The International Journal for Wheat Genetics and Breeding

WIS

Wheat Information Service

1997 No.85

ISSN 0510-3517

Kihara Memorial

Yokohama Foundation for the Advancement of Life Sciences

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Wheat Information Service
Number 85: 1-6 (1997)
Research article

Evaluation of abiotic stress resistance in Hebei winter wheat genetic resources

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Summary

Four hundred and sixty-eight accessions of Hebei winter wheat genetic resources were assessed on abiotic stress resistance in four different agroecological locations. The results showed that 63 accessions, Lang 8519, Kecheng 3, 3053-1, Shi 87-6149-50, Jifu 80-58, 3078-2, Jilang 8190-2 etc. were salinity tolerant, that 116 accessions, Lang 8504, Jimai 22, Kecheng 4, Ji 86 Guan 725, Ji 85-5091 and Jimai 21 etc. were drought resistant, and that 126 accessions, Jinfengl, Ji 82-425 5, Shi 83-5307, Tang 85-5032, Bao 5264 etc. were cold resistant.

Key words: bread wheat, genetic resources, salt tolerance, drought resistance, cold resistance

Introduction

Bread wheat (*Triticum aestivum*) is one of stable food crops in the world. It has played an important role in people's life. However, the shortage of varieties with multiple resistance to abiotic stress affected yield increase so that wheat production does not meet the needs of ever-growing population. It is, therefore, necessary to appraise and screen wheat genetic resources with resistance to abiotic stress for breeders to develop new varieties.

Material and methods

Four hundred and sixty-eight accessions of wheat germplasm resources were evaluated in different agroecological environments from the year 1986 to 1989.

Appraisal of salinity tolerance was conducted in Institute of Cangzhou Agricultural Sciences, which is located in the region of salt stress. Materials were sown in soil bed containing 0.41% salt. The check Keyi 26 was sown once after every 7 accessions, with one row per accession. Salt tolerance coefficient (yield of a material in salt bed / yield of check in salt bed) and salt tolerance

index (salt tolerance coefficient of the material / salt tolerance coefficient of check) were calculated after harvest. Salt tolerance index was indicated in 5 scales for the sake of comparison. Their corresponding relations were indicated as follows:

Scales of salt tolerance:	1	2	3	4	5
Indexes of salt tolerance:	>1.3	>1.1	>0.8	>0.5	<0.5

Each material was compared with neighbor checks. If the materials were classified in lower salt tolerance grade than check Keyi 26 (with average salt tolerance grade 3), we call them salt tolerant genotype.

Drought resistance of each material was tested in Dryland Farming Institute, Hebei Academy of Agricultural and Forestry Sciences. Each material was sown both in irrigated place (under non-stress) and non-irrigated place (under stress). After comparing the evaluation methods of Finlay et al. (1963), Eberhart et al. (1966), Fischer (1978) and Lan et al. (1993), drought resistance coefficient (DRC: variety's yield under stress / variety's yield under non-stress) (Lan et al. 1993) was chosen to evaluate drought resistance. The check was Jimai 6 (DRC = 0.88). The materials with higher DRC than that of the check were drought resistant genotypes.

Appraisal of cold resistance was conducted in both Institute of Baoding Agricultural Sciences (local check variety is Taishan 1 for cold resistance) and Institute of Tangshan Agricultural Sciences (local check variety is Dongfanghong 3 for cold resistance). Both of which are located in the region of coldness. The lowest temperature is minus 30°C in winter. Varieties were sown in field with normal management. After winter, wilting degree was scored in 5 scales and percentage of died tillers was recorded. Cold resistance index (CRI: percentage of winter surviving tillers of a material / the percentage of winter surviving tillers of check) was calculated for eliminating the differences between years so that the materials could be compared with each other in different years. The materials with lower wilting degrees or with higher CRI than the checks were regarded as cold resistant genotypes.

Two hundred and fifty-two accessions (the data of some agronomic characters of other accessions were not recorded) were used for calculating simple correlations between 9 characteristics.

Results and discussion

Salinity tolerance evaluation

Sixty-three accessions, Lang 8519, Kecheng 3, 3053-1, Shi 87-6149-50, Jifu 80-58, 3078-2, and Jilang 8190-2 etc. were classified in salt tolerance grade 1 or grade 2. The varieties with salt tolerance grade 1 were Kecheng 5, Lang 8-7-5-1-3, Lang 767-4-38, Shijiazhuang 10, Shi 4414, Henong 62-8, Hebeinongda 1, Hebei 1, Jiguan 85-5091, and Shi- 86-8107 etc. There are 13 materials in salt tolerance grade 1 or grade 2 with advanced comprehensive agronomic characteristics, such as Jimai 14, Jimai 21 and Lang 8519 etc. (Table 1). In addition, salt tolerance of varieties varies along with developmental stages, such as Ji 85 Guan 680, Tangfu 75005, Bao 412 and Jimai 20 etc. with both salt tolerance and pretty seedlings and higher surviving rate of

Table 1. Means and ranges of 252 Hebei winter wheat accessions

Character	Mean	Range	Variance	Top-ten lines (names of variety)
Height[§]	92.5	58-130	188.5	Shi87-6149-50, Jifu80-58, Shi86-5031, Jinfeng0-3-4, 79-5103, Jizhi4001, 76-4170, Shi81-5071, Ji84Guan777, Ji85-5088
Spi-L	8.78	5.5-12	1.437	Jimai20, Jilang767-4-38, 78-3165-11, Tang76067, Lang8601, Laoting953, 83-4611, 79-5039, 7604170, Bao205
Spi-let	18.4	14-22	2.196	3053-9, Shi86-8107, Bao-5262, Kecheng No.2, Tang76067, Shiliang6261, 76-4170, Jimai24, 87Guan54, Jihan84
TSpi-let	17.2	12-21	2.660	Jimai20, Jimai7, Shijiazhuangdali, 76-4170, 76-4260, Jimai24, Jimai26, Danong7, Ji85guanxuanzhu, Kecheng7
Seed-Spi	46.0	28-69	51.66	Shi81-5071, Jilang7661-2-15-1, Jimai24, Shiliang6261, 76-5200, 76-4170, Jimai20, Shi87-6149-50, Jimai27, Ji855-044
TG-wet	39.2	23-55	37.45	Jiheng8114Xuan 1, Jilang8190-2, Lang8303, Luoting953, Shijiazhuangdali, Danong4, Hebeinongda3, Bao249, Baoding4, Jilang767-4-13-1
Cold	3.5	3-5	0.283	Tang85-5032, Shi81-5090, Heng87-6105, Heng 86-5001, Tang85-6148, Jizi88-4295, Hebei1, Jizixixuan3, Jinfeng1 Tang85-5032
Drought	0.8	0.28-1.2	0.029	Danong4, Ji84-4152, Jishi86-5144, Ji85Guan725, Bao405, Kecheng4, 65-848, 84Guan777, Henong215, Jinfeng1
Salt	3.6	1-5	2.063	Kecheng5, Lang87-5-1-3, Lang767-4-38, Shijiazhuang10, Shi4414, Henong62-8, Hebeinongda1, Hebei1, Jiguan85-5091, Shi86-8107

[§] Height: plant height(cm), Spi-L: spike length(cm), Spi-let: spikelets per spike, TSpi-let: net-spikelets per spike, Seed-Spi: seeds per spike, TG-wet: 1000-grains weight, Cold: wilting degree of coldness, Drought: DRC, Salt: grade of salinity tolerance.

seedlings at seedling stage, but with both intolerance and poor plants at maturing stage. On the contrary, some materials were tolerant in maturing stage and untolerant at seedling stage, such as Shi 86-8107, Lang 8515 and Kecheng 3 etc. Blum (1988) reported the level of salinity resistance changing with plant age and possibly with hardening. This agrees with our views.

Drought resistance evaluation

One hundred and sixteen accessions, Lang 8504, Jimai 22, Ji 86 Guan 725, Ji 85-5091 and Jimai 21 etc. were drought resistant. The materials with both their yield under stress and their DRC were higher than or equal to that of check Jimai 6 were Danong 4, Ji 84-4152, Jishi 86-5144, Ji 85 Guan 725, Bao 405, Kecheng 4, 65-848, 84 Guan 777, Henong 215, and Jinfeng 1 etc. There are 49 materials with-both drought resistance and high comprehensive agronomic characteristics.

Cold resistance evaluation

Wilting degrees of 126 accessions were equal to or lower than that of check Dongfanghong 3 (wilting degree 3). Among them, the CRI of about 86 accessions were equal to or higher than that of check Dongfanghong 3 (CRI=1), such as Jinfeng 1, Ji 82-4255, Shi 83-5307 and Tang 85-5032 etc. Twenty-seven accessions have advanced comprehensive agronomic characteristics, such as Tang 84-6054, Jimai 17, and Luoting 1840 etc. The CRI of about 59 accessions (wilting degree equal to or lower than checks) were equal to or higher than that of both Dongfanghong 3 and Taishan 1, such as Tang 85-5032, Shi 81-5090, Heng 87-6105, Heng 86-5001, Tang 85-6148, Jizi 88-4295, Hebei 1 and Jizixixuan 3 etc.

There are 16 genotypes with both resistance to cold and drought and tolerance to salinity, such as Shi 86-8107, Jimai 22, Bao 436 and Shi 86-5031 etc. (Table 2).

The correlations of abiotic stress and other agronomic characteristics: No any correlation was found between drought resistance and other characters (Table 3). That increasing hydraulic resistance in the seminal root can improve harvest index was first proposed by Passioura (1972). Works subsequently have shown that this can best be achieved by decreasing the diameter of the main xylem vessel in the seminal roots (Richards and Passioura 1981a, b). Richards (1985)

Table 2. Characteristics of the genotypes in salt tolerance grade 1 or grade 2 with both resistance to cold and drought

Names of variety	Height[§]	Spi-L	Spi-let	TSpi-let	Seed-spi	TG-wet	Cold	Drought	Salt
Shi 86-8107	80	9.0	21.0	19.0	46.3	34.6	3	0.96	1
Ji 84-5085	80	9.2	17.3	16.3	36.0	38.9	3	1.07	1
Ji 84-5599-9	83	6.5	16.3	15.6	44.0	36.4	3	0.96	1
Jimai 22	99	8.0	18.0	17.7	52.7	43.6	3	1.02	1
84(3)7-27-5	93	10.0	18.7	16.0	54.7	33.8	3	0.99	1
3053-9	97	10.1	20.7	19.4	50.7	37.5	3	1.00	1
Ji 85-5091	76	9.8	17.3	16.0	42.3	31.4	3	1.07	1
Shijiazhuang 4	115	7.3	16.3	15.3	52.3	32.5	3	0.96	1
9001	105	8.2	19.3	19.3	37.7	42.4	3	1.03	1
Ji 86Guan 725	79	8.0	14.3	13.3	52.0	32.7	3	1.01	1
Shi 87-6149-50	72	8.7	18.7	17.7	58.7	29.0	3	0.96	1
3078-2	99	7.2	17.0	16.7	48.3	43.5	3	0.93	1
Bao 436	90	5.8	15.3	13.6	38.0	42.1	3	1.00	2
Shi 86-5031	66	9.3	17.3	16.3	42.7	31.6	3	0.95	2
3027-3	85	7.5	18.3	18.3	53.0	39.6	3	0.89	2
Hanlin 2	99	7.9	17.0	17.0	44.0	43.2	3	0.99	2

[§]See footnote for Table 1

Table 3. Correlations of abiotic resistance and other agronomic characteristics

Character	Height[§]	Spi-L	Spi-let	TSpi-let	Seed-Spi	TG-wet	Cold	Drought	Salt
Height	1.000								
Spi-L	-0.095	1.000							
Spi-let	-0.075	0.335**	1.000						
TSpi-let	-0.173**	0.382**	0.781**	1.000					
Seed-spi	-0.314**	0.181**	0.370**	0.434**	1.000				
TG-wet	0.309**	0.071	0.099	0.018	-0.123	1.000			
Cold	-0.176**	0.123	0.218**	0.137*	0.042	0.225**	1.000		
Drought	-0.107	-0.020	-0.036	-0.055	0.083	0.077	-0.035	1.000	
Salt	-0.064	0.048	0.000	-0.039	-0.003	-0.051	0.030	-0.104	1.000

*, **Significant at P=0.05 and P=0.01, respectively. [§] See foot note for Table 1.

reported that in all environments lines with small xylem vessels yielded more than lines with larger vessels, and the field advantage was greatest in the driest environments. Higher yields of the determinate tillering cereals over conventional type in dry environments have been found by Donald (1979), Islam and Sedgley (1981) and Richards (1983). Lupton (1987) reported if drought occurs before flowering, the lines with floppy leaves may be drought resistant, and if drought occurs after flowering the lines with erect leaves may be drought resistant.

No any correlation existed between salinity tolerance and other characters. Jones (1981) reported that salinity resistance conditioned by osmoregulation is often recognized by the "succulent" appearance of the plant. Blum (1988) stated seeds germination in saline media is often used as a singular criterion for salinity resistance or in combination with other criteria. The rate of surviving plants associated with salinity tolerance in salt stress conditions (Dewey 1962). In all the reports we know there is no correlation between drought resistance and salinity tolerance.

There is a significantly negative correlation between wilting degree and plant height in coldness condition. It means that the higher the plant is, the lower the wilting degree of the plant is, or the more cold resistant the plant is. Also there is significantly positive correlation between wilting degree and spikelets per spike, net-spikelets per spike and 1000-grain weight. No any correlation was found between cold resistance and other characters (Table 3). Blum (1988) reported that both tissue-water content and plant erectness were highly and negatively correlated with field winter survival index. Dexter et al. (1932) reported that the rate of leakage of electrolytes from plant tissues after a freezing stress was indicated as a potential criterion for freezing tolerance (Quamme 1982). Leakage is considered to be proportional to the rate of damage in living cells. The rate of accumulation of sugar in the hardened tissues was often correlated (Rajki 1972) with survival after freezing. Gusta et al. (1983) found that a moderate correlation between osmotic

potential and winter survival in wheat. Whether osmotic adjustment is evaluated by chemical or psychrometric method it can evidently be evaluated only in a limited number of samples out of the whole population. So, we consider the best selection criteria is the rate of winter survival in the field or CRI mentioned above.

Acknowledgments

The authors are grateful to Mr. Hu Fushun, Mr. Qiao Shiyuan, Ms. Lu Li and Mr. Zhang Xianying for the help in resistance evaluation.

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Wheat Information Service
Number 85: 7–13 (1997)
Research article

Screening of *Aegilops*, *Triticum* and *Hordeum* species for grain weight, protein and lysine content[1)]

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Summary

Grains of four species of *Aegilops* (*Ae. ovata*, *Ae. kotschyi*, *Ae. tauschii*, *Ae. vavilovii*), eight species of *Triticum* (*T. monococcum*, *T. dicoccum*, *T. dicoccoides* (4 accessions), *T. polonicum*, *T. turgidum*, *T. aestivum*, *T. spelta*, *T. sphaerococcum*) and one species of *Hordeum* (*H. vulgare*) were studied for grain weight, protein and lysine contents. *T. polonicum* possessed exceptionally high 100-grain weight (6.5g) almost double the diploid, tetraploid and hexaploid wheats. All the species of *Aegilops* were poor in grain weight. A negative correlation was observed between grain weight and protein and grain weight and lysine content. Species usually having poor grain weight (*Ae. ovata*, *Ae. kotschyi*, *Ae. tauschii* and *T. dicoccoides*) possessed higher protein (>18%) and lysine (>3.65% protein and 6.0 mg/g flour) content. Very strong positive correlations were established between protein content and flour lysine (r= 0.994) and between protein content and protein lysine (r= 0.801). An accession No. 49 of *T. dicoccoides* 'wild emmer' possessed simultaneously better 100-grain weight (2.71g), higher protein (17.42%) and lysine (6.25 mg/g flour and 3.59% protein) content.

Key words: *Aegilops*, *Triticum*, *Hordeum*, protein, lysine

Introduction

The significance of food for biological survival is self-evident. Cereals being the dominating source of food are rich in starch with reasonable amount of protein. The contemporary cultivated species of wheat are the derivatives of the wild grasses, passed through spatial and temporal evolutionary processes. These wild grasses have been successfully used in the improvement of qualitative and quantitative traits in wheat (Sears 1956; Avivi et al. 1983; Grama et al. 1983; Levy and Feldman 1987; Levy et al. 1988; Nevo 1988; Vallega 1992). These wild species though inherently produce low grain yield, yet some of the species, such as *T. dicoccoides* has the potential to produce more

[1)] Contribution No. 38 of AEARC Tandojam, Pakistan.

protein per hectare than contemporary bread wheats. Moreover, Johnson et al. (1985) have proved that the high yielding varieties with substantially higher protein content can be developed. Nevertheless, wheat of stone age is being introduced in Germany by environment conscious farmers (Dunn 1991).

Preliminary results of a study on screening of wild grasses, ancient wheats and barley for grain weight, protein and lysine content are reported in this paper.

Materials and methods

Seeds of following species of *Aegilops*, *Triticum* and *Hordeum* were available at Atomic Energy Agricultural Research Centre (AEARC) Tandojam during 1993-94.

a) *Aegilops*

1. *Ae. ovata* L. Raspail '$C^UC^UM^OM^O$'
2. *Ae. kotschyi* Boiss. '$C^UC^US^VS^V$'
3. *Ae. vavilovii* (Zhuk.) Chenn. '$DDM^{cr}M^{cr}S^pS^p$'
4. *Ae. tauschii* Coss. Schmal 'DD'

b) *Triticum*

5. *T. monococcum* L. 'AA' (small spelt)
6. *T. dicoccum* (Schrank) Schubl. 'AABB' (Emmer)

7–10. *T. dicoccoides* (Körn.) Schweinf. 'AABB' (Wild emmer) (Accession Nos: 49, 53, 54, 60)

11. *T. polonicum* L. 'AABB' (Polish)
12. *T. turgidum* L. 'AABB' (Cone)
13. *T. aestivum* L. Thell. 'AABBDD' (Bread)
14. *T. sphaerococcum* Perc. 'AABBDD' (Indian dwarf or shot)
15. *T. spelta* L. 'AABBDD' (Dinkel).

c) *Hordeum*

16. *H. vulgare* L. 'HH'

Data on following parameters were collected

Grain weight: It was recorded in grams after counting 100 grains at random.

Protein: Protein contents were determined by Udy dye binding capacity method (Udy 1971).

Lysine: Lysine contents were determined by a modified DBC method (100 mg flour, 0.45 mg/ml dye concentration) (Khan 1978). Lysine values were expressed on flour (mg/g) and protein (%) basis.

Whole meal flour was used for analytical purpose and all the data were calculated on dry weight basis.

