shortest tip-awned phenotype; carriers of *B1b* and *B1c* have awns 2 to 3 times longer depending on environment. In F1 hybrids differences between the substitution line combinations are significant.

Boron Tolerance

Bo1.	7B (9409).

Crossability with rye and *Hordeum* spp.

List of wheat/rye crossabilities: 9418.

DNA Markers

Delete *XWx-4A* from the Group 4S listings and delete *XWx-7A* and *XWx-7D* from the Group 7S listings. These loci have been renamed *Wx-B1*, *Wx-A1* and *Wx-D1*, respectively (see 'Waxy Endosperm').

Add the following comment: Two triplicate sets of loci that hybridize to histone-gene probes and four triplicate sets of loci that hybridize to ßZIP class DNA-binding-protein gene probes were located in chromosome arms/ chromosomes by Masuda et al.(9426), the former in the short arms of the homoeologous group 2 chromosomes and in the group 5 chromosomes and the latter in chromosome-arm groups 3S, 3L, 4L, and 6S. A complete listing of these loci will appear in the next supplement.

Elongated glume

Eg (9427).	7AL (9427).	**i:**	Saratovskaya 29*8// Novosibirskaya 67*2/*T. polonicum* (9427).

Glume colour

1. Red (brown/bronze)

Rg3 (9432).	1AS (9432).	**i:**	Saratovskaya 29*3//F2 CS mono1A/Strela (9432).
		V:	Strela *Rg1* (9432).

Rg3 was not linked with *Hg* (9432).

Hairy leaf

H1	**v:**	Artemovka (9434); Caesium 111 (9434); Lutescens 53/12 (9434); Lutescens 62 (9434); Pyrothrix 28 (9434); Poltavka (9434); Sarrubra (9434).

Iron Deficiency

Fe1 (9436).	7DL (9437).	**v:**	Saratovskaya 29 (9436).
Fe2 (9436).	7BS (9437).	**v:**	CS (9437).

Nucleolus Organiser Regions

Nor-H4 7HS (9439).
Nor-H5 2HS (9439).

Proteins

2. Enzymes

IV. <u>α-Amylase</u>

α-Amy-H2 7HL (9439).

α-Amy-S1 (9424). 6SS (9424). **v:** Wembly derivative #31.
al: *Ae. speltoides.*

Response to Vernalization

Vrn2. 5B(9428,9433). The earlier location of 2B(635) was not corrrect.5BL or 7BL (9438).

Vrn2a. *Vrn2* (9428,9433)
i: ANK-18 (9428, 9433).
s: Saratovskaya 29*8/ Mironovskaya 808 5A; Saratovskaya 29*8/Odesskaya 51 5A; Saratovskaya 29*8/ Skorospelka 35 5A
v: Pirothrix 28. Saratovskaya 29 Vrn1.

Vrn2b. *Vrn2* (9428,9433).
s: Diamant 1*8/Mironovskaya 808 5A; Diamant 1*8/Skorospelka 35 5A.
v: Magali; Milturum 321; Milturum 553;Ulyanovka 9 Diamant 1 *Vrn1;* Novosibirskaya 67 *Vrn1.*

Carriers of *Vrn2a* do not react to 15 and 30 days vernalization. Carriers of *Vrn2b* show accelerated heading after 15 and 30 days vernalization (9428, 9433).

Vrn4 5D (9438).

Restorers for cytoplasmic male sterility

<u>Restorers for *T. timopheevii* cytoplasm</u>

Genes *Rfc3* in chromosome 6RL and *Rfc4* in chromosome 4L are reported in 9437.

Ribosomal RNA

<u>5S rRrna genes</u>

5S-Rrna-H3 [*5SDNA-H3* (9439)]. 2H (514), 2HL (9439).
al: Betzes Barley; Sultan barley.

5S-Rrna-H4 [*5SDNA-H4* (9439)]. 3HL (9439).
al: Betzes barley; Sultan barley.

5S-Rrna-H5. [*5SDNA-H5* (9439)]. 4HL (9439).
al: Betzes barley; Sultan barley.

5S-Rrna-H6 [*5SDNA-H6* (9439)]. 4HS (9439).
al: Betzes barley; Sultan barley.

Delete the paragraph that begins 'A single 5S rRNA hybridization site was observed in barley. The chromosome......'

Pathogenic disease/pest reaction

<u>Reaction to *Erysiphe graminis tritici*</u>

Pm8.
v: GR876 (9423).
dv: Cando*2/Veery, KS91WGRC14 (9410).

Pm12 (723). 6BS (T6BS-6SS) (9424,9414).
The earlier location of 6A (723) was not correct.
v: Wembley*6/*Ae. speltoides* #31 (723, 9414).
al: *Ae. speltoides* CL214008 = K (723).

Pm16 — v: Norman lines with resistance from *T. dicoccoides* CL1060025 (719). tv: *T. dicoccoides* CL1060025 (719).

Pm20 (9402). *MlP6L* (9401). 6BL (T6BS.6RL) (9402). v: KSWGRC27 (9402). al: Prolific rye (9401).

Reaction to *Mayetiola destructor*

H3. v: GR876 (9423).
H6. v: Excel (9422).
H22 (848).
H23 (848). 6DL (848).
H24 (848). 3D (848).
H26. 4D (9403). v: KS92WGRC26 (9403). dv: *T. tauschii* TA2473 (9403).

Reaction to *Puccinia graminis*

Sr9a. v: Excel *Sr8a Sr17* (9422).
Sr31. v: GR876 (9423). v: Cando*2/Veery, KS91WGRC14 (9410).
Sr41 (9420). 4D (9420). v: WDR-B1 (9419). Waldron *Sr5*(heterogeneous)*Sr11* (heterogeneous).

Complex genotype: Roblin *Sr5Sr7a?Sr11Sr12?* Enhanced resistance is associated with *Lr34* (9412).

Reaction to *Puccinia recondita*

Lr3bg. i: RL6094 = Tc x 6/T6 (9417). v: T6 *Lr16* (9417).
Lr16. v: T6 *Lr3bg* (9417). i: RL6096 = Tc*6/T6 (9417).
Lr26. v: GR876 (9423). dv: Cando*2/Veery, KS91WGRC14 (9410).
Lr34. v: Others (9421).
Lr38. 6DL. i: RL6097 = Thatcher*6/T7 (9417). v: T7 (265,9417).
Lr44 (9406). 1B (9406). i: Thatcher*6/*T. spelta* 7831 (9406). v: *T spelta* 7831, *T. spelta* 7839 (9406).

Temporary Designations: A series of temporary designations for seedling and adult plant resistance genes in six durums is given in 9415.

Complex genotype: Roblin *Lr1Lr10Lr13Lr34* (9412).

Reaction to *Puccinia striiformis*

Yr9. v: GR876 (9423). dv: Cando*2/Veery, KS91WGRC14(9410).
Yr18. v: Others (9421).

Reaction to *Schizaphis graminum*

Gb6. 1A (1AL.1RS) (9407). v: GRS1201 (9408); GRS1202 (9408); GRS1203 (9408); GRS1204 (9408); GRS1205 (9408). su: Tx4386 (9411). ad: Tx4333 (9411). al: Insave rye.

Reaction to *Tilletia spp.*

Bt10. v: Fairview (9416).

Reaction to *Xanthomonas carpestris pv undulosa*
Disease: Bacterial leaf streak

Bls1 (9413). **v:** Pavon *Bls2*, Mochis T88 *Bls3Bls4*, Angostura F88 *Bls5*.
Bls2 (9413). **v:** Pavon *Bls1*.
Bls3 (9413). **v:** Mochis T88 *Bls1Bls4*.
Bls4 (9413). **v:** Mochis T88 *Bls1Bls3*.
Bls5 (9413). **v:** Turnco F88. Angostura F88 *Bls1*.
bls1 bls2 bls3 bls4 bls5: Alondra (9413).

Waxy Endosperm

Waxy variants are characterised by starch granules containing increased amylopectin and reduced amylase.

Wx-A1 [140,9440]. [*Xwx-7A* (139,140), ***Wx-B1*** (9440,9442)]. 7AS (140,9440). **v:** CS.
  Wx-A1a [9442]. [*Wx-B1a* (9442)]. **v:** CS; Joshuu.
  Wx-A1b [9442]. [*Wx-B1b* (9442)]. **v:** Kanto 79; Kanto 107 (null allele).

