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Research article

The chromosomal distribution of crossability genes in durum wheat cv. Langdon

Liu Deng-Cai, Yen Chi, Yang Jun-Liang, Lan Xiu-Jin, Peng Zheng-Song and Zheng You-Liang

Triticeae Research Institute, Sichuan Agricultural University, Dujiangyan City, 611830, Sichuan, China

Summary

We crossed the 14 D-genome disomic substitutions of durum wheat cv. Langdon with an inbred rye and obtained a large variation in crossability percentages in the 1995-1996 and 1996-1997 growing seasons. The results showed that chromosomes 2A, 2B, 3B and 5B of Langdon carry crossability genes, while chromosomes 4B, 5A, 6A and 7A are involved in a suppressing effect on crossability with rye. Of which, chromosomes 2B and 3B showed a stronger effect on crossability than chromosome 5B, and chromosomes 4B and 7A showed a stronger effect than chromosome 5A. Thus, it was indicated that the tetraploid wheat cv. Langdon has a different *kr* system regulating crossability with rye in comparison with that of hexaploid common wheat.

Key words: Tetraploid wheat, crossability, inheritance

Introduction

The crossability of hexaploid common wheat with rye has been clearly shown to be controlled by four loci, designated *kr*1, *kr*2 (Lein 1943), *kr*3 (Krolow 1970) and *kr*4 (Luo et al. 1989), located on chromosome 5B, 5A (Riley and Chapman 1967), 5D (Krolow 1970) and 1A (Zheng et al. 1992), respectively. Dominant alleles of these crossability genes reduce crossability. The effect of *kr*1 is the greatest and the effect of *kr*4 gene is stronger than *kr*2 but weaker than *kr*1, while the effect of *kr*3 is very weak. Also, Miller et al. (1983) reported that chromosomes 3A and 3B carry genes affecting crossability.

Though as hexaploid wheat, tetraploid wheat has the *kr* system regulating crossability with rye (Krolow 1970), the evolution relationship of *kr* system between tetraploid wheat and hexaploid wheat is still an outstanding issue because data on the inheritance of crossability with rye in tetraploid wheat are quite rare.

Genç et al. (1996) crossed the 14 D-genome disomic substitutions of durum wheat cv. Langdon with rye and found that except 3D(3A) and 4D(4A), each of the remainder 12 substitutions showed

a significant variation in crossability according to the control (Langdon), of which the 7D(7A) line showed the highest crossability and the 2D(2B) showed the lowest. They suggested the variation in crossability involved in the remainder 8 chromosomes, except 1A, 3B, 5A and 5B, was probably caused by the heterozygosity present in the open pollinate rye parent, a Turkish landrace. However, an alternative explanation could be that the variation may have been caused by genes regulating crossability on the 8 chromosomes of Langdon. If the latter explanation is true, it will be indicated that there has a different *kr* system between tetraploid wheat cv. Langdon and hexaploid common wheat. Therefore, it is important that further studies to elucidate the effect of each of the 14 substitutions on the crossability with an inbred rye, rather than an open pollinate rye.

Materials and methods

A set of 14 disomic substitution lines in durum wheat cv. Langdon (*Triticum turgidum* ssp. *turgidum* conv. *durum*), in which each of A and B genome chromosome pairs of tetraploid wheat cultivar Langdon was replaced by a homoeologous pair from the D-genome of Chinese Spring, were pollinated with an inbred Chinese rye (*Secale cereale* L. cv. Qinling), used as male parent.

The emasculation and pollination techniques were the same as the previous paper (Liu et al. 1998). The number of florets with and without seeds for each spike was counted 25 days after pollination in the 1995-1996 season and 15 days after pollination in the 1996-1997 season. Crossability percentages were estimated as the ratio of the number of seed-set to number of florets pollinated. The t-test was adopted to detect the crossability differences between a substitution line and the control (Langdon).

Results and discussion

As seen in Table 1, in the 1995-1996 growing season, crossability percentages of D-genome substitutions of Langdon with rye varied from 1.25 to 54.6. When the crossability percentages were compared, it was shown that the substitution lines 4D(4B), 5D(5A), 6D(6A) and 7D(7A) were significantly higher than the control, while 2D(2A), 2D(2B), 3D(3B) and 5D(5B) were significantly lower than the control. Furthermore, 4D(4B) and 7D(7A) had a higher crossability than 5D(5A), while 2D(2B) and 3D(3B) had a lower crossability than 5D(5B), which was supported by the further studies in the following growing season, as seen in Table 2.

In fact, using an open pollinate rye as male tester, Genç et al. (1996) have found that most of the 14 substitutions of Langdon showed differences according to Langon, of which 7D(7A) had the highest crossability with rye and 2D(2B) had the lowest crossability. They suggested that the variation in crossability involved in the remainder chromosomes, except 1A, 3B, 5A and 5B, was probably caused by the heterozygosity present in the open pollinate rye parent, a Turkish landrace. However, in this paper, because of using an inbred rye as male parent, the variation can not be attributed to the heterozygosity of rye. The previous works have shown that except the weak *kr3* on chromosome 5D, no other crossability genes have been located on D-genome chromosome of cv. Chinese Spring, which provided the substituted D-genome chromosomes for the disomic substitution lines in durum wheat Langdon. Krolow (1970) located *kr3* on chromosome 5D, but other authors, such as Riley and Chapman (1967), reported that *kr3* has no significant effects on crossability with rey. We think that the higher crossability than control in lines 4D(4B), 5D(5A),

Table 1. Crossability of D-genome substitutions of cv. Langdon with rye in the 1995-1996 growing season

Lines	No. of floret pollinated	No. of seed-sets	Crossability percentage
1D(1A)	140	35	25.00
1D(1B)	106	29	27.36
2D(2A)	81	8	9.88*
2D(2B)	80	1	1.25*
3D(3A)	138	53	38.41
3D(3B)	130	3	2.31*
4D(4A)	138	24	17.39
4D(4B)	163	89	54.60*
5D(5A)	178	78	43.82*
5D(5B)	102	9	8.82*
6D(6A)	163	81	49.69*
6D(6B)	36	12	30.00
7D(7A)	112	59	52.68*
7D(7B)	92	31	33.70
Control cv. Langdon	121	35	28.93

*significant at 1% level

Table 2. Crossability of D-genome substitutions of cv. Langdon with rye in the 1996-1997 growing season

Lines	No. of floret pollinated	No. of seed-sets	Crossability percentage
2D(2B)	136	7	5.15*
3D(3B)	143	3	2.10*
4D(4B)	190	120	63.15*
5D(5A)	102	46	45.10*
5D(5B)	114	11	9.65*
7D(7A)	222	159	71.62*
Control cv. Langdon	176	59	33.52

6D(6A) and 7D(7A) indicates that chromosomes 4B, 5A, 6A and 7A of Langdon suppress crossability with rye. The lower crossability in lines 2D(2A), 2D(2B), 3D(3B) and 5D(5B) indicates that chromosomes 2A, 2B, 3B and 5B of Langdon carry crossability genes. Of which, chromosomes 2B and 3B showed a stronger effect on crossability than chromosome 5B, and chromosomes 4B and 7A showed a stronger effect than chromosome 5A.

On the other hand, the crossability genes in hexaploid wheat, *kr*1, *kr*2, *kr*3 and *kr*4 were respectively located on chromosome 5B, 5A, 5D and 1A (Riley and Chapman 1967, Krolow 1970, Zheng et al. 1992), and among them, the effect of *kr*1 on chromosome 5B is the greatest. Thus, it is more logical to suggest that tetraploid wheat cv. Langdon has a different *kr* system regulating crossability with rye in comparison with that of hexaploid wheat.

Meanwhile, the results of present study with regard to specific substitution line show some differences in comparison with those reported by Genç et al. (1996), such as the lines 4D(4B), 5D(5A) were reported to have low crossabiltiy with rye whereas we obtained high crossability. The differences may be caused by the different cultivars of rye in the crosses.

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Research article

Inter- and intravarietal polymorphism in C-banded chromosomes of *Aegilops caudata* L.

Androula Georgiou[1], Stylianos Karataglis[2] and Demetrios Roupakias[3]

[1]Horticultural Section, Agricultural Research Institute, Nicosia, Cyprus
(Georgiou@arinet.ari.gov.cy)
[2]Department of Botany, University of Thessaloniki, GR-54806, Thessaloniki, Greece
[3]Department of Agriculture, University of Thessaloniki, GR-54006, Thessaloniki, Greece

Summary

The chromosome C-banding pattern of two *Ae. caudata* varieties was studied. The two varieties showed a similar basic C-banding pattern, with a restricted inter- and intravarietal heterochromatic polymorphism. The polymorphism observed in var. *typica* concerns the SAT_2 and SM chromosomes while in var. *polyathera* the SM chromosome. In addition, small differences between the two varieties were observed on SAT_1, SAT_2, SM, ST_1 and ST_2 chromosomes. It was concluded that the two varieties had a restricted inter- and intravarietal polymorphism which indicates a close chromosomal similarity between the two varieties.

Key words: *Aegilops caudata* var. *typica*, *Aegilops caudata* var. *polyathera*, C-banding, inter- and intravarietal polymorphism.

Introduction

The genus *Aegilops* L. bears a close and important relationship with the cultivated wheat *Triticum aestivum*. *Aegilops caudata* L. is an annual diploid wild relative of wheat distributed over the Eastern Mediterranean. Eig (1929) described two varieties, var. *typica* and var. *polyathera* Boiss. which in Greece very often grow sympatrically.

Giemsa C-banding has been widely used for identifying wheat chromosomes and wheat-alien chromosome addition, substitution and translocation lines (Gill and Kimber 1974; Endo 1986; Gill et al. 1991). Only limited information is available about the banding pattern of wild relatives of wheat (Gill and Kimber 1974; Friebe and Heun 1989; Dhaliwal et al. 1990; Friebe et al. 1990) and so far a few reports describe the banding pattern of *Ae. caudata* (Gill 1981; Teoh and Hutchinson 1983; Schubert et al. 1987). However, the investigations on intraspecific variation in C-banding pattern of *Aegilops* species are few (Teoh et al. 1983; Friebe et al. 1992) and such work

on natural populations is fewer (Georgiou et al. 1992). Such information is very valuable for identifying chromatin of wild *Aegilops* species in wheat - *Aegilops* derivatives. The present study was undertaken to investigate the C-band polymorphism of the two *Ae. caudata* varieties *typica* and *polyathera* in a single mixed population.

Materials and methods

Plant material

The investigated varieties of *Ae. caudata* L. var. *typica* and var. *polyathera* Boiss. were collected from a natural population located between the villages Kassandrino and Scioni, Chalkidiki, Greece where the two varieties grow sympatrically. Voucher specimens of the plant material are kept at the Department of Botany, Aristotelian University of Thessaloniki, Greece.

Techniques

Cytological studies were carried out on cells from root tips. The C-banding technique used was described by Teoh and Hutchinson (1983). The C-banding patterns of *Ae. caudata* var. *typica* and var. *polyathera* were established from 17 and 13 seedlings, respectively. Each seedling came from an original seed collected from a different mother plant.

Band expression

The size of the C-bands varied from very small to large. The very small did not occur in all chromosomes, but only in less contracted chromosomes. The intensity of the staining varied among different preparations as well as within the same preparation. Bands, which were weak in intensely stained metaphases, were usually absent in weakly stained metaphases. For these reasons, the expression of each band was classified into three classes in the diagram shown in Fig. 3 according to the frequency of its appearance. The bands on each chromosome arm were numbered from centromere to telomere.

Measurements

The C-banding pattern of each plant was established from at least 10 complete metaphases. Complete and well-spread metaphase plates were drawn after magnification. The length of chromosomes and the width and position of each band were also calculated and are expressed in the diagrams. The total percentage of heterochromatin for each chromosome variant and karyotype was estimated. The centromere position was calculated by the arm ratio = S:L (S:short arm, L:long arm). The nomenclature followed Levan et al. (1965). The identification of homologous chromosomes was based on similarities of C-banding patterns and the position of the centromeres.

Results

Karyotype analysis of the two varieties of *Ae. caudata* studied indicated that the chromosome complement of both varieties was similar to that described by Karataglis (1975). Chromosome complement of each variety contains two satellited (SAT_1, SAT_2), one submetacentric (SM) and four subtelocentric (ST_1, ST_2, ST_3 and ST_4) chromosomes. (Figs. 1, 2, 3 and Table 1).

All chromosomes of both varieties had at least one centromeric band and a variable number of intercalary bands. In addition, six out of the seven chromosomes of the haploid set had at least

one terminal band. The position and the width of these bands for each individual chromosome are given in Table 2.

The C-banding pattern of each individual chromosome of the variety *typica* is described below separately (Figs. 1a, 1b, 2a and 3a).

SAT1: Both arms are characterized by the presence of five bands. On the short arm, one of them is centromeric, two intercalary, one terminal and the other is located besides the secondary

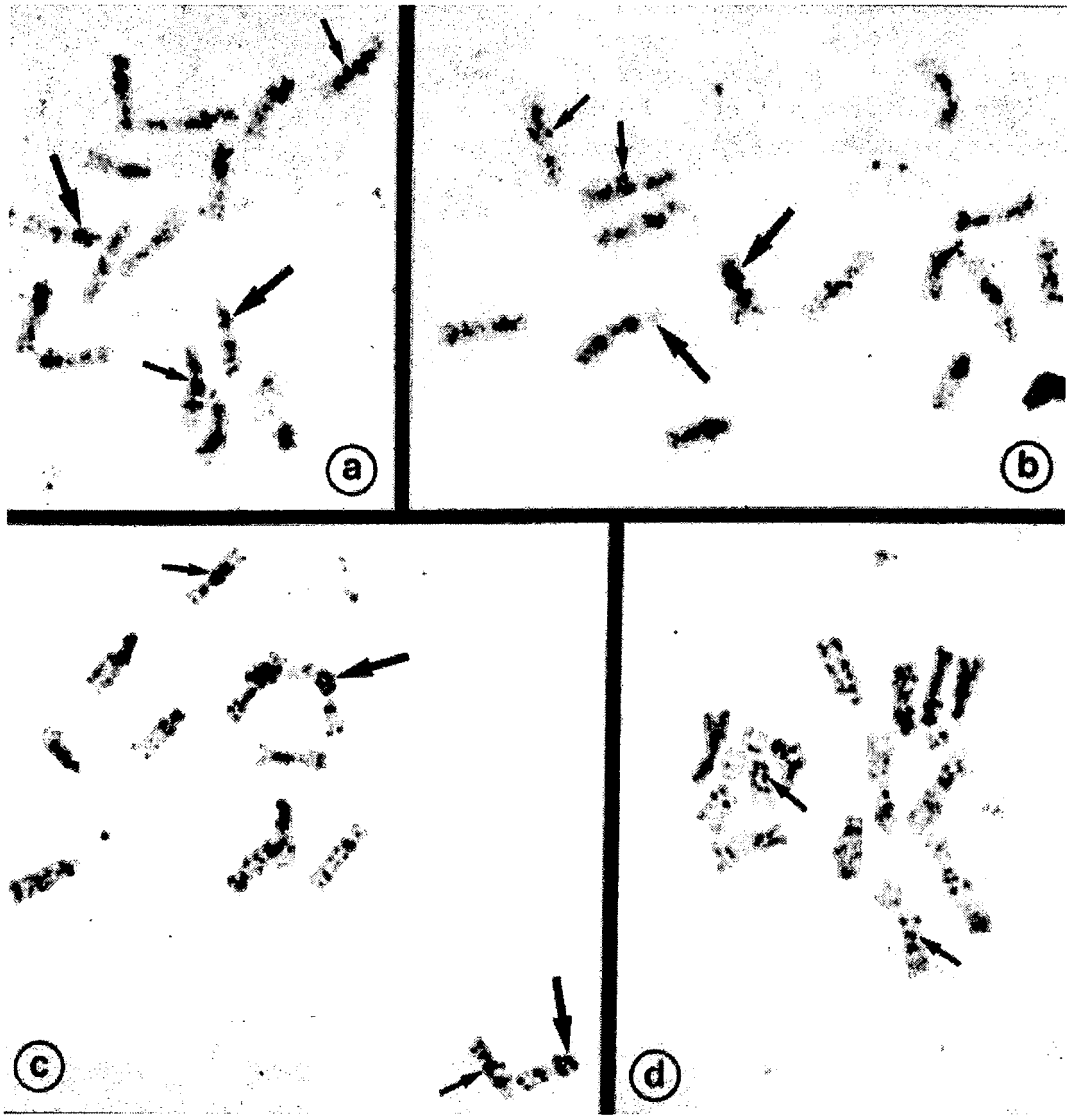

Fig. 1. Giemsa C-banded somatic metaphase plates of *Ae. caudata* var. *typica* (a and b) and var. *polyathera* (c and d). The small and large arrows indicate the chromosome pairs SM and SAT2, respectively.

constriction. The long arm has one terminal and four intercalary bands.

SAT_2: This chromosome is polymorphic with two variants. On the long arm of variant A three intercalary bands are situated between the terminal and the centromeric bands. The short arm of the same variant has two large bands which very often observed as a single band, and one band besides the secondary constriction which is absent from the variant B. The variant A is the most heavily banded chromosome of the complement.

SM: This chromosome has two variants and the polymorphism concerns both the position and the width of the L_2 band. Other two intercalary bands are also present on the long arm. The short arm has one terminal, one intercalary and one centromeric band.

ST_1: On the short arm one intercalary and one terminal band were observed. The long arm is characterized by one centromeric and five intercalary bands.

ST_2: This chromosome is the most heavily banded of all the ST chromosomes. The short arm has two intercalary bands while on the long arm there were one centromeric and six intercalary bands.

ST_3: This chromosome has two centromeric bands with the largest one on the side of the long arm. In addition, the short arm has a very small terminal band. The long arm has four intercalary bands.

ST_4: One centromeric band is observed on the short arm. The long arm has one terminal and three intercalary bands. Two of the intercalary bands are located very close to each other and often they fuse into a single band.

It is worth to be mentioned that in all the 17 plants studied from var. *typica* the chromosome pair SAT_2 was found to be homozygous, either AA (3 plants) or BB (14 plants). In contrast the

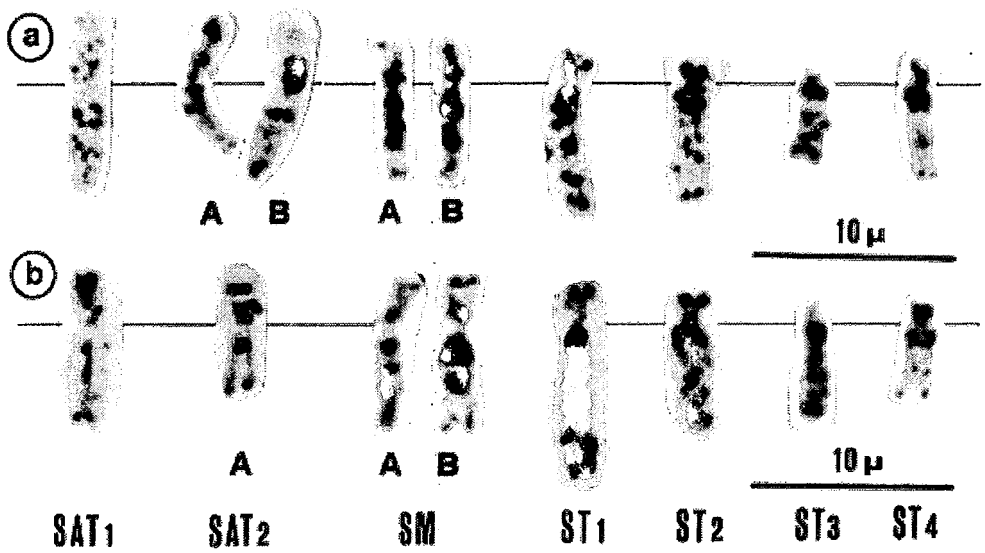

Fig. 2. Giemsa C-banded chromosomes and their variants of *Ae. caudata* var. *typica* (a) and var. *polyathera* (b).