Results and discussion

Wide genetic variability was estimated in the wild species of *Aegilops*, *Triticum* and *Hordeum* for

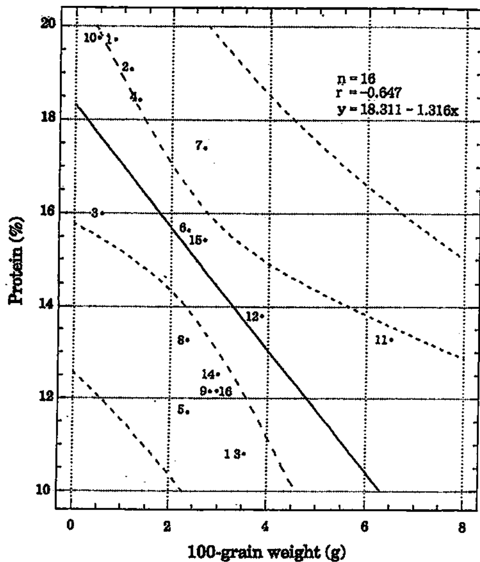
Table 1. Grain weight, protein and lysine content of different cereals

Cereals	100-grain weigh (g)	Protein (%)	Lysine (mg/g flour)	Lysine (%protein)
Aegilops				
1. *Ae. ovata*	0.81 j	19.68 a	7.20 b	3.66 d
2. *Ae. kotschyi*	1.16 i	19.07 b	7.15 b	3.75 b
3. *Ae. vavilovii*	0.58 k	15.97 e	6.19 d	3.89 a
4. *Ae. tauschii*	1.34 h	18.39 c	6.82 c	3.71 c
Triticum				
5. *T. monococcum*	2.40 g	11.66 k	4.01 i	3.45 hi
6. *T. dicoccum*	2.38 g	15.60 f	5.54 e	3.56 ef
T. dicoccoides				
7. Accession No.49	2.71 f	17.42 d	6.25 d	3.59 e
8. Accession No.53	2.36 g	13.27 h	4.64 g	3.49 gh
9. Accession No.54	2.85 e	12.15 j	4.28 h	3.53 fg
10. Accession No.60	0.47 l	19.74 a	7.67 a	3.89 a
11. *T. polonicum*	6.50 a	13.30 h	4.69 fg	3.53 fg
12. *T. turgidum*	3.86 b	13.78 g	4.80 f	3.49 h
13. *T. aestivum*	3.55 c	10.79 l	3.70 j	3.44 i
14. *T. sphaerococcum*	2.96 d	12.53 i	4.35 h	3.47 hi
15. *T. spelta*	2.70 f	15.40 f	5.47 e	3.55 ef
Hordeum				
16. *H. vulgare*	2.95 d	12.15 j	4.20 h	3.46 hi

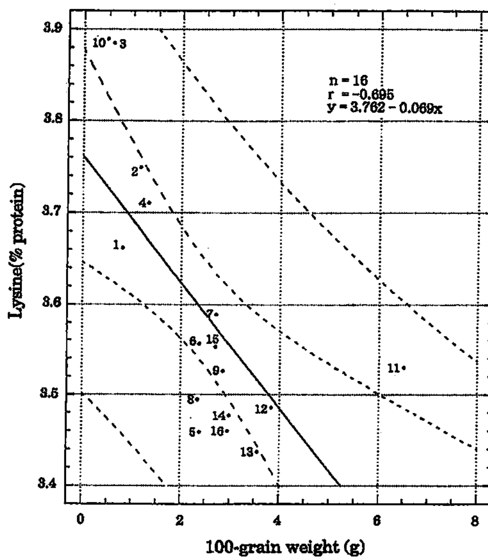
Means followed by different letters are significantly different at 5% level using DMR test.

grain weight, protein and lysine content (Table 1). Wild grasses involving species of *Aegilops* and one accession (No.60) of *T. dicoccoides* possessed lower values for grain weight, but relatively higher values for protein and lysine content establishing a negative relationship. Hundred grain weight of Czechoslovak *Aegilops* collection ranged between 0.34 and 1.70g, *Aegilops tauschii* between 0.86 and 1.70g (Holubee et al. 1992). Similar trend was observed among different species of *Triticum*. *Triticum polonicum* with bold seeds possessed maximum 100-grain weight of 6.5g, which was significantly higher than other species of *Triticum* and *Hordeum* (ranging between 0.47g to 3.86g).

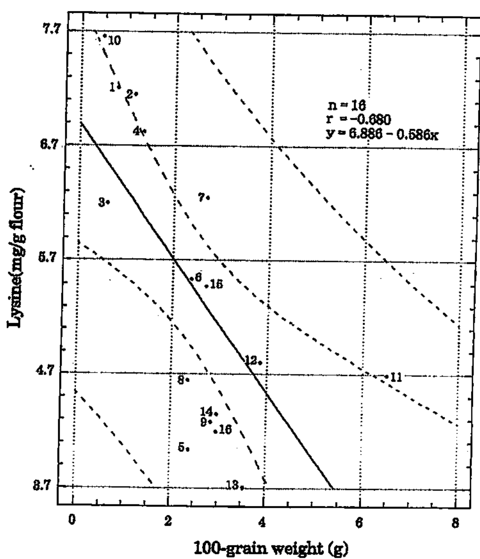
The performance of genotypes may vary under changed environments. For instance, 100-grain weight of small spelt (1.75g), wild emmer (3.13g), cone (5.34g) and bread (3.89g) wheats reported previously (Holubee et al. 1992), deviate from the present results. Having very shrivelled grains, *T. dicoccoides* (No. 60) with 100-grain weight of 0.47g had the protein content of 19.74%



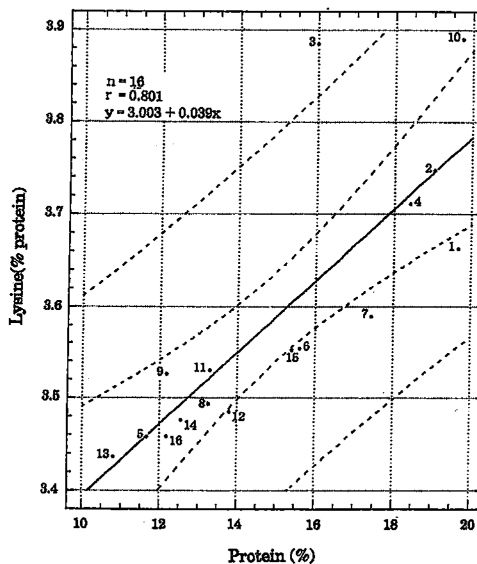
a: Linear regression of protein on grain weight



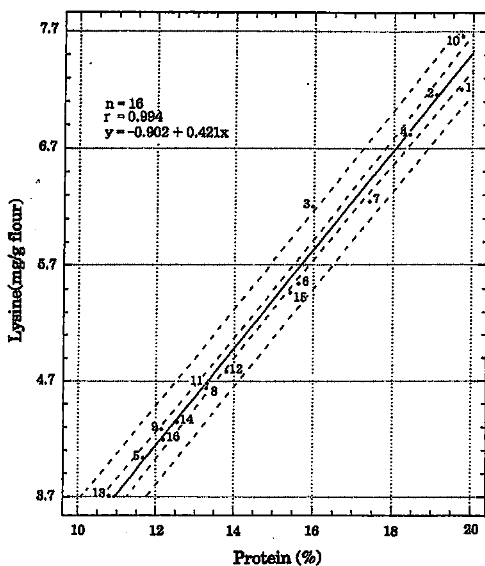
b: Linear regression of lysine (% protein) on grain weight



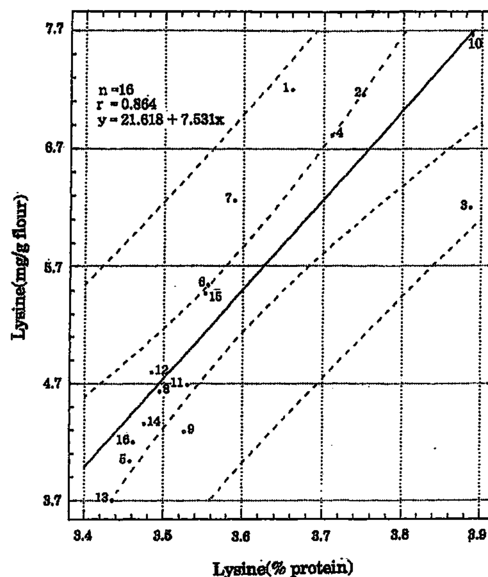
c: Linear regression of lysine (mg/g flour) on grain weight



d: Linear regression of lysine (% protein) on protein



e: Linear regression of lysine (mg/g flour) on protein



f: Linear regression of lysine (mg/g flour) on lysine (% protein)

Fig.1. Linear regression of grain weight, protein and lysine content of different cereals. Numerals in the figures represent material number listed in Table 1. Means were computed using Duncan's multiple range test. Correlation and regression analysis was performed and regression equations were computed and regression lines drawn (a-f). The two lines closer to the regression line show the confidence limits; whereas, the two outer lines are the prediction limits of the values.

and lysine value of 3.89 (percent protein). The accession No.60 could be regarded as an exception in *T. dicoccoides*. High protein content in *Aegilops* accessions (19.1 to 34%), wild emmer (16 to 27%), emmer (14 to 21%), small spelt (11.3 to 18.71%) and other wild/obsolete cultivars have been reported (Dhaliwal 1977; Ciaffi et al. 1992; Damania et al. 1992; Holubee et al. 1992; D'Egidio et al. 1993). Like protein percentage, lysine content of diploids and tetraploids was also higher than that of modern wheats (Rafi et al. 1992; Nevo and Beiles 1992). Grain weight, protein and lysine content seem independent as far as their ploidy level in the genome *Triticum* is concerned. The diploid species *Triticum monococcum* (AA) had significantly similar grain weight as the tetraploid species *T. dicoccoides* (No.53) and *T. dicoccum* (AABB). Comparing the species of *Aegilops*, *Triticum* and *Hordeum*, it was noted that the bread wheat, *Triticum aestivum* had the lowest protein and lysine content. The situation therefore demands concerted efforts for the improvement of protein content and quality particularly in bread wheat (*Triticum aestivum*).

Indeed simultaneous improvement in grain yield and protein content has many limitations, yet positive breakthroughs have also been documented. At Winnipeg, Canada, A.B. Campbell

registered Neepawa hard red spring wheat in 1969, with 7.6% more yield and 0.6% units more protein than Thatcher (De Pauw and Townley-Smith 1988). Similarly Lancota winter wheat also has both elevated yield and protein content (Schmidt et al. 1979). Johnson et al. (1985) have the opinion that because the negative correlations rarely exceed 0.6 and variation in protein content was independent of yield, simultaneous advances in both yield and protein content would be possible.

In the present study, we could not find any positive relationship of grain weight with protein (Fig. 1a), protein lysine (Fig. 1b) and flour lysine (Fig. 1c). The species *T. aestivum* (bread wheat), which is the most widely cultivated species of genus *Triticum* possessed intermediate 100-grain weight and the lowest protein and lysine content. Two species *T. turgidum* and *T. polonicum* were observed to have higher 100-grain weight, better protein and lysine contents. Very strong positive relationships were obtained between protein content and protein lysine (Fig. 1d), protein content and flour lysine (Fig. 1e) and between flour lysine and protein lysine (Fig. 1f).

The positive correlation between protein and lysine content observed in present investigations clearly demonstrates that higher protein content synthesized by wild grasses and old wheat grains was not inferior in quality. This contention is further substantiated by highly significant positive relationship observed between lysine content of flour and protein of different cereals.

The preliminary screening studies provide significant evidence that wild species of *Triticum* and *Aegilops* are bestowed with particular traits such as grain weight (*T. polonicum*), protein content (*T. dicoccoides* No.60, *Ae. ovata*, *Ae. kotschyi* and *Ae. tauschii*), lysine content (*T. dicoccoides* and *Aegilops* spp). One accession No. 49 of wild emmer *T. dicoccoides* may be considered to have simultaneously better grain weight, higher protein and lysine content.

The best hope for future crop improvement lies in the conservation and utilization of genetic diversity of wild species. Wild emmer *T. dicoccoides* easily hybridizes with cultivated tetraploid wheats, whereas gene transfer from wild to hexaploid cultivated wheats is also possible after overcoming the genetic barriers.

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Wheat Information Service
Number 85: 14–20 (1997)
Research article

Removal of green photosynthetic structures and their effect on some yield parameters in bread wheat

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Summary

The studies were carried out to investigate the impact of the removal of green photosynthetic structures including flag leaf, 3rd nodal leaf and awns, on some yield related parameters in two local wheat cultivars (Pasban 90 and Inqalab 91). The experiment was laid out in a triplicated randomized complete block design in split-plot fashion. The two varieties differed significantly for flag leaf area, 3rd nodal leaf area, seed set percentage, grains per spike and grain weight per spike. Effect of the removal of flag leaf (T_2), 3rd nodal leaf (T_3) and awns (T_4) was displayed as reduction in yield components. Removal of flag leaf resulted 16.4, 14.8, 34.5 and 20.0% reduction in seed set percentage, grains/spike, grain weight/spike and 100-grain weight, respectively. Reduction in these traits as a consequence of the removal of 3rd nodal leaf and awns was also significant. However the extent of this reduction was less than that of flag leaf removal. Interaction of varieties and treatment was significant for seed set, grains/spike and 100-grain weight. Both of the varieties presented a marked reduction in the four traits studied when the flag leaf was removed. However, Inqalab 91 proved superior to Pasban 90. The results signified the major contribution of flag leaf towards yield related traits studied. In ranked order maximum contribution occurred from flag leaf followed by 3rd nodal leaf and awns at the last.

Key words: wheat, flag leaf, nodal leaf, awns, photosynthates

Introduction

Economic yield in cereals results from the build up of dry matter in the grains which depends upon potential assimilation of CO_2 and accumulation of photosynthates during the grain filling period. This further depends upon absorption of solar radiation by the green photosynthetic organs of the plant. In wheat major photosynthetic structures are the leaves; specially the flag leaf. Mostly the lower leaves are shaded by the upper leaves and thus maximum solar absorption occurs in flag leaves.

Photosynthates deposited in wheat grain are translocated from major sources which are closer

to, i.e. from the nearest green parts including awns and flag leaf. Then from other green leaves and photosynthetic tissues including leaf sheath and stem itself. The lower leaves supply the needs of lower parts; stem and roots (Lupton 1966; Wardlaw 1968). However, if the top leaves are removed, the lower ones will supply assimilates to the grain, and similarly if the lower leaves are removed, the flag leaf becomes the major transporter of assimilates to stem and roots as well (Marshall and Wardlaw 1973). How much these structures contribute to final grain weight depends upon the environment and genetic potential of the species.

Awns, flag leaf and the very next lower leaf (which is generally a 3rd nodal leaf) are the potentially efficient photosynthetic organs in terms of economic produce of the wheat plant. Of these maximum contribution occurs from the flag leaf. Awns also contribute to the spike, nevertheless, this contribution is not significant. The photosynthetic output of the 3rd and other lower leaves is of significance for the vegetative lower portion of the tiller. However, if the upper leaf, the flag leaf, becomes non-functional (removed or fallen) they also contribute to the grains in spike. The main economic traits which are directly influenced by the non-functioning of the photosynthetic organs include seed set, grain number and grain weight which ultimately produce integrated effects on the total grain yield.

Wheat developed with greater yield has an increased partitioning of photosynthates from upper leaves (Evans and Dunstone 1970). Increasing photosynthesis of small grain heads (spike of wheat) could also increase yield. Therefore awned wheat lines will outyield the awnletted lines under semi-arid or arid environments (McDonough and Gauch 1959). Therefore awn removal can also decrease yield as much as 21% (Saghir et al. 1968). However, awns have shown no yield advantage in humid climates, possibly because of an increased susceptibility of disease or lodging (Mckenzie 1972). Kramer and Didden (1981) considered that awns did not contribute directly to yield but that the effect was through linked genes.

Effect of flag leaf removal has been reported primarily in terms of reduction in grain yield. Duwayri (1984) reported 10.7% reduction in grain yield after flag leaf removal. Singh and Singh (1984) reported that contribution of flag leaf towards grain yield is 17.3%. A loss of grain yield up to 15-25% has been reported by Natt and Hofner (1987) and 16.13% by Mahmood et al. (1991).

This study was conducted to determine the effect of the removal of main photosynthetic parts of wheat plant on some of the yield related characters in two cultivated varieties.

Materials and methods

The experiment was laid out in a triplicated randomized complete block design in split-plot fashion. Inqalab 91 and Pasban 90 are two promising genetically diverse cultivars in Pakistan and are cultivated in different zones. Inqalab 91 is a high yielding variety well suited to irrigated conditions in comparison with Pasban 90. These varieties were planted in main plots consisting of 10 rows of five meter length with 25 cm spacings between rows. The varieties under main plots were subjected to following treatments under split-plots.

T_1 = Control (Intact plants)

T_2 = Flag leaf removed at heading (spike emergence)
T_3 = 3rd nodal leaf removed at heading
T_4 = Awns removed at heading

At spike emergence flag leaves of 10 randomly selected plants, 3rd nodal leaves from other 10 plants and awns from another set of 10 plants were removed and plants were individually tagged. Similarly 10 intact plants were also tagged as control. Flag leaf and 3rd nodal leaf area was measured according to Muller (1991). Observations on spikelets per spike, seed set, grains per spike, grain weight per spike and 100-grain weight were also recorded at maturity. Data collected were subjected to analysis of variance according to Steel and Torrie (1980) to sort out differences among treatments. Treatment means were compared using Duncan's multiple range test as described by Duncan (1955). Percent reduction for significantly affected traits was also calculated in each of the treatment in comparison with control.

Results and discussion

Varieties, in addition to other yield related traits, also differed significantly for flag leaf and 3rd nodal leaf area (Table 1). Mean flag leaf and 3rd nodal leaf area was 19.53 and 23.78 cm^2 in Pasban 90 and 26.20 and 34.32 cm^2 in Inqalab 91, respectively, (Table 2).

A significant effect of the treatments (removal of green photosynthetic parts) was observed for seed set percentage, grains per spike, grain weight per spike and 100-grain weight (Table 1).

The results revealed a prominent overall reduction, 16.4% in seed set, 14.8% in grains per spike, 34.5% in grain weight and 20.0% in 100-grain weight when flag leaf, the main photosynthetic organ, was removed (Table 2).

Table 1. Analysis of variance for flag leaf and 3rd nodal leaf area and other yield related traits in two wheat varieties under study (mean squares)

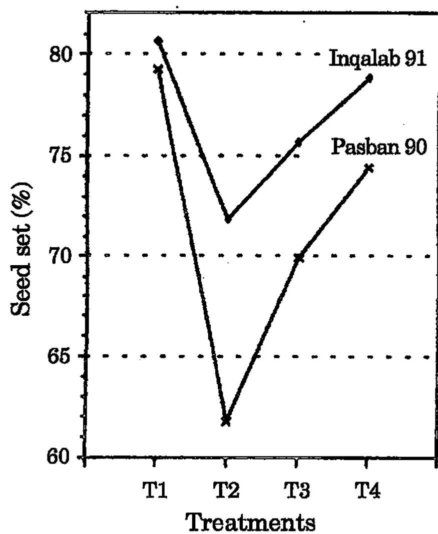
Source	df	Flag leaf area	3rd nodal leaf area	Seed set	Grains per spike	Grain wight per spike	100-grain weight
Replication	2	1.64	0.35	7.69	29.55*	0.03	0.07
Varieties	1	66.73*	166.95**	175.37*	19.44*	0.95*	0.47
Error	2	1.07	1.02	7.70	0.57	0.01	0.41
Treatment	3	-	-	190.51**	80.46**	0.81**	0.81**
V x T	3	-	-	19.57*	24.82**	0.02	0.13*
Error	12	-	-	4.11	2.30	0.17	0.02
C.V%		4.52	3.47	2.74	2.75	6.12	4.17

*$P \leq 0.05$
**$P \leq 0.01$

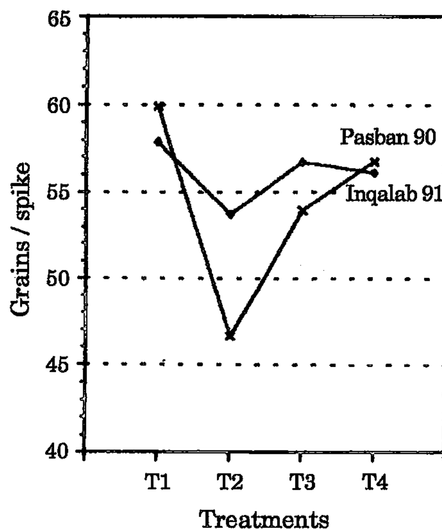
Table 2. Mean values of the traits studied showing statistical significance. Values in parentheses represent the percent decrease as compared to control

	Flag leaf area (cm²)	3rd nodal leaf area (cm²)	Seed set (%)	Grains per spike	Grain weight per spike(g)	100-grain, weight (g)
Varieties						
Pasban 90	19.53 b	23.78 b	71.4b	54.3 b	1.92 b	3.60
Inqalab 91	26.20 a	34.32 a	76.8 a	56.1 a	2.32 a	3.88
S.E	0.84	0.82	0.89	0.22	0.03	0.18
Treatments						
Control (Intact plants)			80.0 a	58.9 a	2.59 a	4.14 a
Flag leaf removerd			66.8 d (16.4)	50.2 c (14.8)	1.69 b (34.5)	3.31d (20.0)
3rd nodal leaf removed			72.8 c (8.9)	55.3 b (6.1)	2.06 b (20.4)	3.57 c(13.8)
Awns removed			76.6 b (4.2)	56.4 b (4.2)	2.15 ab (16.8)	3.92 b (5.3)
S.E			0.83	0.62	0.17	0.06
Interaction (V x T)						
Pasban 90, Control			79.3 ab	59.9 a		4.21 a
Pasban 90, flag leaf removed			61.8 f (22.1)	46.6 d (22.2)		3.03 d(27.9)
Pasban 90, 3rd modal leaf removed			69.9 e (11.8)	53.9c (10.0)		3.41 c (18.9)
Pasban 90, awns removed			74.4cd (6.1)	56.7 b (5.3)		3.74 b (11.1)
Inqalab 91, Control			80.7 a	57.9 ab		4.08 a
Inqalab 91, flag leaf removed			71.9 de (10.9)	53.7 c (7.1)		3.59 bc(11.9)
Inqalab 91, 3rd nodal leaf removed			75.7bc (6.2)	56.7 b (2.0)		3.73 b (8.5)
Inqalab 91, awns removed			78.8 ab(2.3)	56.1 bc (3.0)		4.10 a (0.1)
S.E			1.17	0.88		0.08

Maximum seed set (70.0%) was obtained in intact plants and removal of just a flag leaf reduced this value to minimum (66.8%). Removal of other parts, i.e. awns and 3rd nodal leaf also reduced the seed set significantly but their effect was not so much pronounced as that of removal of flag leaf alone (Fig. 1a). Seed set percentage is directly related to number of grains per spike thus the similar trend was observed in case of grains per spike (Fig. 1b). When the flag leaf was removed, the number of grains reduced to minimum (50.2) in comparison with the maximum (58.9) in intact plants. Removal of 3rd nodal leaf or awns had also depicted a significant impact on grain number per spike. Nevertheless, effect of both of these treatments was statistically at par among themselves for this trait.