Wx-B1 [140,9440]. [*XWx-4B* (139,140), *XWx-4A* (9441), *Wx-A1* (9440,9442)]. 4AL (140,9442). **v:** CS.
  Wx-B1a [9442]. [*Wx-A1a* (9442)]. **v:** CS; Joshuu.
  Wx-B1b [9442]. [*Wx-A1b* (9442)]. **v:** Kanto 79; Kanto 82; Kanto 107; Norin 98 (null allele).

Wx-D1. [140],(9440). [*XWx-7D* (139,140)]. 7DS (140,9440) **v:** CS.
  Wx-D1a (9442). **v:** CS; all wheats.

Genetic Linkages

Chromosome 1B					
	Lr33	-	*Lr44*		9406.
Chromosome 2B					
2BS	*Hst2a-B1*	-	Centromere	20 cM	9426.
Chromosome 3B					
3BS	*Sr12*	-	Centromere	0	9404.
	Lr27	-	*Sr12*	I	9405.
Chromosome 4B					
4BS	*pa*	-	*H1*	29 ± 2.6 cM	9428.
Chromosome 5A					
5AL	*Vrn1*	-	*B1*	31 ± 3.3 cM	9434.
				45 ± 4.1 cM	9434.
				47 ± 4.4 cM	9434.
				50 ± 4.3 cM	9434.
Chromosome 6A					
6AS	*Bza3-A1*	-	Centromere	30 cM	9426.
	Gli-A2	-	Centromere	26.2 cM	9425.
6AL	Centromere	-	*Ep-A1*	1 cM	9425.
	Centromere	-	*α-Amy-A1*	8 cM	9425.

Chromosome 6B

6BS	*Pm12*	-	*α-Amy-S1*	1.1 cM	9424.
	Nor-B2	-	Centromere	4.1 cM	9425.
	XCxp3-6B	-	Centromere	30.1 cM	9425.
	Ep-B2	-	Centromere	33.1 cM	9425.
6BL	Centromere	-	*α-Amy-B1*	4.5 cM	9425.

Chromosome 6D

6DL	*H13*	-	*H23*	25 ± 5.0 cM	9848.

Chromosome 7D

7DS	*Pan1*	-	*Pc2*	13.3 ± 2.3 cM	9428.
				14.4 ± 2.7 cM	9428.

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Guidelines for Nomenclature of Biochemical/Molecular Loci in Wheat and Related Species

Revision of section 5 and new section 6

5 SYMBOLS FOR DNA MARKERS AND ALLELES

This section describes nomenclature for genetic markers that are detected at the DNA level, including those detected by hybridization with DNA probes [e.g., RFLPs (restriction-fragment-length polymorphisms)] and by amplification with primers [e.g., RAPDs (random-amplified-polymorphic DNAs) and STSs (sequence-tagged sites, including loci detected with sequenced RFLP clones, sequenced RAPDs and clones containing micro- and mini-satellites].

5.1 DNA markers of unknown function

5.1.1 *Basic symbol*

The basic symbol for DNA markers of unknown function should be X.

5.1.2 *Locus symbols*

The 'X' should be followed by a laboratory designator (see section 5.6), a number that identifies the probe or primer(s) used to detect the locus, a hyphen (-), and the symbol for the chromosome in which the locus is located. The laboratory designator and number should be assigned by the laboratory that produced the clone or sequenced the primer(s) or, if that laboratory chooses not to do so, then by the laboratory that mapped the locus. The number should consist of one or more Arabic numerals and should begin with a numeral other than zero, i.e., numbers such as '01,' '001,' and '002' should not be used. The number assigned to a probe need bear no relationship to the number name of the clone used to produce the probe and, likewise, the assigned to a primer(s) need bear no relationship to any name that may have been assigned to the primer(s). The letters in the laboratory designator should be lower-case and all characters in the locus symbol should be italicized. For example, *Xpsr119-7A* designates a RFLP locus located in chromosome 7A detected with *P*lant *S*cience *R*esearch probe 119 of the John Innes Centre. DNA markers detected in different chromosomes with the same probe or primer(s) should be assigned the same symbol except for the chromosome designation. For example, *Xpsr119-7D* and *Xpsr119-4A* designate other loci detected with probe 119.

5.1.3 *Locus symbols for DNA markers detected with 'known-function' probes or with primers that amplify genes*

The locus symbols for RFLP markers of unknown function that are detected with 'known-function' probes may include, in parentheses following the probe number, a symbol for the gene from which the probe was obtained. For example, *Xpsr804(Sbp)-3A* designates a chromosome 3A locus detected with a sedoheptulose-1,7-bisphosphatase gene probe. Likewise, when the primers used to amplify a DNA marker of unknown function are of sufficient length and similarity to a known gene to amplify the gene, the DNA-marker symbol may include the gene symbol in parentheses following the number assigned to the primers. For genes for which the Commission on Plant Gene Nomenclature has assigned mnemonic designations, the set number and other numbers assigned by the Commission may also be included inside the parentheses immediately after the gene symbol.

5.2 'Known-function' DNA markers

Loci that are detected with a DNA probe or DNA primers and whose function has been demonstrated should be designated with a symbol that indicates the function of the locus, as described in either section 2 or in the Recommended Rules for Gene Symbolization in Wheat It must be emphasized, however, that some clones and primers are likely to detect both loci whose function is known (proven, for example, by a segregational test against allelic forms of a gene encoding a protein) and additional loci of unknown (i.e., unproven) function (either pseudogenes or unrelated loci whose sequence homology to the probe or primers is sufficient to allow detection by it). In this case, the two types of loci require different nomenclature, namely, that described in section 2 or in the Recommended Rules for Gene Symbolization in Wheat and in section 5.1, respectively.

5.3 Duplicate DNA-marker loci

DNA markers located in the same chromosome that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the addition of a period and an Arabic numeral immediately after the chromosome designation. For example, *Xpsr933-2A.1* and *Xpsr933-2A.2* designate duplicate loci located in 2A that are detected with probe PSR933. As when two or more enzyme or protein protomers are produced by one chromosome arm, multiple DNA fragments from one chromosome arm that hybridize to one probe or that are amplified by one pair of primers (or by one primer) should be assigned to only one locus until recombination evidence indicates otherwise.

As noted in section 5.1, DNA markers located in different chromosomes that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the chromosome designation.

5.4 Allele symbols

Alleles should be designated as outlined in section 2.3 with the exception that restriction-enzyme-specific alleles, e.g., RFLP- and indirect-STS alleles, should be designated with the name of the restriction enzyme followed by a lower-case letter. For example, *Xtam1-5A-HindIIIa* denotes an allele detected with *Hin*dIII. Where possible, Chinese Spring should be the prototype for allele '*a*'. When a double-digest is used to detect an allele, both restriction enzymes should be listed, separated by a slash. The name and source of the probe or primer(s) and the length(s) of the DNA fragment(s) detected normally should be stated in the first publication describing an allele.

5.5 Abbreviation of locus and allele symbols

The chromosome designation is an integral part of the locus symbol for DNA markers. Nevertheless, on chromosome maps and in a limited number of other contexts, the chromosome designation and the hyphen preceding it may be omitted. For example, *Xpsr35-3A* may be abbreviated as *Xpsr35* on a map of chromosome 3A, *Xpsr933-2A.1* and *Xpsr933-2A.2* may be abbreviated as *Xpsr933.1* and *Xpsr933.2*, respectively, on a map of 2A, and *Xpsr804(Sbp)-3A* may be abbreviated as *Xpsr804(Sbp)* on a map of 3A. Also, the chromosome designation and the hyphen preceding it may be omitted on chromosome maps from the symbols for intra-chromosomally duplicated loci that are detected with a 'known-function' probe (or with primers that amplify a gene) but that do not include a gene symbol. For example, if *Xtam200-1A.1* and *Xtam200-1A.2* were the symbols for duplicated loci detected with a 'known-function' clone designated TAM200, then the symbols could be abbreviated as *Xtam200.1* and *Xtam200.2*, respectively, on a map of 1A.
Finally, *Xbg1485(Ger)-4D.2* may be abbreviated on a map of 4D by omission of the hyphen, the chromosome designation and the period, i.e., as *Xbg1485(Ger)2*.