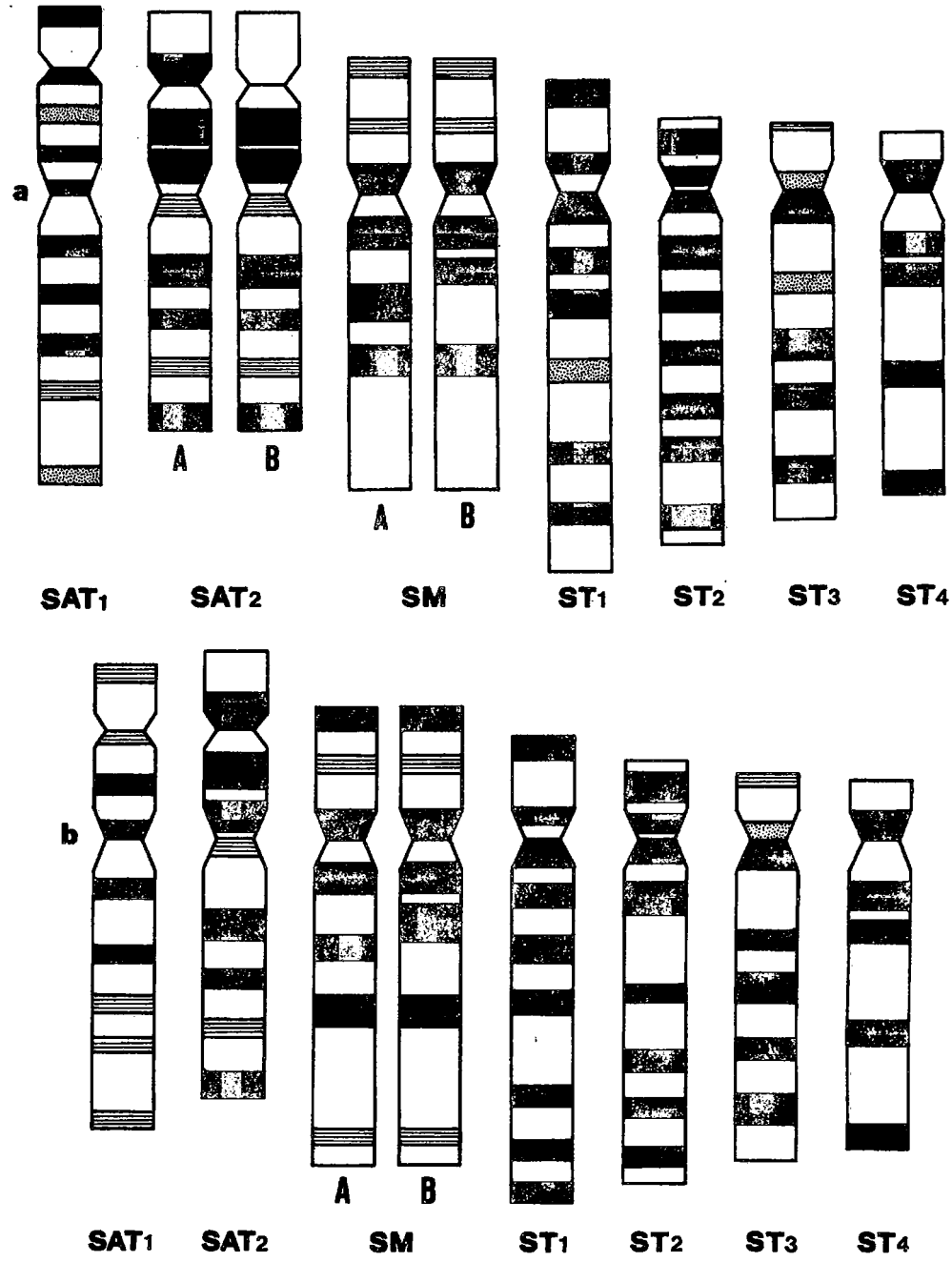

Fig. 3. Diagramic representation of the Giemsa C-banded chromosomes and their variants of *Ae. caudata* var. *typica* (a) and var. *polyathera* (b). Note the frequency of appearance of each band: ▒ 10-30%, ▤ 30-60% and ■ 60-100%.

Table 1. Chromosome arm ratio, number of bands, percentage of heterochromatin in each chromosome variant and percentage of heterochromatin in the diploid genome in *Aegilops caudata* var. *typica* and var. *polyathera*

	Chromosomes and their variants																
	typica									*polyathera*							
Observations	SAT_1	SAT_2		SM		ST_1	ST_2	ST_3	ST_4	SAT_1	SAT_2	SM		ST_1	ST_2	ST_3	ST_4
		A	B	A	B							A	B				
ARM ratio	0.63	0.79		0.44		0.27	0.19	0.20	0.20	0.60	0.75	0.46		0.27	0.23	0.19	0.20
No of bands	10	8	7	6	6	8	9	7	5	9	8	7	7	9	8	7	5
Heterochromatin (%) in each chromosome	45.6	52.2	44.9	40.6	38.0	43.2	48.8	43.0	32.5	41.8	52.2	43.4	46.0	45.0	46.0	45.6	34.8
Heterochromatin (%) in the diploid genome	42.28 (SAT_2:BB) or 43.70 (SAT_2:AA)									44.48 (SM:BB) or 44.48(SM:BB)							

chromosome pair SM in all plants was found to be heterozygous (AB).

The basic C-banding pattern of var. *polyathera* apart from slight differences appears to be same as that of var. *typica*. The most important differences are the following (Figs. 1c, 1d, 2b and 3b):

1. On the short arm of chromosome SAT_1 one intercalary band is absent.
2. Chromosome SAT_2 is not polymorphic and appears to be only the variant A.
3. Chromosome SM has an additional subterminal band on the long arm. In addition, the variant A of this chromosome has a narrower L_2 band than that observed in var. *typica*. The opposite was observed for the L_2 band on the variant B.
4. An additional terminal band was identified on chromosome ST_1.
5. An intercalary band was absent from the long arm of chromosome ST_2.

Table 2. Position (the distance of the band centre from the centromere in % of the chromosome arm on which the band is located) and width (in % of the haploid karyotype length) of the C-bands of *Ae. caudata* var. *typica* and var. *polyathera*

Chromosomes	Bands	Varieties			
		typica		*polyathera*	
		Position	Width	Position	Width
SAT_1	S_1	3.82 ± 1.90	0.49 ± 0.17	5.21 ± 0.28	0.61 ± 0.02
	S_2	21.50 ± 9.28	0.58 ± 0.12	31.42 ± 9.22	0.69 ± 0.15
	S_3	40.76 ± 10.23	0.66 ± 0.12	57.46 ± 0.01	0.53 ± 0.01
	S_4	59.23 ± 5.71	0.58 ± 0.15	92.01 ± 5.50	0.91 ± 0.25
	S_5	92.99 ± 3.38	0.84 ± 0.14		
	L_1	18.99 ± 4.41	0.90 ± 0.17	24.73 ± 5.54	0.69 ± 0.12
	L_2	35.52 ± 1.44	0.81 ± 0.14	40.72 ± 5.65	0.69 ± 0.05
	L_3	51.33 ± 3.90	0.82 ± 0.20	57.78 ± 6.82	0.73 ± 0.04
	L_4	67.14 ± 6.36	0.71 ± 0.34	72.70 ± 2.66	0.68 ± 0.20
	L_5	95.38 ± 3.08	0.82 ± 0.12	95.73 ± 0.32	0.80 ± 0.07
SAT_2	S_1	16.14 ± 4.80	1.03 ± 0.09	10.78 ± 1.11	1.10 ± 0.31
	S_2	36.90 ± 5.40	1.18 ± 0.33	35.27 ± 13.30	1.17 ± 0.31
	S_3	67.71 ± 1.35	1.02 ± 0.07	66.30 ± 4.74	1.20 ± 0.27
	L_1	5.30 ± 1.39	0.83 ± 0.26	4.17 ± 0.11	0.72 ± 0.03
	L_2	32.98 ± 4.98	1.07 ± 0.38	33.49 ± 6.02	1.06 ± 0.24
	L_3	53.39 ± 3.46	0.65 ± 0.12	53.53 ± 3.13	0.68 ± 0.05
	L_4	72.69 ± 1.86	0.56 ± 0.16	74.85 ± 1.74	0.61 ± 0.18
	L_5	93.63 ± 2.03	0.93 ± 0.22	93.63 ± 1.62	0.99 ± 0.19
SM	S_1	11.88 ± 6.47	1.04 ± 0.29	11.01 ± 5.75	0.99 ± 0.22
	S_2	50.22 ± 6.70	0.50 ± 0.15	53.76 ± 0.01	0.73 ± 0.1

Table 2 (continued)

Chromosomes	Bands	Varieties			
		typica		*polyathera*	
		Position	Width	Position	Width
	S_3	85.71 ± 4.24	0.85 ± 0.51	90.49 ± 0.88	0.85 ± 0.07
	L_1	13.77 ± 2.35	1.11 ± 0.31	11.77 ± 2.32	1.12 ± 0.42
	L_2A	37.45 ± 3.26	1.23 ± 0.23	33.18 ± 4.03	0.85 ± 0.09
	L_2B	26.53 ± 2.35	0.87 ± 0.03	26.41 ± 2.59	1.25 ± 0.02
	L_3	57.24 ± 4.69	1.06 ± 0.29	52.18 ± 4.45	1.02 ± 0.22
	L_4			93.51 ± 2.22	0.80 ± 0.02
ST_1	S_1	25.73 ± 3.98	0.75 ± 0.10	23.34 ± 0.01	0.63 ± 0.01
	S_2	88.09 ± 7.50	0.90 ± 0.19	89.00 ± 0.50	0.76 ± 0.01
	L_1	6.94 ± 1.19	1.14 ± 0.12	5.74 ± 0.17	0.96 ± 0.06
	L_2	18.70 ± 0.54	0.82 ± 0.13	15.65 ± 2.33	0.84 ± 0.13
	L_3	29.85 ± 3.01	0.93 ± 0.23	30.39 ± 2.50	0.97 ± 0.07
	L_4	44.22 ± 0.27	1.01 ± 0.09	45.54 ± 0.08	0.78 ± 0.20
	L_5	69.20 ± 2.14	0.77 ± 0.14	71.60 ± 4.16	0.60 ± 0.10
	L_6	85.04 ± 2.57	0.74 ± 0.14	85.43 ± 3.08	0.68 ± 0.27
	L_7			96.42 ± 0.01	0.74 ± 0.01
ST_2	S_1	20.32 ± 4.76	0.58 ± 0.08	16.60 ± 3.02	0.60 ± 0.02
	S_2	63.34 ± 5.45	0.85 ± 0.10	63.77 ± 7.17	1.03 ± 0.15
	L_1	4.59 ± 1.13	0.69 ± 0.31	5.53 ± 0.08	0.81 ± 0.03
	L_2	17.68 ± 3.05	1.12 ± 0.32	17.63 ± 4.38	1.10 ± 0.37
	L_3	32.23 ± 0.51	0.65 ± 0.07	45.35 ± 2.63	0.83 ± 0.24
	L_4	46.52 ± 2.43	0.72 ± 0.10	64.47 ± 4.38	0.77 ± 0.15
	L_5	61.20 ± 0.26	0.75 ± 0.05	78.86 ± 2.37	0.57 ± 0.02
	L_6	74.59 ± 1.80	0.74 ± 0.15	92.54 ± 4.56	0.75 ± 0.20
	L_7	93.22 ± 3.35	0.78 ± 0.13		
ST_3	S_1	15.42 ± 0.02	0.70 ± 0.02	14.86 ± 1.80	0.67 ± 0.09
	S_2	93.83 ± 0.04	0.27 ± 0.02	88.74 ± 1.80	0.48 ± 0.10
	L_1	5.52 ± 2.20	1.20 ± 0.42	5.55 ± 1.03	1.18 ± 0.23
	L_2	28.60 ± 0.92	0.82 ± 0.11	30.60 ± 2.35	0.85 ± 0.03
	L_3	47.02 ± 3.21	1.06 ± 0.16	46.33 ± 6.12	0.91 ± 0.11
	L_4	62.60 ± 2.29	0.85 ± 0.06	65.54 ± 2.92	0.75 ± 0.13
	L_5	83.87 ± 3.12	0.98 ± 0.19	83.61 ± 2.45	1.01 ± 0.19
ST_4	S_1	25.08 ± 1.95	0.99 ± 0.09	22.77 ± 2.98	0.92 ± 0.12
	L_1	18.05 ± 0.29	0.80 ± 0.02	18.85 ± 2.27	0.94 ± 0.33
	L_2	27.32 ± 0.29	0.68 ± 0.12	30.20 ± 3.36	0.78 ± 0.11
	L_3	60.16 ± 3.13	0.77 ± 0.25	62.98 ± 3.55	0.83 ± 0.15
	L_4	96.55 ± 0.79	0.70 ± 0.19	96.25 ± 0.89	0.76 ± 0.18

6. In all the 13 plants studied from var. *polyathera* the chromosome pair SM was found to be homozygous, either AA (8 plants) or BB (5 plants).

Discussion

In spite of the observed inter- and intravarietal C-banding polymorphism in *Ae. caudata* var. *typica* and var. *polyathera*, all chromosomes of the complement show a distinct C-banding pattern allowing precise identification. At both inter- and intravarietal level the polymorphic variation involved variability in the presence of terminal and intercalary bands and those beside the secondary constriction and variability in size and position of intercalary bands. Whereas the intravarietal polymorphism was connected with two chromosomes in var. *typica*, it was more restricted and connected only with one chromosome in var. *polyathera*.

The most important difference between the two varieties was connected with the chromosomes SAT_1, SAT_2, SM, ST_1 and ST_2. Karataglis (1975), based on Feulgen preparations, suggested that the two varieties could be different from each other in the amount of heterochromatic regions. This was not the case in the current work, however, since the amount of heterochromatin found in both varieties was almost the same (Table 1).

Teoh and Hutchinson (1983) and Friebe et al. (1992) studied the C-banding pattern in one and nineteen accessions of *Ae. caudata*, respectively. The overall chromosome morphology and C-banding pattern reported by these authors is similar to that described in the present study. The differences in chromosome morphology concerns the satellited chromosomes. According to Teoh and Hutchinson (1983) the more submetacentric satellited chromosome carries the longest satellite. In this study, as well as in the study of Friebe et al. (1992), the opposite is the case. However, the present C-banding pattern of the SAT_2 chromosome is more similar to that reported by Teoh and Hutchinson (1983) for the more submetacentric and to that reported by Friebe et al. (1992) for the less submetacentric satellited chromosome. Differences in C-banding pattern among the three studies are mainly the presence or the size of some intercalary bands.

In conclusion, the restricted inter- and intravarietal C-banding polymorphism observed in the two varieties of *Ae. caudata* indicates a close chromosomal similarity between *Ae. caudata* var. *typica* and var. *polyathera* and the possibility of intercross between the two varieties at the sympatric population. This is in agreement with the morphological data, the karyotype analysis, and the isozyme similarities reported by other investigators (Kihara 1954; Karataglis 1975; Symeonidis et al. 1979; Tsekos et al. 1981) as well as with the normal fertility of F_1 hybrids from reciprocal crosses between the two varieties collected from sympatric populations (Ohta 1992).

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Research article

Genetical studies and transgressive segregation for field resistance to leaf rust of wheat

B. Yadav, C.S. Tyagi and D. Singh

Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125004, India

Summary

The diallel analysis for combining ability, indicated that large portion of the genetic variation observed for field resistance to leaf rust of wheat was associated with gca effects. In general, the results from diallel analysis were in agreement with the estimates obtained from generation mean analysis. Combining ability analysis along with generation mean analysis appeared to be promising for selecting parents and crosses for transgressive segregants. The present study demonstrated that potential crosses giving transgressive segregants for field resistance to leaf rust were those that showed dispersion of genes among parents, high sca effects and involved at least one of the parents as a good general combiner. The highest frequency of transgressive segregants in F_4 was obtained in WH 377 x HD 2329 which involved WH 377 as a good and HD 2329 as a poor general combiner besides the possibility of having dispersion of genes for field resistance. Prediction for F_{∞} was found to be more accurate from F_3 families than that from generation mean analysis.

Key words: *Triticum aestivum*, cross prediction, transgressive segregation, field resistance

Introduction

Leaf rust of wheat (*Triticum aestivum* L. em. Thell.) caused by *Puccinia recondita* Rob. ex. Desm, is the most common and widely distributed foliar disease of wheat in the world (Statler and Miller 1982: McIntosh et al. 1995). The most effective way of controlling this disease is to develop resistant cultivars. Currently, there is much interest in the type of resistance that is expressed under natural field conditions as opposed to seedling resistance (Kuhn et al. 1980; Knott 1982; Yadav et al. 1992; Knott and Yadav 1993; Broers et al. 1996). This form of resistance usually is longer lasting and quantitative in inheritance. The importance of this disease led plant breeders to attempt new breeding approaches for developing resistant genotypes. The use of transgressive segregants which surpass the best parent has been considered a valuable approach for developing

resistant genotypes (Smith 1966; Wallwork and Johnson 1984; Broers and Jacobs 1989; Yadav et al. 1992). Quantitative genetic theory provides models for predicting frequencies of transgressive segregants in the progeny of crosses between two pure breeding lines. Jinks and Pooni (1976, 1980) have shown how estimates of genetical parameters can be used to predict frequency of transgressive segregants that would appear in later generations. In the present study, attempts were made to predict the frequency of transgressive segregants for field resistance using various mating designs including diallel, generation mean analysis, biparental matings and selfings and to test the validity of the predictions by isolating the transgressive segregants in the different generations.

Materials and methods

Initially, six cultivars (WC 29, WH 291, SGP 14, RAJ. 1972, WH 377 and HD 2329) of spring wheat were crossed in all possible combinations, excluding reciprocals, and their 15 F_1's were grown in a Randomized Block Design with three replications. Five plants in each replication were selected for recording observations. Six basic generations (P_1, P_2, F_1, F_2, BC_1, BC_2) of three crosses viz, WC 29 x WH 291, SGP 14 x RAJ. 1972 and WH 377 x HD 2329 selected on the basis of combining ability were developed to determine gene effects and to predict the frequencies of transgressive segregants. The six basic generations were grown in a Randomized Block Design with three replications. Five plants in each non-segregating generation, 25 in each backcross generation and 50 plants in each F_2 population were taken for recording observations. To predict frequency of transgressive segregants using F_3 family data, a random sample of 30 F_2 plants was taken to produce 30 F_3 families of each cross. The parents and progenies were grown in an Augmented Design with six blocks. Fifteen plants in each F_3 families of each cross and five plants in each of the parents in each block were taken at random for recording observations.

To identify transgressive segregants in the F_2 population, the parents, F_1's and F_2 population of each cross were grown in a Randomized Block Design with three replications. Five plants in each of the non-segregating generations and 350 plants in each of the F_2 population in each replication were selected randomly for recording observations. The F_3 progeny of selected transgressive segregants were grown for progeny testing

To identify transgressive segregants in biparental progenies (BIPs) and F_4 bulks, the parents, BIPs and F_4 of each cross were grown in an Augmented Design with six blocks. Five plants of each parent in each block and 450 plants in each population of each cross were taken at random to identify transgressive segregants.

In each experiment, the row length was 6m, spaced 25 cm apart. The plant to plant distance within rows was 15 cm. To ensure leaf rust development, spreader rows were planted around each replication in each experiment. Spreader rows were inoculated artificially with a mixture of races of leaf rust of wheat. The observation on leaf rust was recorded following Loegering (1959). Field resistance expressed as a coefficient of infection was computed as described by Yadav (1984).

Analysis of variance for Randomized Block Design and Augmented Design was done following Addelman (1969) and Federer (1961), respectively. Combining ability analysis was carried out following Method 4, Model 1 of Griffing (1956). Initially, generation mean analysis following three parameter model as suggested by Cavalli (1952) was carried out. A six parameter model suggested by Hayman (1958) was applied if the three parameter model was found to be inadequate.