(a)



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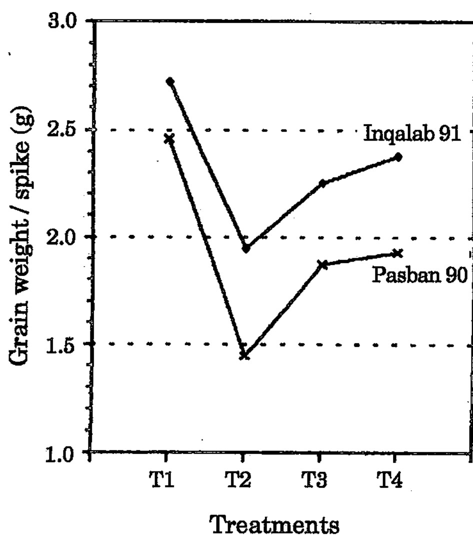

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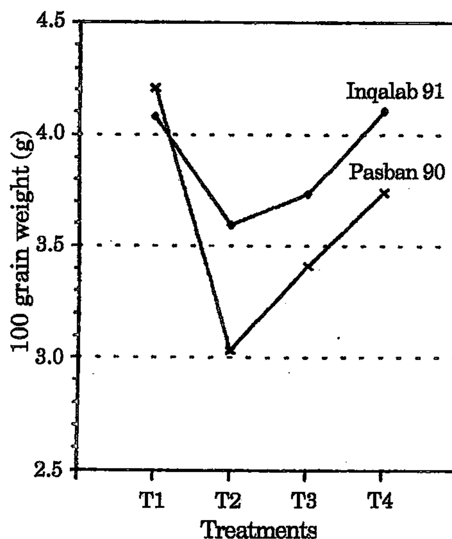

(d)

Fig. 1. Effect of the removal of green photosynthetic parts of wheat plant on (a)seed set, (b)grains per spike, (c)grain weight per spike, and (d)100-grain weight.
(T1) Intact plants, (T2) flag leaf removed, (T3) 3rd nodal leaf removed and (T4) awns removed.

Highest grain weight per spike (2.59 g) in intact plants reduced to lowest (1.69 g) when flag leaf was removed. A reduction of 20.4 and 16.8 % was recorded when 3rd nodal leaf or awns were removed, respectively (Table 2). This trend is evident in Fig. 1c. Ibrahim and Abo Elenein (1977) also found that the flag leaf contributed 41-43% to the grain weight due to increase in kernel weight and number per spike since the flag leaf is photosynthetically the most active leaf during the grain formation period. 100-grain weight is directly related to photosynthetic accumulation and must be altered if any of the photosynthetic organs closer to the grain formation site are removed. This fact was displayed as reduction of 100-grain weight from 4.14 to 3.31 g when flag leaf was removed. Significant reductions were also recorded when 3rd nodal leaf and awns were removed. These reductions, however, were low because of the presence of the flag leaf (Fig. 1d).

Interaction of varieties and treatments was significant for seed set, grains per spike and 100-grain weight where the effect of the removal of the flag leaf was quite prominent in both the varieties (Fig. 1). Both of the varieties presented a marked reduction in the four traits studied when the flag leaf was removed. Removal of 3rd nodal leaf or awns also produced a reasonable amount of reduction. Inqalab 91 was superior to Pasban 90 in respect of all the characters studied. Seed set was higher in Inqalab 91 which resulted in more grain number per spike with greater grain weight per spike and 100-grain weight in Inqalab 91 in comparison with Pasban 90.

A significant reduction of 22.1% in seed set was recorded in Pasban 90 in comparison with 10.9% in Inqalab 91 when flag leaf was removed. While reduction due to the removal of 3rd nodal leaf and awns was 11.8 and 6.1% in Pasban 90 and 6.2 and 2.3% in Inqalab 91, respectively. However, removal of awns in Inqalab 91 depicted a non-significant reduction in seed set percentage (Table 2).

Significant reduction in grains per spike was also recorded due to the removal of the three green parts. Maximum (22.2%) reduction occurred in Pasban 90 as a result of flag leaf removal while this reduction was 7.1% in Inqalab 91. Similarly reduction in other traits due to flag leaf removal was greater in Pasban 90 than in Inqalab 91.

The above cited results signify the major contribution of flag leaf towards yield related traits studied. Thus genotypes with larger flag leaf will produce better than those with smaller one. Enough contribution from awns and 3rd nodal leaf was also observed, nevertheless, this was less than the flag leaf. Olugbemi et al. (1976) also concluded that under absence of severe drought there is a little photosynthetic accumulation through awns in grains rather their presence decreased photosynthesis in the remaining ear structures and flag leaf. Genotypes may differ in their individual response depending upon their genetic architecture and prevailing environmental conditions. Further this response may be of greater extent in one genotype and less in other but the general response is similar. In ranked order maximum contribution occurred from flag leaf followed by 3rd nodal leaf and awns at the last.

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Wheat Information Service
Number 85: 21–24 (1997)
Research article

Chromosome analysis of a hexaploid *Triticum* x *Agropyron* hybrid derivative using Leishman-C-banding[1)]

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Summary

A Leishman-C-banding karyotype of a hexaploid *Triticum turgidum* L. var. *durum* x *Agropyron intermedium* (Host) P.B. derivative, called MT-4-I-I, was analyzed. A total of 48 cells had a stable number of 2n=42 chromosomes. MT-4-1-1 has 7 chromosome pairs from its *A. intermedium* parent which could be identified by their C-banding patterns and morphology.

Introduction

Wide hybridization was accomplished by crossing durum wheat, *Triticum turgidum* L. var. *durum* cv. 'Nodak' (2n=4x=28) with intermediate wheatgrass, *Agropyron intermedium* (Host) P.B. [*Thinopyrum intermedium* (Host) Barkworth and Dewey] (2n=6x=42) (Smith, 1942). The hybrid doubled naturally by unreduced gametes and was received as a partial amphiploid with chromosome numbers of 2n= 58-74 (Schulz-Schaeffer 1970). Selection for chromosome stability was carried out over several generations. An x-ray irradiated octoploid derivative of this partial amphiploid was released in 1987 as MT-2 (Schulz-Schaeffer and Haller 1987). It was characterized by Giemsa-C-banding (Schulz-Schaeffer and Friebe 1992). MT-2 was backcrossed to durum wheat (cv. Wells, C.I. 13333) (Schulz-Schaeffer and McNeal 1977) and selfed for 6 generations after backcrossing. Selfing resulted in the elimination of some *Agropyron* univalents and in others becoming bivalents (Schulz-Schaeffer and Haller 1988). This material was released as MT-4 (Schulz-Schaeffer 1989). MT-4 had 2n=32-44 chromosomes, accounting for 16-21 bivalents and 0-9 univalents (Avg. 18.5 I + 3.5 II). This wide variation in total chromosome number and in degree of chromosome pairing originated from the following breeding approach. After backcrossing MT-2 to durum wheat, all *Agropyron* chromosomes were univalents. In subsequent selfing generations only some chromosomes reestablished pairing relationships, others stayed unpaired, and some were eliminated. Meiotic stabilization of MT-4 by continued selfing, selection for plants

[1)] Contribution No. J-5082 from Montana Agric. Exp. Sta.

FOR EXCHANGE

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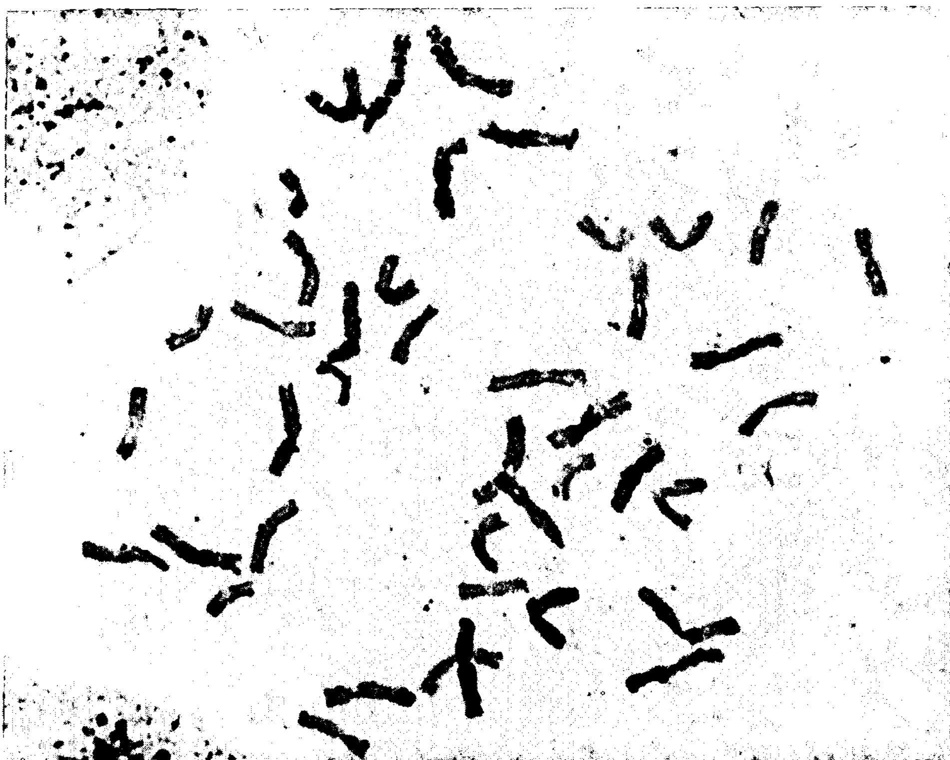
Editor
K.N.



with 7 *Agropyron* chromosome pairs, and selection by single-seed-descent breeding (Brim 1966) was accomplished. The result was a stable line MT-4-1-1. The purpose of this paper is to characterize the chromosome constitution of MT-4-1-1 by Leishman-C-banding analysis which will allow more directed chromosome engineering of this material.

Materials and Methods

Seeds of MT-4-1-1 were placed on moist blotter paper for germination at 23°C. Root tips at lengths of 1.5 to 2.5 cm were collected and pretreated at 0°C for 24 hrs. Root tips were further pretreated in 0°C 45% acetic acid and after excising of the root cap, the meristematic tissue was squeezed out of the epidermal tube. After squashing in 45% acetic acid, the preparations were checked under phase contrast. Cover glasses were frozen on dry ice for 5 minutes and removed with a razor blade. Slides were immediately placed into 99% ethanol for overnight. Leishman-C-banding was carried out according to the method by Gill et al. (1991) except that liquid BDH Wright's Leishman stain (eosin methylene blue, 0.2% w/v solution in methanol) was used instead of Giemsa stain.

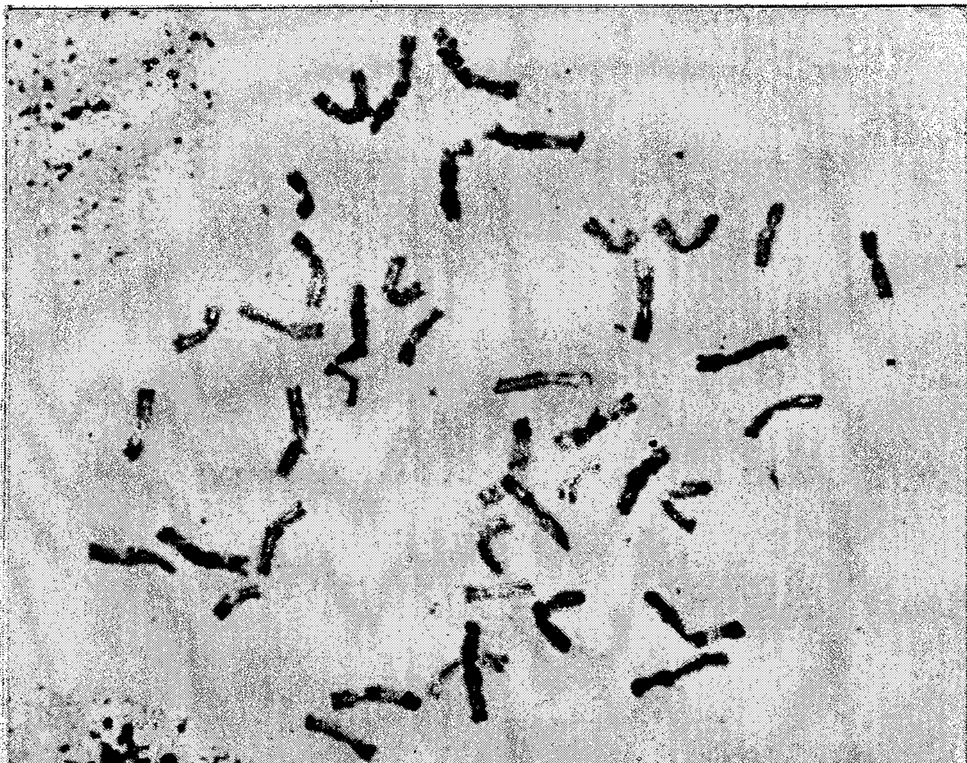


Fig. 1. Mitotic metaphase cell of MT-4-1-1 after Leishman-C-banding (2n = 42). (Magn. 1550x).

Results and discussion

Seed of MT-4 *Agrotriticum* was grown in the field during 1988. Selection of plants with a high number of *Agropyron* chromosome pairs was carried out by morphological observations. Plants with grass-like appearance are expected to have more *Agropyron* chromosomes than plants with wheat-like appearance. Analysis of 15 cells in mitosis showed an average of 2n=42 chromosomes (range 40-46). Further field selection was carried out in 1989 and 1990. MT-4-1 is a single seed progeny of MT-4 and MT-4-1-1 a single seed progeny of MT-4-1. Forty-eight cells of 22 plants of MT-4-1-1 were studied in mitosis. All had 2n=42 chromosomes. The karyotype indicated that chromosomes 3A and 4B which were missing in MT-2 are replaced in MT-4-1-1. MT-4-1-1 was selected for its karyotype stability and its euploid nature.

MT-4-1-1 carries 7 chromosome pairs derived from its *A. intermedium* parent which can be identified by their C-banding patterns and morphology (Fig. 1). The C-banding patterns of these chromosomes are similar to those reported earlier (Aizatulina et al. 1989; Friebe et al. 1992). However, the large extent of polymorphic variation as well as structural rearrangements in *A. intermedium* itself make it presently difficult to assign these chromosomes to the homoeologous groups of the Triticeae. So far, the homoeologous relationships of nine *A. intermedium*

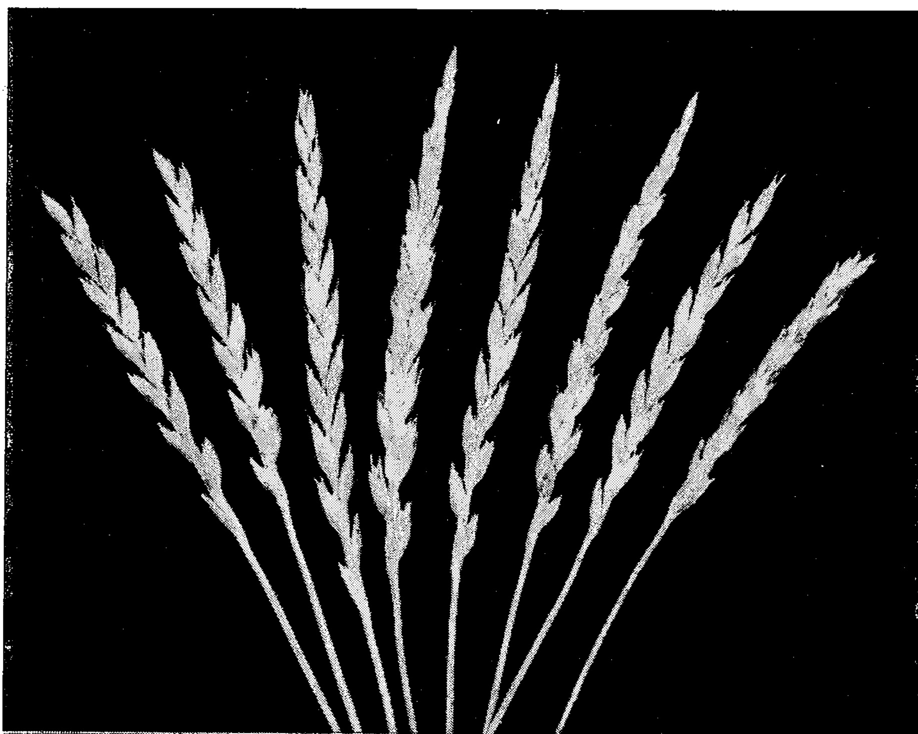


Fig. 2. Spikes of MT-4-1-1.

chromosomes have been established (Foster et al. 1987, Friebe et al. 1992). The C-banding analysis of MT-4-1-1 confirms earlier reports of the hexaploid nature of MT-4. A picture of MT-4-1-1 spikes shows the morphology of this plant type which has wheat and grass characteristics (Fig. 2). Seed of MT-4-1-1 is available from the author for research purposes.

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Wheat Information Service
Number 85: 25–30 (1997)
Research article

Rubisco activity vs photosynthetic CO_2 assimilation rate in the alloplasmic hybrids of common wheat cv. Chinese Spring

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Summary

In vitro Rubisco activity was measured in 15 alloplasmic lines of common wheat (*Triticum aestivum* L.) cv. Chinese Spring (CS) based on the rate of incorporation of $NaH^{14}CO_3$ in acid-precipitable fraction. Five alloplasmic lines with cytoplasms of *T. boeoticum*, *Ae. heldreichii*, *Ae. uniaristata*, *Ae. speltoides*, and *T. timopheevi* showed significantly higher Rubisco activities than CS. Rubisco activity was compared with the available data on the photosynthetic capacity that was measured by the rate of incorporation of $^{13}CO_2$. The comparison showed no correlation between the two parameters. A possible experimental approach to solve this inconsistency between *in vitro* Rubisco activity and *in vivo* photosynthetic CO_2 assimilation rate was discussed.

Key words: Rubisco activity, CO_2 assimilation rate, *Triticum*, *Aegilops*, alloplasmic lines

Introduction

Photosynthesis is the most important function of the chloroplast genome, that is regulated through the interaction with the nuclear genome. In wheat, there are two forms of large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (EC 4.1.1.39, abbreviation: Rubisco); one with the lower isoelectric point (L-type) and the other with higher isoelectric point (H-type) (Chen et al. 1975; Hirai and Tsunewaki 1981). L-type is found in diploid species with A or D genomes, while H-type is found in some diploid *Aegilops* species of the section Sitopsis and in all tetraploid and hexaploid species with B or G genomes. Evans and Seemann (1984) and Evans and Austin (1986) showed an association of *in vitro* Rubisco activity with the isoelectric property of its large subunit: Rubisco

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with L-type large subunit shows low *in vitro* specific activity, while that of H-type is high. Terachi et al. (1987) further suggested, based on the sequences of the genes (*rbcL*) encoding L- and H-type large subunits, that the replacement of glutamine in L-type by lysine in H-type is responsible for the higher *in vitro* specific activity of Rubisco with H-type than L-type subunit.

It was, however, shown that the higher *in vitro* Rubisco activity did not result in different *in vivo* CO_2 assimilation rate measured under light-saturated and CO_2-limiting conditions (Austin et al. 1984; Evans 1986). *In vivo* maximum rate of CO_2 assimilation measured by the rate of $^{13}CO_2$ incorporation also showed no correlation with the large subunit types in alloplasmic common wheat (Nakamura et al. 1991). In this communication, we report the result of re-examination of *in vitro* Rubisco activity using the same set of alloplasmic lines and compared it with the previous data on the CO_2 assimilation rate (Nakamura et al. 1991).