In some contexts it will also be possible to abbreviate the symbols for alleles as, for example, *BamHIb*, or even simply *b*.

5.6 Laboratory designators

Laboratory designators should consist of from two to four and preferably three letters. When used in locus symbols, all of the letters should be lower-case and italicized (see section 5.1.2).
Laboratory designators should be chosen carefully to insure that they differ both from those used by other laboratories and from those that compose gene symbols. As an aid in this regard, a list of laboratory designators that have appeared in the literature is available electronically via the Internet Gopher from host greengenes.cit.cornell.edu, port 70, menu "Grains files to browse" / "Reserved Laboratory Designators for DNA Probes, Primers and Markers".
Laboratories that are investigating DNA markers in different species and/or of different types, e.g., RFLPs, STSs, and RAPDs, may choose to use more than one designator. For example, oat and barley cDNA clones isolated at Cornell University have been designated with the prefixes CDO and BCD, respectively, and *cdo* and *bcd*, respectively, are appropriately used as laboratory designators in symbols for loci detected with these clones. Likewise, *tam* and *txs*, respectively, are being used as laboratory designators in symbols for loci detected with wheat and sorghum DNA clones isolated at Texas A&M University, and the John Innes Centre is using *psr* and *psm* as laboratory designators in the symbols for DNA markers detected with wheat and millet probes, respectively, and *psp* for wheat PCR markers.

5.7 Clone designations

Clone designations should minimally identify the type of vector, the species from which the cloned DNA was obtained, and the source laboratory and cloned DNA, in that order. p = plasmid, l = lambda, c = cosmid, and m = M13 should be used to identify vectors. Initials of the species name, e.g., Ta = *Triticum aestivum* and *Secale cereale*, should be used to designate the source of the cloned DNA and a unique letter-number combination chosen by the source laboratory should be used to designate the source laboratory and the cloned DNA.

6 SYMBOLS FOR LOCI AND ALLELES CONTROLLING QUANTITATIVE CHARACTERS

6.1 Genes identified by segregational analysis

Symbols for loci and alleles controlling quantitative characters that are identified by segregational analysis should be in accord with the Recommended Rules for Gene Symbolization in Wheat.

6.2 Quantitative trait loci (QTLs)
QTLs are loci controlling quantitative characters whose allelic classes do not exhibit discontinuous variation or clear segregational patterns. They are identified by association with one or more linked markers.

6.2.1 *Basic symbol*
The basic symbol for QTLs should be 'Q'.

6.2.2 *Locus symbols*
The 'Q' should be followed by a trait designator, a period, a laboratory designator (see section 5.6), a hyphen (-), and the symbol for the chromosome in which the QTL is located. The trait designator should consist of no more than four and preferably three letters, the first of which is capitalized. Different QTLs for the same trait that are identified in one chromosome should be assigned the same symbol except for the addition of a period and an Arabic numeral after the chromosome designation. All characters in the locus symbol should be italicized. For example, *QYld.psr-7B.1* and *QYld.psr-7B.2* would designate two yield QTLs identified in chromosome 7B by the John Innes Centre. On a map of 7B, these could be abbreviated as *QYld.psr.1* and *QYld.psr.2*

6.2.3 *Allele symbols*
Alleles at QTL loci should be designated by a lower-case italic letter following the locus designation.

Guidelines for Nomenclature of Genes for Reaction to Pathogenic Diseases and Pest

1. All genes for resistance (low reaction) will be designated with a capital letter, even though they behave as recessive alleles. Moreover, the dominance of individual alleles may vary with the environment, the genetic background and the particular culture of the pathogen. Symbols for disease/pest-reaction genes are used by people of many disciplines, and since they are frequently communicated verbally, dominance relationships are not clear. Those alleles initially designated with a lower-case letter have tended to be miswritten with a capital. For example, the usually recessive resistance allele *Sr17* was initially designated *sr17*, but its presentation in some reports was confusing.

2. Where no recombination occurs between genes conferring resistance to more than one pathogen, the gene(s) segment shall be designated separately for each disease; e.g., *Pm1*, *Sr15* and *Lr20*.

3 . Where recombination occurs between two closely linked factors for reaction to a pathogen, the recombined 'allele' may be designated as a combination of the separate alleles; e.g., the recombined 'allele' obtained by combining *Lr14a* and *Lr14b* was designated as *Lr14ab*. The decision as to whether a designation should be as a combination or as separate genes shall be at the discretion of particular workers. A maximum value of 1 crossover unit for designation as an 'allele' is suggested.

Although the need to consider uniform symbolization of corresponding genes in pathogens is recognized, no recommendations are proposed.

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IV. Recent publications on wheat genetics

It is great pleasure that Wheat Information Service was authorized to publish a list of bibliographic references on wheat genetics by *Cambridge Scientific Abstracts.* Following references are selected from the original database using key words, WHEAT AND GENETICS. They attribute to *Life Sciences Collection* of CSA as the secondary source for the references. The present list includes a half of the publications on wheat genetics issued in 1993. Another half and those in 1994 will appear in the future issues of WIS. The editor appreciates CSA.

(1)
ACCN:001166449 CTLN:2913641
ABSJ:G (Genetics Abstracts)
AUTH:Hammond-Kosack, M.C.U.;Holdsworth, M.J.;Bevan, M.W.
AFFN:Cambridge Lab., John Innes Cent. Plant Sci. Res., Colney Lane, Norwich NR4 7UJ, UK
TITL:In vivo footprinting of a low molecular weight glutenin gene (LMWG-1D1) in wheat endosperm.
HTIL:EMBO J.
HYER:1993.
HCOL:vol. 12, no. 2, pp. 545-554

(2)
ACCN:001168483 CTLN:2917153
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); J (Microbiology Abstracts Section B: Bacteriology)
AUTH:Zaghmout, O.M.-F.;Trolinder, N.L.
AFFN:USDA-ARS, Cropping Syst. Res. Lab., Route 3, P.O. Box 215, Lubbock, TX 79401, USA
TITL:Simple and efficient method for directly electroporating Agrobacterium plasmid DNA into wheat callus cells.
HTIL:NUCLEIC ACIDS RES.
HYER:1993.
HCOL:vol. 21, no. 4, p. 1048

(3)
ACCN:001170338 CTLN:2919273
ABSJ:G (Genetics Abstracts); W2(Agricultural & Environmental Biotechnology Abstracts)
AUTH:Hernould, M.;Suharsono, S.;Litvak, S.;Araya, A.;Mouras, A.
AFFN:Univ. Bordeaux II, Lab. Biol. Cell., Ave. des Facultes, 33405 Talence Cedex, France
TITL:Male-sterility induction in transgenic tobacco plants with an unedited atp9 mitochondrial gene from wheat.
HTIL:PROC. NATL. ACAD. SCI. USA.
HYER:1993.
HCOL:vol. 90, no. 6, pp. 2370-2374

(4)
ACCN:001179344 CTLN:2933435
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts); L (Biochemistry Abstracts Part 3: Amino Acids, Peptides and Proteins)
AUTH:Zhuo, Degen;Bonen, L.
AFFN:Dep. Biol., Univ. Ottawa, 30 George Glinski St., Ottawa, ON K1N 6N5, Canada
TITL:Characterization of the S7 ribosomal protein gene in wheat mitochondria.
HTIL:MOL. GEN. GENET.
HYER:1993.
HCOL:vol. 236, no. 2-3, pp. 395-401

(5)
ACCN:001191700 CTLN:2953846
ABSJ:A (Microbiology Abstracts Section A: Industrial and Applied
Microbiology); K (Microbiology Abstracts Section C: Algology, Mycology
and Protozoology); G (Genetics Abstracts)
AUTH:Chen, Xianming;Line, R.F.
AFFN:Dep. Plant Pathol., Washington State Univ., Pullman, WA 99164-6430,
USA
TITL:Inheritance of stripe rust resistance in wheat cultivars postulated to
have resistance genes at Yr3 and Yr4 loci.
HTIL:PHYTOPATHOLOGY.
HSSN:0031-949X
HYER:1993.
HCOL:vol. 83, no. 4, pp. 382-388