Table 1. Analysis of variance for coefficient of infection to leaf rust of wheat

Source of variation	d.f.	Mean squares
Replication	2	0.5
Treatment	14	502.1**
Error	28	1.9
gca	5	285.8**
sca	9	101.6**
Error	28	0.6
General predictability ratio		1.9

**Significant at 1% level of probability

The frequency of transgressive segregants was predicted from generation mean analysis and F_3 family alone following Jinks and Pooni (1976, 1980).

Results and discussion

Significant mean square due to general combining ability (gca) and specific combining ability (sca) indicated the importance of both additive and non-additive gene effects (Table 1). However, general predictability ratio as suggested by Baker (1978) indicated that additive gene effects were predominant and prediction for crosses to obtain desirable segregants could be made on the basis of gca effects. The parents WH 291 and WH 377 were found to be good general combiners whereas RAJ. 1972 was found to be an average general combiner (Table 2). Other parents showed poor gca effects. Paroda and Joshi (1970) and Gill et al. (1972) argued that crosses involving one of the parents as good general combiner can be expected to throw desirable segregants. Therefore, three crosses WC 29 x WH 291, SGP 14 x RAJ. 1972 and WH 377 x HD 2329 which involved one of the parents as good or average general combiner and had good to poor sca effects were selected for further studies.

The joint scaling test of Cavalli (1952) revealed that the additive-dominance model was inadequate in all three crosses (Table 3). The failure of the model may be due to linkage, or two or many genes that may also involve higher order epistasis. Therefore, the six parameter model in each cross was applied. In general, there was a close agreement between the results of joint scaling test and six parameter model. However, the dominance component estimated through joint scaling test in WC 29 x WH 291 was found to be non-significant in six parameter model. This may be attributed to either sampling error leading to a high standard error of the estimate or internal cancellation of the gene effects in the presence of epistasis. Similar discrepancies between the results of joint scaling test and six parameter model were reported by Tonk (1988). The additive effect was higher in magnitude than dominance effect in WC 29 x WH 291 and SGP 14 x RAJ. 1972. In such cases, intermating and mass selection in early generation followed by single plant selection in later generations could be useful to derive desirable segregants (Bhatt 1972). In WH 377 x HD 2329, dominance effect was higher in magnitude than additive effect.

Table 2. Estimates of general combining ability (gca) and specific combining ability (sca) effects for coefficient of infection to leaf rust of wheat

Parents/ crosses	WC 29	WH 291	SGP 14	RAJ. 1972	WH 377	HD 2329
WC 29	4.8	-3.6	-5.2	-3.4	2.1	10.1
WH 291		-8.3	-2.0	7.6	7.1	-9.1
SGP 14			3.1	-6.7	-2.6	16.5
RAJ. 1972				-4.9	6.7	- 4.2
WH 377					-7.7	- 13.3
HD 2329						13.1

l.s.d. (gca)=1.1
l.s.d. (sca)=1.6

Table 3. Estimate of gene effects for coefficient of infection to leaf rust of wheat in three crosses of wheat

Model	Parameter	WC 29 x WH 291	SGP14 x RAJ. 1972	WH 377 x HD 2329
Three	m	40.7 ± 0.5	39.1 ± 0.4	13.6 ± 0.8
parameter	[d]	-31.9 ± 0.5**	- 33.2 ± 0.4**	-11.4 ± 0.7**
	[h]	-35.8 ± 0.8**	- 37.7 ± 0.5**	-12.5 ± 0.8**
χ^2(3d.f.)		25.1**	253.2**	101.2**
	m	18.2 ± 1.7	22.9 ± 2.1	19.9 ± 2.1
	[d]	-27.1 ± 2.1**	19.2 ± 1.9**	-4.1 ± 1.3**
	[h]	3.3 ± 8.0	-15.3 ± 3.4**	-22.3 ± 8.9*
	[i]	32.9 ± 8.0**	-7.3 ± 9.4	-17.3 ± 8.9
	[j]	4.9 ± 2.2*	-15.1 ± 2.0**	8.1 ± 1.3**
	[1]	-48.2 ± 11.0**	6.0 ± 11.5	-31.2 ± 9.9**
	Epistasis	C	-	C

* and ** Significant at 5% and 1% level of probability, respectively
C=Complementary epistasis

Table 4. Predicted and observed frequencies of transgressive segregants for field resistance to leaf rust of wheat in different population of three crosses

Population	WC 29 x WH 291	SGP 14 x RAJ. 1972	WH 377 x HD 2329	Source of prediction
1	2	3	4	5
F_2				
No. of plants studied	1050	1050	1050	
No. of plants selected	48	22	12	
No. of F_3 families selected	4	-	8	
No. of plants predicted	-	177	-	
Observed frequency (%)	0.38	-	0.76	
Expected frequency (%)	-	16.86	-	Generation mean analysis
χ^2 (1 d.f.)	-	-	-	
BIP				
No. of plants studied	450	450	450	
No. of plants selected	35	17	7	
No. of plants predicted	-	76.0	-	
Observed frequeny (%)	7.78	3.78	1.56	
Expected frequency (%)	-	16.86	-	Generation mean analysis
χ^2 (1d.f.)	-	45.80**	-	
F_4				
No. of plants studied	450	450	450	
No. of plants selected	3	3	11	
No. of plants predicted	3	2	20	
Observed frequency (%)	0.67	0.76	2.44	
Expected frequency (%)	0.76	0.43	44.43	Generation mean analysis
χ^2(1 d.f.)	0.00	0.50	178.61	
F_∞				
No. of plants expected / 450	5	-	122.0	
Expected frequency (%)	1.04	-	27.09	
χ^2 in relation to F_4	0.80	-	100.99	
No. of plants predicted / 450	5	2	10	
Expected frequency (%)	1.13	0.42	2.12	F_3 progeny
(1 d.f.) in relation to F_4	0.80	0.50	0.10	

** Significant at 1% level of probability

This revealed the possibility of dispersion of genes for field resistance among the parents. In such a situation, transgressive segregants could be expected in later generations. Negative value of dominance effect exhibited to directional dominance of increasing alleles imparting field resistance. Contradictory results were reported by Singh et al. (1988). A perusal of epistatic gene effect indicated the preponderance of additive x additive gene effects in WC 29 x WH 291 whereas in other two crosses it was non-significant. Other types of non-fixable epistatic gene effects were also noted in different crosses. Under such situations, in order to get transgressive segregants and break undesirable linkages intermating followed by selection in early generations has been advocated by Gill et al. (1974) and Singh et al. (1986).

In the present study, a higher frequency of transgressive segregants was observed in the BIPs than F_2 and F_4 populations in WC 29 x WH 291 and SGP 14 x RAJ. 1972 (Table 4). In WH 377 x HD 2329, frequency of transgressive segregants was higher in F_4 than F_2 and BIPs. In general more plants were selected in F_2 than F_4 but majority of them were discarded on progeny testing because they showed either a low mean value or segregation. This was not unexpected because of high level of heterozygosity in the F_2 population. Significant differences between predicted and observed frequencies of transgressive segregants in the F_2 and BIPs were recorded. This may be due to the failure of the model. Prediction for the F_∞ generation was found to be more accurate from F_3 families than that from generation mean analysis. This was evident from non-significant values of χ^2 between observed frequencies in F_4 and predicted frequencies in F_∞. The present results are in conformity with the findings of Jinks and Pooni (1980) in tobacco. The highest frequency of transgressive segregants in F_4 was obtained in WH 377 x HD 2329 and gave good fit to the predicted frequencies in F_4.

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Research article

Chromosomal location of genes controlling final coleoptile length in wheat using chromosome substitution lines

T. Matsui[1], S. Inanaga[1], Y. Sugimoto[1] and N. Nakata[2]

[1]Arid Land Research Center, Tottori University, Hamasaka 1390, Tottori 680-0001, Japan
[2]Faculty of Agriculture, Tottori University, Koyama, Tottori 680-0945, Japan

Summary

Seedling emergence in wheat is closely associated with the final coleoptile length. This association is important when considering cultivars suitable for deep sowing cultivation in arid regions. The study reported in this paper was designed to investigate differences in the final coleoptile length among seven selected wheat cultivars and to determine chromosomal locations of genes controlling the final coleoptile length by using Cheyenne disomic substitution lines in Chinese Spring. Differences among cultivars in final coleoptile length were evident. Hongwangmai had the longest coleoptile, while Cheyenne had the shortest. The difference in the final coleoptile length between Chinese Spring and Cheyenne was highly significant. The substitution line 4D had a longer coleoptile than Chinese Spring, while 15 lines had significantly shorter coleoptiles. Four (1A, 4A, 5A and 5B) of the 15 lines showed remarkable reductions in the final coleoptile length. It was concluded, therefore, that the most influential genes controlling the final coleoptile length are located on the 5 chromosomes.

Key words: Cheyenne, Chinese Spring, Chromosome substitution line, Coleoptile, Deep sowing

Introduction

In the arid regions, surface soils dry rapidly resulting in a water deficit that constitutes a major constraint to crop production. Crops often suffer serious losses in stand due to poor germination and emergence. To avoid poor germination and/or emergence, crops in the dry regions are sown deeper than those in the wet regions. This sowing method, known as deep sowing cultivation, is made feasible by the relative stability in water content of the deep soil layers. Deep sowing has limitations as it may impair crop emergence (Martin et al. 1976). The limits imposed by sowing depth are, however, different for each crop and cultivar (Kudair and Adary 1982, Martin et al. 1976, Matsui et al. in press). The other studies indicated usual positive correlation between coleoptile length in wheat (*Triticum aestivum* L.) and seedling emergence (Feather et al. 1968;

Nayyar and Josum 1978). This correlation is more remarkable under deep sowing (Burleigh et al. 1965; Sunderman 1964).

Varietal differences in coleoptile length were reported in many studies (Ashraf and Taylor 1974; Kudair and Adary 1982; Matsui et al. 1998; Nayyar and Josum 1978). Coleoptile length is basically inheritable character and controlled by several genes (Allan et al. 1961; Chowdhry and Allan 1963). In most experiments on inheritance of coleoptile length in wheat, plants were raised under shallow sowing. Furthermore, coleoptile length, and not the final coleoptile length, was referred to in most publications (Allan and Vogel 1964; Allan et al. 1962; Allan et al. 1961; Chowdhry and Allan 1963). In this study, final coleoptile length is defined as the length after which no elongation takes place. The final coleoptile length is more important character than coleoptile length for emergence under deep sowing and is determinant for tolerance to deep sowing.

Inadequate information is available on inheritance and chromosomal location of genes controlling final coleoptile length. Using chromosome substitution lines, this investigation was undertaken to determine the chromosomal locations of the genes controlling final coleoptile length in wheat.

Materials and methods

Two separate experiments were conducted. In the first experiment, seven cultivars, namely Hongwangmai, Ninchun No.10 and Mianyang No.11 from China, Sv 85131 from Sweden, Haruhikari from Japan, Chinese Spring and Cheyenne were used. In the second experiment, the Cheyenne disomic substitution lines in Chinese Spring and their parents, maintained by the Plant Genetics and Breeding Laboratory of Tottori University Japan, were employed. Planting was done in vinyl pots (diameter 8.3 cm x height 44.0 cm) filled with vermiculite. The pots were placed at 22°C in a dark room. Twenty wheat seeds were sown in each pot at a depth of 15 cm.

Table 1. Final coleoptile length of seven cultivars in wheat

Cultivar[1)]	Mean final coleoptile length (cm)	SE
Hongwangmai	14.6 a[2)]	±0.2
Chinese Spring	13.1 b	±0.2
Haruhikari	13.1 b	±0.6
Mianyang No. 11	10.6 c	±0.1
Ninchun No, 10	10.3 cd	±0.4
Sv 85131	9.3 de	±0.2
Cheyenne	9.0 e	±0.2

1) A total of 100 seedlings of each variety was examined: 20 seedlings x 5 replications.

2) Means followed by the same letters are not significantly different at 1% level according to Duncan's Multiple Range Test.

Water potential was adjusted to -0.18 MPa. Treatments were arranged in a complete randomized design with 5 replications. Final coleoptile length was measured after cessation of elongation, 12 days after sowing. Data were evaluated by analysis of variance and means were tested for significance by the Duncan Multiple Range Test.

Results and discussion

In the first experiment, varietal differences in the final coleoptile length were, invariably, significant and each cultivar had a characteristic final coleoptile length (Table 1). Hongwangmai, which has been successfully used in deep sowing cultivation in the Loess Plateau in China, had the longest coleoptile, while Cheyenne had the shortest. Relationship between the final coleoptile

Table 2. Final coleoptile length of Chinese Spring and its Cheyenne chromosome substitution lines

Line	Mean final coleoptile length (cm)
1A	10.7 a [1)]
1B	12.4 d
1D	13.2 ef
2A	12.8 e
2B	11.4 b
2D	12.3 d
3A	11.5 bc
3B	11.9 cd
3D	12.8 eg
4A	11.0 a
4B	11.6 bc
4D	14.0 g
5A	10.9 a
5B	10.6 a
5D	12.3 d
6A	11.9 cd
6B	12.8 e
6D	13.3 f
7A	11.4 b
7B	11.5 bc
7D	11.7 bc
Chinese Spring	13.1 ef

1) Means followed by the same letters are not significantly different at 5% level according to Duncan's Multiple Range Test using student's t.

length and emergence under deep sowing showed a highly positive correlation (Matsui 1998). Furthermore, the final coleoptile length of Chinese Spring, grown under deep sowing condition, was about twice that under shallow sowing reported by Allan and Vogel (1964). Therefore, the results confirmed that the final coleoptile length is more suitable criterion of tolerance to deep sowing than coleoptile length reported by several workers (Burleigh et al. 1965; Feather et al. 1968; Nayyar and Josum 1978; Sunderman 1964).

The difference in final coleoptile length between Chinese Spring (recipient) and Cheyenne (donor) was highly significant. In the second experiment, fifteen of the 21 substitution lines had significantly shorter coleoptiles than Chinese Spring (Table 2). However, four substitutions of the chromosomes 1A, 4A, 5A and 5B, of the 15 lines resulted in remarkable reductions in the final coleoptile length (Table 2). On the other hand, substitution of the chromosome 4D showed the longest final coleoptile length. These results indicate that the final coleoptile length is controlled by many genes. And, the most influential genes are located on the 5 chromosomes. Repressor genes of final coleoptile elongation are located on the chromosome 4D of Chinese Spring, while stimulatory genes reside on the chromosomes 1A, 4A, 5A and 5B. Allan and Vogel (1964), based on F_2 monosomic analysis involving Chinese Spring monosomic series with Norin 10-Brevor and Olympia, concluded that genes promoting coleoptile elongation are located on the chromosomes, 1A, 2A, 3A, 5A, 6A, 2B and 2D, while inhibitory genes reside on the chromosomes 4A, 7A and 6D.

This study suggests that the final coleoptile length is interactively influenced by many genes. Furthermore, the results, in conformity with those of Allan and Vogel (1964), emphasize the importance of the A genome in controlling coleoptile length. However, contrary to their findings, the results in the present study indicate the importance of chromosomes 4A, 5B and 4D. This discrepancy may be attributed to differences in the donor cultivars used and /or to the method of assessment. Allan and Vogel (1964) used Norin 10-Brevor and Olympia, while the cultivar Cheyenne was used in this study. Finally, the study implies the possibility of development of cultivars with longer coleoptiles by manipulating the inhibitory genes on the 4D chromosome.

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Research article

Seedling copper tolerance and cytogenetic characterization of wheat-*Aegilops ovata* hybrid lines

S. Landjeva[1], M. Merakchijska[2], and G. Ganeva[1]

[1]Institute of Genetics, [2]Institute of Plant Physiology, Bulgarian Academy of Sciences, Sofia 1113, Bulgaria (E-mail: landjev@bgearn.acad.bg)

Summary

Two wheat-*Aegilops ovata* advanced backcross-derived lines showed good tolerance at seedling stage to high concentrations of copper ions in solution (10^{-6} M and 10^{-5} M $CuSO_4.8H_2O$). Both lines were established to carry a pair of sub-metacentric *Ae. ovata* chromosomes as substitution for wheat D-genome chromosomes. The alien chromosome pair is supposed to be 3U according to its specific N-banding pattern.

Key words: wheat, *Aegilops ovata*, copper tolerance, N-banding

Introduction

Many wild relatives of wheat have been reported as donors of metal stress tolerance and have been exploited for wheat improvement (reviewed in Manyowa and Miller 1991; Mujeeb-Kazi et al. 1995). *Aegilops ovata* L. (syn. *Aegilops geniculata* Roth., *Triticum ovatum* (L.) Raspail, 2n=28, UUM^0M^0) was involved in breeding programmes as a donor of genes for early maturity, winter hardiness, high grain protein content, and disease resistance (Bochev 1988). Several wheat-*Aegilops ovata* addition and substitution lines have been developed in bread wheat cultivar Chinese Spring (Landjeva and Ganeva 1997). The present study deals with the tolerance of six of them to high concentrations of Cu ions. An *Aegilops ovata* chromosome is supposed to contribute to the better tolerance of two of lines.

Material and methods

Six wheat-*Aegilops ovata* hybrid lines derived from the BC_3F_3-population of the *Triticum aestivum* Chinese Spring x *Aegilops ovata* amphiploid (Ganeva et al. 1992) were studied. Both parents were also included. The excess Cu tolerance was assessed at seedling stage at two concentrations

of Cu ions in $CuSO_4$ solution ($CuSO_4.8H_2O$): 10^{-6} M and 10^{-5} M. Plant growth was estimated by measuring the length and fresh weight of roots, shoots and the whole plant. To measure tolerance the tolerance index (TI) was calculated as a ratio: growth in metal solution / growth in control solution (water) (Macnair 1993). Chromosome counts and arm ratio measurements were made in root tip cells on N-banded chromosome spreads. N-banding was conducted according to Gill et al. (1991).

Results and discussion

The roots length reduction in *Aegilops ovata* was significantly less than in Chinese Spring at both low and high Cu concentrations (Fig. 1). There was no significant difference between the two parental genotypes regarding the shoots growth at concentration of 10^{-6} M. At the higher concentration the performance of Chinese Spring was better.

The performance of two of lines, ADL-18 and ADL-33, was better at both concentrations of Cu ions in comparison with the parents and the rest of lines. They combined the better roots growth of the wild species with the better shoots growth of 'Chinese Spring' at stress conditions (Fig. 1).