Materials and methods

Fifteen alloplasmic lines of *Triticum aestivum* cv Chinese Spring (CS) with cytoplasms of *Triticum*

Table 1. Alloplasmic lines used in the study

Nucleus donor	Plasma type
Triticum aestivum cv. Chinese Spring(CS)	B
Cytoplasm donor	**Plasma type**
T. boeoticum	A
Aegilops caudata	C
Ae. umbellulata	Cu
Ae. squarrosa	D
Ae. heldreichii	Mh
Ae. uniaristata	Mu
Ae. speltoides	S
Ae. sharonensis	Sl
Ae. bicornis	Sb
Ae. mutica	Mt
Ae. mutica	Mt2
T. timopheevi	G
Ae. ovata	Mo
Ae. kotschyi	Sv
Ae. crassa 4X	D2

Lines having A, C, Mh, Mt2 and G cytoplasm are male sterile

and *Aegilops* were used in this study (Table 1). CS was used as control. Seeds were imbibed for 5 h under tap water, placed in 4 °C overnight, planted in pots and grown under natural light with day-night temperatures of 25-20 °C. At 14th day after sowing, plants were harvested, fresh and dry weights were measured, and leaves were frozen with liquid nitrogen.

Rubisco activity of 6-9 samples per line was measured based on the rate of $NaH^{14}CO_3$ incorporation (Keys and Parry 1990). Briefly, leaf tissues (ca. 0.5 g fresh weight) were ground in 1.5 ml of extraction buffer containing 100 mM Bicine (pH 8.2), 20 mM $MgCl_2$, 5 mM dithiothreitol and 0.025 mM polyclar AT, and centrifuged at 15,000 x g for 20 sec. The reaction was initiated in capped vials by adding 10 μl of the supernatant to a reaction mixture containing 100 mM Bicine (pH 8.2), 20 mM $MgCl_2$, 50 mM mercaptoethanol, 20 mM $NaH^{14}CO_3$ (4.44 x 10^7 Bq/mmol) and 20 mM ribulose-1,5-bisphosphate. The vials were incubated at 25 °C for 10 min. The reaction was stopped by the addition of 30 ml of 4N HCl and unincorporated $NaH^{14}CO_3$ was allowed to be trapped by NaOH overnight in an oven at 50 °C. The amount of incorporated ^{14}C was measured by liquid scintillation counter and means were compared by t-test. All solutions used in the experiment were prepared as CO_2-free using boiled-distilled water and gassed with N_2 just before activity measurements.

Chlorophyll was extracted with ice-cold 80% acetone and the concentration was determined according to Arnon (1949). Protein content was determined by Bradford's method (Bradford 1976) using BioRad protein reagent. Data were based on 9 samples per line and mean separation was made by t-test.

Results

Chlorophyll content: Five alloplasmic lines with cytoplasms of *Ae. caudata, Ae. umbellulata, Ae.*

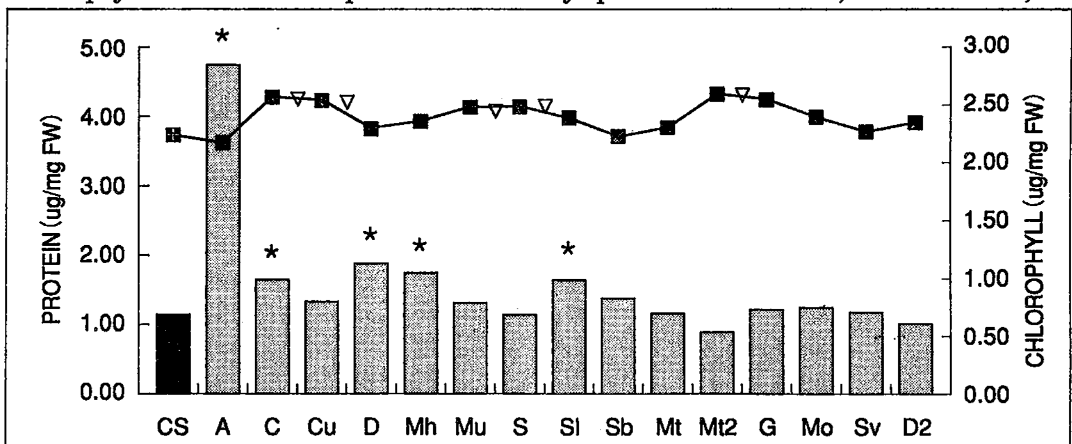

Fig. 1. Protein and chlorophyll contents of 2-week-old plants of CS and the alloplasmic lines. Protein contents are shown by bars and chlorophyll contents by square marks. * (for protein) and ∇ (for chlorophyll) indicate the lines showing significantly higher mean values than CS (α=0.05).

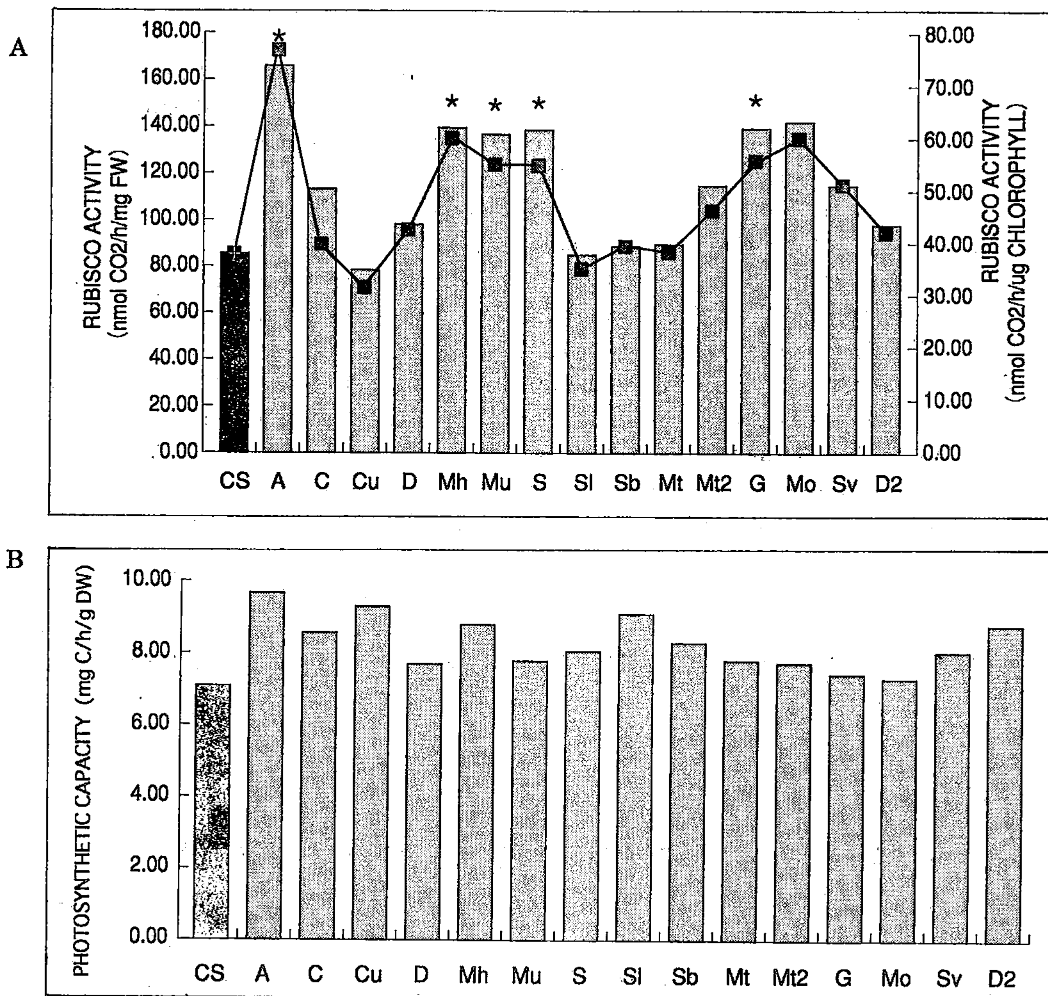

Fig. 2. Rubisco activity and CO_2 assimilation rate.

(A) Rubisco activities of 2-week-old plants of CS and the alloplasmic lines; per fresh weight values are shown by bars and per chlorophyll content by square marks. * indicates the lines showing significantly higher mean values than CS (α=0.05). (B) Photosynthetic capacity (maximum activity) of 3-week-old plants of CS and the alloplasmic lines (Nakamura et.al. 1991).

uniaristata, Ae. speltoides and *Ae. mutica* showed significantly higher chlorophyll contents than CS (Fig. 1). An alloplasmic line with *Ae. squarrosa* cytoplasm showed a higher chlorophyll-a/b ratio than CS (data not shown).

Protein content: Five alloplasmic lines with cytoplasms of *T. boeoticum, Ae. caudata, Ae. squarrosa, Ae. heldreichii* and *Ae. sharonensis* showed significantly higher protein contents than CS (Fig. 1).

Protein content was markedly high in the alloplasmic line with cytoplasm of *T. boeoticum* that shows severe growth depression.

Rubisco activity: No alloplasmic lines showed lower Rubisco activity than CS, but five alloplasmic lines with cytoplasms of *T. boeoticum, Ae. heldreichii, Ae. uniaristata, Ae. speltoides* and *T. timopheevi* showed significantly higher Rubisco activity than CS, based on both fresh weight and chlorophyll content (Fig. 2). No significant correlation was found between Rubisco activity and photosynthetic capacity measured by the rate of $^{13}CO_2$ assimilation (Nakamura et al. 1991).

Discussion

Rubisco is the key enzyme for the photosynthetic CO_2 assimilation (Johal et al. 1980; Lorimer 1981). It has been known that Rubisco activity is the rate-limiting factor under light-saturated and low CO_2 environments (Stitt and Schulze 1994). We compared *in vitro* Rubisco activity and *in vivo* CO_2 assimilation rate in 15 alloplasmic lines of CS with cytoplasms of *Triticum* and *Aegilops* species. All alloplasmic lines showed either equivalent or higher levels of Rubisco activity on both fresh weight and chlorophyll bases as compared with CS. Significantly higher Rubisco activity was observed in 5 lines (Fig. 2). Although the line with *T. boeoticum* cytoplasm showed a markedly higher Rubisco activity and the highest CO_2 assimilation rate, the line exhibits highly depressed plant vigor. The high Rubisco activity, therefore, does not result in good plant vigor in this line. Two alloplasmic lines with H-type large subunit of *Ae. speltoides* and *T. timopheevi* showed higher Rubisco activities than CS, but those in two other lines with *Ae. sharonensis* and *Ae. bicornis* subunit were equivalent to that of CS. Moreover, no correlation was found between the Rubisco activity and the photosynthetic CO_2 assimilation rate.

A question remains how one can approach towards solving this inconsistent result, i.e., high Rubisco activity does not necessarily associate with high CO_2 assimilation rate. Apparently some other factor(s) is involved in the regulation of *in vivo* photosynthetic CO_2 assimilation. Somerville et al. (1982) found a mutant of *Arabidopsis* that could survive only under high (5 %) CO_2. The mutant was later shown to lack an enzyme that activates Rubisco; thus it was named Rubisco activase (Salvucci et al. 1985). Rubisco activase encoded by nuclear gene(s) interacts with the catalytic site of the large subunit of Rubisco (Yokota and Tsujimoto 1992). It is now well known that Rubisco and Rubisco activase play central roles in the regulation of photosynthetic CO_2 assimilation, thus suggesting the necessity of studying the interaction of Rubisco with Rubisco activase in wheat and related species. A study on other factors, particularly the quantity and quality of chlorophyll-protein complexes in photosystem II (Watanabe et al. 1991) might also help understand the photosynthetic property of wheat.

Acknowledgments

This research was supported in part by Grant-in-Aid for JSPS Fellow (to KK). The authors would like to thank Prof. Tsunewaki for providing us with the alloplasmic lines used in this study.

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Wheat Information Service
Number 85: 31–34 (1997)
Research article

Agronomic performance of plant height near-isolines of Nugaines wheat

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Summary

Semidwarf wheat production escalated in the U.S. Pacific Northwest after the development of Gaines and Nugaines. Nugaines replaced Gaines and became widely grown because of its high yield capacity and heavy test weight. This study examines the contribution of semidwarf genes (*Rht1* and *Rht2*) and background genes to the agronomic performance of Nugaines. Near isogenic lines (NILs) representing each of the four possible genotypes of the *Rht1* and *Rht2* loci were selected from a backcross-derived population of Chugoku 81/5*Nugaines; Nugaines has *Rht2* while Chugoku 81 has *Rht1*. The agronomic performance of the four sets of NILs revealed that the Nugaines genetic background is uniquely compatible with the *Rht1* and *Rht2* genes. The three semidwarf genotypes had mean yields of 22 to 36% greater than the nonsemidwarf genotype. In other genetic backgrounds, yield increases associated with semidwarf genotypes averaged 2 to 16% greater than nonsemidwarf NILs. Contrary to results with other genetic backgrounds, the *Rht2* gene did not significantly lower test weight in the Nugaines genetic background. Test weight received special emphasis in the breeding program of O.A. Vogel because it affects market price and milling quality.

Introduction

Semidwarf wheat production began in North America in 1961 with the release of Gaines (Vogel 1964). Gaines is a Norin 10 derived semidwarf. The transition to semidwarf wheat production, especially in the U.S. Pacific Northwest was rapid and had major economic impact for the region (Patterson and Allan 1981; Dalrymple 1980). While Gaines was the first semidwarf variety to be grown, its sister line, Nugaines, released in 1965 had even greater impact because it had improved quality, stripe rust resistance, and higher test weight (Vogel and Peterson 1974). Nugaines was the most widely grown soft white winter wheat variety in the U.S. Pacific Northwest (PNW) for over 10 years. It is estimated that semidwarf wheat increased PNW wheat production by 30%. This study attempts to determine the contribution of Norin 10-derived semidwarf gene(s) to yield

and other agronomic characteristics of Nugaines.

Materials and methods

Four sets of F_6 : F_9 near-isogenic lines (NILs) were developed from Chugoku 81/5* Nugaines. The sets represented three semidwarf genotypes (*Rht1 Rht1 Rht2 Rht2, Rht1 Rht1 rht2 rht2, rht1 rht1 Rht2 Rht2*) and the nonsemidwarf genotype (*rht1 rht1 rht2 rht2*). Sets comprised 3 to 10 lines each. The genotype of Nugaines is *rht1 rht1 Rht2 Rht2* and the genotype of Chugoku 81 must be *Rht1 Rht1 rht2 rht2* because progeny with nonsemidwarf and two-gene semidwarf phenotypes were obtained from this population. Seed of Chugoku 81 was obtained from Byung Hee Hong, Korea University, Seoul, Korea. Chugoku 81 is an early maturing selection having facultative growth habit developed at the Chugoku National Agricultural Experiment Station, Fukuyama, Japan (Takashi Nagamine, personal communication).

The genotypes of NILs having plant heights similar to Chugoku 81 and Nugaines were determined by test crossing to Nugaines (*Rht2* tester) and Stephens (*Rht1* tester). The lines were tested in 7 replicated trials at 3 eastern Washington locations during 1991 to 1993. Individual plots were $2.97m^2$. Locations represented irrigated, summer fallow and annual crop management systems.

Agronormic data were obtained for the nine traits shown in Table 1. Analyses of variance were performed for each trait and trial. Combined analyses across trials were also performed and these statistics are given in Table 1.

Results and discussion

Means and ranges of nine agronomic traits for NILs representing the four plant height genotypes appear in Table 1. Except for spike number, significant ($P \leq 0.05$) mean trait differences occurred among the plant height genotypes.

Comparisons between the *Rht1* (*Rht1 Rht1 rht2 rht2*) and *Rht2* (*rht1 rht1 Rht2 Rht2*) NILs were of main interest. The *Rht1* NILs had higher overall mean grain yields, kernel weights, and plant heights than *Rht2* NILs while the *Rht2* NILs had heavier test weights than *Rht1* NILs (Table 1). An earlier study (Allan 1989) found no differences in grain yield or kernel weight between *Rht1* and *Rht2* NILs, while NILs with *Rht1* had heavier test weights than *Rht2* sibs in some populations. The current and earlier study showed the *Rht1* NILs were slightly taller than their *Rht2* sibs. The grain yield advantage of the *Rht1* and *Rht2* genes in the Nugaines genetic background was generally greater than that obtained when these genes were transferred into genetic backgrounds of nonsemidwarf wheat varieties. In the Nugaines genetic background *Rht1* and *Rht2* NILs yielded 36 and 28%, respectively, greater than their nonsemidwarf *rht1 rht1 rht2 rht2* sibs while in three nonsemidwarf genetic backgrounds the yield increases associated with *Rht1* and *Rht2* averaged only 16% greater than their *rht1 rht2* sibs (Allan 1989).

Table 1. Means and ranges for nine agronomic traits of Chugoku 81/5*Nugaines near-isolines (NIL) representing four plant height genotypes

Parameter	Plant height[a]	Heading	Grain yield	Test weight	Kernel weight	Spike number	Kernels/ spike	Harvest index	Lodging
	cm	days	kg/ha	kg/hl	mg	m^2	no.	%	%
Rht1 Rht1 Rht2 Rht2									
High NIL	55	150	6670	80.1	34.7	672	29.1	49.8	9
Low NIL	51	149	5769	79.1	31.1	604	38.1	45.6	2
Av. (3)[b]	53 d	150 a	6293 b	79.7 c	32.8 d	646 a	33.4 ab	48.1 a	5 c
Rht1 Rht1 rht2 rht2									
High NIL	81	149	7580	81.7	36.4	731	40.1	46.6	14
Low NIL	78	147	6347	80.9	30.7	626	32.5	42.7	3
Av.(10)	80b	148b	6992a	81.1b	34.2b	689a	36.5a	45.0b	8bc
rht1 rht1 Rht2 Rht2									
High NIL	82	150	6925	82.9	31.2	731	37.6	48.6	14
Low NIL	74	147	6297	81.1	35.4	649	32.0	42.7	7
Av. (8)	78 c	148 b	6576 b	81.9 a	33.6 c	686 a	35.8 ab	45.0 b	10 b
rht1 rht1 rht2 rht2									
High NIL	103	149	5228	82.6	36.4	659	33.9	40.3	30
Low NIL	99	144	5020	80.1	34.4	630	27.6	34.9	22
Av. (3)	101 a	147b	5144c	81.8a	35.4a	643 a	31.1 b	37.8c	26a
Nugaines	79	149	6881	82.3	35.3	735	32.2	44.9	7
Trials	7	6	7	7	4	4	4	4	7

[a] Trait means of plant height genotypes with the same letter do not differ at $P \leq 0.05$.

[b] Number of NILs in the mean.

Yield component differences between Nugaines *Rht1* NILs vs *rht1 rht2* NILs were similar to results obtained in the earlier study. In both studies the *Rht1* gene was associated with reduced test weight and kernel weight but increased kernels/spike; it was neutral for spike number. In the case of *Rht2* vs *rht1 rht2* NILs, the two studies differed. Unlike the earlier study, with Nugaines, the *Rht2* gene was neutral for test weight, kernels per spike and spike number. In the earlier study, the *Rht2* gene was associated with enhanced spike number and kernels/spike but with

reduced test weights among all nonsemidwarf genetic backgrounds.

When *Rht1 Rht2* (*Rht1 Rht1 Rht2 Rht2*) NILs were compared to *rht1 rht2* NILs, this genotype significantly enhanced grain yield (22%) and harvest index (27%) but was neutral for kernels/spike and spike number, while reducing test weight and kernel weight. These results were in agreement with the earlier study for test weight and kernel weight. In the earlier test, the *Rht1 Rht2* genotype generally enhanced spike number and kernels/spike but caused inconsistent effects on grain yield (Allan 1989).

Lodging was inversely related to plant height (Table 1). Higher yields of the three semidwarf genotypes over the nonsemidwarf genotype were only partly due to their superior lodging resistance. The percentage yield increase of semidwarf NILs compared to nonsemidwarf NILs in tests sustaining significant versus minor lodging were: *Rht1* NILs (45 versus 30%), *Rht2* NILs (33 versus 24%) and *Rht1 Rht2* NILs (24 versus 21%), respectively.

These results may explain the exceptional performance of Nugaines in the PNW of USA. Background genes of Nugaines appear to be especially compatible with *Rht1* or *Rht2* genes allowing for maximum grain yield increase. Furthermore, the *Rht2* gene does not reduce test weight in the Nugaines background whereas it has consistently reduced test weights in all other genetic backgrounds. Nugaines was a sib of Gaines and was released to replace Gaines because it had higher test weight and flour yield.

The grain yield superiority of *Rht1* compared to *Rht2* was unexpected since Nugaines contributed the *Rht2* allele while Chugoku 81 contributed the *Rht1* allele. One explanation could be that favorable yield genes of Chugoku 81 remained linked to *Rht1* when backcrossed to Nugaines. That *Rht1 Rht2* NILs had unusually high mean grain yields which were comparable ($P>0.05$) to *Rht2* NILs supports this possibility. O.A. Vogel selected Nugaines from a cross of Sel 14/50-3 and Burt. Sel 14/50-3 had the *Rht2* gene while Burt had neither semidwarf gene. Hence there was no possibility of obtaining selections with *Rht1* from the cross that produced Nugaines.