(6)
ACCN:001194513 CTLN:2958251
ABSJ:G (Genetics Abstracts)
AUTH:Kim, N.-S.;Armstrong, K.;Knott, D.R.
AFFN:Plant Res. Cent., Agric. Canada, Ottawa, ON K1A 0C6, Canada
TITL:Molecular detection of Lophopyrum chromatin in wheat-Lophopyrum
recombinants and their use in the physical mapping of chromosome 7D.
HTIL:THEOR. APPL. GENET.
HYER:1993.
HCOL:vol. 85, no. 5, pp. 561-567

(7)
ACCN:001198477 CTLN:2964612
ABSJ:G (Genetics Abstracts)
AUTH:Fernandez-Calvin, B.;Orellana, J.
AFFN:Dep. Genet., E.T.S.I. Agron., Univ. Politec., 28040 Madrid, Spain
TITL:Metaphase-I bound-arm frequency and genome analysis in wheat-Aegilops
hybrids. 2. Cytogenetical evidence for excluding Ae. sharonensis as
the donor of the B genome of polyploid wheats.
HTIL:THEOR. APPL. GENET.
HYER:1993.
HCOL:vol. 85, no. 5, pp. 587-592

(8)
ACCN:001199239 CTLN:2966245
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics
Abstracts); L (Biochemistry Abstracts Part 3: Amino Acids, Peptides
and Proteins)
AUTH:Apsit, V.;Freeberg, J.A.;Chase, M.R.;Davis, E.A.;Ackerman, S.
AFFN:Biol. Dep., Univ. Massachusetts, 100 Morrissey Blvd., Boston, MA 02125,
USA
TITL:Wheat TFIID TATA binding protein.
HTIL:NUCLEIC ACIDS RES.
HYER:1993.
HCOL:vol. 21, no. 6, p. 1494

(9)
ACCN:001201241 CTLN:0047893
ABSJ:W4(Bioengineering Abstracts)
AUTH:Dardoize, F.;Goasdoue, N.;Goasdoue, C.;Couffignal, R.
AFFN:Universite Pierre et Marie Curie, Paris, France
TITL:High-performance liquid chromatography of chemical hybridizing agent
in wheat.
HTIL:J LIQ CHROMATOGR.
HSSN:0148-3919
HYER:1993.
HCOL:vol. 16, no. 7, pp. 1517-1528

(10)
ACCN:001206945   CTLN:2978602
ABSJ:G (Genetics Abstracts)
AUTH:Rathburn, H.;Song, J.;Hedgcoth, C.
AFFN:Dep. Biochem., Willard Hall, Kansas State Univ., Manhattan, KS 66506-3702, USA
TITL:Cytoplasmic male sterility and fertility restoration in wheat are not associated with rearrangements of mitochondrial DNA in the gene regions for cob, coxII, or coxI.
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 21, no. 1, pp. 195-201

(11)
ACCN:001206980   CTLN:2978637
ABSJ:G (Genetics Abstracts)
AUTH:Reddy, P.;Appels, R.
AFFN:Wheat Res. Unit, Div. Plant Ind., CSIRO, P.O. Box 7, North Ryde, NSW 2113, Australia
TITL:Analysis of a genomic DNA segment carrying the wheat high-molecular-weight (HMW) glutenin Bx17 subunit and its use as an RFLP marker.
HTIL:THEOR. APPL. GENET.
HYER:1993.
HCOL:vol. 85, no. 5, pp. 616-624

(12)
ACCN:001215608   CTLN:2988711
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Ouellet, F.;Houde, M.;Sarhan, F.
AFFN:Dep. Sci. Biol., Univ. Quebec Montreal, C.P. 8888, Succ. "A", Montreal, PQ H3C 3P8, Canada
TITL:Purification, characterization and cDNA cloning of the 200 kDa protein induced by cold acclimation in wheat.
HTIL:PLANT CELL PHYSIOL.
HSSN:0032-0781
HYER:1993.
HCOL:vol. 34, no. 1, pp. 59-65

(13)
ACCN:001220657   CTLN:2995758
ABSJ:V (Virology Abstracts); N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Shirako, Y.;Wilson, M.A.
AFFN:Div. Biol., CA Inst. Tech., Pasadena, CA 91125, USA
TITL:Complete nucleotide sequence and organization of the bipartite RNA genome of soil-borne wheat mosaic virus.
HTIL:VIROLOGY.
HSSN:0042-6822
HYER:1993.
HCOL:vol. 195, no. 1, pp. 16-32

(14)
ACCN:001220970   CTLN:2996135
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Singh, N.K.;Donovan, G.R.;Carpenter, H.C.;Skerritt, J.H.;Langridge, P.
AFFN:Cent. Cereal Biotechnol., Waite Agric. Res. Inst., Glen Osmond, S.A. 5064, Australia
TITL:Isolation and characterization of wheat triticin cDNA revealing a unique lysine-rich repetitive domain.

HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 22, no. 2, pp. 227-237

(15)
ACCN:001221014 CTLN:2996179
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Ainsworth, C.;Clark, J.;Balsdon, J.
AFFN:Dep. Biol. Sci., Wye Coll. (Univ. London), Wye, Kent TN25 5AH, UK
TITL:Expression, organisation and structure of the genes encoding the waxy protein (granule-bound starch synthase) in wheat.
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 22, no. 1, pp. 67-82

(16)
ACCN:001223859 CTLN:3003390
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Mukai, Y.;Friebe, B.;Hatchett, J.H.;Yamamoto, M.;Gill, B.S.
AFFN:Dep. Plant Pathol., Throckmorton Hall, Kansas State Univ., Manhatten, KS 66505-5502, USA
TITL:Molecular cytogenetic analysis of radiation-induced wheat-rye terminal and intercalary chromosomal translocations and the detection of rye chromatin specifying resistance to Hessian fly.
HTIL:CHROMOSOMA.
HSSN:0009-5915
HYER:1993.
HCOL:vol. 102, no. 2, pp. 88-95

(17)
ACCN:001226148 CTLN:2995758
ABSJ:V (Virology Abstracts)
AUTH:Shirako, Y.;Wilson, M.A.
AFFN:Div. Biol., CA Inst. Tech., Pasadena, CA 91125, USA
TITL:Complete nucleotide sequence and organization of the bipartite RNA genome of soil-borne wheat mosaic virus.
HTIL:VIROLOGY.
HSSN:0042-6822
HYER:1993.
HCOL:vol. 195, no. 1, pp. 16-32

(18)
ACCN:001230229 CTLN:3011707
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Nagy, F.;Fejes, E.;Wehmeyer, B.;Dallman, G.;Schafer, E.
AFFN:Friedrich-Miescher Inst., P.O. Box 2543, CH-4002 Basel, Switzerland
TITL:The circadian oscillator is regulated by a very low fluence response of phytochrome in wheat.
HTIL:PROC. NATL. ACAD. SCI. USA.
HSSN:0027-8424
HYER:1993.
HCOL:vol. 90, no. 13, pp. 6290-6294

(19)
ACCN:001234880 CTLN:3019421
ABSJ:A (Microbiology Abstracts Section A: Industrial and Applied Microbiology); K (Microbiology Abstracts Section C: Algology, Mycology and Protozoology); D (Ecology Abstracts)
AUTH:Hetrick, B.A.D.;Wilson, G.W.T.;Cox, T.S.