The chromosome N-banding analysis showed that both tolerant lines, ADL-18 (2n=40+4t) and ADL-33 (2n=40+3t) carry one and the same pair of submetacentric (arm ratio 2.45) *Aegilops*

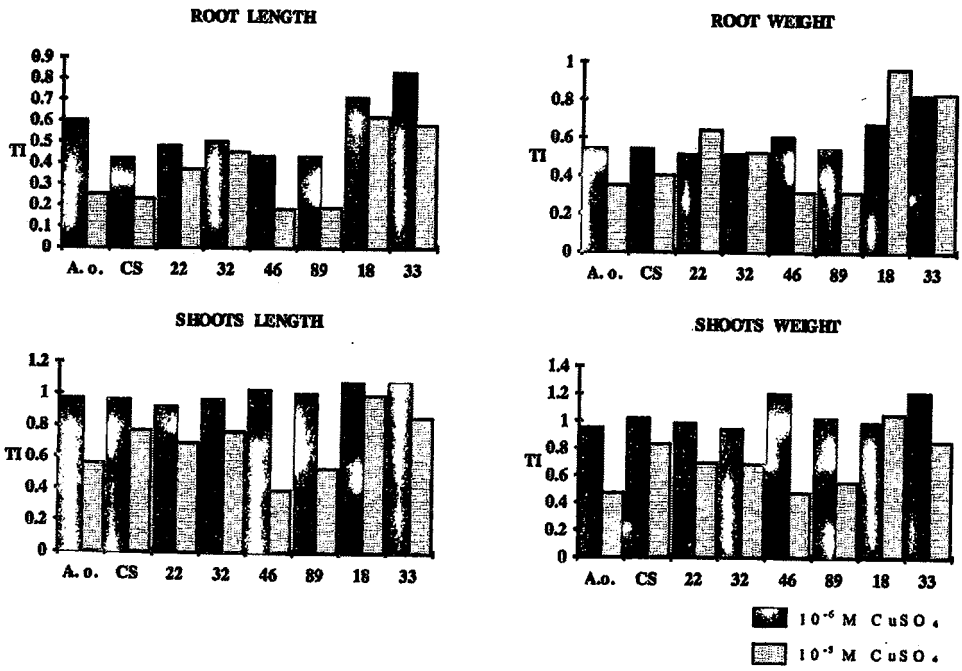

Fig. 1. Tolerance index at two concentrations of copper ions in *Aegilops ovata* (A.o.), *Triticum aestivum* cv. Chinese Spring (CS) and wheat-*Aegilops ovata* hybrid lines, ADL-22, ADL-32, ADL-46, ADL-89, ADL-18 and ADL-33.

ovata chromosomes substituted for wheat D-genome chromosomes (Fig. 2). The N-banded karyotype of the parental *Aegilops ovata* accession is given for comparison (Fig. 3). The rest of lines do not carry this alien chromosome. The telocentrics are supposed to be the short and the long arm of wheat chromosome 4A, which is missing in the complement of both lines. The

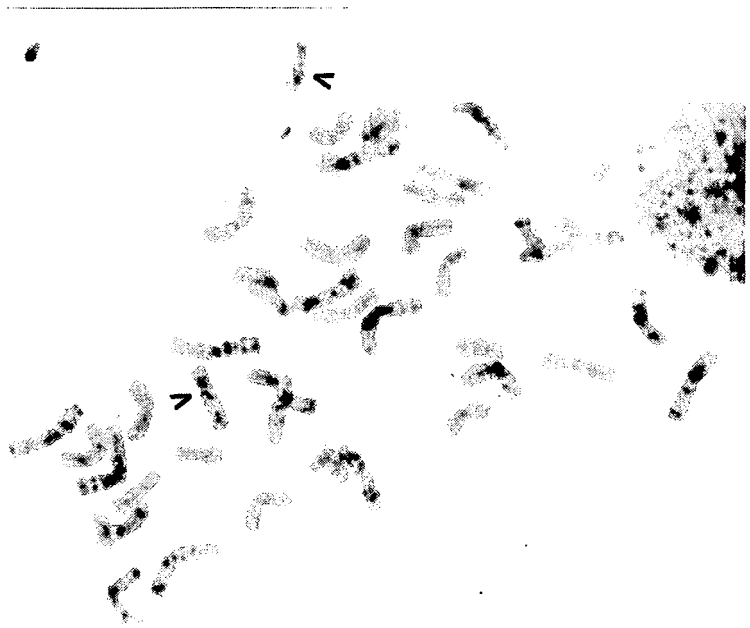

Fig. 2. N-banded somatic metaphase chromosomes in copper tolerant wheat-*Aegilops ovata* line ADL-33 (2n=40+3t). The *Aegilops ovata* chromosomes are marked by arrows.

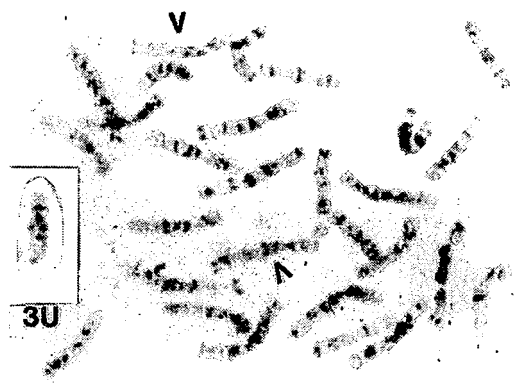

Fig. 3. N-banded karyotype of *Aegilops ovata* (2n=28). The chromosomes which are present in the copper tolerant lines are marked by arrows. N-banded chromosome 3U of *Aegilops umbellulata* is given for comparison.

comparison with the C-banded (Friebe et al. 1995) and N-banded (our unpublished results) chromosomes of the U-genome donor, *Aegilops umbellulata*, suggests that the alien chromosome pair is 3U (Fig. 3). Studies on the genetical control of mineral stress tolerance indicated the major effect of homoeologous groups 5 and 2 chromosomes in the members of Triticeae (Manyowa and Miller 1991). The role of group 3 chromosomes has also been reported. Aluminum tolerance has been transferred into bread wheat through chromosome 3N of *Aegilops uniaristata* (Miller et al. 1992). Modifying genes for excess boron tolerance were found on chromosome 3R in rye, 3S in *Aegilops sharonensis* and 3E in *Agropyron elongatum* (Manyowa 1989, cited in Manyowa and Miller 1991). We suppose that the *Aegilops ovata* chromosome 3U contribute to the excess Cu tolerance through its effect on the growth of roots. In wheat, the effect of group 3 chromosomes on root development has been established (Sears 1954). Both ADL-18 and ADL-33 lines had slower root growth in control solution compared with the rest of lines and the parents (data not shown). This opinion is also in agreement with the observation that in most cases tolerant ecotypes have slower growth than the typical non-tolerant ones (Macnair 1993).

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Research article

Combining ability analysis of scab resistance for F1 and F2 in 4 x 5 factorial cross of common wheat

Guo-Liang Jiang

Wheat Research Laboratory, Department of Agronomy, Nanjing Agricultural University, Nanjing 210095, China

Summary

Nine genotypes with different levels of resistance and genetic backgrounds were crossed in a 4 x 5 factorial cross to make a choice and effective use of excellent parents in wheat breeding program for resistance to scab. A field trial including parents, F_1's and F_2's was conducted in a 3-replicate randomized block design at Nanjing. The number of diseased spikelets was observed to assess the fungal-spread resistance by single-floret inoculation with *Fusarium graminearum*. Average numbers of diseased spikelets of F_1 and F_2 were less than midparent values for most combinations, indicating dominance effects of the resistance genes. The 'parent versus F_1' effects and average degree of dominance showed that the midparent heterosis in F_1 was mainly attributed to overdominance. General and specific combining ability effects were significant for both F_1 and F_2. For inheritance of the resistance, the additive effects of resistance genes in F_2 played a more important role than those in F_1. Hence, parent selection in breeding pure lines should be mainly based on combining ability analysis for F_2 rather than for F_1. The effects of resistance levels of parents and their interaction on the performance of offsprings should be considered. It is suggested that two new resistant resources could be used in breeding program.

Key words: *Triticum aestivum*, scab resistance, combining ability, factorial cross, breeding

Introduction

Scab or head blight caused by *Fusarium graminearum* Schwabe with the perfect stage *Gibberella zeae* (Schw.) is a world-wide disease in common wheat (*Triticum aestivum* L.) (Mesterhazy 1983; Wu 1990; Wilcoxson et al. 1992; Van Eeuwijk et al. 1995). It occurs frequently in temperate humid and semi-humid regions, and is especially destructive in the middle and lower reaches of the Yangtze River Valley and the South China (King 1996). Development of resistant cultivars is the most economical and effective approach controlling this disease. In general, however, high yielding and semidwarf genotypes tend to be rather susceptible to scab, and most of resistant

germplasm resources do not possess desirable agronomic traits (Jiang 1992; Liu et al. 1992). In China, for a long time, very few resistance resources were utilized in wheat breeding programs and the strategy and methodology of breeding for resistance were not approached quite well (Wu et al. 1984; Liu et al. 1992). Although certain progresses were made in breeding for scab resistance, the resistance has not been incorporated into superior cultivars and any resistant cultivar has been hardly planted in wheat production up to now (Jiang 1992). Wu et al. (1984) proposed that a gene pool with improved resistance to scab could be developed through recurrent selection by using the single dominant male-sterile gene *Ta1* (*ms2*), and it was expected that superior resistant cultivars integrated with high-yielding capacity or excellent germplasm with improved resistance would be obtained from the improved population. After more than ten years of experiment, the population of the gene pool has been significantly improved in resistance and some new resistant strains with improved resistance and desired agronomic characteristics have been developed jointly by this method and conventional selection (Jiang and Wu 1996). Four resistant genotypes selected from the gene pool and the well-known resistant cultivar Sumai 3 were used to cross with a set of testers and a genetic study was made. The objective of this study was: (1) to evaluate the combining ability of these resistant genotypes; (2) to explore if their resistance can be transmitted to offsprings; and (3) to analyze the relationships between parents, F_1's and F_2's.

Materials and methods

Host and field trial

Nine winter wheat genotypes with different levels of resistance to scab were selected and a factorial design was adopted to investigate the inheritance of the resistance. Four resistant genotypes TFSL037, Changjiang 8809, W14 and Nantai 7 bred at Nanjing Agricultural University through recurrent selection and conventional selection during the development of scab-resistant gene pool in wheat (Jiang and Wu 1996) and the well-known resistant cultivar Sumai 3 were selected as resistant parents or paternal ones. Four cultivars with different genetic backgrounds from Yangtze River Valley, Yangmai 5, Mianyang 11, Changjiang 8853 and Aiganzao representing high-yielding capacity, early maturity, good quality and from moderate to high susceptibility to scab, respectively, were used as maternal parents or testers. During 1992-1993, all possible crosses were made in a 4 x 5 factorial design or NCII mating design. In 1993-1994, a field trial including 9 parents, 20 F_1's and 20 F_2's was established in a 3-replicate randomized block design at Nanjing. Each plot, with the row length of 1.5m and a space of 0.2m, consisted of 1 row for each of parents and F_1's and 5 rows for each of F_2's. 40 seeds were sown per row.

Assessment of resistance to scab

In general, scab resistance in wheat consists of two components: resistance to initial penetration and resistance to fungal spreading within plant tissue after infection (Schroeder and Christensen 1963), and the expression of resistance is attributable mostly to the latter (Wu 1990). Therefore, the single-floret inoculation was made to evaluate the fungal-spread resistance. The experimental inoculation was conducted by injecting 20μl of conidiospore suspension of *Fusarium graminearum* into a single basipetal floret in the middle part of heads which were to flower or had just flowered. The concentration of the inoculum was about 1×10^4 conidia/ml. About 15 plants for the parent and F_1, only one spike per plant, and about 80 plants for the F_2 were inoculated per plot,

respectively. When the symptoms were clearly identified and the differences between genotypes were quite distinct, head blight, expressed as number of diseased spikelets, was observed 25 days after inoculation. The experimental data were recorded based on the fungal spread and symptoms on the inoculated heads as follows:

0.5: only inoculated floret showed symptom;
1.0: inoculated spikelet showed symptom;
1.8: one spikelet and the main axis of inoculated spike showed symptom;
2, 3, ...,n: the number of total diseased spikelets on the inoculated spike.

Statistical analysis

10 observed values for parent and F_1 and 50 ones for F_2 were sampled randomly per plot, respectively, and plot means were calculated. Analysis of variance on a plot mean basis was conducted for parents, F_1's and F_2's, respectively. Since differences between their error variances were not significant, analysis of variance and combining ability was carried out for the F_1 and parents, and F_2 and parents, respectively (Singh and Chaudhary 1979; Guo 1993). Genetic parameters such as heritability and average degree of dominance were estimated on the random model or Model II in Table 3 (Guo 1993). Additionally, simple correlations were computed for parent versus F_1, parent versus F_2 and F_1 versus F_2, on the basis of genotype means and combining ability effects.

Results

Performance of genotypes in resistance to scab

The averages of scab-diseased spikelets for the parents, F_1 crosses and F_2 populations are given in Table 1. Overall generation means for the diseased spikelets were 3.92, 3.40 and 3.82 for parent, F_1 and F_2, respectively, and the coefficients of variation were 24.04% for F_1 and 25.28% for F_2. Of all parents, W14 was the most resistant, superior to Sumai 3. For most combinations, averages of numbers of diseased spikelets of F_1 and F_2 were less than mid-parent values, indicating that dominance for resistance existed. The average number of diseased spikelets of F_2 was larger than that of F_1 though differences between both generation means and error variances were not significant. On average of all combinations, number of diseased spikelets of F_1's was significantly less than that of midparent values. However, there was no significant difference between F_2's and midparent values. Analysis of variance showed that there were highly significant differences in scab resistance among parents, among F_1's and among F_2's (Table 2). The 'female versus male' effect and 'parent versus F_1' effect were also highly significant but the 'parent versus F_2' effect was insignificant.

Combining ability analysis and effects of combining ability

As shown in Table 3, general combining ability (GCA) effects were highly significant for both F_1 and F_2. It indicates that both maternal and paternal parents have great influences on the performance of their cross offsprings in resistance to *Fusarium graminearum*. Relatively speaking, the effects of the paternals were larger than those of the maternals. Specific combining ability (SCA) effects were also highly significant in F_1 and F_2. It is shown that the performance of specific combination in resistance depends upon the resistance level of two parents as well as the interaction of parents.

Table 1. Averages of the parents, F_1's (above) and F_2's (below) and the effects of GCA ($g_{i.}$ and $g_{.j}$) in 4 x 5 factorial cross of winter wheat for number of diseased spikelets inoculated with *Fusarium graminearum*

Parent number [a]		5	6	7	8	9	$x_{i.}$ [b]	$g_{i.}$
	Diseased spikelets	1.49	1.07	1.51	1.26	0.93	1.25	
1	6.44	3.94	2.26	3.15	4.03	2.69	3.21	-0.19
		3.87	3.33	3.36	3.09	1.50	3.03	0.79**
2	5.24	2.83	3.39	2.29	4.77	1.48	2.95	0.45**
		3.69	4.63	3.06	4.86	2.23	3.69	-0.13
3	9.81	3.42	3.35	4.15	3.63	2.89	3.49	0.08
		4.11	5.64	3.98	4.64	3.05	4.28	0.47**
4	7.50	4.54	3.79	3.62	4.17	3.70	3.96	0.56**
		4.35	4.92	4.20	4.17	3.68	4.26	0.45**
$x_{.j}$ b)	7.25	3.68	3.20	3.30	4.15	2.69	3.40	
		4.01	4.63	3.65	4.19	2.61	3.82	
$g_{.j}$		0.28*	-0.21	-0.10	0.75**	-0.72**		
		0.19	0.81**	-0.17	0.37**	-1.20**		

a) Parent numbers 1-9 represent Yangmai 5 (1), Changjiang 8853 (2), Aiganzao (3), Mianyang 11 (4), Nantai 7 (5), Sumai 3 (6), TFSL037 (7), Changjiang 8809 (8) and W14 (9), respectively.
b) $x_{i.}$ and $x_{.j}$ represent row and column means, for F_1 and F_2, respectively.
* and ** Significant at 5% and 1%, respectively.

GCA effects of parents are given in Table 1. Among the resistant or paternal parents, W14 was of the highest resistance, and greatest and significant GCA effects in both F_1 and F_2. Clearly, it should be a good parent for breeding for resistance to scab in wheat. The well-known resistant cultivar Sumai 3 possessed higher resistance (only second to W14), but did not have good GCA effect in F_2 although its relative value of GCA for F_1 was 6.07% in decreasing diseased spikelets of offsprings. Relative values of GCA of TFSL037 were 3.06% and 4.36% in F_1 and F_2, respectively. Compared with W14 and TFSL037, the GCA effects of Changjiang 8809 and Nantai 7 were disadvantageous to increasing resistance in F_1 and F_2. For the maternal parents or testers, Yangmai 5 and Changjiang 8853 had higher resistance and general combining ability. Aiganzao and Mianyang 11 had negative effects on performance of the offsprings in the resistance.

Estimation of genetic parameters

Based on random model, variance between combinations, GCA variance of maternal and paternal parents and SCA variance of their interaction for F_1 and F_2, except GCA variance of maternals and paternals in F_1, were significant or highly significant (Tables 2 and 3). Then genetic parameters were estimated. Of the genetic variance, SCA variance accounted for 55.22% and 50.91%, respectively, in F_1 and F_2, and GCA variance accounted for 44.78% and 49.09%. Average degree of dominance was 1.111 and 1.018 for F_1 and F_2, respectively, indicating that there was dominance

Table 2. Mean squares from analysis of variance of diseased spikelets for 4 x 5 factorial cross of winter wheat inoculated with Fusarium gramineantm

F_1 and parent Source	DF	MS	F_2 and parent Source	DF	MS
Block	2	0.105	Block	2	0.150
Genotype	28	11.340**	Entry	28	11.704**
Parent	8	34.303**	Parent	8	34.303**
Female	3	11.329**	Female	3	11.329**
Male	4	0.196	Male	4	0.196
Female vs. male	1	239.653**	Female vs. male	1	239.653**
Parent vs. F_1	1	4.909**	Parent vs. F_2	1	0.186
F_1	19	2.010**	F_2	19	2.795**
Error	56	0.227	Error	56	0.226

** Significant at 1%

Table 3. Mean squares from combing ability analysis of diseased spikelets for 4 x 5 factorial cross of winter wheat inoculated with *Fusarium graminearum*

Source	F_1 DF	MS	EMS (Model II)	F_2 DF	MS	EMS (Model II)
Combinations	19	2.010**	$\sigma_e^2+3\sigma_g^2$	19	2.795**	$\sigma_e^2+3\sigma_g^2$
Female g.c.a.	3	2.805**	$\sigma_e^2+3\sigma_{fm}^2+15\sigma_f^2$	3	5.261**	$\sigma_e^2+3/4\sigma_{fm}^2+15\sigma_f^2$
Male g.c.a.	4	3.604**	$\sigma_e^2+3\sigma_{fm}^2+12\sigma_m^2$	4	6.921**	$\sigma_e^2+3/4\sigma_{fm}^2+12\sigma_m^2$
s.c.a. (F x M)	12	1.280**	$\sigma_e^2+3\sigma_{fm}^2$	12	0.803**	$\sigma_e^2+3/4\sigma_{fm}^2$
Error	38	0.188	σ_e^2	38	0.176	σ_e^2

$\sigma_g^2=\sigma_f^2+\sigma_m^2+\sigma_{fm}^2$

** Significant at 1% based on the fixed model or Model I

or superdominance in F_1 and F_2. Estimates of broad-sense and narrow-sense heritability were 77.86% and 34.86% in F_1, and 90.34% and 44.35% in F_2, respectively. It is indicated that, in the inheritance of the resistance to scab in wheat, the additive effects of resistance genes in F_2 played a more important role than those in F_1.

Correlation

Analysis of simple correlation on parent mean versus combination mean showed that correlations between four maternals and F_1 crosses and F_2 populations, between five paternals and F_1 and F_2, between mid-parent values and F_1's and F_2's, and between parent mean and GCA effects for F_1 and F_2 were not significant. Simple correlation coefficients between maternal means and GCA effects were 0.558 and 0.639 for F_1 and F_2, and 0.564 and 0.315 between paternal means and GCA effects for F_1 and F_2, respectively. There was a significant correlation between F_1 and F_2 for

combination means (r=0.616**) and for SCA effects (r=0.643**). For GCA effects, however, correlation between F_1 and F_2 was not significant (r=0.631).

Discussion

Since 1980s, genetic studies on resistance in wheat to scab or Fusarium head blight have been reported in China (Jiang and Wu 1989; Lin et al. 1992) and abroad (Tomasovic 1989; Snijders 1990a, 1990b; Ittu et al. 1997). Most researches indicated that the resistance was quantitatively inherited and affected largely by additive gene effects although the results obtained were not completely consistent and even contradictory (Buerstmayr et al. 1997; Ban and Suenaga 1997). In this study, the fact that mean numbers of diseased spikelets of F_1 and F_2, for most combinations, were less than the mid-parent values indicated that the dominance effects existed. The effect of parents versus crosses tests the mean deviation of the hybrids from their midparent value. It reflects average heterosis contributed by all parents in the crosses and is attributable entirely to non-additive effects (Snijders 1990b). The 'parent versus F_1' effect was highly significant but the 'parent versus F_2' effect was not significant. This means that there were dominance effects in F_1's, predominantly in the direction of resistance. Average degree of dominance showed that there was dominance or overdominance in F_1 and F_2. The midparent heterosis of F_1 may mainly lie in superdominance effects.

Combining ability analysis for scab resistance in wheat was done mostly with F_1 crosses following Griffing's methods in the earlier studies. F_2 populations were included in very few experiments (Snijders 1990b). For hybrid breeding, information about F_1's is undoubtedly suitable. For breeding pure lines, however, F_2's should be more valuable than F_1's. Because selection of superior genotypes is conducted in F_2 population and progenies rather than F_1 crosses, higher average resistance of F_2 population means greater opportunity of obtaining resistant individuals. This study indicated that SCA effect was more important than GCA among F_1 generations, while among F_2 generations GCA had nearly the same effect as SCA. The additive effects of resistance genes for F_2's played a more important role than those for F_1's in the inheritance of the resistance to scab in wheat. In breeding resistant pure lines, therefore, parent selection based on combining ability analysis for F_2's should be more reliable than for F_1's.