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Wheat Information Service
Number 85: 35–42 (1997)
Research article

DNA amplification fingerprinting (DAF) as a new source of molecular markers in bread wheat

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Summary

Polymorphism in seven bread wheat genotypes (differing for four quality traits) was studied using DAF. Ten arbitrary, 8-mer, GC rich, linear primers and ten 11-mer minihairpin primers, each having a 3-mer core sequence at 3' end, were utilized for DNA amplification. Nine linear primers and four mini-hairpin primers produced characteristic fingerprinting patterns involving polymorphism. The remaining primers gave poor DAF profiles with high background smear, which was associated with relatively higher GC content of these primers. It could partly also be due to large genome size of bread wheat. Both linear as well as mini-hairpin primers producing good DAF profiles, also revealed polymorphic DAF products, some of which were unique to a genotype. Contrary to earlier claims, neither the average number, nor the proportion of polymorphic products obtained with mini-hairpin primers suggested their superiority over the linear primers. In view of our earlier unpublished results with RAPDs and MP-PCR on the same set of genotypes, giving no reproducible polymorphism, we conclude that DAF technology may be a useful tool for detecting polymorphism in a difficult crop such as bread wheat.

Key words: arbitrary primers, DAF, fingerprinting, PAGE, bread wheat

Introduction

A variety of molecular markers are available for detecting DNA polymorphism among animal and plant materials. In crop plants, their use in tagging genes for marker aided selection has been demonstrated (for a review see Mohan et al. 1997). These markers may be hybridization based markers or PCR based markers and include (i) RFLPs using various types of probes, (ii) microsatellites or simple sequence repeats (SSRs) (Jefferys et al. 1985; Weber and May 1989; Litt

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and Luty 1989; Tautz, 1989; Akkaya et al. 1992; Morganty and Oliviari 1993), (iii) minisatellites (Jefferys et al. 1988; Vassart et al. 1987; Broun et al. 1992; Stockton et al. 1992), and (iv) RAPDs (Williams et al. 1990), AP-PCR (Welsh and McClelland 1990) and DAF (Caetano-Anolles et al. 1991). The last category of markers are also collectively called as MAAP (Multiple Arbitrary Amplicon Profiling) (Caetano-Anolles et al. 1991). The lack of prior knowledge of DNA sequences and lack of characterization of the probes restricts the use of RFLPs for detecting polymorphism. Similarly, the requirement of prior knowledge of flanking sequences for designing primers limits the use of minisatellites and microsatellites. Markers of MAAP family, however, make use of arbitrary primers and therefore, can be used without any prior knowledge of DNA sequences. However, among these markers of MAAP family also, markers like RAPDs proved to be of limited value in a crop like bread wheat due to detection of low polymorphism (Penner et al. 1995). DNA Amplification Fingerprinting (DAF) has recently been found to be promising in many plant materials. DAF makes use of very short (may be 5-mer but typically 7–8-mer) GC rich primers. The utility of short oligonucleotides for DNA amplification, producing genotype specific, characteristic DNA profiles was first demonstrated by Caetano-Anolles et al. (1991). It was shown that these complex DNA profiles can detect genetic differences in a wide variety of organisms including bacteria, fungi, plants (soybean, bermudagrass, centipedegrass, etc.) and humans (Caetano-Anolles et al. 1991, 1995; Gresshoff and MacKenzie 1994; Prabhu and Gresshoff 1994; Weaver et al. 1995; Gresshoff et al. 1997). Following PCR amplification, DAF products can be separated on polyacrylamide gel. Silver staining of the gels reveals DNA amplification profiles with high multiplex ratio (Caetano-Anolles et al. 1991, 1995; Prabhu and Gresshoff 1994; Caetano-Anolles and Gresshoff, 1996). A new class of DAF primers referred to as minihairpin primers have also been used and a few recent reports suggested their superiority over linear DAF primers (Caetano-Anolles and Gresshoff 1994; 1996). In view of the above, and due to failure of RFLPs and RAPDs to detect polymorphism among wheat varieties (Chao et al. 1989; Penner et al. 1995), we utilized DAF technology in bread wheat for the first time to check its suitability for detection of polymorphism and for their subsequent use in tagging of some quality traits for molecular marker aided selection in plant breeding.

Materials and methods

Plant materials

Seven bread wheat genotypes differing for protein content, leaf rust resistance, grain size and pre-harvest sprouting tolerance were used in the present study (Table 1).

DNA isolation

DNA was isolated from young leaves collected from 30 day old field grown plants using a modified CTAB method (Weising et al. 1995).

DAF primers

A total of 20 DAF primers (procured from G. Caetano-Anolles and P.M. Gresshoff, University of Tennessee, USA) including 10 unstructured (linear) (Table 1) and 10 mini-hairpin primers were

Table 1. Details of linear primers and abundance of polymorphism in bread wheat

Primer code number	Primer sequence	GC/AT ratio	Average number of bands/primer (<2kb)	Total polymorphic bands (<2kb)	Unique bands	Polymorphic bands obtained with pairs of genotypes differing for a trait[1]			
						A/B	B/C	D/E	F/G
8-2	CCTGTGAG	5:3	26.4	8	4	8	3	1	ND[2]
8-4	GTAACGCC	5:3	25.0	14	3	5	5	10	7
8-5	GACGTAGG	5:3	22.0	13	5	12	2	5	1
8-8	GAAACGCC	5:3	27.2	21	3	10	10	9	17
8-10	GTATCGCC	5:3	25.8	15	3	5	5	4	1
8-26	GCAGGTGG	6:2	25.4	3	1	2	0	0	1
8-30	GCTGGTCG	6:2	31.0	17	3	7	2	9	3
8-36	GCAGGTGC	6:2	34.7	8	0	1	0	5	3
8-45	GGACCCGC	7:1	27.6	8	4	7	1	3	ND
8-47	GCCCGCCC	8:0	S[3]	–	–	–	–	–	–

[1]Genotypes are marked for different quality traits: A(PH 132) for high protein content; B(WL711) for low protein content and leaf rust susceptibility; C(WL711 + *Lr24*) for leaf rust resistance; D(Rye selection 111) for large grain size; E(Chinese Spring) for small grain size; F(SPR 8198) for pre-harvest sprouting tolerance and G(HD 2329) for pre-harvest sprouting susceptibility)
[2]Not determined
[3]Smear

used for DNA amplification (Table 2).

DNA amplification and electrophoresis

DNA amplification was performed in 20 μl volume containing 3 μM primer, 0.15U/μl (in case of linear primers) and 0.2U/μl (in case of mini-hairpin primers) of *Taq* DNA polymerase (Bangalore Genei Limited, India), 0.2 ng/μl template DNA, 200 μM each of dNTPs, 1.5 mM of $MgCl_2$ and 10x PCR buffer (supplied by the manufacturer of *Taq* polymerase) at a final concentration of 1x. Amplification was conducted in a Perkin-Elmer DNA Thermal Cycler for 35 cycles using temperature profiles of 96°C for 30 sec, 30°C for 30 sec and 72°C for 30 sec with a ramp time of 3 min from 30°C to 72°C in case of linear primers. In case of mini-hairpin primers, the temperature profiles included 95°C for 30 sec, 55°C for 2 min and 72°C for 30 sec. The final extension in both the cases was 5 min at 72°C. Amplification products obtained with linear primers were electrophoresed on 7% polyacrylamide-7M urea denaturing gel applying 7.5 V/cm for 12 h while amplification products primed with mini-hairpin primers were resolved on 10% polyacrylamide supergel (Gresshoff et al. 1997). Silver staining of gel was done following Tegelstrom (1992).

Table 2. Details of mini-hairpin primers and abundance of polymorphism in bread wheat

Primer code number	Primer sequence	GC/AT ratio[1]	Total number of bands (<2kb)	Polymorphic bands obtained with pairs of genotypes differing for a trait		
				A/B[2]	D/E	F/G
HPC 17	GCGAGAGC-TCC	2:1	S[3]	–	–	–
HPC 19	GCGAGAGC-TCG	2:1	S	–	–	–
HPC 23	GCGAGAGC-TTG	1:2	54	3	ND[4]	ND
HPC 26	GCGAGAGC-TGT	1:2	60	ND	ND	5
HPC 27	GCGAGAGC-TGG	2:1	S	–	–	–
HPC 29	GCGAGAGC-TAC	1:2	57	ND	2	ND
HPC 33	GCGAGAGC-GCC	3:0	S	–	–	–
HPC 41	GCGAGAGC-GGC	3:0	S	–	–	–
HPC 43	GCGAGAGC-GGG	3:0	S	–	–	–
HPC 44	GCGAGAGC-GGA	2:1	56	ND	ND	5

[1]Ratio of the core sequence only (see text)
[2]Genotypes are same as in Table 1
[3]Smear
[4]Not determined

Evaluation of fragment patterns

Amplified fragments in each primer-genotype combination were scored in two ways. Firstly, for each primer, the number of polymorphic fragments included all those fragments which were absent in at least one genotype. Secondly, polymorphism was examined between each pair of the genotypes having contrasting phenotypes for a single trait (e.g. protein content, leaf rust resistance, etc.). Polymorphism in these cases was scored on the basis of presence or absence of fragments between the two genotypes. The amplification fragment(s) present in only one genotype and absent in the remaining genotypes was classified as unique band(s).

Results and discussion

Nine out of ten linear primers tested using seven genotypes of bread wheat, gave characteristic fingerprinting patterns. The DAF profiles contained 20-35 scorable bands (<2kb) in all the seven bread wheat genotypes examined (Fig. 1, Table 1). These results were utilized for a comparison of the DAF profiles with the GC/AT ratio in the sequences of the corresponding DAF primers. For this purpose, it may be noted from Table 1, that in five primers the GC/AT ratio is 5 : 3, in three other primers, the ratio is 6 : 2, in one primer, the ratio is 7 : 1, while the remaining one primer

has a GC/AT ratio of 8 : 0. When these GC/AT ratios are compared with DAF profiles, it becomes apparent that the primers with low GC content gave better DAF profiles with distinct bands and low background smear (Fig. 1). For instance, the primer 8-47 with all GC gave smear with faint non-scorable bands. The average number of DAF products (25.4 to 34.7) with primers having 6 : 2 and 7 : 1 GC/AT ratio was higher in comparison to that (22.0 to 27.2) obtained with the primer having 5 : 3 GC/AT ratio (Table 1). However, the utility of a primer depends not so much on number of distinct products it gives, but on the degree of polymorphism, it detects. In this connection, in general, the primer with 5 : 3 GC/AT ratio proved to be more useful giving more polymorphic DAF products than the remaining primers with high GC ratios (Table 1). For instance, the primers 8-8, 8-10, 8-4 and 8-5 having 5 : 3 GC/AT ratio respectively gave 21, 15, 14 and 13 polymorphic products. Out of the remaining primers with high GC content, only one primer (8-30) gave comparable number of polymorphic DAF products (Table 1). Therefore, with the limited number of linear primers used in this study, it may be concluded that the DAF primers with low GC content (60%) may be more suitable for revealing polymorphism in bread wheat.

The above results differ from some earlier reports, which suggested that the GC content of the primer had no correlation with either the amplification itself or with the total number of distinct DAF products obtained or with the frequency of polymorphism detected (Caetano-Anolles and Gresshoff 1994; Prabhu and Gresshoff 1994). However, the present results do support another earlier study involving *Staphylococcus aureus*, soybean and Caucasian human (Caetano-Anolles et al. 1991), where it was suggested that the number of DAF products depended both on the genome size of the species being examined and on the GC content of the primer used. In the present study, it is possible that a large genome of bread wheat and 100% GC content of the primer 8-47 contributed to the smear obtained. A few unique bands (1-5 per primer) were obtained in one or the other genotype tested with all the primers except with the primer 8-36 (Table 1). These specific bands may help in cultivar identification.

In addition to the ten linear DAF primers utilized in the present study as above, ten additional mini-hairpin primers (Hirao et al. 1992; Caetano-Anolles and Gresshoff 1994) were also evaluated for their utility in detecting polymorphism. Mini-hairpin primers form a loop of 3-4 nucleotides, a stem of only two nucleotides and a core arbitrary sequence of variable length (1-8 nucleotides) at the 3' terminal end. This loop-stem region closes during early ramping (Caetano-Anolles and Gresshoff 1994; Gresshoff et al. 1997). In the present study, mini-hairpin primers are each made up of a core arbitrary sequence of 3 bases (in earlier studies, a core sequence of 3 bases was found most appropriate) at the 3' terminus and a loop stem of 8 bases. Each of the ten mini-hairpin primers listed in Table 2 could be tried, each only on a single pair of genotypes of bread wheat differing for one quality trait. Four of these primers (HPC 23, HPC 26, HPC 29 and HPC 44) gave excellent DAF profiles with distinct scorable amplified products (Fig. 2; Lanes 1, 2, 5 and 6). The remaining six mini-hairpin primers, however, gave only a few faint bands superimposed on high background smear, suggesting their limited utility in detecting polymorphism in a crop like bread wheat (Fig. 2; Lanes 3 and 4).

The mini-hairpin primers were also examined for their utility in relation to their GC/AT ratio as done above for linear DAF primers. In this case also, higher GC content in the core

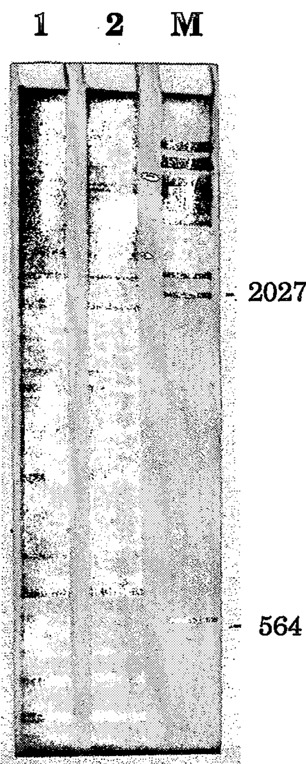

Fig. 1. DAF profiles of two bread wheat genotypes obtained using linear primer 8-4.
Lane 1, SPR 8198; lane 2, HD 2329 and M, λ-HindIII molecular weight (bp) marker

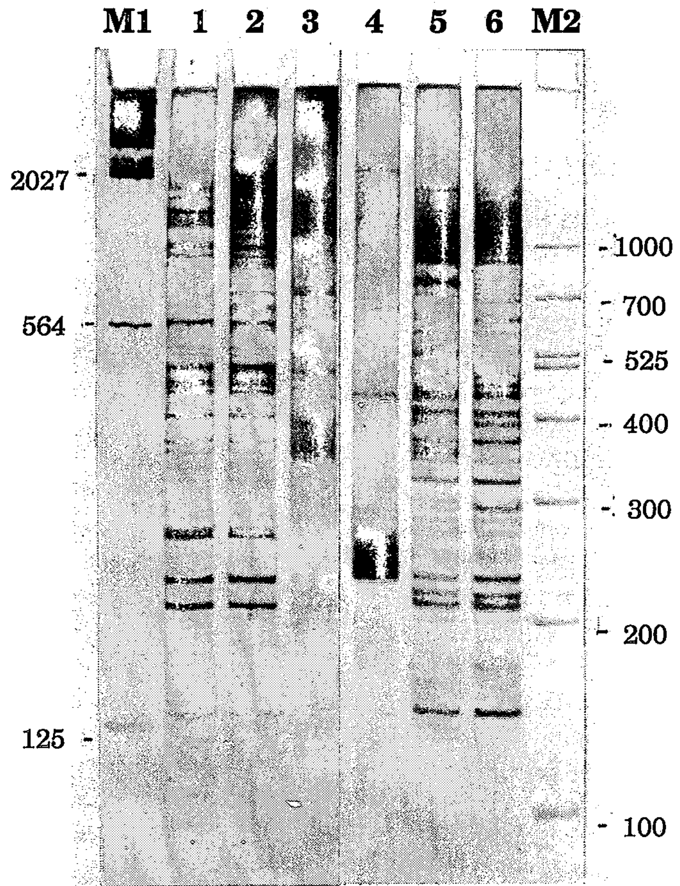

Fig. 2. DAF profiles of five bread wheat genotypes obtained using four mini-hairpin primers.
Lane M_1, λ-*Hin*dIII molecular weight (bp) marker; lanes 1 and 2, Rye Selection 111 and Chinese Spring (primer HPC 29); lane 3, WL 711 (primer HPC 33); lane 4, HD 2329 (primer HPC 43); lanes 5 and 6, SPR 8198 and HD 2329 (primer HPC 44); M_2, PCR molecular weight (bp) marker.

sequence seems to give a smear rather than distinct scorable DAF profile (Fig. 2; Lanes 3 and 4). However, the presence of A or T nucleotide at the 3' end of the core sequence of the mini-hairpin primer, despite high GC content (GC/AT=2 : 1) gave excellent scorable DAF profiles (Fig. 2; Lanes 5 and 6). The number of amplification products (total number of bands of <2kb) obtained with mini-hairpin primers, was almost double to that obtained with a linear primer even at an annealing temperature of 55°C (Tables 1 and 2). This may be due to a smaller core sequence (3-mer) of the primer involved in annealing, which is provided with greater thermostability by the hairpin loop during annealing (Caetano-Anolles and Gresshoff 1994; Gresshoff et al. 1997).

While making an overall assessment of the utility of DAF primers in bread wheat in terms of producing polymorphic bands, during the present study, we found that neither the average number, nor the proportion of polymorphic DAF products obtained with the mini-hairpin primers was greater than those obtained with linear primers in bread wheat (Tables 1 and 2). These results thus do not support the earlier contention, that for detecting polymorphism, the mini-hairpin primers are superior over the linear primers. Since these earlier results pertain to smaller genome of centipedegrass (Caetano-Anolles and Gresshoff 1994), bermudagrass (Caetano-Anolles et al. 1995) and soybean (Caetano-Anolles and Gresshoff 1996), it is possible that the relative utility of mini-hairpin primers differs in different plant systems.

The genotypes of bread wheat utilized in the present study were also earlier analyzed by us using RAPDs and microsatellite primed PCR (MP-PCR), both of which failed to detect reproducible polymorphism among the above genotypes. DAF, on the other hand, revealed polymorphism between pairs of genotypes differing for individual traits e.g. protein content, grain size, pre-harvest sprouting tolerance and, leaf rust resistance (Tables 1 and 2). Similar conclusions were earlier drawn by Prabhu and Gresshoff (1994), while examining two species of *Glycine*. Using DAF they obtained three fold increase in polymorphism per primer between *G. max* and *G. soja* over the polymorphism revealed using RAPDs on the same *Glycine* species (Williams et al. 1990). We therefore, conclude that DAF technology may become a useful tool for detecting polymorphism and for developing molecular markers for tagging genes for molecular marker aided selection in plant breeding even for a difficult crop like bread wheat.

Acknowledgments

We gratefully acknowledge the financial support from the Department of Biotechnology, Government of India, for carrying out this study. Thanks are also due to Drs. G. Caetano-Anolles and P.M. Gresshoff for supplying DAF primers, and Drs. Harjit Singh and H S Dhaliwal for seed materials.

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Wheat Information Service
Number 85: 43–44 (1997)
Research information

Combining ability analysis in relation to heat stress for yield, its components and some growth durations in wheat

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The wheat crop in India matures in March/April and wide temperature fluctuations expose the crop to heat stress during the grain filling stage. Eight wheat purelines viz., Hindi 62(1), Narmada 4(2), Kalyansona(3), Kharchia 65(4), Sonalike (5), WH 283(6), DWR 39(7), HI 1011(8) and their all possible cross combinations excluding reciprocals were used to generate combining ability information and identify suitable parents and cross combinations for further exploitation. The material was sown on 25.10.89 (S_1) and 1.12.89 (S_2). The S_1 exposed the material to relatively higher temperature stress during vegetative growth, whereas S_2 exposed the post flowering phase to high temperature stress (Table 1). Data were recorded on days to appearance of first node (FN), days to ear emergence (EE), days to maturity (DM), duration from anthesis to maturity (AM), number of effective tillers per plant (TP), grains per spike (GS), 1000-grain weight (GW) and grain yield per plant (GY). The data were subjected to Grriffing's combining ability analysis

Table 1. Mean temperatures (°C) prevailing during various growth phases under the two sowing conditions

Growth phase	FN	EE	DM	AM
Sowing condition				
S_1	19.0	15.7	16.8	18.0
S_2	14.7	15.3	17.8	22.3

method II, model 1.