AFFN:Dep. Plant Pathol., Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:Mycorrhizal dependence of modern wheat cultivars and ancestors: A synthesis.
HTIL:CAN. J. BOT./REV. BOT. CAN.
HSSN:0008-4026
HYER:1993.
HCOL:vol. 71, no. 3, pp. 512-518

(20)
ACCN:001244385 CTLN:3027902
ABSJ:G (Genetics Abstracts)
AUTH:Kota, R.S.;Gill, K.S.;Gill, B.S.;Endo, T.R.
AFFN:Dep. Plant Pathol., Wheat Genet. Resour. Cent., Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:A cytogenetically based physical map of chromosome 1B in common wheat.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 3, pp. 548-554

(21)
ACCN:001245634 CTLN:3029375
ABSJ:G (Genetics Abstracts)
AUTH:Josephides, C.M.
AFFN:Agric. Res. Inst., Nicosia, Cyprus
TITL:Analysis of adaptation of barley, triticale, durum and bread wheat under Mediterranean conditions.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 65, no. 1, pp. 1-8

(22)
ACCN:001245666 CTLN:3029407
ABSJ:G (Genetics Abstracts)
AUTH:Reddy, V.R.K.;Edwin, R.;Suganthi, C.P.
AFFN:Cytogenet. Lab., Dep. Bot., Bharathiar Univ., Coimbatore-641 046, India
TITL:Behaviour of wheat and rye genome chromosomes in triticale-A review.
HTIL:CYTOLOGIA.
HSSN:0011-4545
HYER:1993.
HCOL:vol. 58, no. 1, pp. 1-8

(23)
ACCN:001245680 CTLN:3029421
ABSJ:G (Genetics Abstracts)
AUTH:Motzo, R.;Attene, G.;Deidda, M.
AFFN:Ist. Agron. e Coltivazioni Erbacee, Fac. Sci. Agrarie, Univ. Sassari, Via E. De Nicola, 07100 Sassari, Italy
TITL:Genotypic variation in durum wheat root systems at different stages of development in a Mediterranean environment.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 66, no. 3, pp. 197-206

(24)
ACCN:001245713 CTLN:3029454
ABSJ:G (Genetics Abstracts)
AUTH:Joshi, C.P.;Nguyen, H.T.
AFFN:Plant Mol. Genet. Lab., Dep. Agron., Hortic., and Entomol., Mail Stop 2122, Texas Tech Univ., Lubbock, TX 79409, USA

TITL:Application of the random amplified polymorphic DNA technique for the detection of polymorphism among wild and cultivated tetraploid wheats.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 3, pp. 602-609

(25)
ACCN:001245799 CTLN:3029540
ABSJ:G (Genetics Abstracts)
AUTH:Mukai, Y.;Nakahara, Y.
AFFN:Lab. Plant Mol. Genet., Div. Nat. Sci., Osaka Kyoiku Univ., 4-698-1 Asahigaoka, Kashiwara, Osaka 582, Japan
TITL:Simultaneous discrimination of the three genomes in hexaploid wheat by multicolor fluorescence in situ hybridization using total genomic and highly repeated DNA probes.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 3, pp. 489-494

(26)
ACCN:001245817 CTLN:3029558
ABSJ:G (Genetics Abstracts)
AUTH:Stelmakh, A.F.
AFFN:Plant Breed. and Genet. Inst. (SGI), 270036 Odessa, Ukraine
TITL:Genetic effects of Vrn genes on heading date and agronomic traits in bread wheat.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 65, no. 1, pp. 53-60

(27)
ACCN:001250210 CTLN:3033469
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Krishnan, H.B.;Pueppke, S.G.
AFFN:Dep. Plant Pathol., 108 Waters Hall, Univ. Missouri, Columbia, MO 65211, USA
TITL:Nucleotide sequence of an abundant rice seed globulin: Homology with the high molecular weight glutelins of wheat, rye and triticale.
HTIL:BIOCHEM. BIOPHYS. RES. COMMUN.
HYER:1993.
HCOL:vol. 193, no. 1, pp. 460-466

(28)
ACCN:001250264 CTLN:3033523
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Lai, D.M.L.;Hoj, P.B.;Fincher, G.B.
AFFN:Dep. Plant Sci., Univ. Adelaide, Waite Campus, Glen Osmond, SA 5064, Australia
TITL:Purification and characterization of (1 arrow right 3, 1 arrow right 4)- beta -glucan endohydrolases from germinated wheat (Triticum aestivum).
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 22, no. 5, pp. 847-859

(29)
ACCN:001253413 CTLN:3037796
ABSJ:G (Genetics Abstracts); J (Microbiology Abstracts Section B: Bacteriology)

AUTH:Duveiller, E.;Van Ginkel, M.;Thijssen, M.
AFFN:CIMMYT, Lisboa 27, Apdo-Postal 6-641, Col. Juarez, Del. Cuauhtemoc, 06600 Mexico D.F., Mexico
TITL:Genetic analysis of resistance to bacterial leaf streak caused by Xanthomonas campestris pv. undulosa in bread wheat.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 66, no. 1-2, pp. 35-43

(30)
ACCN:001254423 CTLN:3039052
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Puterka, G.J.;Black, W.C.,IV;Steiner, W.M.;Burton, R.L.
AFFN:USDA-ARS, Appalachian Fruit Res. Stn., 45 Wiltshire Rd., Kearneysville, WV 25430, USA
TITL:Genetic variation and phylogenetic relationships among worldwide collections of the Russian wheat aphid, Diuraphis noxia (Mordvilko), inferred from allozyme and RAPD-PCR markers.
HTIL:HEREDITY.
HSSN:0018-067X
HYER:1993.
HCOL:vol. 70, no. 6, pp. 604-618

(31)
ACCN:001254491 CTLN:3039124
ABSJ:G (Genetics Abstracts)
AUTH:Banks, P.M.;Xu, S.J.;Wang, R.R.-C.;Larkin, P.J.
AFFN:CSIRO, Div. Plant Ind., GPO Box 1600, Canberra, ACT 2601, Australia
TITL:Varying chromosome composition of 56-chromosome wheat x Thinopyrum intermedium partial amphiploids.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 2, pp. 207-215

(32)
ACCN:001254497 CTLN:3039130
ABSJ:G (Genetics Abstracts)
AUTH:Luo, M.C.;Yen, C.;Yang, J.L.
AFFN:Triticeae Res. Inst., Sichuan Agric. Univ., Dujiangyan City, Sichuan 611830, China, People's Rep.
TITL:Crossability percentages of bread wheat landraces from Shaanxi and Henan provinces, China with rye.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 67, no. 1-2, pp. 1-8

(33)
ACCN:001254500 CTLN:3039133
ABSJ:G (Genetics Abstracts)
AUTH:Hohmann, U.;Lagudah, E.S.
AFFN:CSIRO Div. Plant Ind., P.O. Box 1600, Canberra, A.C.T. 2601, Australia
TITL:C-banding polymorphism and linkage of nonhomoeologous RFLP loci in the D genome progenitor of wheat.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 2, pp. 235-243

(34)
ACCN:001254507 CTLN:3039140
ABSJ:G (Genetics Abstracts)
AUTH:Jiang, Jiming;Chen, Peidu;Friebe, B.;Raupp, W.J.;Gill, B.S.

AFFN:Wheat Genet. Resour. Cent. and Dep. Plant Pathol., Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:Alloplasmic wheat - Elymus ciliaris chromosome addition lines.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 2, pp. 327-333

(35)
ACCN:001254538 CTLN:3039171
ABSJ:G (Genetics Abstracts)
AUTH:Sirkka, A.;Immonen, T.;Varughese, G.;Pfeiffer, W.H.;Mujeeb-Kazi, A.
AFFN:Int. Maize and Wheat Improvement Cent. (CIMMYT), Apdo. Postal 6-641, 06600 Mexico, D.F., Mexico
TITL:Crossability of tetraploid and hexaploid wheats with ryes for primary triticale production.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 65, no. 3, pp. 203-210

(36)
ACCN:001254543 CTLN:3039176
ABSJ:G (Genetics Abstracts)
AUTH:Murai, K.;Tsunewaki, K.
AFFN:Agric. Sci. Lab., Takarazuka Res. Cent., Sumitomo Chem. Co., Ltd., Takarazuka, Hyogo 665, Japan
TITL:Photoperiod-sensitive cytoplasmic male sterility in wheat with Aegilops crassa cytoplasm.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 67, no. 1-2, pp. 41-48

(37)
ACCN:001254545 CTLN:3039178
ABSJ:G (Genetics Abstracts)
AUTH:Suenaga, K.;Nakajima, K.
AFFN:Natl. Inst. Agrobiol. Resour., Kan-non-dai 2-1-2, Tsukuba, Ibaraki 305, Japan
TITL:Segregation of genetic markers among wheat doubled haploid lines derived from wheat x maize crosses.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 65, no. 2, pp. 145-152