Heritability estimated showed that the expression of resistance to scab was mainly controlled by genetic factors. There was a significant correlation between F_1's and F_2's for generation means and for specific combining ability. However, correlations between parent means or mid-parent values and the averages of F_1's or F_2's and between parent means and combining ability effects were not statistically significant. It is concluded that the inheritance of resistance in wheat to scab is complex. The performance of offsprings in resistance to scab was not absolutely expected by the resistance levels of parents. The interaction between parents should be considered.

The cultivar Sumai 3 has been proved to have high and stable resistance to scab and been widely used in combining ability analysis and breeding program for the resistance. Its general combining ability based on F_1's was high and obviously increased the resistance of hybrids (Jiang and Wu 1989). However, its undesirable agronomic traits have negative effects on the offsprings. So far, no cultivars derived from Sumai 3 have been applied in production because of their lacking desired agronomic traits and high-yielding capacity. In the present study, Sumai 3 did not have good GCA effect for F_2's although it possessed higher resistance and GCA value of 6.07% for F_1's

in decreasing diseased spikelets of offsprings. Relatively, the recurrent selection strain W14 had not only the highest resistance but also greatest GCA effects both in F_1's and F_2's. Clearly, it. should be an excellent parent for breeding for resistance to scab in wheat. The recurrent selection strain TFSL037 had positive GCA effects on performance of resistance to scab in F_1's and F_2's. As compared with Sumai 3, W14 and TFSL037 have improved agronomic traits such as shorter plant height, higher biomass, grain yield, harvest index and 1000-grain weight, and more grains per spike (Jiang and Wu 1996). It is suggested they could be used as excellent resistant parents in breeding program for scab resistance. It is also demonstrated that the development of a gene pool through recurrent selection integrated with conventional breeding methods using the dominant male-sterile gene *Ta1* (*ms2*) is entirely feasible and effective in developing excellent scab-resistant germplasm of wheat (Jiang et al. 1994; Jiang and Wu 1996). Among the maternal parents, Yangmai 5 and Changjiang 8853 had higher resistance and general combining ability. In practice, some good lines with resistance and desired agronomic characters have been obtained from the cross Yangmai 5/W14.

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Research information

Combining ability analysis in bread wheat adapted to the East African highlands

William W. Wagoire, Olav Stølen, and Rodomiro Ortiz*

Department of Agricultural Sciences, The Royal Veterinary and Agricultural University, 40 Thorvaldsenvej, DK-1871 Frederiksberg C, Copenhagen, Denmark

The Uganda Wheat Development Project (UWDP) aims to develop widely adapted, high yielding, cultivars with good resistance to diseases. The objective of this study was to determine the combining ability for days to heading, plant height and grain yield of cultivars widely tested in Uganda but whose yellow rust resistance varied from very resistant to very susceptible.

Sixty-four genotypes, derived from a full diallel cross among eight cultivars were assessed for agronomic characteristics. The parental genotypes were selected for their good agronomic characteristics but with varying responses to yellow rust (Wagoire et al. 1998a). The experiments were planted in two cropping seasons (A and B) at two locations (Kalengyere and Buginyanya), both having bimodal rainfall. Kalengyere (1° 15' S, 29° 45' E) is at 2400 m.a.s.l, has an Andosol with pH 5.7, and an average temperature of 16 °C throughout the year. The high rainfall (750 mm) season (B) lasts from September to March and the relatively low rainfall (480 mm) season (A) from March to August. Buginyanya (1° 1' N, 34° 2' E) is at 2100 m.a.s.l., has an Andosol with pH 5.5, and an average temperature of 18 °C. The high rainfall (560 mm) season (B) occurs from September to March and the relatively low rainfall (470 mm) season (A) occurs from March to August (470 mm). The study was carried out in three growing seasons from August 1994 to March 1996. An additional environment was obtained by applying fungicide to control yellow rust at Kalengyere in 1995 (B) season. All plots were fertilized at a rate of 50 kg N ha^{-1} prior to planting. The combining ability effects were calculated using Griffing's (1956) method. The phenotypic stability of all the characters was investigated using Eberhart and Russell's procedures (1966). In addition, correlations between combining ability values of days to heading, plant height and grain yield and their stability parameters were calculated.

The diallel analysis revealed the predominant role of additive gene action for days to heading, plant height and grain yield (Table 1). Parental genotypes showed significant general combining ability (GCA) for days to heading, plant height, and grain yield (Table 2). Similarly, there was significant specific combining ability for the same characters. A highly significant genotype-by-environment interaction affected all the characters, which suggests that selection for specific environments could maximize the use of available germplasm. The significance of environmental effects in our investigation was attributed to the abiotic and biotic differences. For example, the

Table 1. Analysis of variance mean squares for days to heading, plant height (cms) and grain yield (g m^{-2}) for a full 8 x 8 F_1 wheat diallel cross grown in seven environments in Uganda from 1994 to 1996.

Source of variation	df†	Days to heading	Plant height	Grain yield
Environment (E)	6	6291.531***	8509.509***	1532738.103***
Replications/E	7	45.650	399.820	21626.555
Genotypes (G)	63	99.897***	595.753***	17940.426***
GCA‡	7	766.743***	4084.723***	80969.455***
SCA§	28	18.787**	241.689***	12211.377***
REC¶	28	14.321*	73.755**	7932.092*
GxE interaction	378	13.909***	88.566**	6776.905***
GCA x E	42	39.018***	393.195***	19839.655***
SCA x E	168	10.901	47.323	5116.710
REC x E	168	10.635	50.032	5166.876
Error	441	8.695	40.482	3080.750

†degrees of freedom. ‡General combining ability. §Specific combining ability. ¶Reciprocal differences.
*P < 0.05, ** P < 0.01, *** P < 0.001

Table 2. Estimates for general combining ability for days to heading, plant height (cm) and grain yield (gm^{-2}) in an 8 x 8 F_1 wheat diallel grown in seven environments in Uganda from 1994 to 1996. Parents were resistant (R), moderately resistant (MR), moderately susceptible (MS) or susceptible (S) to yellow rust.

Parent (Yellow rust reaction)	Days to heading	Plant height	Grain yield
Buri (R)	-0.1496	+3.6719	+21.1538
K. Chiriku (R)	-1.6674	-0.7031	+4.9395
Esda/Lira (R)	+0.6629	+0.6808	+17.6092
VEE"S"/JUP73/EMU"S"//GJO"S" (MR)	+2.3504	+7.3504	+5.9663
Attila (MS)	+1.4219	-2.6585	+12.0556
CY8801 (S)	-3.5513	+0.3862	-15.1408
F60314.76/4/CNO76/7C//KAL/BB/3/ PCI"S"/5/CNO79 (S)	+0.2165	-1.7299	-16.3641
CAR853/COC//VE"S"/3/E7408/PAM"S"/ HORK"S"/PF73226 (S)	+0.7165	-6.9978	-30.2194
S.E(g_i)†	0.2364	0.5873	5.2437
S.E(g_i-g_j)‡	0.3574	0.8878	7.9200

†Standard error of the mean of the general combining ability of i^{th} parent.
‡Standard error of difference between the general combining ability of i^{th} and j^{th} parents.

amount of precipitation received in each season as well as the annual total precipitation per site were different. Also, Kalengyere had a lower mean temperature as compared to Buginyanya. In addition, one of the experiments in 1995 (B) season at Kalengyere was sprayed with a fungicide in order to control yellow rust. The yellow rust significantly affected the phenotypic performance for grain yield and plant height (Wagoire et al. 1998b).

Significant genotypic effects were expected since the parental lines had been selected to provide a full range of reaction types to yellow rust (Wagoire et al. 1998a). This also explained to some extent the observed genotype-by-environment effects for all the characters. The experiments at Buginyanya were yellow rust-free during the test period while those at Kalengyere always had yellow rust infestation which varied in severity between seasons. The yellow rust severity (coefficient of infection) at Kalengyere averaged 7.89 % in 1994 (B) season, 30.17 % in 1995 (A) season and 24.05 % in 1995 (B) season.

GCA was correlated with the phenotypes of the parents across locations ($r \leq 0.94$, $P < 0.001$), suggesting that phenotypic selection may be adequate for choosing parents. However, GCA was not correlated with phenotypic stability, thereby multilocational testing would be required to select stable genotypes. Specific combining ability (SCA) was only correlated with yield stability across environments ($r = 0.53$, $P < 0.001$). We suggest that a stable wheat cultivar for Uganda should be defined as one with a high mean yield (above the national average of 1.8 t ha^{-1}), regression coefficient for performance across environments (b) equal to 1, and almost nil deviations from the regression slope. These criteria were used because Uganda relies on wheat germplasm introductions that were bred for high yielding environments (Braun et al. 1996).

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Record

The 26th Japanese Wheat Genetics Symposium, June 19-21, 1998

Introductary remarks

Koichiro Tsunewaki (Fukui Prefectural University)

The 26th Japanese Wheat Genetics Symposium was held at the Fukui Prefectural University in June 19-21, 1998. The Local Organizing Committee consisting of K. Tsunewaki (Chairman), S. Ohta and Y. Matsuoka was in charge of its organization and management. The symposium involved three special lectures, six sessions of 24 research papers in total, open-discussion session, business session, and a post-symposium tour. Total number of the attendants were 113 belonging to 21 different institutions, including seven researchers from five foreign countries.

The special lectures delivered are; "Gene analysis on sex determination and sexual organ development from liverwort, *Marchantia polymorpha*" by K. Ohyama, Kyoto University, "Complete sequence of wheat chloroplast DNA" by Y. Ogihara, Yokohama City University, and "Examining genetic structure and history of species through DNA analysis: Case studies in marine biology" by M. Nishida, Fukui Prefectural University. The titles of the six oral sessions were; (1) structural stability of mitochondrial genome (two papers), (2) structure of wheat chloroplast genome (two papers), (3) analysis of stress-responsive genes and haploid breeding (three papers), (4) genetic control of reproduction and viability in Triticeae (six papers), (5) genome differentiation revealed from the studies on repetitive sequences (four papers), and (6) polymorphism and intraspecific differentiation in Triticeae (six papers). The abstracts of all research papers are presented in this issue of Wheat Information Service.

In the evening of June 19, a free-talking session was held. Its topic was "Future breakthrough of wheat genetics". In the business session, five agenda were discussed and agreement was made as follows; (1) version-up of the Japanese wheat stock database, "KOMUGI", was proposed by T. Sasakuma and the member substations agreed to up-to-date their data in "KOMUGI", (2) T. R. Endo asked opinion of the attendants on his idea to propose the establishment of an international database network at the workshop on wheat stock maintenance, that is scheduled during the 9th International Wheat Genetics Symposium, and a suggestion was made not to consider a world-scale network at present, but to form a network between the existing databases and to connect new ones whenever they are established, (3) change of the present name of the symposium to "Triticeae Genetics Symposium" was proposed by T. Kawahara, and the agreement was made that it is not suitable to make decision at this symposium and should wait until the next symposium, (4) necessity for an adjustment on the time when the Wheat Genetics Symposium and the Workshop on Triticeae Molecular Biology would be held was pointed out by K. Tsunewaki, and an agreement was made that the former symposium is held once for every two years while the latter workshop every year, and that the former should be planned at the same site and in an adjacent period to the latter when both are held in the same year, and (5) site of the 27th Wheat Genetics Symposium was decided to be Gifu University and Y. Furuta, professor there, addressed his willingness to become its host.

Abstract

Special lecture

Kanji Ohyama, Hideya Fukuzawa and Katsuyuki Yamato (Grad. Schl. Agr., Div. Appl. Life Sci., Kyoto Univ.)

Gene analysis on sex determination and sexual organ development from liverwort *Marchantia polymorpha*.

(1) We have constructed the respective genome libraries from the male and female liverwort using PAC vector. In order to isolate the clones which are specific either male or female sex chromosomes (X and Y chromosomes, respectively), we are approaching to it by FISH method and genome subtraction using PAC libraries. (2)We have made cDNA libraries derived from female sexual organ. In order to investigate the gene expression specific sexual organ, we have sequences approximately 1000 cDNA and obtained several sex related cDNA clones.

Y. Ogihara, K. Isono, T. Kojima, H. Tsuzuki and A. Endo (Kihara Inst. for Biol. Res., Yokohama City Univ.), R. Murai and K. Murai (Res. Inst. of Agr. Res., Ishikawa Agr. Coll.), M. Hanaoka and T. Shiina (Grad. Schl. Human and Environ. Studies, Kyoto Univ.), T. Terachi (Dept. of Biotech., Fac. of Engineer., Kyoto Sangyo Univ.), S. Utsugi and M. Murata (Res. Inst. for Biores., Okayama Univ.), N. Mori and S. Takumi (Dept.of Biol. and Environ. Sci., Fac. Agr., Kobe Univ.), K. Ikeo and T. Gojobori (Cent. Inform. Biol., Natl. Inst. Genet.), Y. Matsuoka, Y. Ohnishi, H. Tajiri and K. Tsunewaki (Dept. Biosci., Fukui Pref. Univ.)

Complete sequence of wheat chloroplast DNA

The complete sequence of chloroplast (cp) DNA of common wheat, *Triticum aestivum* cv. Chinese Spring, have been determined. The wheat chloroplast genome has 134,363bp, in total. The basic structure and gene content of wheat cp DNA were similar to its relatives, rice and maize. In the inverted repeat regions, 23S, 16S, 4.5S and 5S ribosomal RNA genes were involved. 30 tRNA genes were dispersed in the plastome. 63 genes encoding functional proteins reported in rice cpDNA were also found in wheat cpDNA. Some structural alterations of wheat cpDNA in comparison to the arrangement of rice cpDNA were detected.

M. Nishida (Dept. Mar. Biosci., Fukui Pref. Univ.)

Examining genetic structure and history of species through DNA analysis: Case studies in marine biology

Most marine organisms inhabit coastal areas sedentarily as adults, but spend their early life stages as planktonic larvae. Though the sedentary adult stage appears the phase of genetic divergence among populations, the planktonic larval stage is that of genetic homogenization. These two life stages, therefore, have opposite functions to form genetic population structure. It is intriguing to understand patterns of genetic structure of populations in typical marine organisms with such life history. Here I introduce examples of studies to examine those patterns through DNA analysis in the hope that these case studies in marine biology would provide some insight for terrestrial plant geneticists.

Session 1: Structural stability of mitochondrial genome

N. Tsukamoto[1], N. Asakura[2], Y. Igarashi[1], S. Takumi[1], N. Mori[1], I. Ohtsuka[2] and C. Nakamura[1] ([1]Fac. Agr., Kobe Univ., [2] Fac. Engineer., Kanagawa Univ.)

The presence of maternal, paternal and novel paternal-like copies of the mitochondrial *nad3-orf156* region in the nucleus-cytoplasm hybrids of tetraploid wheat with *A e. squarrosa* cytoplasm.

Chromosome 1D of *Ae. squarrosa* and 1A of timopheevi wheat respectively possess a nuclear gene, *Ncc-sqr1D* and *Ncc-tmp1A*, which confers compatibility with the cytoplasm of *Ae. squarrosa* on the NC hybrids. Mitochondrial DNA organization was studied in three tetraploid NC hybrids with *Ae. squarrosa* cytoplasm and compared with that in the nucleus and cytoplasm donors. PCR-RFLP analysis revealed notable polymorphisms in the *nad3-orf156* region. The comparative sequence analysis demonstrated the presence of both maternal and paternal copies of this region in the NC hybrids. One novel paternal-like copy was also detected. Our results suggest possible paternal transmission of mtDNA sequence(s) in these NC hybrids.

G.-Z. Wang, Y. Matsuoka and K. Tsunewaki (Fac. Biosci., Fukui Pref. Univ.)

Organellar RFLP markers for plasmon distinction in *Triticum* and *Aegilops*

To develop molecular markers for plasmon distinction, RFLP of 28 alloplasmic common wheats representing 22 plasmons has been analyzed. Total DNAs were digested with a restriction enzyme (*Bam*HI, *Hin*dIII or *Pst*I), and then subjected to hybridization. Two chloroplast and seven mitochondrial probes were used. Twenty plasmon types successfully were distinguished by three probe-enzyme combinations, *cox1-Pst* I, *cox2-Hin* dIII and *cob-Bam* HI. No polymorphism was detected between C and C^2 plasmons, and between G and G^2 plasmons despite the differences in phenotypic effects. Close relationship between the plasmons of polyploid wheats and *Ae. speltoides* was supported by phylogenetic analysis.

Session 2: Structure of wheat chloroplast genome

T. Kojima[1], A. Endo[1], H. Tsuzuki[1], K. Isono[2] and Y. Ogihara[1] ([1]Kihara Inst. Biol. Res., Yokohama City Univ., [2]Perkin-Elmer)

Chloroplast genome organization of the region between *psbA* and *psbC* in wheat

The nucleotide sequence of wheat chloroplast (cp) DNA with region between *psbA* and *psbC*, in which a part of inverted repeat-A (IR-A) is included, has been completed. This region consists of 11,523 base-pairs and contains 12 genes (8 peptide-encoding genes, 3 tRNAs and a putative open reading frame). The 11 genes, except one open reading frame, are identical with the those of rice and maize. The junction point between large single copy (LSC) region and IR-A is determined by comparing with the sequence of wheat cp IR-B. The numbers of nucleotides from this junction point to *rps19* (within IR-A) and *psbA* (LSC) are 50 bp and 90 bp, respectively, and are slightly longer than rice and maize.

Y. Ohnishi, H. Tajiri, Y. Matsuoka and K. Tsunewaki (Fac. Biosci., Fukui Pref. Univ.)
Organization and evolutionary properties of a 21.1kb *Pst*I fragment of the wheat chloroplast DNA with emphasis on RNA polymerase subunit genes.

The entire nucleotide sequence of a 21.1kb *Pst*I fragment of the wheat chloroplast DNA has been determined. This fragment contained 18 genes, including *rpoB, rpoC1* and *rpoC2* that encode b, b' and b" subunits of RNA polymerase, respectively. Comparison of the wheat genes to those of other plants indicated that they are highly conserved especially among grass species. The following four distinct structural alterations, however, were detected in wheat *rpo* genes; absence of the intron in *rpoC1*, deletions in the middle (81bp) and 3' terminal (ca. 30bp) regions of *rpoC2* and the presence of an insertional sequence (408bp) in *rpoC2*.

Session 3: Analysis of stress-responsive genes and haploid breeding

Y. Nemoto[1], N. Kawakami[2] and T. Sasakuma[1] ([1]Kihara Inst. Biol. Res., Yokohama City Univ., [2]Meiji Univ.)
Novel salt stress responding genes isolated from common wheat

We isolated five novel cDNAs that responded to 0.15M NaCl treatment from common wheat (*Triticum aestivum* L. cv Chinese Spring) by an improved differential display method. The clones were collectively named as WESR (wheat early salt-responding gene) since the clones were isolated from the salt treated seedlings only for 2 hours. They showed different patterns of transcript accumulation during exposure to salt stress. Analysis of nucleotide and deduced amino acid sequence indicated that WESR4 showed homology to a barley cDNA clone containing zinc finger motif, WESR5 was for glucose-6-phosphate dehydrogenase (G6PDH). Other clones did not show significant homology to known genes.

S. Tsvetanov[1], K. Tsuda[2], S. Takumi[2], N. Mori[2], A. Atanassov[1] and C. Nakamura [2] ([1] Inst. Genet. Engineer., Bulgaria, [2]Fac. Agr., Kobe Univ.)
Cloning and characterization of novel members of a cold-responsive gene family, *Wcor*, in wheat.