Both gca and sca mean squares were significant, however, a greater importance of gca was revealed (Table 2). This indicated immense scope for selection to improve these characters, except number of tillers per plant under S_1 and grain yield per plant under S_2. The best positive combiners

Table 2. Combining ability mean squares and best combiners for the different relevant characters under two sowing conditions

Characater / Parameter		FN	TP	AM	GS	GW	GY
gca mean squares	S1	50.5**	2.6**	37.2**	135.6**	54.1**	9.9**
	S2	41.4 **	14.1**	22.1**	145.2**	81.1**	9.9**
sca mean squares	S1	16.1**	4.7**	14.6**	75.0**	33.2**	11.9**
	S2	9.9**	6.1**	19.7**	50.3**	25.3**	5.5**
Best postive combiners	S1	8,1,4#	1,4,6	7,6	7,3,4	2,6,4	7,5,4
	S2	8,3,1	1,4,6	2,7	3,7	4,6,5	7,4
Best negative combiners	S1	5,1,3	8,3,2	8,2,4	1,6	3,1	3,2
	S2	6,2,5	3,8,2	3,8	4,1,2	3,7,2	1,3,2

**Significant at 1% level

1: Hindi 62, 2: Narmada 4, 3: Kalyansona, 4: Kharchia 65, 5: Sonalike, 6: WH 283, 7: DWR 39, 8: HI 1011

for further breeding work are listed in Table 2. Since additive as well as non-additive components of genetic variability determined the inheritance of the relevant characters, an efficient breeding plan would be the one which can exploit both these components.

Wheat Information Service
Number 85: 45–46 (1997)
Research information

Screening of spontaneous translocations in cultivated Emmer wheat

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Although many spontaneous translocations have been reported in tetraploid Emmer wheat (Nishikawa et al. 1986; Schlegel 1996), the overall frequency of rearranged types is unknown. In this study, the translocations in cultivated Emmer wheat was screened and the translocation frequency was estimated.

Twenty five strains of cultivated Emmer wheat were intercrossed and chromosome pairings were observed in F_1 hybrids (for strain number, see Table 1). They consist of 6 strains of *Triticum dicoccum* Schübl., 5 of *T. durum* Desf., 4 of *T. carthlicum* Nevski, three each of *T. abyssinicum* Vav. and *T. paleocolchicum* Men. and one each of *T. orientale* Perc., *T. polonicum L.*, *T. pyramidale* (Del.) Perc. and *T. turgidum* L. (for detailed passport data, see Tanaka 1983). Several translocation tester strains of wild Emmer (Taketa and Kawahara 1996), *T. dicoccoides* Körn. were also used in the crossings. The chromosome pairings of the hybrids were observed at the first meiotic metaphase of the pollen mother cells by the aceto-orcein squash method.

The strains examined were classified into four groups based on the presence or absence of translocations; those without translocations (E1a type), and those with one (E7 type) and two translocations (E21 and E22 type) as shown in Table 1. Three strains with one translocation were intercrossed and the hybrids showed normal meiosis with 14 bivalents. They were then crossed with the translocation testers, E2 to E6, of *T. dicoccoides* and pairings were observed as shown in Table 2. Since this translocation is different from those already found in *T. dicoccoides,* the rearranged chromosome structure was named E7 type. One of the two strains with two translocations, KU-185, shared one translocation in common with the E7 type (Table 2) and was called the E21 type. The other, KU-111, had two different translocations from E21 (detailed data not shown) and was named E22. The present results are in agreement with those obtained by

Table 1. Classification of cultivated Emmer wheat strains based on the presence or absence of chromosomal translocations.

No translocation (Ela type):	*T.dicoccum* (*KU-114,* 115, 118, 119, 124), *T. durum* (KU-125, 126, 127, 128-1, 128-2,) *T. carthlicum* (KU-138, 139-1, 139-2), *T. paleocolchicum* (KU-156, 190-1, 190-2), *T. orientale* (KU-137), *T. polonicum* (KU-141), *T. pyramidale* (KU-146), *T. turgidum* (KU-147)
One translocation (E7 type):	*T. abyssinicum* (KU-186, 188), *T. carthlicum* (KU-187)
Two translocations (E21 type):	*T. abyssinicum* (KU-185)
Two translocations (E22 type):	*T. dicoccum* (KU-111)

Table 2. Multivalents observed among eight chromosome types in the Emmer wheat.

	E1a	E2	E3	E4	E5	E6	E7
E7	IV	2 IV	2 IV	VI	2 IV	2 IV	–
E21	VI	VIII	IV+VI	VIII	IV+VI	IV+VI	IV

Table 3. Chromosomes involved in translocations of the Emmer wheat

Type	Chromosomes
Ela (LD 222) *	standard
E2	2B-3B
E3	5B-7B
E4	3B-4B
E5	6B-7B
E6	1A-5A
E7 (Ethiopicum)	2A-4B
E21 (Abyssinicum)	2A-4B : 2A-2B
E22 (Liguiforme)	7A-5B, –

*Types reported by Nishikawa et al. 1986.

Nishikawa et al. (1986). From the chromosome pairing among strains and the detailed information on strains used, the types reported by Nishikawa et al. (1986) corresponded to those used in this study. Chromosomes involved in translocations of wild and cultivated Emmer wheat have been identified by using telosomics or C-banding (Nishikawa et al. 1986; 1994, Taketa and Kawahara 1996) and the available data are summarized in Table 3. Observed multivalents shown in Table 2 are in agreement with those expected from Table 3.

The standard type, E1a, was found in both wild and cultivated Emmer but E2 to E6 in wild type only and E7, E21 and E22 in cultivated form. All three strains of *T. abyssinicum*, KU-185, 186 and 188, had a common 2A-4B translocation, suggesting the fixation of this structural rearrangement in *T. abyssinicum*.

In summary, of 25 strains examined 20 were of the standard type, three had one translocation and two had two translocations. The average number of translocations (total number of translocations detected/number of strains examined) in cultivated Emmer wheat was 0.280. This is in good agreement with that of 0.202 reported for Israeli wild populations of *T. dicoccoides* (Kawahara and Nevo 1996). Therefore, the present value can be regarded to be a good estimation of the frequency of spontaneous chromosomal mutation in cultivated Emmer.

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Wheat Information Service
Number 85: 47–48 (1997)
Research information

Transfer of rust resistance genes into high temperature and moisture stress tolerant genotype

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Kanchan and MP 938 are commercial, good yield potential, resistance to yellow rust and rainfed genotypes of wheat. Hindi 62 is a highly rust susceptible but high temperature and moisture stress tolerant genotype. An attempt was made to transfer unidentified yellow rust resistance from two hexaploid wheat genotypes of Kanchan and MP 938 into Hindi 62.

Cross of Kanchan and MP 938 with Hindi 62, were made at Wheat Research Experimental Area, Department of Plant Breeding and Genetics, Jawaharlal Nehru Agricultural University, Jabalpur (M.P.) during the year 1993-94. Resistant hybrids were back-crossed to recurrent parent (Hindi 62) and genotypes showing moderately resistance to leaf rust were constituted after two successive back crosses. Screening for rust resistance were made under natural epiphytotic conditions at Indira Gandhi Agricultural University, Regional Agricultural Research Station, Sarkanda, Bilaspur (M.P.) during rabi (winter season) 1996-97.

Table 1. Reaction of Kanchan, MP 938, Hindi 62 and their derivatives to rust and yield contributing characters.

Cross/varieties	Reaction to yellow leaf rust	Tillers per plant	Spike length (cm)	No.of grains per spike	1000 grain weight (g)
Kanchan	MR	4.00	11.41	54.72	42.50
MP 938	MR	4.47	10.40	55.72	35.89
Hindi 62	S	3.50	6.08	53.47	45.00
Hindi 62 / Kanchan	MR	7.90	11.82	58.19	32.19
Hindi 62 / MP 938	S	7.97	11.05	56.18	32.53

MR: Moderately resistance
S: Susceptible

The lines constituted from the respective cross between Hindi 62 and Kanchan was exhibited moderately resistance to yellow leaf rust.

It has been reported that rust resistance provided by single gene is not effective and durable resistance is provided only by a few gene combination (McIntosh 1988; Roelfs 1988; Roelfs et al. 1992).

Since the new line i.e. Hindi 62 x Kanchan was moderately resistant to leaf rust, it is possible that the resistance genes for leaf rust derived from the donor parents, i.e. Kanchan and MP 938 are linked to each other. While, Hindi 62 x MP 938 was still susceptible to leaf rust. The lines also indicated maximum values for yield contributing characters (Table 1).

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Wheat Information Service
Number 85: 49–51 (1997)
Research information

A reliable protocol for doubled haploid accelerated wheat breeding

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Doubling the chromosome number of haploids produces instant homozygotes called doubled haploids (DHs). These give rise to pure breeding lines that advance breeding programmes aimed at homozygosity by four to six generations. Furthermore, the recovery of a specific recombinant from x independently segregating loci is 2^x times more efficient with the DH method than with conventional genetic methods (Jensen 1977). The production of DHs from heterozygous material therefore became the preferred method for breeding autogamous crops (Bajaj 1990).

Wheat haploids can be produced by means of anther culture (Henry and De Buyser 1990) or by chromosome elimination following wide crosses (Barclay 1975, Laurie and Bennett 1988, Inagaki and Tahir 1990, Matzk and Mahn 1994). The 'wheat x maize' method is usually more reliable than anther culture (Kisana et al. 1993, Mujeeb-Kazi et al. 1995). Unfortunately most South African wheats responded poorly to the protocols generally employed.

The following protocol was developed over the past five years after evaluating 250 growth regulator solutions as wheat haploidizers (WHs), and 50 embryo rescue media (ERM) for their ability to regenerate plants from the induced haploid embryos. The method of Laurie and Reymondie (1991) served as control. This protocol resulted in up to 25 haploid embryos and 15 haploid plants per spike.

Protocol for DH production by the wheat x maize method

1. Plant the heterozygous wheat kernels in moistened, sand-filled 2-liter pots (2 kernels/pot) in a greenhouse with a 12-14 hour photoperiod on a 18°C day/12°C night cycle.
2. Plant the maize parent likewise in a greenhouse with a 16 hour photoperiod on a 28°C day/18°C night cycle. (We use a maize line developed from Seneca 60. Two pots are planted twice weekly. Anthesis occurs six weeks later. Four plants produce sufficient pollen per day for 20 wheat spikes).
3. After germination micro-irrigate (40 ml) the pots three to five times a day (depending on plant size and greenhouse temperature) with the nutrient solution of Maree (pers. commun.) to obtain luxuriant plants. This nutrient solution is made up by stirring 13 liters (l) of each of two stock solutions into a tank containing 1000 l water. Stock solution A consists of 540 g KNO_3, 1746 g KH_2PO_4, 1331 g K_2SO_4, 3375 g $MgSO_4$, 150 g Microplex (a commercial micro-element complex), and 1.5 l liquid NH_4NO_3 (19%) in 100 l water, whereas stock solution B consists of 5775 g $CaNO_3$ in 100 l water). Aphids are controlled with 2 g l^{-1} Gaucho 70 WS (Bayer), thrips with 2 g l^{-1} Mesurol (Bayer) plus 3 g sucrose, red spider with 0.35 ml l^{-1} Agrimec (Merck), and powdery mildew with 1g l^{-1} BAS-49015 (BASF) or 1 ml l^{-1} Afugan (AgrEvo) plus 1 ml l^{-1} Sporkill (Hygrotech) alternated with 2 g l^{-1} Diathane M.45 (Rohm & Haas). All sprays are

deleterious to embryo development and should be discontinued at least one week before pollination. Cover the wheat plants with a 50% shade screen during summer.

4. As soon as the primary spikes of healthy, vigorous plants have emerged from the boot, emasculate the two outer florets of their 15 best spikelets (enter from the side with the forceps). Remove the upper and the two basal spikelets as well as all the other florets. Cover the emasculated spikes with glassine or plastic bags and record the date of emasculation on the bags.
5. Remove the upper halves of the florets at the stage anthesis would normally have commenced, i.e. when the florets of the central spikelets begin to open (usually 3-5 days after emasculation).
6. Collect fresh maize pollen by tapping the tassels over a smooth sheet. Transfer the pollen and some dehisced anthers (to prevent pollen clogging) immediately to a small receptacle with a lid. Pollinate the wheat pistils liberally using a fine brush (0 Rolfes 279 Oron VC 1372, England, being the best). Replace the glassine or plastic bags with brown paper bags and record the date of pollination on the bags.
7. After 24-30 hours fill all the floral cups with the WH growth regulator solution by means of an insulin syringe to induce embryo formation (wear protective clothing). Cover the spikes again with the brown paper bags and record the treatment date. (The WHs which induce the most regenerable embryos are:

   WH10 = 30 mg l^{-1} picloram + 4 mg l^{-1} BA

   WH12 = 20 mg l^{-1} picloram + 25 mg l^{-1} 2,4,5-T + 6 mg l^{-1} BA

   WH13 = 50 mg l^{-1} 2,4-D + 100 mg l^{-1} GA_3.

   The WHs containing dicamba, e.g. WH6 (30 mg l^{-1} dicamba + 10 mg l^{-1} BA), induce high frequencies of embryos, but their regeneration is very poor).
8. Harvest the treated spikes 16-20 days after pollination if the greenhouse temperature is > 22°C, but at 21-25 days if it is < 18°C. (The spikes may be kept at 6°C for 24 hours in a plastic bag).
9. Remove the green parthenocarpic caryopses (GPCs) from the florets by bending them backwards with a forceps. This prevents damage to the attachment site; damage causes microbial contamination of the embryos. Discard the white and necrotic caryopses as they contain no embryos.
10. Surface sterilize the GPCs in sterile McCartney bottles by rinsing in 70% ethanol for 1 minute and then in 1% sodium hypochlorite for 10 minutes. Rinse four times in sterile distilled water, each lasting 3 minutes. (Changing solutions is facilitated by placing sterilized gauze over the mouths of the bottles).
11. Wearing sterile latex gloves, a mask and a watchmaker's 2x headband enlarger, excise the haploid embryos from the disinfected GPCs under a laminar flow hood. (Fine scalpels fashioned from discarded dentist's needles are best for this purpose; their surgical steel enables repeated flaming, and cooling in cold sterile water. Lift each green caryopsis from the McCartney bottle by inserting the sterilized scalpel into its attachment end. Hold the brush end between the thumb and forefinger and cut along the lateral grooves at the attachment end, fold back the dorsal pericarp and green integuments, and lift out the haploid embryo).
12. Five excised embryos are placed in each 100 ml tissue culture jar containing 20 ml of autoclaved ERM (the barley anther culture medium of Olsen (1987) modified by Daniel (1990) and us. This modified MS-medium contains 165 mg l^{-1} instead of 1650 mg l^{-1} NH_4NO_3, 20000 mg l^{-1} sucrose, 100 mg l^{-1} myo-inositol, 0.4 mg l^{-1} thiamine HCl, 0.5 mg l^{-1} BA, 1 mg l^{-1} IBA and 2300 mg l^{-1} Gelrite; the pH is adjusted to 5.8 with KOH).
13. Seal the transparent lids of the tissue culture jars containing the rescued embryos with clear plastic

wrap. Place the jars in the dark for 10 days at 6-8°C and then at 25°C until the regenerating shoots are 1 cm long. Transfer them to a 25°C growth cabinet with cool white fluorescent tubes on a 10 h light/14 h dark cycle. The regenerating plantlets reach the three leaf stage after four to six weeks.

14. Transplant the plantlets in micro-irrigated, sand-filled 2-liter pots (6-8 per pot) in a 16°C growthroom on a 10 h light/14 h dark cycle, and water once with a dilute seaweed extract (2 ml/l Kelpak) to stimulate growth. (Plantlets transplanted in a greenhouse should be covered with a 50% shade screen for a week).
15. Lift the plants from the pots as soon as they have developed two to three sprouts (usually after a month), and trim their washed roots to 10 cm. Treat the plants in an aerated (use an aquarium pump) aqueous solution of 0.05% colchicine (BDH), without DMSO, for 24 hours at 22°C. Rinse the plants in running water for an hour and transfer them to aerated water in a refrigerator at 4°C for three days. (The colchicine solution can be used again; filter and store in a refrigerator).
16. The shoots of the treated plants are cut back to 15 cm and the plants repotted (2-3 per pot) in the 16°C growthroom. Water once with the Kelpak solution.
17. After 4-6 weeks the ± 95% plants that survived the colchicine treatment will have formed new shoots. Transfer the potted spring wheats to a greenhouse on a 18°C day/12°C night cycle, but vernalize the winter wheats first for at least six weeks at 4°C.
18. Nearly all the colchicine treated plants will produce a few spikes with fertile doubled haploid (DH) sectors. Cover the fertile spikes to prevent cross pollination. These spikes will give rise to homozygous DH lines from which new cultivars can be selected.

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Wheat Information Service
Number 85: 52–55 (1997)
Proposal

Nomenclature in Triticeae with emphasis on D genome diploid species

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Yen et al. (1997), in the latest issue of WIS (No. 84: 56-59), discussed the issue of nomenclature of D genome diploid species of the tribe Triticeae. This was necessitated to clarify the confusion due to the common usage of two different names, namely *Aegilops squarrosa* L. and *Triticum tauschii* (Cosson) Schmal for the same species (D genome diploid species). The issue is also partly relevant to a bigger question asking whether *Aegilops* L. be retained as a separate genus or merged in an enlarged genus *Triticum* L. emend Bowden. We earlier discussed this issue in some detail (Gupta and Baum 1986), which escaped the attention of Yen et al. (1997), while dealing with the problem. Therefore, we like to add to the present discussion, the genesis of the recent usage of the name *T. tauschii* for D genome species in preference to *Ae. squarrosa* by a group of cytogeneticists during the last more than 35 years. Yen et al. (1997), while outlining the history of the nomenclature of D genome species, emphasized that *Ae. tauschii* and *T. tauschii* are both valid scientific names for the D genome diploid species. However, the usage of *T. tauschii* for the D genome diploid species in recent years is neither due to the validity and/or priority of this name, nor due to rejection of *Ae. squarrosa* as an illegitimate name. Instead, the known evolutionary history of bread wheat, and the nomenclature of hybrids, were used to suggest that the complete genus *Aegilops* be merged in an enlarged genus *Triticum*. Consequently, *T. tauschii* was suggested as the new name for the erstwhile popular, though illegitimate name, *Ae. squarrosa*.

As discussed by us earlier (Gupta and Baum 1986), Bowden (1959) regarded hexaploid wheat, *T. aestivum* L. as a hybrid for nomenclatural purposes. Since at that time the three diploid progenitors of hexaploid bread wheat were known to be *T. monococcum*, *Ae. speltoides* and *Ae. squarrosa* with some certainty, Bowden (1959) argued as follows: "the parents of hybrids or the parents of species of hybrid origin and the hybrids or the species of hybrid origin must be included in separate taxa at the same rank". Therefore, he had two options, either to place tetraploid wheat, hexaploid wheat and the three diploid progenitors in separate genera (same rank at the generic level), or in separate species of the same genus (same level at the species level). He accepted the latter alternative to allow minimum disturbance to the existing species of the genus *Triticum*. Consequently, he proposed that *Ae. speltoides* and *Ae. squarrosa* be treated as species within the genus *Triticum*. This was done by merging the whole genus *Aegilops* into an enlarged genus *Triticum* L. emend Bowden. Consequently, new names were proposed for all diploid and polyploid *Aegilops* species. We realized that the above argument used by Bowden (1959) was

applicable only to nothogenera, and not to the established botanical genera like *Triticum* L. and *Aegilops* L. (Gupta and Baum 1986). We, therefore, believed that it was neither necessary nor appropriate to merge *Aegilops* with *Triticum*, by treating *Triticum aestivum* as a hybrid that originated from three diploid species. Our contention found support from a note in the Article H.3.4. of the code, which reads as follows: "taxa, which are believed to be of hybrid origin need not be designated as nothotaxa".

In view of the above, as emphasized by us earlier (Gupta and Baum 1986), we support the view that *Aegilops* L. be recognized as a valid independent genus. Therefore, the question remains whether the D genome diploid species is *Ae. tauschii* Cosson or *Ae. squarrosa* L. Since *Ae. squarrosa* L. is an illegitimate name for D genome diploid species as pointed out by Yen et al. (1997), *Ae. tauschii* Cosson is the only correct name for D genome species, if *Aegilops* is retained as an independent genus, and if D genome diploid species are included in this genus. However, since in scientific literature and also in text books, *Ae. squarrosa* is being used for a long time as a popular name for the D genome diploid species, it will again cause lot of confusion, if this popular name is replaced by the botanically correct name *Ae. tauschii* Cosson. We, therefore, suggest that for D genome diploid species, the name *Ae. squarrosa* with a new type specimen be conserved and *Ae. tauschii* with its type specimen be rejected. This should be possible under Article 14 of the code, which allows conservation against both homotypic as well as against rejected heterotypic synonyms. Fortunately, in the Tokyo code the scope of conservation of taxa at the species level has been widened to allow conservation of even those species that are of no economic value. Earlier, while conserving the name *T. aestivum* for bread wheat, against *T. hybernum*, which had priority, rules of nomenclature under ICBN were modified to allow for the conservation of names of only the economically important species (Karguelen 1980). The Tokyo code also provides for rejection of any name (irrespective of rank), that would cause disadvantageous nomenclatural change. Therefore, it should be possible to reject *Ae. tauschii* Cosson, since its adoption as the valid name for D genome diploid species will certainly cause disadvantageous nomenclatural change. Actually. at the Tokyo congress, the Nomenclature Section made it clear that "indulging in futile name changes (in the present case from *Ae squarrosa* to *Ae. tauschii*) in the future is reprehensible unless the new conservation/rejection avenues have previously been explored and found to be unhelpful" (Nicolson and Greuter 1994).