(38)
ACCN:001254556 CTLN:3039189
ABSJ:G (Genetics Abstracts)
AUTH:Dvorak, J.;Di Terlizzi, P.;Zhang, Hong-Bin;Resta, P.
AFFN:Dep. Agron. and Range Sci., Univ. California, Davis, CA 95616, USA
TITL:The evolution of polyploid wheats: Identification of the A genome donor species.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 1, pp. 21-31

(39)
ACCN:001254557 CTLN:3039190
ABSJ:G (Genetics Abstracts)
AUTH:Talbert, L.E.;Kimber, G.;Magyar, G.M.;Buchanan, C.B.
AFFN:Dep. Plant and Soil Sci., Montana State Univ., Bozeman, MT 59717, USA
TITL:Repetitive DNA variation and pivotal-differential evolution of wild

wheats.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 1, pp. 14-20

(40)
ACCN:001254559 CTLN:3039192
ABSJ:G (Genetics Abstracts)
AUTH:Yen, Yang;Baenziger, P.S.
AFFN:Dep. Agron., Univ. Nebraska, P.O. Box 830915, Lincoln, NE 68583-0915
TITL:Identification, characterization, and comparison of RNA-degrading enzymes of wheat and barley.
HTIL:BIOCHEM. GENET.
HSSN:0006-2928
HYER:1993.
HCOL:vol. 31, no. 3-4, pp. 133-145

(41)
ACCN:001254562 CTLN:3039195
ABSJ:G (Genetics Abstracts)
AUTH:Conner, R.L.;Whelan, E.D.P.;Laroche, A.;Thomas, J.B.
AFFN:Agric. Canada Res. Stn., Lethbridge, AB, T1J 4B1 Canada
TITL:Reaction of alien chromosome substitution and addition lines of hard red spring wheat to common root rot and black point.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 1, pp. 173-180

(42)
ACCN:001255079 CTLN:3039712
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics Abstracts); W2(Agricultural & Environmental Biotechnology Abstracts)
AUTH:Ainsworth, C.;Tarvis, M.;Clark, J.
AFFN:Dep. Biol. Sci., Wye Coll., Univ. London, Wye, Kent, TN25 5AH, UK
TITL:Isolation and analysis of a cDNA clone encoding the small subunit of ADP-glucose pyrophosphorylase from wheat.
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 23, no. 1, pp. 23-33

(43)
ACCN:001255413 CTLN:3040052
ABSJ:G (Genetics Abstracts)
AUTH:Takumi, S.;Nasuda, S.;Liu, Y.-G.;Tsunewaki, K.
AFFN:Lab. Genet., Fac. Agric., Kyoto Univ., Sakyo-ku, Kyoto 606-01, Japan
TITL:Wheat phylogeny determined by RFLP analysis of nuclear DNA. 1. Einkorn wheat.
HTIL:JAP. J. GENET.
HSSN:0021-504X
HYER:1993.
HCOL:vol. 68, no. 1, pp. 73-79

(44)
ACCN:001255415 CTLN:3040054
ABSJ:G (Genetics Abstracts)
AUTH:Tsunewaki, K.
AFFN:Lab. Genet., Fac. Agric., Kyoto Univ., Sakyo-ku, Kyoto 606-01, Japan
TITL:Genome-plasmon interactions in wheat.
HTIL:JAP. J. GENET.
HSSN:0021-504X
HYER:1993.
HCOL:vol. 68, no. 1, pp. 1-34

(45)
ACCN:001255424 CTLN:3040063
ABSJ:G (Genetics Abstracts)
AUTH:Nasuda, S.;Liu, Yao-Guang;Sakamoto, A.;Nakayama, T.;Iwabuchi, M.;
Tsunewaki, K.
AFFN:Lab. Genet., Fac. Agric., Kyoto Univ., Sakyo-ku, Kyoto 606-01, Japan
TITL:Chromosomal locations of the genes for histones and a histone gene-
binding protein family HBP-1 in common wheat.
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 22, no. 4, pp. 603-614

(46)
ACCN:001255495 CTLN:3040134
ABSJ:G (Genetics Abstracts)
AUTH:Barnes, W.C.;McKenzie, E.A.
AFFN:NSW Agric., Agric. Res. Cent., RMB 944, Tamworth, 2340, NSW, Australia
TITL:Dough mixing tolerance in non-1BL/1RS translocation wheats.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 66, no. 3, pp. 187-195

(47)
ACCN:001255496 CTLN:3040135
ABSJ:G (Genetics Abstracts)
AUTH:Balatero, C.H.;Darvey, N.L.
AFFN:Plant Breed. Inst., Cobbitty, NSW 2570, Australia
TITL:Influence of selected wheat and rye genotypes on the direct synthesis
of hexaploid triticale.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 66, no. 3, pp. 179-185

(48)
ACCN:001255708 CTLN:3040475
ABSJ:G (Genetics Abstracts)
AUTH:Bariana, H.S.;McIntosh, R.A.
AFFN:CSIRO Div. Plant Ind., Grain Qual. Res. Lab., P.O. Box 7, North Ryde,
N.S.W. 2113, Australia
TITL:Cytogenetic studies in wheat. XV. Location of rust resistance genes in
VPM1 and their genetic linkage with other disease resistance genes in
chromosome 2A.
HTIL:GENOME.
HYER:1993.
HCOL:vol. 36, no. 3, pp. 476-482

(49)
ACCN:001255771 CTLN:3040538
ABSJ:G (Genetics Abstracts)
AUTH:Kawahara, T.
AFFN:Plant Germ-plasm Inst., Fac. Agric., Kyoto Univ., Mozume, Muko, Kyoto
617, Japan
TITL:Genetic analysis of Cs chlorosis in tetraploid wheats.
HTIL:JAP. J. GENET.
HSSN:0021-504X
HYER:1993.
HCOL:vol. 68, no. 2, pp. 147-153

(50)

ACCN:001255869   CTLN:3040652
ABSJ:N (Biochemistry Abstracts Part 2: Nucleic Acids); G (Genetics
Abstracts)
AUTH:Curry, J.;Walker-Simmons, M.K.
AFFN:U.S. Dep. Agric., Agric. Res. Serv., Wheat Genet., Qual., Physiol. and
Dis. Res., Washington State Univ., Pullman, WA 99164-6420, USA
TITL:Unusual sequence of group 3 LEA (II) mRNA inducible by dehydration
stress in wheat.
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993.
HCOL:vol. 21, no. 5, pp. 907-912

(51)
ACCN:001257138   CTLN:3050013
ABSJ:G (Genetics Abstracts); Z (Entomology Abstracts)
AUTH:Papp, M.;Mesterhazy, A.
AFFN:Cereal Res. Inst., Div. Wheat Breed., Group Dis. and Insect Resistance,
H-6701 Szeged, P.O. Box 391, Hungary
TITL:Resistance to bird cherry-oat aphid (Rhopalosiphum padi L.) in winter
wheat varieties.
HTIL:EUPHYTICA.
HSSN:0014-2336
HYER:1993.
HCOL:vol. 67, no. 1-2, pp. 49-57

(52)
ACCN:001261533   CTLN:3053777
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental
Biotechnology Abstracts)
AUTH:Ghaemi, M.;Sarrafi, A.;Alibert, G.
AFFN:Lab. Biotechnol. et Amelioration des Plantes (BAP) INP-ENSAT 145, Ave.
Muret 31076, Toulouse, France
TITL:Influence of genotype and culture conditions on the production of
embryos from anthers of tetraploid wheat (Triticum turgidum)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1993
HCOL:vol. 65, no. 2, pp. 81-85

(53)
ACCN:001261676   CTLN:3053927
ABSJ:G (Genetics Abstracts)
AUTH:Ceoloni, C.;Donini, P.
AFFN:Dep. Agrobiol. and Agrochem., Univ. Tuscia, 01100 Viterbo, Italy
TITL:Combining mutations for the two homoeologous pairing suppressor genes
Ph1 and Ph2 in common wheat and in hybrids with alien Triticeae
HTIL:GENOME
HYER:1993
HCOL:vol. 36, no. 2, pp. 377-386