Five *Wcor* cDNAs were selected using a library constructed from a cold-acclimated Russian winter wheat cv. 'Mironovska 808'. The screening was based on the homology with three barley cold-responsive and/or ABA-responsive cDNAs. One novel clone *Wcor35* was chimeric consisting of a 5' half region homologous with cold- and light-responsive barley *T59* and wheat *Wcs19* and a 3' half region homologous with a hedydrin group, *Wcs66* and *Wcs120*. *Wcor35* expression was specific to low temperature acclimation. Three other clones were homologous to several reported cold and/or ABA-responsive cDNAs.

M. N. Inagaki (Biol. Resour. Div., Japan Intern. Res. Cent. Agr. Sci. (JIRCAS))
Application of doubled haploids to wheat breeding programs

The breeding method using wheat doubled haploids (DHs) has advantages in reducing the time

required to obtain recombinant inbred genotypes ready for yield evaluation. Field experiments suggested that genetic advance obtained in DH method were comparable to that observed in the conventional methods. A methodology for producing wheat haploids using wide crosses followed by chromosome elimination has been developed over the last two decades. Significant technical advances on crossability have been made by using pollen donors selected from different subfamily species and by applying plant growth regulators. Efficient crossing techniques were developed using stored pollen and detached-tiller culture, resulting in considerable savings in terms of labor and space required for growing parent plants. Production efficiency of doubled haploid lines has been improved to a level allowing their utilization in breeding programs.

Session 4: Genetic control of reproduction and viability in Triticeae

K. Murai[1], R. Murai[1], S. Takumi[2] and Y. Ogihara[3] ([1]Res. Inst. Agr. Resour., Ishikawa Agr. Coll. [2]Fac. Agr., Kobe Univ., [3]Kihara Inst. Biol. Res., Yokohama City Univ.)

Cloning and characterization of cDNAs corresponding to the wheat MADS box genes

To clarify the function of MADS box genes in wheat (*Triticum aestivum* L.), we have isolated and characterized cDNA clones corresponding to MADS box genes from wheat. Seven cDNA clones were isolated by screening 2.2×10^4 plaques of a cDNA library from young spike (3-10 mm in length) using degenerate PCR products of MADS box region as probes. Each clone contains an open reading frame encoding a putative protein with a MADS box region. Based on the deduced amino acid sequence, seven clones were classified into three groups, i.e., *AP1*-like (4 clones), *AP3*-like (2 clones) and *AGL6*-like (1 clone) groups. Analyses of gene expression patterns suggested that they play different roles in spike/spikelet/ floret development in wheat.

S. Ito, Y. Nakahira, T. Shiina and T. Toyoshima (Grad. Schl. Human and Environ. Studies, Kyoto Univ.)

Circadian expression of a nuclear-encoded chloroplast sigma factor gene in wheat.

The light-responsive promoter (LRP) of the plastid *psbD* gene encoding photosystem II D2 protein is recognized by the eubacterial-type RNA polymerase (PEP). The level of mRNAs derived from the LRP oscillates diurnally for three cycles in continuous light condition. In vitro transcription in chloroplast extracts revealed that the *psbD* LRP mRNA level is controlled by an endogenous circadian clock through transcription. In this study, we revealed that mRNA level of a nuclear-encoded chloroplast sigma factor gene (*sigA*) is controlled by the circadian clock in wheat, that may be involved in the circadian behavior of the psbD LRP .

T. Sugiura, K. Naito, K. Tsunewaki, T. Asahi, and H. Suzuki (Fac. Biosci., Fukui Pref. Univ.)

Repressed expression of the *defender against apoptotic cell death 1* (*dad1*) gene in leaves of necrotic wheat

The *dad1* gene is the only identified as an apoptotic cell death suppresser in higher plants. We have cloned an *Arabidopsis thaliana dad1* cDNA (*Atdad1*). We examined the mRNA level of its

homologue in leaves of necrotic wheat (*Triticum aestivum* cv. S-615) that undergoes growth stage-specific necrosis caused by two complementary genes, *Ne1* and *Ne2*. We found that the transcript level was extremely low in the necrotizing region where many dead cells were histochemically observed, in comparison with the level of control wheat (S-615). This suggests that reduction of the *dad1* transcript could be associated with cell demise in necrotic wheat.

T. Koba, T. Suzuki, M. Hayashi and Y. Iguchi (Fac. Hort., Chiba Univ.)
Detection of cDNA fragments responsible for crossability of common wheat with alien species by means of Differential Display method

Crossability of common wheat cultivars with alien species are controlled by *Kr* genetic system. cDNAs were isolated from pistils of cv. Chinese Spring (*kr1kr1*) and its chromosome substitution lines having chromosome 5B of cvs. Hope and Cheyenne (*Kr1Kr1*). After amplification of the cDNAs by using combinations of five decamer arbitrary primers, eleven cDNA fragments were found to be specific for chromosome 5B of Hope and Cheyenne, and two were specific for chromosome 5B of Chinese Spring. Some of the fragments are thought to correspond to the gene *Kr1*. Cloning of the fragments and their characterization are now in progress.

N. Asakura[1], C. Nakamura[2] and I. Ohtsuka[1] ([1]Fac. Engineer., Kanagawa Univ., [2]Fac. Agr., Kobe Univ.)
Mapping of nucleus-cytoplasm compatibility gene, *Ncc-tmp1A*, from *Triticum timopheevi* for the cytoplasm of *Aegilops squarrosa* and its origin

Tetraploid wheat species have been classified into three groups based on the nuclear compatibility with the cytoplasm of *Ae. squarrosa*. Nuclear genomes of emmer wheat are incompatible or partially compatible, while nuclear genomes of timopheevi wheat are fully compatible, indicating the presence of nucleus-cytoplasm compatibility (*Ncc*) gene for the cytoplasm of *Ae. squarrosa*. *Ncc-tmp1A* from *T. timopheevi* was mapped near the centromere of chromosome 1A using (*sqr*)-Langdon with it. In the nuclear genome of *T. timopheevi* only *Ncc-tmp1A* was functional for the cytoplasm of *Ae. squarrosa*. The origin of *Ncc-tmp1A* was discussed, comparing with the wheat phylogeny.

Y. Furuta (Fac. Agr., Gifu Univ.)
Propagation properties and flowering habit of *Hordeum bulbosum*

The wild barley species, *Hordeum bulbosum*, consists of diploid and autotetraploid cytotypes. In hybrids of *H. bulbosum* with cultivated barley or wheat, elimination of the bulbosum chromosomes occurs resulting in haploid plants. *H. bulbosum* can be propagated both sexually by seeds and vegetatively by bulbs. Its flowering habit is characterized by monoecy but heterogamy, and by female sterile but male fertile lateral florets, which enforce a predominantly out-crossing behavior. However, the male floral organ in the lateral florets contains long filaments and big anthers with a large amount of pollen grains, effecting self-pollination of the male-sterile central florets.

Session 5: Genome differentiation revealed from the studies on repetitive sequence

M. Yamamoto[1] and Y. Mukai[2] ([1]Kansai Women's Coll., [2]Osaka Kyoiku Univ.)
High-resolution mapping in wheat and rye by two-color fluorescence in situ hybridization to extended DNA fibers

Fluorescence in situ hybridization to extended DNA fibers (EDFs) from interphase nuclei is a powerful technique in high-resolution mapping. The fiber FISH technique is useful for determining the size of target DNA sequences, the order of genes or clones and their distances in a large chromosome region. We succeeded in high resolution FISH mapping of multigene families, repeated DNA sequences, lambda phage clones, and BACs on EDFs in wheat and rye. The hybridization signals of DNA sequences in EDFs were traced with length of up to 2.0 Mb on single DNA fibers. The lower limit of the detection was 1.0 kb.

K. Nagaki, M. Kishii, H. Tsujimoto, and T. Sasakuma (Kihara Inst. Biol.Res., Yokohama City Univ.)
Analysis of Afa-family repetitive sequence from *Leymus racemosus*

We isolated Afa-family repetitive sequences from *Leymus racemosus* (2n = 4x = 28, Genome NNXX). These sequences repeat tandem in *L. racemosus* using 340-bp as one unit. In situ hybridization using the Afa-family sequence revealed that the sequences locate on the subtelomeric and interstitial regions of all *L. racemosus* chromosomes. This repetitive family occupied about 1 % of *L. racemosus* genomes. The restriction sites, *Afa*I and *Alu*I, were conserved as seen in the Afa-family sequences of the other species. Phylogenic analysis indicated that the Afa-family sequences of *L. racemosus* clustered near those of Ht genome of *Elymus trachycaulus*.

Y. Mukai (Osaka Kyoiku Univ.)
Repetitive DNA sequences present near useful genes in wheat

Agronomically important genes in wheat are mostly isolated from large-insert genomic DNA libraries such as lambda phage clones, cosmids, and BACs. These DNA clones usually contain highly repeated sequences. From distribution patterns on chromosomes by fluorescence in situ hybridization (FISH), repetitive DNA sequences were classified into several types: uniformly dispersed type; localized (dotted) type; telomeric (terminal) type; and centromeric (proximal) type. These repeated sequences were also visualized on extended DNA fibers by FISH. Biological function and evolutionary significance of repeated sequences were discussed.

Y. Matsuoka and K. Tsunewaki (Dept. Biosci., Fukui Pref. Univ.)
Characterization of *copia*-like retrotransposon families in grass

Four grass *copia*-like retrotransposon families (named G1, G2, G3, and G4) have been identified by phylogenetic analysis of 177 reverse transcriptase clones obtained from several grass species including wheat, rice and maize. Elements of G1 and G2 were detected in various subfamilies of Poaceae by Southern hybridization, whereas elements of G3 and G4 were restricted to a few given subfamilies. Comparative analyses of two well sampled families (G1 and G4) showed that the percentage of elements carrying non-functional reverse transcriptase domain is high in G4, suggesting that this family may employ a non-autonomous mechanism for amplification.

Session 6: Polymorphism and intraspecific differentiation in Triticeae

T. Sasanuma and N. T. Miyashita (Fac. Agr., Grad. Schl. Agr., Kyoto Univ.)

Amplified fragment length polymorphism (AFLP) analysis of five *Aegilops* species in the section of Sitopsis

To investigate the level of intra- and interspecific variation of five *Aegilops* Sitopsis species, we conducted AFLP analysis for 32 accessions by using three pairs of selective primers. A total of 441 bands were scored. On an average 23.9 bands were detected per accession per primer pairs. Phylogenetic analysis showed that the five Sitopsis species were classified into two distinct groups: *Ae. speltoides* and the other four. Among the five species, *Ae. speltoides* had the highest level of intraspecific variation. Estimates of nucleotide variation obtained by AFLP analysis was similar to those in our previous RFLP analysis.

S. Nasuda (Grad. Schl. Agr., Kyoto Univ.)

Fluorescent AFLP (amplified fragment length polymorphism) analysis in hexaploid wheat.

Fluorescent AFLP technique was employed to investigate polymorphisms between *Triticum aestivum* cv. Chinese Spring (CS) and *T. spelta* var. *duhamelianum* (Splt). Of 2322 bands generated by 32 primer combinations, 286 were polymorphic between CS and Splt. The polymorphism rate (0.123) was lower than that previously revealed by RFLP (0.174). Aneuploid analysis of those bands detected in CS indicated unequal distribution of AFLP markers within the wheat genome. Polymorphism survey was also made in two CS derived gametocidal (Gc) lines having a Gc gene from *Aegilops speltoides* or *Ae. sharonensis*. Gc lines showed gain or loss of bands compared to CS.

A. Kawabe, S. Nasuda, and N. T. Miyashita (Grad. Schl. Agr., Kyoto Univ.)

An analysis of codon usage in common wheat (*Triticum aestivum*): a possibility of natural selection on synonymous substitution

Codon usage in 223 wheat nuclear genes was analyzed. Codon bias varied among genes. The frequency distribution of codon bias in wheat was similar to those of maize and barley. Codon bias was correlated with GC content at the third position of codon. Genes which showed high codon bias in wheat had high codon bias in maize and barley. Between wheat and maize, codon bias was significantly correlated with the number of synonymous substitutions per site i. e., high biased genes had low synonymous substitutions. This result suggested that synonymous substitutions were not selectively neutral in the Poaceae.

Getachew Belay (Fac. Agr., Gifu Univ.)

C-band polymorphism and chromosomal rearrangements in Ethiopian tetraploid wheats

C-band polymorphism was studied in seven tetraploid (2n=3D4x=3D28) wheat (*Triticum turgidum*

L.) landraces of Ethiopian origin, and an attempt was made to localize chromosomal breakpoints in five of them that carry one reciprocal translocation each, relative to the variety "Senatore Cappelli" (SC). Most chromosomes showed C-banding variation, which was not associated with spike morphology or collection locality. None of the genotypes showed a similar C-banding pattern to SC for chromosome arms 3BL, 5AL and 5BL. Unusual bands or banding patterns were observed on 2AS, 7AL, 5BL and 7BS. Generally, unequivocal localization of translocation breakpoints by C-banding alone proved difficult. Nevertheless, it is plausible that most of the translocations have non-centromeric breakpoints.

Kaz. Noda[1], Y. Amano[2], and T. Fukase[3] ([1]Res. Inst. Biores., Okayama Univ., [2]Kitami Agr. Exp. Stn., [3]Tokachi Agr. Exp Stn.)

Premature a-amylase production in de-embryonated seeds of wheat

Preharvest sprouting and seeds with high α-amylase activity without germination have been observed every three years in Japan and on average, 20 percent or more of the seeds are classified as out of the standard grade. Two periods during seed development are responsive to these phenomena. 1) Frequent rainfalls during the ripe stage of seeds. 2) Humid and cool temperature in the maturing stage (between yellow ripe and full ripe). In respect to premature α-amylase production, de-embryonated half seeds of some wheat lines showed to have a potential to synthesize α-amylase when imbibed.

H. Tsujimoto, T. Yamada, and T. Sasakuma (Kihara Inst. Biol. Res., Yokohama City Univ.)

***Leymus racemosus* chromosome addition lines of common wheat (preliminary report)**

Leymus racemosus (2n=4x=28, NNXX) was crossed as male with common wheat (*Triticum aestivum*) cultivar "Chinese Spring" (abbrev. CS). The hybrid was rescued by embryo culture and treated with colchicine for chromosome doubling. The amphidiploid was further crossed with CS, and a plant with genomes AABBDDNX was obtained. The offspring (26 plants) by the cross between the octoploid and CS carried from 41 to 52 chromosomes. Most of the *L. racemosus* chromosomes were distinguished from each other and from common wheat chromosomes by C-banding. Since all of the alien chromosomes appeared in the offspring, complete set of addition lines will be possibly bred.

Wheat Information Service
Number 87: 51–61 (1998)
Recent publications

Recent publications on wheat genetics

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

1997

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(92)
ACCN:001899534 CTLN:4244131
ABSJ:G (Genetics Abstracts)
AUTH:Rengel, Z.;Hawkesford, M.J.
AFFN:Soil Sci. and Plant Nutr., Fac. Agric., Univ. Western Australia, Nedlands, WA 6907, Australia
TITL:Biosynthesis of a 34-kDa polypeptide in the root-cell plasma membrane of a Zn-efficient wheat genotype increases upon Zn deficiency
HTIL:AUST. J. PLANT PHYSIOL.
HSSN:0310-7841
HYER:19970000
HCOL:vol. 23, no. 3, pp. 307-315

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(93)
ACCN:001899812 CTLN:4244430
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Wood, D.W.;Gong, F.;Daykin, M.M.;Williams, P.;Pierson, L.S.,III*
AFFN:Dep. Plant Pathol., Univ. Arizona, Tucson, AZ 85721, USA
TITL:N-acyl-homoserine lactone-mediated regulation of phenazine gene expression by Pseudomonas aureofaciens 30-84 in the wheat rhizosphere
HTIL:J. BACTERIOL.
HSSN:0021-9193
HYER:19971200
HCOL:vol. 179, no. 24, pp. 7663-7670

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(94)
ACCN:001900260 CTLN:4244954
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts)
AUTH:Keller, S.M.;Wolfe, M.S.;McDermott, J.M.;McDonald, B.A.*
AFFN:Dep. Plant Pathol. and Microbiol., Texas A&M Univ., College Station, TX 77845-2132, USA
TITL:High genetic similarity among populations of Phaeosphaeria nodorum across wheat cultivars and regions in Switzerland
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:19971100
HCOL:vol. 87, no. 11, pp. 1134-1139

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(95)
ACCN:001901649 CTLN:4248035
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Liu, J.Q.;Kolmer, J.A.*
AFFN:Agric. and Agri-Food Canada, Cereal Res. Cent., 195 Dafoe Rd., Winnipeg, MB, Canada R3T 2M9
TITL:Genetics of leaf rust resistance in Canadian spring wheats AC Domain and AC Taber
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:19970700
HCOL:vol. 81, no. 7, pp. 757-760

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(96)
ACCN:001910864 CTLN:4265863
ABSJ:Z (Entomology Abstracts)
AUTH:Sharma, H.C.;Ohm, H.W.;Patterson, F.L.;Benlhabib, O.;Cambron, S.
AFFN:Dep. Agron., Purdue Univ., West Lafayette, IN 47907, USA
TITL:Genetics of resistance to Hessian fly (Mayetiola destructor) [Diptera: Cecidomyiidae] biotype L in diploid wheats
HTIL:PHYTOPROTECTION
HSSN:0031-9511
HYER:19970000
HCOL:vol. 78, no. 2, pp. 61-65

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(97)
ACCN:001918511 CTLN:4274482
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Calonec, A.;Johnson, R.;De Vallavieille-Pope,

C.
AFFN:INRA, Stn. de Pathologie Vegetale, Domaine de la Grande Ferrade, BP 81, 33883 Villenave d'Ornon, France
TITL:Identification and expression of the gene Yr2 for resistance to Puccinia striiformis in the wheat differential cultivars Heines Kolben, Heines Peko and Heines VII
HTIL:PLANT PATHOL.
HSSN:0032-0862
HYER:19970600
HCOL:vol. 46, no. 3, pp. 387-396

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(98)
ACCN:001918512 CTLN:4274481
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Calonnec, A.;Johnson, R.;De Vallavieille-Pope, C.
AFFN:INRA, Stn. de Pathologie Vegetale, Domaine de la Grande Ferrade, BP 81, 33883 Villenave d'Ornon Cedex, France
TITL:Genetic analysis of resistance to Puccinia striiformis in the wheat differential cultivars Heines VII, Heines Peko and Strubes Dickkopf
HTIL:PLANT PATHOL.
HSSN:0032-0862
HYER:19970600
HCOL:vol. 46, no. 3, pp. 373-386

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(99)
ACCN:001924273 CTLN:4282676
ABSJ:G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Broers, L.H.M.
AFFN:Nunhems Zaden BV, P.O. Box 4005, NL-6080 AA Haelen, The Netherlands
TITL:Components of quantitative resistance to yellow rust in ten spring bread wheat cultivars and their relations with field assessments
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 96, no. 2, pp. 215-223

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(100)
ACCN:001924524 CTLN:4282927
ABSJ:G (Genetics Abstracts)
AUTH:Miralles, D.J.;Slafer, G.A.
AFFN:Catedra de Cerealicultura, Depto. de Produccion Vegetal, Fac. de Agronomia, Univ. de Buenos Aires, Av. San Martin 4453, 1417, Buenos Aires, Argentina
TITL:Radiation interception and radiation use efficiency of near-isogenic wheat lines with different height
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 97, no. 2, pp. 201-208

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(101)
ACCN:001924533 CTLN:4282936
ABSJ:G (Genetics Abstracts)
AUTH:Rerkasem, B.;Jamjod, S.
AFFN:Agron. Dep., Fac. Agric., Chiang Mai Univ., Chiang Mai, 50200 Thailand
TITL:Boron deficiency induced male sterility in wheat (Triticum aestivum L.) and implications for plant breeding
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 96, no. 2, pp. 257-262

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(102)
ACCN:001924541 CTLN:4282944
ABSJ:G (Genetics Abstracts)
AUTH:Murai, K.;Koba, T.;Shimada, T.
AFFN:Res. Inst. Agric. Resour., Ishikawa Agric. Coll., Nonoichi-machi, Ishikawa 921, Japan
TITL:Effects of barley chromosome on heading characters in wheat-barley chromosome addition lines
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 96, no. 2, pp. 281-287