While examining the question of nomenclature of the D genome diploid species, we also need to address to the question of large scale destabilization of generic names in the tribe Triticeae. We recognized two main reasons for destabilization of names in the Triticeae (Gupta and Baum 1989); the first is due to changing taxonomy and the second is due to application of the rules laid down in ICBN. One would accept that continuous generation of information and its desired input in taxonomy may require changes in classification and therefore in the names of taxa.. Therefore, we should strive for a stable classification that would require minimum changes in the names of taxa . This is possible only when maximum information from all disciplines is used for classification. Unfortunately, this has not been done and cytogeneticists in the past always suggested newer classifications with altered names of taxa. The most conspicuous of these classifications are the genomic systems of classification suggested by Love (1984) and Dewey (1984), who suggested

that each taxon with a novel genomic constitution be recognized as a separate genus. Consequently, Love (1984) defined 38 independent genera in the tribe Triticeae. In this classification, Love (1984) grouped diploid wheats (A genome) into a separate genus *Crithodium* Link, and tetraploid wheats (AB genomes) into the new genus *Gigachilon* Seidl, thus leaving only hexaploid wheats in the genus *Triticum*. The 38 genera of Triticeae proposed in this genomic system of classification included 13 new genera to accommodate the different species of the traditional genus *Aegilops* L., which on the other extreme, was once merged with *Triticum*. Under this new system, *Ae. squarrosa* L., the D genome diploid species, has been placed in a new genus *Patropyrum* A. Love. However, we criticized earlier this genomic system of classification (Baum et al. 1987), and fortunately as a relief to the non-taxonomist users of these taxa, the new names did not find any wide usage. It is, thus, obvious that major destabilization in the common traditional names can sometimes be caused by a new system of classification. It is, therefore, suggested that changes in classification, if absolutely necessary, be proposed on the basis of maximum information, and not on the basis of limited information as done in genomic system of classification. Therefore, any destabilization in the names due to changes in classification may be difficult to control, but needs to be restricted by not using such classifications.

The second reason for destabilization of names is the application of nomenclatural rules, which have been modified from time to time, to provide for stability in the names of taxa. For instance, in Tokyo code, a provision has been made for conservation of names of species without any restriction (earlier the names of only species of economic importance could be conserved). As a means to provide stability of names , Brummitt (1987) also proposed the preparation of lists of "Names in Common Use or NCUs", which would take precedence over any names not so listed. At least three such lists of NCUs have already been published. The issue of NCUs, which was deferred in Tokyo congress, is likely to be approved in 1999 congress to be held at St. Louis, Missouri, USA.

In conclusion we may like to say, that although there is lot of confusion in the tribe Triticeae due to frequent changes in the names of taxa, the steps being taken by the Nomenclature Section of the International Botanical Congress will go a long way in providing stability of names by discouraging changes in names, wherever the new conservation/rejection avenues and the lists of NCUs can be helpful. It may be useful to give a call to wheat workers through the medium of WIS that only the name *Ae. squarrosa* be used for the D genome species and that restrain may be exercised in using altered names, whenever proposed. It may also be desirable to persuade the organizers of the 9th International Wheat Genetics Symposium (IX IWGS, to be held in Saskatoon, Canada, during August 2-7, 1998), to organize a workshop on the nomenclature and taxonomy of the tribe Triticeae, so that the nontaxonomist users of nomenclature become aware of the dangers and implications of using new names.

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Wheat Information Service
Number 85: 56–81 (1997)
Gene symbol

Catalogue of gene symbols for wheat: 1997 Supplement

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The most recent edition of the Catalogue (9441) appears in the Proceedings of the 8th International Wheat Genetics Symposium held in Beijing, China, 1993, pp. 1333-1500. Revised Guidelines for Nomenclature of Biochemical/Molecular Loci (including QTLs) in Wheat and Related Species were included with the 1994 Supplement. Further proposals were included in the 1995 and 1996 Supplements.

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

As the Catalogue evolves, the co-ordinators do not always make appropriate changes to past entries. Researchers and readers are encouraged to advise updatings and errors to make the Catalogue more useful to others. This is now particularly important as a complete review of the Catalogue is planned for 1998.

Additions and revisions to symbols list ('Summary Table 1' in the 1995 Catalogue of Gene Symbols for Wheat):

Ald	Chloroplastic aldolase
Alt	Aluminum tolerance
bh	Branched spike
Caa	Carbonic anhydrase
Cat0	Catalase isozyme 1
Cdu	Cadmium uptake: low cadmium uptake
Cyc	Cyclophilin
Fbpa	Fructose bisphosphatase aldolase
Fedr	Ferredoxin $NADP^+$ reductase
Gapd3	Glyceraldehyde-3-phosphate dehydrogenase
GapA	Cytosolic mRNA of chloroplast glyceraldehyde-3-phosphate dehydrogenase
Gdd	P subunit of glycine decarboxylase multi-enzyme complex
Glp3	Germin-like protein 3
Gpc	Grain protein content
Hmgp	High mobility group protein
Hrp	NAPH-dependent hydroxypyruvate reductase
Hsp70	Heat shock protein 70
Hsp82	Heat shock protein 82
Lhcb1	Light harvesting chlorophyl a/b binding protein
Lhcb3	Light harvesting complex for type III LHCII CAB precursor protein
Lhcb4	Chlorophyl a/b-binding protein (Lhcb4 gene)

Lhcb5	CP29 precursor for core chlorophyll a/b binding protein of PS II
L13	Chloroplast ribosomal protein L13
Pgk1-1	Replaces '*Pgk1*'
Pgk2-1	Replaces '*Pgk2*'
Pp	P protein
Prk	Ribulose-5-phosphate kinase
Psah	10.2kDa PS I polypeptide
Psk-1	Chloroplast photosytem I PSK-I subunit
PuiA	Puroindoline-a
Rbca	Rubisco activase
Sam	S-adenosylmethionine decarboxylase
Sdh	Succinate dehydrogenase
Sgp	Starch granule protein
Tel	Telomere
Tsc	Reaction to *Pyrenophora tritici-repentis*: resistance to chlorosis induction
Xdh	Xanthine dehydrogenase
17kD	17kDa protein
60S	60S ribosomal protein

Additions to Laboratory Designators List

scs (*S. cereale* SSRs)
Gustafson, P.
Dept. of Agronomy
208 Curtis Hall
University of Missouri-Columbia
Columbia, Missouri 6521
USA

wmc (wheat microsatellites)
Isaac, Peter G.
Agrogene
620 rue Blaise Pascal
Z.I. 77550
Moissy Cramayel
France

Gross Morphology

Spelt

Q was physically mapped in 5AL to fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23 (9756).

Branched spike

Synonymns: branched head, four-rowed spike, supernumerary spikelet, tetrastichon spikelet.
bh (9701). 2AS (9701). **dv:** PI 349056 (9701).

Elongated Glume (Revised section)

Elongated glume is the phenotype associated with the polonicum group of tetraploid wheats. Expression in hexaploid wheat is much reduced compared with tetraploids. Matsumura (9537) reported linkage of gene *P* and a gene for red coleoptiles implicating chromosomes 7A or 7B.

P (9537). *Eg* (9427). 7AL (9427; 9727). **i:** Saratovskaya29*8//Novsibirskaya 67*2/*T. polonicum* (9427).

itv: P-LD222 = LD222*11/*T. turgidum* var. *polonicum* (9538, 9727).

Aluminum Tolerance

Alt2 (9757). [Alt_{BH} (9758)]. 4DL (9757). **su:** *T. turgidum* cv. Langdon 4D(4B) (9757).
ma: *Alt2* was mapped to a 4 cM interval flanked by *Xpsr914* and *Xpsr1051* (9757) on a consensus 4B-4D map of *T. aestivum*.
ma: *Alt2* and *Xbcd1230* are linked by 1.1 cM (9758).

Anthocyanin Pigmentation

3. Red/purple coleoptiles

Add below the *Rc3* section:
'**ma:** *Rc3* was mapped 3 cM distal of *Xpsr108* (140).'

4. Purple/red culm/straw/stem.

Add below the *Pc1* section:
'**ma:** *Pc* was mapped 5.7 cM proximal of *Xpsr490*(*Ss1*) (9739)[2].'

Blue Aleurone

Add:
'4A^{m}L (96119)[3].'
'The *Ba* allele in *T. monococcum* spp. *aegilopoides* acc. G3116 determines a half-blue seed phenotype and is different from the solid blue allele present in *Elytrigia pontica* (96119).'
'**ma:** Cosegregation was observed between *Ba, Xcdo1387, Xmwg677* and *Xbcd1092.*'

Cadmium Uptake

Low Cadmium Uptake

Cdu1 (9705). *Cdu1* (9704). **dv:** Biodur (9704); Hercules(9704); Nile (9704).

Cdu1 (9705). *cdu 1* (9704). **dv:** Kyle (9704).

ma: *Cdu1 - OPC-20* 4.6cM (9704).
Cdu1 - UBC-180 21.2 cM (9704).

Chlorophyll Abnormalities

2. Chlorina

cn-A1d (9701). **dv:** CDd6 (9701, 9702).
cn-B1a (9701). **dv:** CDd1 (9701, 9702); CBC-CDd1 (9701).

cn-B1b (9701). dv: CDd2 (9701, 9702).

Crossability with Rye and *Hordeum* spp

kr1 kr2 v: Martonvársári 9*4/Chinese Spring (9724).

Kr1 Kr2/Kr1 kr2 (heterogeneous). v: Martonvársári 9 (9724).

Meiotic Characters

2. Pairing homoeologous

Ph1 was physically mapped in 5BL to fraction length 0.55, bracketed by deletions 5BL-1 and *ph1b* (9756).

DNA Markers:

Add at the end of the preamble:
'a' Designates primer pairs that identify loci that cap the genetic maps. The forward primer is a degenerate telomeric sequence and the reverse primer is a specific sequence. Each primer combination identified multiple loci; however, only telomeric (*Tel*) loci are included (9742).'
'b' Designates loci whose functions were identified through homology with known genes in the EMBL database (9754).'

STS's from RFLP clones: Several new STS markers are listed this year using sequences from previously listed RFLP clones. The convention adopted is to add a '*p*' to the later descriptor. The 'References' to PCR markers refer, however, to the paper(s) which reported the first chromosomal location detected by this PCR marker.

Group 1S

Revise:
Xcdo388; Add '5D' in the last column.
Xpsr161-1A,B,D; Replace with '*Xpsr161(Hsp70)-1A,B,D* [950][b]' and add '[*Xpsr161-1A,B,D* (950)].' in second column.
Xpsr168-1A,B,D; Replace with '*Xpsr168(Hmgp)-1A,B,D* [1130,1129][b]' and add '[*Xpsr168-1A,B,D* (1130,1129)].' in second column.

Add:

Xpsp2530(Tel)-1B.1 (9742).	T4/PSP2530R[a].	
Xpsp3003-1A (9741,9743).	PSP3003F/PSP3003R.	(7D).
Xpsp3027-1A (9741,9743).	PSP3027F/PSP3027R.	
Xpsp3151-1A (9741,9743).	PSP3151F/PSP3151R.	
Xwms30-1A (9736).	WMS30F/WMS30R.	
Xwms33-1A (9736).	WMS33F/WMS33R.	

Group 1L

Revise:

Xbcd508; Add '5D' in the last column.
Xpsr159-1A,B,D; Replace with '*Xpsr159(Psah)-1A,B,D* [1130,1129][b].' and add '[*Xpsr159-1A,B,D* (1130,1129)].' in second column.
Xpsr462(Pgk1)-1A,B,D; Replace with '*Xpsr462(Pgk1-1)-1A,B,D* [138].' and add '[*Xpsr462(Pgk1)-1A,B,D*].' to second column.

Add:

Xpsp3100-1B (9741,9743).	PSP3100F/PSP3100R.	
Xpsp3137-1D (9741,9743).	PSP3137F/PSP3137R.	
Xpsp3139-1D (9743).	PSP3139F/PSP3139R.	
Xpsr172(Lhcb1)-1A (9754).	PSR172.	(5A,B,D, 7A,B,D).
Xwms11-1B (9736).	WMS11F/WMS11R.	
Xwms24-1B (9736).	WMS24F/WMS24R.	
Xwms33-1B (9736).	WMS33F/WMS33R.	

Group 1

Add:

XGluTR-1A,B,D (9735).	BHA87.	
Xabcp158-1D (9744).	ABC158F/ABC158R.	(3D, 6D).
Xabcp253-1A (9744).	ABC253F/ABC253R.	(3B, 4B,D).
Xabgp358-1A (9744).	ABG358F/ABG358R.	
Xabgp712-1A (9744).	ABG712F/ABG712R.	(2A,B,D).
Xcdop312-1A (9744).	CDO213F/CDO213R.	(4B, 7D).
Xcdop673-1A (9744).	CDO673F/CDO673R.	
XksupD15-1D (9744).	KSUD15F/KSUD15R.	(5B,D, 7B,D).
XksupM148-1B (9744).	KSUM148F/KSUM148R.	(2A, 4B,D, 6B).
Xpsp3004-1D (9741).	PSP3004F/PSP3004R.	
Xpsp3136-1A (9741).	PSP3136F/PSP3136R.	

Group 2S

Revise:
Xpsr100-2A,B,D; Replace with '*Xpsr100(60S)-2A,B,D* [186][b].' and add '[*Xpsr100-2A,B,D* (186)].' in second column.
Xpsr107-2A,B,D; Replace with '*Xpsr107(Lhcb4)-2A,B,D* [186][b].'and add '[*Xpsr107-2A,B,D* (186)].' in second column.
Xpsr108-2A,B,D; Replace with '*Xpsr108(Glp3)-2A,B,D* [952,9547][b].' and add '[*Xpsr108-2A,B,D* (952,9547)].' in second column.
Xpsr135-2A,B,D; Replace with '*Xpsr135(17kD)-2A,B,D* [950,186][b].' and add '[*Xpsr135-2A,B,D* (950,186)].' in second column.
Xpsr143-2A; Replace with '*Xpsr143(Lhcb3)-2A* [186][b].'and add '[*Xpsr143-2A* (186)].' in second column.
Xpsr150-2A,B,D; Replace with '*Xpsr150(Hsp82)-5A,B,D* [186][b].' and add '[*Xpsr150-2A,B,D* (186)].' in second column.

Add:

Xpsp2152(Tel)-2D.1 (9742).	T4/PSP2152R[a].	
Xpsp2152(Tel)-2B.10 (9742).	PSP2159F/PSP2152R[a].	
Xpsr2152(Tel)-2D.1 (9742).	PSR2152.	(3B).
Xpsp3058-2D (9743).	PSP3058F/PSP3058R.	(4A, 6D).
Xpsp3142-2A (9743).	PSP3142/PSP3142R.	(4A).
Xpsp3153-2A (9741,9743).	PSP3153/PSP3153R.	
Xwms10-2A (9736).	WMS10F/WMS10R.	

Group 2L

Revise:
Xcdo388: Add '5D' in the last column.
XksuF1: Add '2B,D' to the last column entry.
Xpsr101-2A,B,D; Replace with '*Xpsr101(Psk-1)-2A,B,D* [950][b].' and add '[*Xpsr101-2A,B,D* (950,9754)].' in second column.
Xpsr102-2A,B,D; Replace with '*Xpsr102(Sam)-2A,B,D* [952,186][b].'and add '[*Xpsr102-2A,B,D* (952,186)].' in second column.
Xpsr151-2A,B,D; Replace with '*Xpsr151(GapA)-2A,B,D* [186][b].' and add '[*Xpsr151-2A,B,D* (186).' in second column.

Add:

Xglkp605-2B (9738).	AWP1-U,AWP2-U,AWP3-U/AWP1-L, AWP2-L,AWP3-L.	
Xpsp2151(Tel)-2A.3 (9742).	PSP2159F/PSP2151R[a].	
Xpsp3029-2A (9743).	PSP3029F/PSP3029R.	(6AS,AL).
Xpsp3034-2B (9743).	PSP3034F/PSP3034R.	(7B).
Xpsp3039-2A (9743).	PSP3039F/PSP3039R.	
Xpsp3088-2A (9741,9743).	PSP3088F/PSP3088R.	
Xwms10-2B (9736).	WMS10F/WMS10R.	
Xwms30-2D (9736).	WMS30F/WMS30R.	

Group 2

Revise:
Xglk222-2D; Add '(5B).' in the last column.
Xpsr148-2A,B,D; Replace with '*Xpsr148(Cat0)-2A,B,D* [27][b].' and add '[*Xpsr148-2A,B,D* (274)].' in second column.

Add:

Xabgp58-2B (9744).	BG058F/ABG058R.	(5B, 7B).
Xabgp317-2D (9744).	ABG317F/ABG317R.	
Xabgp602-2B,D (9744).	ABG602F/ABG602R.	
Xabgp712-2A,B,D (9744).	BG712F/ABG712R.	(1A).
Xbcdp129-2B (9744).	BCD129F/BCD129R.	
Xbcdp175-2B,D (9744).	BCD175F/BCD175R.	
XksupE8-2B (9744).	SUE8F/KSUE8R.	(4D, 6B, 7D).

XksupF15-2A,B (9744).	SUF15F/KSUF15R.	(3A, 6A,B,D).
XksupG12-2B,D (9744).	KSUG12F/KSUG12R.	
XksupM148-2A (9744).	SUM148F/KSUM148R.	(1B, 4B,D, 6B).
Xpsp3023-2A (9741).	PSP3023F/PSP3023R.	
Xpsp3030-2B (9741,9743).	PSP3030F/PSP3030R	.(3B, 4B).
Xwms47-2 (9736).	WMS47F/WMS47R.	

Group 3S

Delete:

Xabg395-3A (96119)[3].	ABG395.	

Add:

Xpsp2152(Tel)-3B.3 (9742).	PSP2153F.1/PSP2152R[a].	
Xpsr2152(Tel)-3B.2 (9742).	PSR2152.	(2D).
Xpsp3030-3B (9741,9743).	PSP3030F/PSP3030R.	(2B, 4B).
Xpsp3047-3A (9741,9743).	PSP3047F/PSP3047R.	
Xwms2-3A (9736).	WMS2F/WMS2R.	
Xwms5-3A (9736).	WMS5F/WMS5R.	
Xwms10-3A (9736).	WMS10F/WMS10R.	

Group 3L

Revise:

Xpsr56-3A,B,D; Replace with '*Xpsr56(Caa)-3A,B,D* [182][b].' and add '[*Xpsr56-3A,B,D* (182)].' in second column.

Xpsr116-3A,B,D; Replace with '*Xpsr116(Pp)-3A,B,D* [182][b].' and add '[*Xpsr116-3A,B,D* (182)].' in second column.

Xpsr156-3A,B,D; Replace with '*Xpsr156(L13)-3A,B,D* [950,949][b].' and add '[*Xpsr156-3A,B,D* (950,949)].' in second column.

Xpsr170-3A,B,D; Replace with '*Xpsr170(Fbpa)-3A,B,D* [182][b].' and add '[*Xpsr182-3A,B,D* (182)]'. in second column.

Add:

Xpsp3001-3B (9743).	PSP3001F/PSP3001R.	(7AS,AL).
Xpsp3035-3B (9741,9743).	PSP3035F/PSP3035R.	(7D).
Xpsp3078-3B (9741,9743).	PSP3078F/PSP3078R.	(4B).
Xpsp3144-3B (9741,9743).	PSP3144F/PSP3144R.	
Xpsr138(Sbp)-3A,B,D (9754).	PSR138.	
Xpsr171(Gdd)-3A,B,D (9754).	PSR171.	
Xwms3-3D (9736).	WMS3F/WMS3R.	

Group 3

Add:

Xabcp158-3D (9744).	ABC158F/ABC158R.	(1D, 6D).
Xabcp253-3B (9744).	ABC253F/ABC253R.	(1A, 4B,D).