(54)
ACCN:001262721   CTLN:3500526
ABSJ:G (Genetics Abstracts); N (Biochemistry Abstracts 2: Nucleic Acids)
AUTH:Coulthart, M.B.;Spencer, D.F.;Gray, M.W.*
AFFN:Program Evol. Biol., Canadian Inst. Adv. Res., Dep. Biochem.,
Dalhousie Univ., Halifax, NS B3H 4H7, Canada
TITL:Comparative analysis of a recombining-repeat-sequence family in the
mitochondrial genomes of wheat (Triticum aestivum L.) and rye (Secale
cereale L.)
HTIL:CURR. GENET.
HSSN:0172-8083
HYER:1993
HCOL:vol. 23, no. 3, pp. 255-264

(55)
ACCN:001265131 CTLN:3503020
ABSJ:G (Genetics Abstracts); N (Biochemistry Abstracts 2: Nucleic Acids)
AUTH:Sardana, R.;O'Dell, M.;Flavell, R.*
AFFN:John Innes Inst. AFRC Inst. Plant Sci. Res., John Innes Cent., Colney Lane, Norwich, NR4 7UH, UK
TITL:Correlation between the size of the intergenic regulatory region, the status of cytosine methylation of rRNA genes and nucleolar expression in wheat
HTIL:MOL. GEN. GENET.
HYER:1993
HCOL:vol. 236, no. 2-3, pp. 155-162

(56)
ACCN:001266128 CTLN:3504046
ABSJ:G (Genetics Abstracts)
AUTH:Nkongolo, K.K.;Lapitan, N.L.V.*;Quick, J.S.;Muhlmann, M.D.
AFFN:Dep. Agron., Colorado State Univ., Fort Collins, CO 80523, USA
TITL:An optimized fluorescence in situ hybridization procedure for detecting rye chromosomes in wheat
HTIL:GENOME
HYER:1993
HCOL:vol. 36, no. 4, pp. 701-705

(57)
ACCN:001266177 CTLN:3504095
ABSJ:G (Genetics Abstracts)
AUTH:D'Ovidio, R.
AFFN:Dip. Agrobiol. e Agrochim., Univ. Studi Tuscia, Via San Camillo de Lellis, 01100 Viterbo, Italy
TITL:Single-seed PCR of LMW glutenin genes to distinguish between durum wheat cultivars with good and poor technological properties
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1993
HCOL:vol. 22, no. 6, pp. 1173-1176

(58)
ACCN:001266178 CTLN:3504096
ABSJ:G (Genetics Abstracts)
AUTH:Metakovsky, E.V.;Ng, P.K.W.;Chernakov, V.M.;Pogna, N.E.;Bushuk, W.
AFFN:Ist. Sper. Cerealicoltura, 20079 S. Angelo Lodigiano, Milano, Italy
TITL:Gliadin alleles in Canadian western red spring wheat cultivars: Use of two different procedures of acid polyacrylamide gel electrophoresis for gliadin separation
HTIL:GENOME
HYER:1993
HCOL:vol. 36, no. 4, pp. 743-749

(59)
ACCN:001266183 CTLN:3504101
ABSJ:G (Genetics Abstracts)
AUTH:Bilang, R.;Zhang, Shibo;Leduc, N.;Iglesias, V.A.;Gisel, A.;Simmonds, J.;Potrykus, I.;Sautter, C.
AFFN:Dep. Crop and Soil, Michigan State Univ., East Lansing, MI 48824, USA
TITL:Transient gene expression in vegetative shoot apical meristems of wheat after ballistic microtargeting
HTIL:PLANT J.
HSSN:0960-7412
HYER:1993
HCOL:vol. 4, no. 4, pp. 735-744

(60)
ACCN:001266512 CTLN:3504483
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Friebe, B.;Jiang, J.;Gill, B.S.;Dyck, P.L.
AFFN:Dep. Plant Pathol., Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506-5501, USA
TITL:Radiation-induced nonhomoeologous wheat-Agropyron intermedium chromosomal translocations conferring resistance to leaf rust
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 2-3, pp. 141-149

(61)
ACCN:001274620 CTLN:3513041
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Albani, D.;Cote, M.-J.;Armstrong, K.C.;Chen, Q.;Segal, A.;Robert, L.S.*
AFFN:Plant Res. Centre, Agric. Canada Res. Branch, K.W. Neatby Bldg., Central Experimental Farm, Ottawa, ON K1A 0C6, Canada
TITL:PCR amplification of microdissected wheat chromosome arms in a simple 'single tube' reaction
HTIL:PLANT J.
HSSN:0960-7412
HYER:1993
HCOL:vol. 4, no. 5, pp. 899-903

(62)
ACCN:001283148 CTLN:3521565
ABSJ:G (Genetics Abstracts)
AUTH:Brett, G.M.;Mills, E.N.C.*;Tatham, A.S.;Fido, R.J.;Shewry, P.R.;Morgan, M.R.A.
AFFN:Dep. Agric. Sci., Univ. Bristol, AFRC Inst. Arable Crops Res., Long Ashton Res. Stn., Bristol, BS18 9AF, UK
TITL:Immunochemical identification of LMW subunits of glutenin associated with bread-making quality of wheat flours
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 4, pp. 442-448

(63)
ACCN:001283152 CTLN:3521569
ABSJ:G (Genetics Abstracts)
AUTH:Ciaffi, M.;Lafiandra, D.;Porceddu, E.;Benedettelli, S.
AFFN:Dep. Agrobiol. and Agrochem., Univ. Tuscia, 01100 Viterbo, Italy
TITL:Storage-protein variation in wild emmer wheat (Triticum turgidum ssp. dicoccoides) from Jordan and Turkey. I. Electrophoretic characterization of genotypes
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 4, pp. 474-480

(64)
ACCN:001283176 CTLN:3521593
ABSJ:G (Genetics Abstracts)
AUTH:Jolly, C.J.;Rahman, S.*;Kortt, A.A.;Higgins, T.J.V.
AFFN:CSIRO Div. Plant Ind., Grain Quality Res. Lab., PO Box 7, North Ryde, N.S.W. 2113, Australia
TITL:Characterisation of the wheat Mr 15 000 "grain-softness protein" and

analysis of the relationship between its accumulation in the whole
seed and grain softness
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 5, pp. 589-597

(65)
ACCN:001283279 CTLN:3521696
ABSJ:G (Genetics Abstracts)
AUTH:Torabinejad, J.;Mueller, R.J.*
AFFN:Dep. Biol., Utah State Univ., Logan, UT 84322-5305, USA
TITL:Genome analysis of intergeneric hybrids of apomictic and sexual
Australian Elymus species with wheat, barley and rye: Implication for
the transfer of apomixis to cereals
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 2-3, pp. 288-294

(66)
ACCN:001285866 CTLN:3524788
ABSJ:G (Genetics Abstracts)
AUTH:Silvela, L.;Ayuso, M.C.;Gil-Delgado, L.G.;Salaices, L.
AFFN:INIA, Ctra. de la Coruna, Km 7 Apdo 8111, 28040 Madrid, Spain
TITL:Genetic and environmental contributions to bread-wheat flour quality
using the SDS sedimentation test as an index
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 7, pp. 889-894

(67)
ACCN:001285873 CTLN:3524795
ABSJ:G (Genetics Abstracts)
AUTH:Vahl, U.;Mueller, G.;Boehme, T.
AFFN:KAI-e.V. Projectgroup Biotech. Bernburg, Strenzfelder Allee, D-O 4351
Bernburg, FRG
TITL:Electrophoretic protein analysis for the identification of doubled
haploid 1A-1R, 1B-1R wheat-rye double translocation lines and for the
assessment of their genetic stability
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 5, pp. 547-556

(68)
ACCN:001285879 CTLN:3524801
ABSJ:G (Genetics Abstracts)
AUTH:Kim, N.-S.;Armstrong, K.C.*;Fedak, G.;Fominaya, A.;Whelan, E.W.P.
AFFN:Plant Res. Cent., Res. Branch, Agric. Canada, Ottawa, K1A 0C6, Canada
TITL:Cytological and molecular characterization of a chromosome interchange
and addition lines in Cadet involving chromosome 5B of wheat and 6Ag
of Lophopyrum ponticum
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 7, pp. 827-832