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(103)
ACCN:001924542 CTLN:4282945
ABSJ:G (Genetics Abstracts)
AUTH:Ehdaie, B.;Waines, J.G.
AFFN:Dep. Botany and Plant Sci., Univ. California, Riverside, CA 92521-0124, USA
TITL:Chromosomal location of genes influencing plant characters and evapotranspiration efficiency in bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 96, no. 3, pp. 363-375

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(104)
ACCN:001924548 CTLN:4282951
ABSJ:G (Genetics Abstracts)
AUTH:Labuschagne, M.T.;Claassen, A.;Van Deventer, C.S.
AFFN:Dep. Plant Breeding, Univ. Free State, P.O. Box 339, Bloemfontein, 9300, South Africa
TITL:Biscuit-making quality of backcross derivatives of wheat differing in kernel hardness
HTIL:EUPHYTICA
HSSN:0014-2336

HYER:19970000
HCOL:vol. 96, no. 2, pp. 263-266

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(105)
ACCN:001924567 CTLN:4282970
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Bommineni, V.R.;Jauhar, P.P.*;Peterson, T.S.
AFFN:USDA-ARS, Northern Crop Sci. Lab., Fargo, ND 58105-5677, USA
TITL:Transgenic durum wheat by microprojectile bombardment of isolated scutella
HTIL:J. HERED.
HSSN:0022-1503
HYER:19971200
HCOL:vol. 88, no. 6, pp. 475-481

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(106)
ACCN:001924580 CTLN:4282983
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Koba, T.;Takumi, S.;Shimada, T.
AFFN:Lab. Genet. and Plant Breeding, Fac. Horticulture, Chiba Univ., Matsudo, Chiba 271, Japan
TITL:Isolation, identification and characterization of disomic and translocated barley chromosome addition lines of common wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:19970000
HCOL:vol. 96, no. 2, pp. 289-296

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(107)
ACCN:001929512 CTLN:4250361
ABSJ:G (Genetics Abstracts)
AUTH:Gornicki, P.;Faris, J.;King, I.;Podkowinski, J.;Gill, B.;Haselkorn, R.
AFFN:Department of Molecular Genetics and Cell Biology, University of Chicago, 920 East 58th Street, Chicago, IL 60637, USA
TITL:Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded by a single gene on each of the three ancestral chromosome sets
HTIL:Proc. Natl. Acad. Sci. USA
HSSN:0027-8424
HYER:19971209
HCOL:vol. 94, no. 25, pp. 14179-14184

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(108)
ACCN:001934580 CTLN:4292475
ABSJ:G (Genetics Abstracts)
AUTH:Feldman, M.;Liu, B.;Segal, G.;Abbo, S.;Levy, A.A.;Vega, J.M.
AFFN:Dep. Plant Genet., Weizmann Inst. Sci., Rehovot 76100, Israel
TITL:Rapid elimination of low-copy DNA sequences in polyploid wheat: A possible mechanism for differentiation of homoeologous chromosomes
HTIL:GENETICS
HSSN:0016-6731
HYER:19971100
HCOL:vol. 147, no. 3, pp. 1381-1387

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(109)
ACCN:001934598 CTLN:4292493
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Kurek, I.;Ezra, D.;Begu, D.;Erel, N.;Litvak, S.;Breiman, A.*
AFFN:Dep. Botany, George S. Wise Fac. Life Sci., Tel Aviv Univ., Tel Aviv 69978, Israel
TITL:Studies on the effects of nuclear background and tissue specificity on RNA editing of the mitochondrial ATP synthase subunits alpha , 6 and 9 in fertile and cytoplasmic male-sterile (CMS) wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971200
HCOL:vol. 95, no. 8, pp. 1305-1311

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(110)
ACCN:001934602 CTLN:4292497
ABSJ:G (Genetics Abstracts)
AUTH:Sarhan, F.;Ouellet, F.;Vazquez-Tello, A.
AFFN:Dep. des Sci. Biologiques, Univ. du Quebec a Montreal, C.P. 8888, Succ. Cent.-Ville, Montreal, PQ, H3C 3P8, Canada
TITL:The wheat wcs120 gene family. A useful model to understand the molecular genetics of freezing tolerance in cereals
HTIL:PHYSIOL. PLANT.
HSSN:0031-9317
HYER:19971000
HCOL:vol. 101, no. 2, pp. 439-445

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(111)
ACCN:001934617 CTLN:4292512
ABSJ:G (Genetics Abstracts)
AUTH:Lee, J.-H.;Yen, Y.*;Arumuganathan, K.;Baenziger, P.S.
AFFN:Dep. Biol./Microbiol., South Dakota State Univ., Brookings, SD 57007, USA
TITL:DNA content of wheat monosomics at interphase estimated by flow cytometry
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971200
HCOL:vol. 95, no. 8, pp. 1300-1304

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(112)
ACCN:001934632 CTLN:4292527
ABSJ:G (Genetics Abstracts)
AUTH:Appleford, N.E.J.;Lenton, J.R.
AFFN:IACR-Long Ashton Res. Stn., Dep. Agric. Sci.,

Univ. Bristol, Long Ashton, Bristol BS18 9AF, UK
TITL:Hormonal regulation of alpha -amylase gene expression in germinating wheat (Triticum aestivum) grains
HTIL:PHYSIOL. PLANT.
HSSN:0031-9317
HYER:19970700
HCOL:vol. 100, no. 3, pp. 534-542

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(113)
ACCN:001934653 CTLN:4292548
ABSJ:G (Genetics Abstracts)
AUTH:Tsujimoto, H.;Mukai, Y.;Akagawa, K.;Nagaki, K.;Fujigaki, J.;Yamamoto, M.;Sasakuma, T.
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., 641-12 Maioka-cho, Totsuka-ku, Yokohama 244, Japan
TITL:Identification of individual barley chromosomes based on repetitive sequences: Conservative distribution of Afa-family repetitive sequences on the chromosomes of barley and wheat
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19971000
HCOL:vol. 72, no. 5, pp. 303-309

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(114)
ACCN:001934655 CTLN:4292550
ABSJ:G (Genetics Abstracts)
AUTH:Murai, K.;Murai, R.;Ogihara, Y.
AFFN:Res. Inst. Agric. Resour., Ishikawa Agric. Coll., Nonoichi-machi, Ishikawa 921, Japan
TITL:Wheat MADS box genes, a multigene family dispersed throughout the genome
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19971000
HCOL:vol. 72, no. 5, pp. 317-321

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(115)
ACCN:001934660 CTLN:4292555
ABSJ:G (Genetics Abstracts)
AUTH:Chhina, G.S.;Kler, D.S.
AFFN:Dep. Agron., Punjab Agric. Univ., Ludhiana 141004, India
TITL:Evaluation of the performance of genotypes in different wheat canopies through relative crowding index
HTIL:ENVIRON. ECOL.
HSSN:0970-0420
HYER:19971200
HCOL:vol. 15, no. 4, pp. 739-742

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(116)
ACCN:001935097 CTLN:4293247
ABSJ:G (Genetics Abstracts)
AUTH:Mauch, F.;Kmecl, A.;Schaffrath, U.;Volrath, S.;Goerlach, J.;Ward, E.; Ryals, J.;Dudler, R.
AFFN:Inst. fuer Pflanzenbiologie, Univ. Zuerich, Zollikerstrasse 107, CH- 8008 Zuerich, Switzerland
TITL:Mechanosensitive expression of a lipoxygenase gene in wheat
HTIL:PLANT PHYSIOL.
HSSN:0032-0889
HYER:19970800
HCOL:vol. 114, no. 4, pp. 1561-1566

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(117)
ACCN:001935565 CTLN:4294550
ABSJ:G (Genetics Abstracts)
AUTH:D'Ovidio, R.;Simeone, M.;Masci, S.;Porceddu, E.
AFFN:Dipartimento di Agrobiologia e Agrochimica, Universita della Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:Molecular characterization of a LMW-GS gene located on chromosome 1B and the development of primers specific for the Glu-B3 complex locus in durum wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971100
HCOL:vol. 95, no. 7, pp. 1119-1126

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(118)
ACCN:001935658 CTLN:4294643
ABSJ:G (Genetics Abstracts)
AUTH:Mori, N.;Moriguchi, T.;Nakamura, C.
AFFN:Laboratory of Plant Genetics, Faculty of Agriculture, Kobe University, 1 Rokkodai-cho, Nada-ku, Kobe 657, Japan
TITL:RFLP analysis of nuclear DNA for study of phylogeny and domestication of tetraploid wheat
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19970600
HCOL:vol. 72, no. 3, pp. 153-161

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(119)
ACCN:001935865 CTLN:4294850
ABSJ:G (Genetics Abstracts)
AUTH:Nieto-Taladriz, M.T.;Ruiz, M.;Martinez, M.C.;Vazquez, J.F.;Carrillo, J. M.
AFFN:Unidad de Genetica, E.T.S. Ingenieros Agronomos, Universidad Politecnica, 28040-Madrid, Spain
TITL:Variation and classification of B low-molecular-weight glutenin subunit alleles in durum wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971100
HCOL:vol. 95, no. 7, pp. 1155-1160

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(120)

ACCN:001935866 CTLN:4294851
ABSJ:G (Genetics Abstracts)
AUTH:Boerner, A.;Roeder, M.;Korzun, V.
AFFN:Institut fuer Pflanzengenetik und Kulturpflanzenforschung (IPK), Correnssstrasse 3, D-06466 Gatersleben, Germany
TITL:Comparative molecular mapping of GA insensitive Rht loci on chromosomes 4B and 4D of common wheat (Triticum aestivum L.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971100
HCOL:vol. 95, no. 7, pp. 1133-1137

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(121)
ACCN:001935869 CTLN:4294854
ABSJ:G (Genetics Abstracts)
AUTH:Dubcovsky, J.;Echaide, M.;Giancola, S.;Rousset, M.;Luo, M.C.;Joppa, L. R.;Dvorak, J.
AFFN:Department of Agronomy and Range Science, University of California, Davis, CA 95616-8515, USA
TITL:Seed-storage-protein loci in RFLP maps of diploid, tetraploid, and hexaploid wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971100
HCOL:vol. 95, no. 7, pp. 1169-1180

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(122)
ACCN:001935871 CTLN:4294856
ABSJ:G (Genetics Abstracts)
AUTH:Qi, L.L.;Wang, S.L.;Chen, P.D.;Liu, D.J.;Friebe, B.;Gill, B.S.
AFFN:Department of Agronomy, Nangjing Agricultural University, Nangjing, 210095, P.R. China
TITL:Molecular cytogenetic analysis of Leymus racemosus chromosomes added to wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971100
HCOL:vol. 95, no. 7, pp. 1084-1091

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(123)
ACCN:001936791 CTLN:4295940
ABSJ:G (Genetics Abstracts)
AUTH:Prins, R.;Marais, G.F.;Pretorius, Z.A.;Janse, B.J.H.;Marais, A.S.
AFFN:Agric. Res. Counc. (Small Grain Inst.), P/a Dep. Genet., Univ. Stellenbosch, 7600 Stellenbosch, South Africa
TITL:A study of modified forms of the Lr19 translocation of common wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970800
HCOL:vol. 95, no. 3, pp. 424-430

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(124)
ACCN:001936815 CTLN:4295965
ABSJ:G (Genetics Abstracts)
AUTH:Thomas, J.;Chen, Qin;Howes, N.
AFFN:Lethbridge Res. Cent., Box 3000, Lethbridge, AB T1J 4B1, Canada
TITL:Chromosome doubling of haploids of common wheat with caffeine
HTIL:GENOME
HSSN:0831-2796
HYER:19970800
HCOL:vol. 40, no. 4, pp. 552-558

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(125)
ACCN:001936837 CTLN:4295987
ABSJ:G (Genetics Abstracts)
AUTH:Joshi, C.P.;Klueva, N.Y.;Morrow, K.J.;Nguyen, H.T.*
AFFN:Plant Mol. Genet. Lab., Dep. Plant and Soil Sci., Texas Tech. Univ., Lubbock, TX 79409-2122, USA
TITL:Expression of a unique plastid-localized heat-shock protein is genetically linked to acquired thermotolerance in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971000
HCOL:vol. 95, no. 5-6, pp. 834-841

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(126)
ACCN:001936840 CTLN:4295990
ABSJ:G (Genetics Abstracts)
AUTH:Giroux, M.J.;Morris, C.F.*
AFFN:USDA-ARS Western Wheat Quality Lab., E-202 Food Sci. and Hum. Nutr. Facil. East, Washington State Univ., Pullman, WA 99164-6394, USA
TITL:A glycine to serine change in puroindoline b is associated with wheat grain hardness and low levels of starch-surface friabilin
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971000
HCOL:vol. 95, no. 5-6, pp. 857-864

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(127)
ACCN:001936845 CTLN:4295995
ABSJ:G (Genetics Abstracts)
AUTH:Sun, Gen-Lou;Salomon, B.;Bothmer, R.
AFFN:Dep. Plant Breeding Res., Swedish Univ. Agric. Sci., S-268 31 Svaloev, Sweden
TITL:Analysis of tetraploid Elymus species using wheat microsatellite markers and RAPD markers
HTIL:GENOME
HSSN:0831-2796
HYER:19971200

HCOL:vol. 40, no. 6, pp. 806-814

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(128)
ACCN:001936857 CTLN:4296007
ABSJ:G (Genetics Abstracts)
AUTH:Mingeot, D.;Jacquemin, J.M.
AFFN:Cent. de Recherches Agronomiques, Stn. d'Amelioration des Plantes, 4 Rue du Bordia, 5030 Gembloux, Belgium
TITL:A wheat cDNA coding for a thaumatin-like protein reveals a high level of RFLP in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971000
HCOL:vol. 95, no. 5-6, pp. 822-827

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(129)
ACCN:001938507 CTLN:4300611
ABSJ:G (Genetics Abstracts)
AUTH:Aragon-Alcaide, L.;Reader, S.;Miller, T.;Moore, G.*
AFFN:John Innes Cent., Norwich Research Park, Colney, Norwich NR4 7UH, UK
TITL:Centromeric behaviour in wheat with high and low homoeologous chromosomal pairing
HTIL:CHROMOSOMA
HSSN:0009-5915
HYER:19970000
HCOL:vol. 106, no. 5, pp. 327-333

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(130)
ACCN:001938575 CTLN:4300679
ABSJ:G (Genetics Abstracts)
AUTH:Matsuoka, Y.;Tsunewaki, K.
AFFN:Dep. Biosci., Fukui Prefect. Univ., Matsuoka-cho, Yoshida-gun, Fukui 910-11, Japan
TITL:Presence of wheat retrotransposons in Gramineae species and the origin of wheat retrotransposon families
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19971200
HCOL:vol. 72, no. 6, pp. 335-343

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(131)
ACCN:001938576 CTLN:4300680
ABSJ:G (Genetics Abstracts)
AUTH:Matsuoka, Y.;Tsunewaki, K.
AFFN:Dep. Biosci., Fukui Prefect. Univ. Matsuoka-cho, Yoshida-gun, Fukui 910-11, Japan
TITL:Origin and the transmission of some types of family 1 wheat retrotransposons in the two related genera Triticum and Aegilops
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19971200
HCOL:vol. 72, no. 6, pp. 345-351

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(132)
ACCN:001938577 CTLN:4300681
ABSJ:G (Genetics Abstracts)
AUTH:Kojima, T.;Tsujimoto, H.;Ogihara, Y.*
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., Maioka-cho 641-12, Yokohama 244, Japan
TITL:High-resolution RFLP mapping of the fertility restoration (Rf3) gene against Triticum timopheevi cytoplasm located on chromosome 1BS of common wheat
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19971200
HCOL:vol. 72, no. 6, pp. 353-359

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(133)
ACCN:001940619 CTLN:4250893
ABSJ:G (Genetics Abstracts)
AUTH:Shi, Fang;Endo, T.R.
AFFN:Laboratory of Plant Genetics, Graduate School of Agriculture, Kyoto University, Kyoto 606-01, Japan
TITL:Production of wheat-barley disomic addition lines possessing an Aegilops cylindrica gametocidal chromosome
HTIL:Genes Genet. Syst.
HSSN:1341-7568
HYER:19970800
HCOL:vol. 72, no. 4, pp. 243-248

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(134)
ACCN:001941102 CTLN:4258743
ABSJ:G (Genetics Abstracts)
AUTH:Wang, Gui-Zhi;Miyashita, N.T.;Tsunewaki, K.
AFFN:Department of Bioscience, Fukui Perfectural University, 4-1-1, Kenjyojima, Matsuoka, Yishida-gun, Fukui 910-11, Japan
TITL:Plasmon analyses of Triticum (wheat) and Aegilops: PCR-single-strand conformational polymorphism (PCR-SSCP) analyses of organellar DNAs
HTIL:Proc. Natl. Acad. Sci. USA
HSSN:0027-8424
HYER:19971223
HCOL:vol. 94, no. 26, pp. 14570-14577

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(135)
ACCN:001944909 CTLN:4301212
ABSJ:G (Genetics Abstracts)
AUTH:Rahman, S.;Abrahams, S.;Abbott, D.;Mukai, Y.;Samuel, M.;Morell, M.; Appels, R.
AFFN:Cooperative Research Centre for Plant Sciences, Australian National University, P.O. Box 475, Canberra ACT 2601, Australia
TITL:A complex arrangement of genes at a starch branching enzyme I locus in the D-genome donor of wheat
HTIL:GENOME

HSSN:0831-2796
HYER:19970800
HCOL:vol. 40, no. 4, pp. 465-474

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(136)
ACCN:001944913 CTLN:4301216
ABSJ:G (Genetics Abstracts)
AUTH:David, J.L.;Zivy, M.;Cardin, M.L.;Brabant, P.
AFFN:INRA, Station de Genetique et d'Amelioration des Plantes, Domaine de Melgueil, F-34130 Mauguio, France
TITL:Protein evolution in dynamically managed populations of wheat: Adaptive responses to macro-environmental conditions
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971000
HCOL:vol. 95, no. 5-6, pp. 932-941

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(137)
ACCN:001944915 CTLN:4301218
ABSJ:G (Genetics Abstracts)
AUTH:Huang, X.Q.;Hsam, S.L.K.;Zeller, F.J.*
AFFN:Technische Universitaet Muenchen, Institut fuer Pflanzenbau und Pflanzenzuechtung, D-85350 Freising-Weihenstephan, Germany
TITL:Chromosomal location of genes for resistance to powdery mildew in common wheat (Triticum aestivum L. em. Thell.) 4. Gene Pm 24 in Chinese landrace Chiyacao
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19971000
HCOL:vol. 95, no. 5-6, pp. 950-953

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(138)
ACCN:001944920 CTLN:4301223
ABSJ:G (Genetics Abstracts)
AUTH:Lukaszewski, A.J.
AFFN:Department of Botany and Plant Sciences, University of California, Riverside, CA 92521, USA
TITL:Construction of midget chromosomes in wheat
HTIL:GENOME
HSSN:0831-2796
HYER:19970800
HCOL:vol. 40, no. 4, pp. 566-569

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(139)
ACCN:001948572 CTLN:4309910
ABSJ:G (Genetics Abstracts)
AUTH:Basu, U.;McDonald-Stephens, J.L.;Archambault, D.J.;Good, A.G.;Briggs, K.G.;Taing-Aung,;Taylor, G.J.
AFFN:Dep. Biol. Sci., Univ. Alberta, Edmonton, Alberta, T6G 2E9, Canada
TITL:Genetic and physiological analysis of doubled-haploid, aluminium- resistant lines of wheat provide evidence for the involvement of a 23 kD, root exudate polypeptide in mediating resistance
HTIL:PLANT SOIL
HSSN:0032-079X
HYER:19971000
HCOL:vol. 196, no. 2, pp. 283-288

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(140)
ACCN:001948585 CTLN:4309923
ABSJ:G (Genetics Abstracts)
AUTH:Cakmak, I.;Derici, R.;Torun, B.;Tolay, I.;Braun, H.J.;Schlegel, R.
AFFN:Dep. Soil Sci. and Plant Nutr., Cukurova Univ. 01330 Adana, Turkey
TITL:Role of rye chromosomes in improvement of zinc efficiency in wheat and triticale
HTIL:PLANT SOIL
HSSN:0032-079X
HYER:19971000
HCOL:vol. 196, no. 2, pp. 249-253