(69)
ACCN:001285887 CTLN:3524809
ABSJ:G (Genetics Abstracts)
AUTH:Mena, M.;Orellana, J.;Lopez-Brana, I.;Garcia-Olmedo, F.;Delibes, A.*

AFFN:Dep. Biochem. and Mol. Biol., E. T. S. Ingenieros Agron.-UPM, E-28040 Madrid, Spain
TITL:Characterization of wheat/Aegilops ventricosa introgression and addition lines with respect to the M super(v) genome
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 2-3, pp. 197-204

(70)
ACCN:001285893 CTLN:3524815
ABSJ:G (Genetics Abstracts)
AUTH:Hsam, S.L.K.;Zeller, F.J.
AFFN:Tech. Univ. Muenchen, Inst. Pflanzenbau und Pflanzenzuechtung, D-85350 Freising-Weihenstephan, FRG
TITL:Haploid production in durum wheat by the interaction of Aegilops kotschyi cytoplasm and 1BL/1RS chromosomal interchange
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 8, pp. 951-954

(71)
ACCN:001285895 CTLN:3524817
ABSJ:G (Genetics Abstracts)
AUTH:Hartl, L.;Weiss, H.;Zeller, F.J.;Jahoor, A.*
AFFN:Lehrstuhl Pflanzenbau und Pflanzenzuechtung, Tech. Univ. Munich, D-85350 Freising-Weihenstephan, FRG
TITL:Use of RFLP markers for the identification of alleles of the Pm3 locus conferring powdery mildew resistance in wheat (Triticum aestivum L.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 8, pp. 959-963

(72)
ACCN:001285917 CTLN:3524839
ABSJ:G (Genetics Abstracts)
AUTH:King, I.P.;Purdie, K.A.;Rezanoor, H.N.;Koebner, R.M.D.;Miller, T.E.; Reader, S.M.;Nicholson, P.
AFFN:Cambridge Lab., IPSR, JI Cent., Colney, Norwich, Norfolk NR4 7UJ, UK
TITL:Characterization of Thinopyrum bessarabicum chromosome segments in wheat using random amplified polymorphic DNAs (RAPDs) and genomic in situ hybridization
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 8, pp. 895-900

(73)
ACCN:001285924 CTLN:3524846
ABSJ:V (Virology & AIDS Abstracts); G (Genetics Abstracts)
AUTH:Jiang, J.;Friebe, B.;Dhaliwal, H.S.;Martin, T.J.;Gill, B.S.*
AFFN:Dep. Plant Pathol., Wheat Genet. Resour. Cent., Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:Molecular cytogenetic analysis of Agropyron elongatum chromatin in wheat germplasm specifying resistance to wheat streak mosaic virus
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 1, pp. 41-48

(74)

ACCN:001285933   CTLN:3524855
ABSJ:G (Genetics Abstracts)
AUTH:Lukaszewski, A.J.;Curtis, C.A.
AFFN:Dep. Bot. and Plant Sci., Univ. California, Riverside, CA 92521-0124,
USA
TITL:Physical distribution of recombination in B-genome chromosomes of
tetraploid wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 1, pp. 121-127

(75)
ACCN:001285939   CTLN:3524861
ABSJ:G (Genetics Abstracts)
AUTH:Dachkevitch, T.;Redaelli, R.*;Biancardi, A.M.;Metakovsky, E.V.;Pogna,
N.E.
AFFN:Sez. S. Angelo Lodigiano, Ist. Sper. Cerealicolt., via Mulino 3, 20079
S. Angelo Lodigiano, Milano, Italy
TITL:Genetics of gliadins coded by the group 1 chromosomes in the high-
quality bread wheat cultivar Neepawa
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1993
HCOL:vol. 86, no. 2-3, pp. 389-399

V. Information

7th International Symposium on Preharvest Sprouting in Cereals (July 2-7, 1995; Abashiri, Japan)

Specific topics will include: Physiology and molecular biology of grain development and germination; influence of environmental, physical and agronomic factors on sprouting; genetics and plant breeding; effects of sprouting damage on cereal end products. To receive a second announcement contact: Secretariat, 7th International Symposium on Preharvest Sprouting in Cereals, Kitami Agricultural Experiment Station, Kunneppu, Hokkaido 099-14, Japan; telephone 0157-47-2146, fax 0157-47-2774 or M. K. Walker-Simmons, USDA-ARS, 209 Johnson Hall, Washington State University, Pullman, WA 99164-6420; telephone 509-335-8696, fax 509-335-8674, e-mail simmons@wsuvm1.edu.

ITMI Worksession of Plant Genome III (January 18, 1995; San Diego, California)

The International Plant Genome III Conference will take place January 15-19, 1995 at the Town and Country Hotel in San Diego, California. A 2.5 hour worksession for ITMI has been scheduled on Wednesday, Jan. 18, 3:30 to 6:00 pm. The session is designed to provide a forum for open discussion of application and problems involved with tools and technologies relevant to genome mapping in the Triticeae. Several individuals will make brief introductions to specific tools or practices, such as PCR techniques (RAPDs, microsatellites, STS, AFLP) or gene tagging, and their applications to mapping in the Triticeae. After each, discussion and comments from participants will be encouraged.

No specific registration for the worksession is required, but participants must be registered for Plant Genome III. For registration costs and procedures and program information for Plant Genome III, contact: Scherago International, Inc. at 212-643-1750 (telephone), 212-643-1758 (fax), or scherago@biotechnet.com (e-mail).

ITMI International Public Workshop (September 1-3, 1995; Norwich, England)

First announcement. The 1995 ITMI International Public Workshop will be held September 1-3 (finish 12:30 pm) at Norwich, England, hosted by the John Innes Centre following the annual meeting of the Society for Experimental Biology (SEB), August 29-31, 1995, at Queen's College, Cambridge. Direct transport from Cambridge to Norwich will be available. The Workshop agenda will include progress reports by ITMI coordinators on the status of genome mapping in wheat and other species of Triticeae and oral and poster presentations on research results in mapping and application of mapping technology. Please respond to the ITMI Management Office (address and communication information is given above), if you wish further information on the Workshop as it is developed.

For program and registration information for the SEB meeting, contact: Society for Experimental Biology, Burlington House, London W1V 0LQ, United Kingdom; Tel: 44 171 439 8732/ FAX 44 171 287 4786.

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VI. Editorial Remarks

During the last year, many contributions and suggestions have been sent to the office to propose further improvement of Wheat Information Service. We should appreciate Drs. McIntosh, Hart and Gale for their continuous effort to review gene symbol catalogue which is included in the present issue for 1994 supplement. From this volume, we start to enclose the bibliographical information of recent publications on wheat genetics which are kindly provided by Cambridge Scientific Abstracts. This is followed by one of proposals from subscripting members. Some articles are printed directly from computer floppy disk or photocopy to avoid editorial error. General Tables of Contents and Author Index are, also, listed in this volume.

Among those suggestions, followings are some of important examples, which should be discussed:

1) According to the original stand-point of WIS, non-reviewed articles should be included for idea, research information, and proposal as Research Note.

2) Donation system should be introduced for financial support, because we should contribute certain payment for benefit of ourself and for further improvement of WIS, although, at the same time, we have to consider economical difficulties in certain counties. For mutual support among world-wide wheat researches, certain donation system rather than membership payment is reasonable. (It is true that raising fund is necessary to cover increasing publication and postal costs and further service)

3) Changing name of the journal world extend the reputation of WIS, like Wheat Science, Wheat Research, or Wheat Genetics, so on.

The editorial committee will welcome for your opinion.

The next issue will be published in June, 1995. The articles for strain list, information, book advertisement and announcement should be mailed not later than the end of April, 1995. Research articles are accepted anytime.

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Explanation of the picture on the cover

C-banding pattern of 3A and 7A of Chinese Spring and the translocated chromosome of a Japanese common wheat variety, Saitama 27. See the article by A. M. Ali et al for the details.

WIS No.79

編集 国際小麦研究連絡会議
西 川 浩 三

発行所 木原記念 横浜生命科学振興財団
〒232 横浜市南区六ツ川 3-122-20
Tel. (045) 721-0751

発行日 1994年12月21日

印刷 株式会社 野 毛 印 刷
Tel. (045) 252-2511

Wheat Information Service No. 79

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