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(141)
ACCN:001950102 CTLN:4314529
ABSJ:W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts)
AUTH:Menon, U.;Sharma, S.N.
AFFN:Dep. Genet. & Plant Breeding, RAU Agric. Res. Stn., Durgapura, Jaipur 302 018, India
TITL:Phenotypic stability in hexaploid wheat
HTIL:CROP IMPROV.
HSSN:0256-0933
HYER:19970600
HCOL:vol. 24, no. 1, pp. 132-134

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(142)
ACCN:001951759 CTLN:4317709
ABSJ:G (Genetics Abstracts)
AUTH:Klindworth, D.L.;Klindworth, M.M.;Williams, N.D.
AFFN:USDA Agricultural Research Service, Northern Crop Science Lab., P.O. Box 5677, State University Station, Fargo, ND 58105, USA
TITL:Telosomic mapping of four genetic markers in durum wheat
HTIL:J. HERED.
HSSN:0022-1503
HYER:19970600
HCOL:vol. 88, no. 3, pp. 229-232

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(143)
ACCN:001959422 CTLN:4320839
ABSJ:G (Genetics Abstracts)
AUTH:Rana, V.;Sharma, S.C.
AFFN:Department of Plant Breeding and Genetics, H. P. Agricultural University, Palampur (H. P.), India
TITL:Inheritance of yield and its components in bread wheat under moisture stress conditions

HTIL:ANN. AGRI BIO RES.
HYER:19970700
HCOL:vol. 2, no. 1, pp. 59-62

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(144)
ACCN:001960771 CTLN:4327382
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Cruz-Ortega, R.;Cushman, J.C.;Ownby, J.D.*
AFFN:Department of Botany, Oklahoma State University, Stillwater, OK 74078, USA
TITL:cDNA clones encoding 1,3- beta -glucanase and a fimbrin-like cytoskeletal protein are induced by Al toxicity in wheat roots
HTIL:PLANT PHYSIOL.
HSSN:0032-0889
HYER:19970800
HCOL:vol. 114, no. 4, pp. 1453-1460

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(145)
ACCN:001961111 CTLN:4327742
ABSJ:G (Genetics Abstracts)
AUTH:Sun, G.L.;Fahima, T.*;Korol, A.B.;Turpeinen, T.;Grama, A.;Ronin, Y.I.; Nevo, E.
AFFN:Institute of Evolution, University of Haifa, Mount Carmel, Haifa 31905, Israel
TITL:Identification of molecular markers linked to the Yr15 stripe rust resistance gene of wheat originated in wild emmer wheat, Triticum dicoccoides
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970900
HCOL:vol. 95, no. 4, pp. 622-628

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(146)
ACCN:001961125 CTLN:4327756
ABSJ:G (Genetics Abstracts)
AUTH:Kato, K.;Mori, Y.;Beiles, A.;Nevo, E.
AFFN:Faculty of Agriculture, Okayama University, Okayama 700, Japan
TITL:Geographical variation in heading traits in wild emmer wheat, Triticum dicoccoides. I. Variation in vernalization response and ecological differentiation
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19970900
HCOL:vol. 95, no. 4, pp. 546-552

1998

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(1)
ACCN:001923952 CTLN:4282178
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Niewoehner, A.S.;Leath, S.
AFFN:Dep. Plant Pathol., North Carolina State Univ., Raleigh, NC 27695, USA
TITL:Virulence of Blumeria graminis f. sp. tritici on winter wheat in the eastern United States
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:19980100
HCOL:vol. 82, no. 1, pp. 64-68

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(2)
ACCN:001924614 CTLN:4283017
ABSJ:G (Genetics Abstracts)
AUTH:Jiang, J.;Gill, B.S.
TITL:Preferential male transmission of an alien chromosome in wheat
HTIL:J. HERED.
HSSN:0022-1503
HYER:19980200
HCOL:vol. 89, no. 1, pp. 87-89

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(3)
ACCN:001928120 CTLN:4277079
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Keon, J.;Hargreaves, J.
AFFN:IACR-Long Ashton Research Station, Department of Agricultural Sciences, University of Bristol, Long Ashton, Bristol BS18 9AF, UK
TITL:Isolation and heterologous expression of a gene encoding 4- hydroxyphenylpyruvate dioxygenase from the wheat leaf-spot pathogen, Mycosphaerella graminicola
PBSR:Elsevier Science B.V.
HTIL:FEMS MICROBIOL. LETT.
HSSN:0378-1097
HYER:19980415
HCOL:vol. 161, no. 2, pp. 337-343

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(4)
ACCN:001930794 CTLN:4286926
ABSJ:G (Genetics Abstracts)
AUTH:Law, C.N.;Suarez, E.;Miller, T.E.;Worland, A.J.
AFFN:41 Thornton Close, Cambridge CB3 ONF, UK
TITL:The influence of the group 1 chromosomes of wheat on ear-emergence times and their involvement with vernalization and day length
HTIL:Heredity
HSSN:0018-067X
HYER:19980100
HCOL:vol. 80, no. 1, pp. 83-91

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(5)
ACCN:001930986 CTLN:4288055
ABSJ:K (Microbiology Abstracts C: Algology,

Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Liu, J.Q.;Kolmer, J.A.*
AFFN:Agric. and Agri-Food Canada, Cereal Res. Cent., 195 Dafoe Rd., Winnipeg, MB, Canada R3T 2M9
TITL:Genetics of stem rust resistance in wheat Cvs. Pasqua and AC Taber
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:19980200
HCOL:vol. 88, no. 2, pp. 171-176

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(6)
ACCN:001930988 CTLN:4288057
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Shi, A.N.;Leath, S.*;Murphy, J.P.
AFFN:USDA-ARS and Dep. Plant Pathol., North Carolina State Univ., Raleigh, NC 27695-7616, USA
TITL:A major gene for powdery mildew resistance transferred to common wheat from wild einkorn wheat
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:19980200
HCOL:vol. 88, no. 2, pp. 144-147

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(7)
ACCN:001936770 CTLN:4295919
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Zheng-Song, Peng;Deng-Cai, Liu;Chi, Yen;Jun-Liang, Yang
AFFN:Triticeae Res. Inst., Sichuan Agric. Univ., Dujiangyan City, Sichuan 611830, P.R. China
TITL:Crossability of tetraploid wheat landraces native to Sichuan, Shaanxi, Gansu and Xinjiang provinces, China with rye
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:19980200
HCOL:vol. 45, no. 1, pp. 57-62

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(8)
ACCN:001936771 CTLN:4295920
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Figliuolo, G.;Jones, S.S.*;Murray, T.D.;Zeuli, P.L.S.
AFFN:Dep. Plant Pathol., Washington State Univ., Pullman, WA 99164-6420, USA
TITL:Characterization of tetraploid wheat germplasm for resistance to Pseudocercosporella herpotrichoides, cause of eyespot disease
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:19980200
HCOL:vol. 45, no. 1, pp. 47-56

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(9)
ACCN:001936803 CTLN:4295952
ABSJ:G (Genetics Abstracts); V (Virology & AIDS Abstracts)
AUTH:Chen, Q.;Friebe, B.;Conner, R.L.;Laroche, A.;Thomas, J.B.;Gill, B.S.
AFFN:Res. Cent., Agric. and Agri-Food Canada, P.O. Box 3000, Lethbridge, T1J 4B1, AB Canada
TITL:Molecular cytogenetic characterization of Thinopyrum intermedium- derived wheat germplasm specifying resistance to wheat streak mosaic virus
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980100
HCOL:vol. 96, no. 1, pp. 1-7

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(10)
ACCN:001936821 CTLN:4295971
ABSJ:G (Genetics Abstracts)
AUTH:Van Campenhout, S.;Sagi, L.;Vander Stappen, J.;Volckaert, G.*
AFFN:Lab. Gene Technol., Katholieke Universiteit Leuven, Willem de Croylaan 42, B-3001 Leuven, Belgium
TITL:Characterisation of type-I thionin loci from the A, B, D and R genomes of wheat and rye
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980100
HCOL:vol. 96, no. 1, pp. 80-86

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(11)
ACCN:001936823 CTLN:4295973
ABSJ:G (Genetics Abstracts)
AUTH:Kojima, T.;Nagaoka, T.;Noda, K.;Ogihara, Y.*
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., Maioka-cho 641-12, Yokohama 244, Japan
TITL:Genetic linkage map of ISSR and RAPD markers in Einkorn wheat in relation to that of RFLP markers
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980100
HCOL:vol. 96, no. 1, pp. 37-45

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(12)
ACCN:001936829 CTLN:4295979
ABSJ:G (Genetics Abstracts)
AUTH:Peil, A.;Korzun, V.;Schubert, V.;Schumann,

E.;Weber, W.E.;Roeder, M.S.
AFFN:Inst. fuer Pflanzenzuechtung und Pflanzenschutz, Martin-Luther-Univ. Halle-Wittenberg, Berlinerstrasse 2, D-06188 Hohenthurm, Germany
TITL:The application of wheat microsatellites to identify disomic Triticum aestivum-Aegilops markgrafii addition lines
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980100
HCOL:vol. 96, no. 1, pp. 138-146

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(13)
ACCN:001936835 CTLN:4295985
ABSJ:G (Genetics Abstracts)
AUTH:Zhang, H.;Jia, J.;Gale, M.D.;Devos, K.M.
AFFN:John Innes Cent., Norwich Research Park, Colney, Norwich NR4 7UH, UK
TITL:Relationships between the chromosomes of Aegilops umbellulata and wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980100
HCOL:vol. 96, no. 1, pp. 69-75

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(14)
ACCN:001936917 CTLN:4296120
ABSJ:G (Genetics Abstracts)
AUTH:Baum, M.;Beier, H.*
AFFN:Inst. fuer Biochemie, Bayerische Julius-Maximilians-Univ., Biozentrum, Am Hubland, D-97074 Wuerzburg, Germany
TITL:Wheat cytoplasmic arginine tRNA isoacceptor with a U*CG anticodon is an efficient UGA suppressor in vitro
HTIL:NUCLEIC ACIDS RES.
HSSN:0305-1048
HYER:19980300
HCOL:vol. 26, no. 6, pp. 1390-1395

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(15)
ACCN:001938141 CTLN:4299985
ABSJ:G (Genetics Abstracts)
AUTH:Paull, J.G.;Chalmers, K.J.;Karakousis, A.;Kretschmer, J.M.;Manning, S.; Langridge, P.
AFFN:Dep. Plant Sci., Waite Campus, Univ. Adelaide, South Australia 5064, Australia
TITL:Genetic diversity in Australian wheat varieties and breeding material based on RFLP data
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980000
HCOL:vol. 96, no. 3-4, pp. 435-446

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(16)
ACCN:001938149 CTLN:4299993
ABSJ:G (Genetics Abstracts)
AUTH:Qu, L.-J.;Foote, T.N.;Roberts, M.A.;Money, T.A.;Aragon-Alcaide, L.; Snape, J.W.;Moore, G.
AFFN:Natl. Lab. Protein Eng. and Plant Genetic Eng., Peking Univ., Beijing 100871, P.R. China
TITL:A simple PCR-based method for scoring the ph1b deletion in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980000
HCOL:vol. 96, no. 3-4, pp. 371-375

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(17)
ACCN:001938565 CTLN:4300669
ABSJ:G (Genetics Abstracts)
AUTH:Vega, J.M.;Feldman, M.
AFFN:Dep. Plant Sci., Weizmann Inst. Sci., Rehovot 76100, Israel
TITL:Effect of the pairing gene Ph1 on centromere misdivision in common wheat
HTIL:GENETICS
HSSN:0016-6731
HYER:19980300
HCOL:vol. 148, no. 3, pp. 1285-1294

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(18)
ACCN:001951395 CTLN:4317345
ABSJ:G (Genetics Abstracts)
AUTH:Metakovsky, E.V.;Branlard, G.
AFFN:INRA Station d'Amelioration des Plantes, 63039 Clermont-Ferrand, France
TITL:Genetic diversity of French common wheat germplasm based on gliadin alleles
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:19980000
HCOL:vol. 96, no. 2, pp. 209-218

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(19)
ACCN:001952132 CTLN:4318363
ABSJ:G (Genetics Abstracts)
AUTH:Giroux, M.J.;Morris, C.F.
AFFN:Plant, Soil and Environmental Sciences Department, P.O. Box 173120, Montana State University, Bozeman, MT 59717-312 (contribution no. J- 5188 of the Montana Agricultural Experiment Station)
TITL:Wheat grain hardness results from highly conserved mutations in the friabilin components puroindoline a and b
HTIL:Proc. Natl. Acad. Sci. USA
HSSN:0027-8424
HYER:19980526
HCOL:vol. 95, no. 11, pp. 6262-6266

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(20)
ACCN:001959401 CTLN:4320818
ABSJ:G (Genetics Abstracts)
AUTH:Gent, M.P.N.;Kiyomoto, R.K.

AFFN:Department of Forestry and Horticulture, The Connecticut Agricultural Experiment Station, POB 1106, New Haven, CT 06504-1106, USA
TITL:Physiological and agronomic consequences of Rht genes in wheat
HTIL:J. CROP PROD.
HSSN:1092-678X
HYER:19980000
HCOL:vol. 1, no. 1, pp. 27-46

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(21)
ACCN:001961065 CTLN:4327696
ABSJ:G (Genetics Abstracts)
AUTH:Kojima, T.;Ogihara, Y.*
AFFN:Kihara Institute for Biological Research, Yokohama City University, Maioka-cho 641-12, Yokohama 244-0813, Japan
TITL:High-resolution RFLP map of the long arm of chromosome 5A in wheats and its synteny among cereals
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19980200
HCOL:vol. 73, no. 1, pp. 51-58

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(22)
ACCN:001961067 CTLN:4327698
ABSJ:G (Genetics Abstracts)
AUTH:Yamazaki, Y.;Tsujimoto, H.;Kawahara, T.
AFFN:Center for Genetic Resource Information, National Institute of Genetics, Mishima, Shizuoka 411-8540, Japan
TITL:KOMUGI database — wheat genetics resources database
HTIL:GENES GENET. SYST.
HSSN:1341-7568
HYER:19980200
HCOL:vol. 73, no. 1, pp. 75-77

Wheat Information Service
Number 87: 62–63 (1998)
Information

Information

1. Mendel Centenary Congress (March 7–9, 2000, Brno, Czech Republic)

On the occasion of the rediscovery of the Mendelian Law of Inheritance in 1900, the Mendel University of Agriculture and Forestry, Brno, and the Gesellschaft für Pflanzenzüchtung (GPZ) will hold an International Congress with the topic,

100 years of Genetics for Plant Breeding–Mendel, Meiosis and Marker

at the city of Mendel, Brno, in Czech Republic, on March 7_9, 2000.

First circulars is available from: Mendel Centenary Congress, Gesellschaft für Pflanzenzüchtung, Sekretariat, c/o Prof. Röbbelen, Von Sieboldstr. 8, D–37075, Göttingen, GERMANY. Send registration by December 31, 1998. Date: Mon, 23 Nov 98 18:19:39 EST

2. The Percival Symposium: Wheat - Yesterday, Today & Tomorrow

A meeting to celebrate the life and work of John Percival (1863-1949)
Organised by the School of Plant Sciences, The University of Reading, UK
12-13 July 1999

First circular and call for poster presentations
John Percival (1863-1949) was a driving force behind the creation of agricultural botany as a scientific discipline and Professor of Agricultural Botany at the University of Reading from 1907 to 1932. His monumental treatment of wheat "The Wheat Plant: a Monograph" (1921) still serves as a standard reference, having been reprinted as recently as 1974. Percival was the consummate agricultural scientist - botanist, taxonomist, geneticist, germplasm collector, curator, breeder, agronomist, historian and teacher. On the occasion of the 50th anniversary of Percival's death, the University's School of Plant Sciences is hosting a meeting to celebrate his life and work. Reflecting the scope of Percival's scientific view, invited speakers will survey research progress during the last half-century in the archaeobotany, systematics, genetics and breeding of the wheat plant. The two-day event offers a unique opportunity for a multi-disciplinary gathering of experts who share a common interest in wheat studies.

Participants are invited to offer poster presentations on relevant aspects of wheat research. The symposium will feature displays of Percival's work and his wheat collection. There will also be a tour of the University's Rural History Centre, and an exhibition of current work at the School of Plant Sciences. A Proceedings volume of invited speaker papers will also include Percival's unpublished treatment of the genus *Aegilops*. Since John Percival's time, activity in agricultural botany has flourished at Reading. The Department's tradition of research at both a fundamental and applied level over a wide range of aspects of crop plants continues, with Professor Peter

Caligari being the current Professor of Agricultural Botany. The Department is now one of the three constituent members of The University of Reading's School of Plant Sciences is ranked as one of the UK's major centres of plant science, and the only one given the highest possible rating (5*) in the latest Research Assessment Exercise.

Participants will be lodged on the campus of The University of Reading. Located in the Thames Valley, west of London. Reading has excellent rail (25 minutes) and bus (1 hour) links with London. There are also direct bus and rail links to the major international airports of Heathrow and Gatwick.

Sponsored by the Linnean Society of London
Percival Symposium, The University of Reading, 1999

To receive the second circular, please complete and mail, email or fax this form as soon as possible to Dr. Geoff Hewitt, at the address below.

Title/Name: _____
Institution: _____
Address: _____
_____
_____
Telephone: _____
Fax: _____
Email: _____

I am/am not interested in presenting a poster (delete as appropriate)

Provisional title: _____
_____

Contact Address:
Dr Geoff Hewitt e-mail: h.g.hewitt@reading.ac.uk
School of Plant Sciences Tel: +44 (0) 118 931 8294
The University of Reading Fax: +44 (0) 118 975 0630
Whiteknights, P.O. Box 221
Reading RG6 6AS, UK

Organising Committee:
Professor Peter D S Caligari - Chairman (The University of Reading, UK)
Dr Geoff Hewitt (The University of Reading, UK)
Dr Stephen L Jury (The University of Reading, UK)
Dr Terry E Miller (John Innes Centre, UK)
Dr Laura A Morrison (Oregon State University, USA)
Dr Mark Nesbitt (University College London, UK)

Website:http:/www.reading.ac.uk/AcaDepts/sb/Courses/courses-short.html
Sponsored by the Linnean Society of London

Wheat Information Service
Number 87: 64 (1998)

Editorial remarks

The 9th International Wheat Genetics Symposium was successfully held in Aug.2-8, 1998 at beautiful wheat land of Saskatchewan. We enjoyed a lot of, various kinds of program, project, information, and people. Thanks to the organizing committee. The formal records will be announced later, but contact for the details including purchase of five volumes of proceedings and a independent volume of formal gene symbol catalog.

WIS has accepted about 50 newly-jointed members during 9IWGS. Just sending your mailing address through general mail or e-mail; yamabosi@yokohama-cu.ac.jp will be enough to be registered. Subscribers contributed to the financial donation (2,000 Japanese Yen or US$25) will receive a nice greeting card for the receipt, and, of cause, will be very much appreciated for the next year.

In the present volume of WIS, the record from 26th Wheat Genetic Symposium of Japan is printed with abstracts. If you have such information or record of any academic meetings related to wheat genetics and breeding, please send them to the office to be published in WIS, although suitability and the page limitation (within 10 printed pages) should be considered by the editorial board.

Dr. Kozo Nishikawa has retired from Kihara Memorial Foundation last spring, but he will continue to work as an editor in chief of Wheat Information Service. Thanks for his effort.

T. S.

Business Office

Wheat Information Service
c/o Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
641-12 Maioka-cho, Totsuka-ku, Yokohama 244, Japan.
Phone: +81-45-825-3487. Fax: +81-45-825-3307, E-mail: yamabosi@yokohama-cu.ac.jp
Mr. F. Maji (Chief officer), Ms. K. Furukawa (Publication secretary)

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編　集　西　川　浩　三
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Tel : (045)825-3487
Fax: (045)825-3307
E-mail: yamabosi@yokohama-cu.ac.jp
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Contents