Xabcp309-3D (9744).	ABC309F/ABC309R.	(6A).
Xabcp602-3B,D (9744).	ABC602F/ABC602R.	
Xabgp378-3B,D (9744).	ABG378F/ABG378R.	
XbarpG10-3B (9744).	BarG10F/BarG10R	(4B).
XksupF15-3A (9744).	KSUF15F/KSUF15R.	(2A,B, 6A,B,D).
Xpsp3012-3B (9741).	PSP3012F/PSP3012R.	
Xpsp3019-3D (9741,9743).	PSP3019F/PSP3019R.	
Xpsp3059-3B (9741).	PSP3059F/PSP3059R.	
Xpsp3080-3A (9741).	PSP3080F/PSP3080R.	
Xpsp3107-3A (9741).	PSP3107F/PSP3107R.	

Group 4AL : 4BS : 4DS

Revise:
XksuG12: Add '5D' in the last column.
Xpsr144-4A,B,D; Replace with '*Xpsr144(Lhcb5)-4A,B,D* [949][b].' and add '[*Xpsr144-4A,B,D* (949)].' in second column.
Xpsr147-4A,B,D; Replace with '*Xpsr147(Ald)-4A,B,D* [585][b].' and add '[*Xpsr147-4A,B,D* (585)].' in second column.
Xpsr155-4A,B,D; Replace with '*Xpsr155(Rbca)-4A,B,D* [9541][b].' and add '[*Xpsr155-4A,B,D* (9541)].' in second column.

Add:

Xmgb343-4B (9739)[2].	MGB343.	
Xpsp3078-4B (9741,9743).	PSP3078F/PSP3078R.	(3B).
Xpsp3079-4D (9743).	PSP3079F/PSP3079R.	(6B, 7D).
Xpsp3103-4D (9741,9743).	PSP3103F/PSP3103R.	
Xpsp3142-4A (9743).	PSP3142F/PSP3142R.	(2A).
Xpsr622-4A (96125),4B (9739)[2].	PSR622.	
Xwms18-4B (9736).	WMS18F/WMS18R.	

Group 4AS : 4BL : 4DL

Revise:
Xcdo1312; Add '5B' in the last column.
Xpsr104-4A,B,D; Replace with '*Xpsr104(Fbp)-4A,B,D* [952][b].' and add '[*Xpsr104-4A,B,D* (952)].' in second column.

Add:

Xpsp2152(Tel)-4B.9 (9742).	PSP2159F/PSP2152R[a].	
Xpsp2152(Tel)-4B.12 (9742).	PSP2156F/PSP2152R[a].	
Xpsp3007-4D (9743).	PSP3007F/PSP3007R.	
Xpsp3030-4B (9741,9743).	PSP3030F/PSP3030R.	(2B, 3B).
Xpsp3058-4A (9743).	PSP3058F/PSP3058R.	(2D, 6D).
Xpsp3112-4D (9741,9743).	PSP3112F/PSP3112R.	
Xwms6-4B (9736).	WMS6F/WMS6R.	
Xwms6-4D (9736).	WMS6F/WMS6R.	

Group 5AL : 4BL : 4DL

Revise:
Xpsr164-5A,4B,D; Replace with '*Xpsr164(Gadp3)-5A,4B,D* [585,1189][b].' and add '[*Xpsr164-5A,4B,D* (585,1189)].' in second column.

Group 4

Revise:
Xglk354; Add '5D' in the last column.

Add:

Xabcp253-4B,D (9744).	ABC253F/ABC253R.	(1A, 3B).
Xabgp391-4A (9744).	ABG391F/ABG391R.	(5A,B,D).
Xabgp618-4A (9744).	ABG618F/ABG618R.	(7D).
Xabgp704-4A (9744).	ABG704F/ABG704R.	(7A).
Xabgp715-4A,B (9744).	ABG715F/ABG715R.	
XbarpG10-4B (9744).	BarG10F/BarG10R.	(3B).
Xcdop213-4B (9744).	CDO213F/CDO213R.	(1A, 7D).
XksupD16-4A (9744).	KSUD16F/KSUD16R.	(5B).
XksupE8-4D (9744).	KSUE8F/KSUE8R.	(2B, 6B, 7D).
XksupG49-4A (9744).	KSUG49F/KSUG49R.	(7D).
XksupM148-4B,D (9744).	KSUM148F/KSUM148R.	(1B, 2A, 6B).
Xpsp3061-4A (9741).	PSP3061F/PSP3061R.	
Xpsp3124-4D (9741).	PSP3124F/PSP3124R.	
Xpsp3159-4A (9741).	PSP3159F/PSP3159R.	
Xpsp3163-4B (9741).	PSP3163F/PSP3163R.	
Xwgp181-4B (9744).	WG181F/WG181R.	
Xwgp232-4A,D (9744).	WG232F/WG232R.	(6B, 7A).
Xwgp530-4A (9744).	WG530F/WG530R.	
Xwgp564-4B,D (9744).	WG564F.2/WG564R.2.	

Group 5AS : 5BS : 5DS

Delete previous entry and substitute:

Xcdo677-5A (96119)[3],(9756)[1], *5D* (9756)[1].	CDO677 (24). [*pAscnlcdo677* (9756)].

Revise:
Xabg705; add '(9756)[1]' as reference for *Xabg705-5A,* add '*Xabg705-5D* (9756)[1]' as another locus, and add '[*pHvabg705* (9756)].' to the last column.
XksuG44; add the following comment, 'In physical mapping studies of *T. aestivum* (9756), no *XksuG44* loci were detected in the 5S arms but *XksuG44-5A, XksuG44-5B.1, XksuG44-5B.2,* and *XksuG44-5D* were located in the 5L arms.
XksuH8: add '*XksuH8-5B* (9756)[1]' as another locus, add '[*pHvksuH8* (9756)].' to the last column and add '(5B).' in the last column for the 4A, 7AS, 7AL, 7BS, and 7DL *XksuH8* entries.
Xpsr118-5A,B,D; Replace with '*Xpsr118(Ald)-5A,B,D* [949,1179][b].' and add '[*Xpsr118-5A,B,D* (949,1179)].' in second column.

Xpsr170-5A,B,D; Replace with '*Xpsr170(Fbpa)-5A,B,D* [182,1179][b].' and add '[*Xpsr170-5A,B,D* (182,1179].' in second column.

Add:

Xabg395-5A (96119)[3]. ABG395.

Xcdo687-5B (9756). CDO687. [*pAscnlcdo687* (9756)].

Xcdo1335-5A,B,D (9756). CDO1335 [*pAscnlcdo1335* (9756)].

XcsSR3(Gsp)-5A (96119)[3]. pGsp (9753).

Xgsp-5A,B,D (9756). pgsp (9756).

Xglk317-5A.1,.2 (594), 5A(9756). [*Xglk217a,b* (594), *Tag317* (9756)]. pTag317 (594). (6A).

Xglk319-5A (9756), *5B* (594,9756), *5D* (9756). [Tag319 (9756)]. pTag319.

XksuG60-5B (9756). [*ksug60-6B* (9756)]. pTtksuG60. [*pTtksug60* (9756)].

XksuI26-5B (9756)[1], 5D (309)[4],(9756)[1]. [*ksui26* (9756)]. pTtksuI26 (309). [*pTtksui26* (9756)].

Xpsp2152(Tel)-5D.2 (9742). T4/PSP2152R[a].

Group 5AL : 5BL : 5DL

Revise:

Xbcd157; Add '*Xbcd157-5D* (9756).' in the first column and add '[*pHvcnlbcd157* (9756)].' as a snyonym for the probe.

Xbcd351; Add '*Xbcd351-5B,D* (9756).' to the first column, add '[*pHvcnlbcd351* (9756)].' as a synonym for the probe, and add the following comment, 'Two *Xbcd351-5A* loci were reported in 9756.'

Xbcd450; Add '*Xbcd450-5A* (9756)' in the first column and add '[*pHvcnlbcd450* (9756)].' as a synonym for the probe.

Xbcd508; Add '*Xbcd508-5D.1,.2* (9756)' to the first column and add '[*pHvcnlbcd508* (9756)]' as a synonym for the probe.

Xcdo57; add'*Xcdo57-5B* (9756)' to the first column, add '[*pAscncdo57* (9756)].' as a snyonym for the probe, and add '(5B).' in the last column for the 2A, 7A, 7B, and 7D *Xcdo57* entries.

Xcdo504-5A,B; Add '(96119)[3]' as a reference for *Xcdo504-5A*.

Xcdo786; Add '*Xcdo786-5D* (9756)' in the first column and add '[*pTscnlcdo786* (9756)].' as a snyonym for the probe.

Xcsc2(Dhn2); Add '*Xcsc2(Dhn2)-5B,D* (9756)' in the first column, add '*dhn-5B,D* (9756)' in the second column and add '[*dhn2* (9756)].' as a synonym for the probe.

XksuF1; Add '*XksuF1-5B,D* (9756)[1]' in the first column.

XksuG7; Add '*XksuG7-5A* (9756)[1]' in the first column.

XksuG14: Add '*XksuG14-5B,D* (9756)[1]' in the first column.

Xmwg522; Add '*pTamwg522-5B* (9756)' in the first column and add '[*pTamwg522* (9756)].' as a snyonym for the probe.

Xwg530; Add '*Xwg530-5B,D* (9756)' in the first column and add'[*pTacnlwg530* (9756)].' as a synonym for the probe.

Xpsr100-5A,B,D; Replace with '*Xpsr100(60S)-5A,B,D* [186][b].' and add '[*Xpsr100-5A,B,D* (186)].'

in second column.
Xpsr145-5A,B,D; Replace with '*Xpsr145(Xdh)-5A,B,D* [585,1179][b].' and add '[*Xpsr145-5A,B,D* (585,1179)].' in second column.
Xpsr147-5A,B,D; Replace with '*Xpsr147(Ald)-5A,B,D* [274][b].' and add '[*Xpsr147-5A,B,D* (274)].' in second column.
Xpsr150-5A,B,D; Replace with '*Xpsr150(Hsp82)-5A,B,D* [585][b].' and add '[*Xpsr150-5A,B,D* (585)].' in second column.
Xwg644; add '*Xwg644-5B,D* (9756)' in the first column and add '[*pTacnlwg644* (9756)].' as a synonym for the probe.
Xwg889; add '*Xwg889-5D* (9756)' in the first column and add '[*pTacnlwg889* (9756)].' as a snyonym for the probe.
Xwg908; add '*Xwg908-5B.1,.2, 5D* (9756)' in the first column, add [*Xwg908-5Ba,5Bb* (9756)].' in the second column, and add '[*pTacnlwg908* (9756)].' as a synonym for the probe.
Xwg1026; add '*Xwg1026-5B,D* (9756)' in the first column and add '[*pTacnlwg1026* (9756)].' as a synonym for the probe.

Delete corresponding previous entries and substitute:

Xbcd204-5A (96119)[3],(9756)[1], 5B.1,5B.2,5D (9756)[1].		BCD204 (24). [*pHvcnlbcd204* (9756)].	
Xcdo1049-5A (96119)[3],(9756), 5B,D (9756)[1].		CDO1049 (24). [*pAscnlcdo1049* (9756)].	
Xcdo388-5A (96119)[3],(9756)[1], 5D (9756)[1].	[*cdo388-5Db* (9756)].	CDO388 (24). [*pAscnlcdo388* (9756)].	
XksuD30-5A,B (9756), *5D* (9657,9756).	[*ksud30* (9756)].	pTtksuD30. [*pTtksud30* (9756)].	
Xpsr628-5A,B,D (9756).		PSR628. [*pTapsr628* (9756)].	
Xwg909-5A (9756), *5B* (9657,9756), *5D* (9756).		WG909 (96124). [*pTacnlwg909* (9756)].	(7B).
Xwg583-5A (9756), *5B* (9657), *5D* (9756).		WG583. [*pTacnlwg583* (9756)].	

Add:

Xabc309-5B,D (9756).		ABC309. [*pHvabc309* (9756)].
Xbcd1087-5D (9756).		BCD1087. [*pHvcnlbcd1087* (9756)].
Xcdo213-5B,D (9756).		CDO213. [*pAscnlcdo213* (9756)].
Xcdo400-5A,B,D (9756).		CDO400. [*pAscnlcdo400* (9756)].
Xcdo484-5B,D (9756).		CDO484. [*pAscnlcdo484* (9756)].
Xcdo1312-5B (9756).		CDO1312. [*pAscnlcdo1312* (9756)].
Xglk69-5A (9756).	[*Tag69-5A* (9756)].	pTag69.

Xglk165-5B (594),*5D.1,.2* (9756). [*Tag165-5Da,5Db* (9756)].
pTag69.
The arm location of *Xglk165-5B* was not reported in 594.
Xglk222-5B (9756). [*Tag222-5B* (9756)]. pTag222. (2D).
Xglk251-5A (9756), *5D* (594). [*Tag251-5A* (9756)]. pTag251.
The arm location of *Xglk251-5D* was not reported in 594.
Xglk354-5B (594,9756), *5D* (9756).
[*Tag354-5D* (9756)]. pTag354.
Xglk614-5A (594,9756), *5B,D* (9756).
[*Tag614-5B,D* (9756)]. pTag614 (594).
Xglk621-5D (594,9756). [*Tag621-5D* (9756)]. pTag621.
Xglk644-5A (594), *5B,D* (9756). [Tag644-5B,D (9756)]. pTag644 (594).
The arm location of *Xglk644-5A* was not reported in 594.
Xglk651-5B,D (9756). [*Tag651-5B,D* (9756)]. pTag651. (7A).
Xglk695-5B.1,.2, (9756), *5D* (594), *5D.1,.2* (9756).
[*Tag695-5Ba,5Bb,5Da,5Db* (9756)].
pTag695 (594).
Xglk754-5B (9756). [Tag754-5B (9756)]. pTag754.
Xksup8-5A,B,D (9737). pHvksu8F/pHvksu8R.
Xksu8-5A.1,.2, 5B.1,.2,.3, 5D.1,.2 (9756).
[*ksu8-5Aa,b,5Ba,b,c,5Da,b* (9756)].
pHvksu8.
Xksu26-5D (9756). pHvksu26.
XksuA3-5A.1,.2, 5B (9756)[1], 5D (309)[4],(9756)[1].
[*ksua3,ksua3b* (9756)]. pTtksuA3.
[*pTtksua3* (9756)].
XksuD42-5A,B (9756)[1], *5D* (309)[4],(9756)[1].
[*ksud42* (9756)]. pTtksuD42 (309).
[*pTtksud42* (9756)].
XksuD16-5A,B (9756)[1], *5D* (309)[4],(9756)[1].
[*ksud16* (9756)]. pTtksuD16 (309).
[*pTtksud16* (9756)].
XksuG12-5D (9756). pTtksuG12.
[*pTtksug12* (9756)]. (4A, 7A).
XksuG44-5A,B.1,B.2,D (9756). [*ksug44* (9756)]. pTtksuG44 (309).
[*pTtksug44* (9756)].
The 5AS, 5BS, and 5DS *XksuG44* loci reported in 9547 (see Group 5S) were not detected in the physical mapping studies reported in 9756.
XksuM2-5A,B (9756), *5D* (309)[4],(9756)[1].
[*ksum2* (9756)]. pTtksuM2 (309).
[*pTtksum2* (9756)].
XksuS1-5A,B,D (9756). pTtksuS1.
[*pTtksus1* (9756)].
Xpsp3037-5B (9743). PSP3037F/PSP3037R.

Xpsp3065-5B (9743).	PSP3065F/PSP3065R.	
Xwg419-5A,B,D (9756).	WG419. [*pTacnlwg419* (9756)].	
Xmwg602-5A,D (9756).	MWG602. [*pTamwg419* (9756)].	
Xwg564-5A,B,D (9756).	WG564. [*pTacnlwg564* (9756)].	

Group 4AL : 5BL : 5DL

Revise:
Xpsr115-4A,5B,D; Replace with '*Xpsr115(Pk)-4A,5B,D* [585][b].' and add '[*Xpsr115-4A,5B,D* (585)].' in second column.

Group 7BS : 5BL : 5DL

Revise:
XksuG7; Add '5B' in the last column.

Group 5

Note: The following markers were moved to the 5S group.
Xglk317, Xglk319, XksuA3, and XksuI26.

Note: The following markers were moved to the 5L group.
Xglk165, Xglk251, Xglk614, Xglk644, Xglk695, XksuD16, XksuD42, XksuG7 and XksuM2.

Revise:
Xpsr167-5B; Replace with '*Xpsr167(Hpr)-5B* [950][b].' and add '[*Xpsr167-5B* (950)].' to second column.

Add:

Xabgp58-5B (9744).	ABG058F/ABG058R.	(2B, 7B).
Xabgp391-5A,B,D (9744).	ABG391F/ABG391R.	(4A).
XksupD15-5B,D (9744).	KSUD15F/KSUD15R.	(1D, 7B,D).
XksupD16-5B (9744).	KSUD16F/KSUD16R.	(4A).
XksupG44-5B,D (9744).	KSUG44F/KSUG44R.	
Xpsp3090-5D (9741).	PSP3090/PSP3090R.	
Xpsr172(Lhcb1)-5A,B,D (9754).	PSR172.	(1A, 7A,B,D).

Group 6S

Revise :
XksuG8-6B,D; Replace first column with '*XksuG8-6A*(9739)[2], *6B* [96114][1],(9596)[2], *6D* (309)[4],(96114)[1],(9589)[1]' in first column.'
Xpsr106-6A,B,D; Replace with '*Xpsr106(Cyc)-6A,B,D* [429][b].' and add '[*Xpsr106-6A,B,D* (429)].' in second column.

Xpsr141-6A,B,D; Replace with '*Xpsr141(Pgk1-2)-6A,B,D* [429][b].' and add '[*Xpsr141-6A,B,D* (429)].' in second column.
Xpsr167-6A,B,D; Replace with '*Xpsr167(Hpr)-6A,B,D* [950][b].' and add '[*Xpsr167-6A,B,D* (950)].' in second column.
Xpsr477(Pgk2)-6A,B,D; Replace with '*Xpsr477(Pgk1-2)-6A,B,D* [138].' and add '[*Xpsr477(Pgk2)-6A,B,D*].' in second column.

Add:

Xmgb56-6A (9739)[2].	MGB56.	
Xmwg573-6A.2 (96119)[3].	MWG573.	(6AL).
Xpsp3009-6B (9741,9743).	PSP3009F/PSP3009R.	
Xpsp3029-6A.2 (9743).	PSP3029F/PSP3029R.	(2A, 6AL).
Xpsp3058-6D (9743).	PSP3058F/PSP3058R.	(2D, 4A).
Xpsp3071-6A (9741,9743).	PSP3071F/PSP3071R.	
Xpsp3079-6B (9743).	PSP3079F/PSP3079R.	(4D, 7D).
Xpsp3200-6D (9743).	PSP3200F/PSP3200R.	

Group 6L

Revise:
Xmwg573-6A; Change '*Xmwg573-6A*' to '*Xmwg573-6A.1*' and add '($6A^m$)' in last column.

XksuD17-6A,B,D: delete previous entry and substitute
'*XksuD17-6A,B* (96114), *6D* (96114,96113). pTtksuD17.'
XksuG48-6D and *XksuG48-6A,D:* delete both entries and substitute
'*XksuG48-6A* (96113), *6D* (9589,96113).
[XksuG48(A) (9589)].
pTtksuG48 (309).
[DG G48 (9589)].'
Xpsr142-6A,B,D; replace with '*Xpsr142(Prk)-6A,B,D* [429][b].' and add '[*Xpsr142-6A,B,D* (429)].' to second column.

Add:

Xpsp3029-6A.1 (9743).	PSP3029F/PSP3029R.	(2A, 6AS).
Xpsp3131-6B (9741,9743).	PSP3131F/PSP3131R.	
Xpsp3152-6A (9741,9743).	PSP3152F/PSP3152R.	

Group 6

Add:

Xabcp158-6D (9744).	ABC158F/ABC158R.	(1D, 3D).
Xabcp309-6A (9744).	ABC309F/ABC309R.	(3D).
XksupE8-6B (9744).	KSUE8F/KSUE8R.	(2B, 4D, 7D).
XksupF15-6A,B,D (9744).	KSUF15F/KSUF15R.	(2A,B, 3A).
XksupM148-6B (9744).	KSUM148F/KSUM148R.	(1B, 2A, 4B,D).
Xpsp3070-6A (9741).	PSP3070F/PSP3070R.	(7D).
Xpsp3139-6B (9741).	PSP3139F/PSP3139R.	

Xwgp232-6B (9744). WG232F/WG232R. (4A,D, 7A).

Group 7S

Revise:
Xglk651; Add '(5B,D).' in the last column.
Xwg909; Add '(5A,D).' in the last column.
Xpsr108-7A,B,D; Replace with '*Xpsr108(Glp3)-7A,B,D* [140][b].' and add '[*Xpsr108-7A,B,D* (140)].' in second column.
Xpsr150-7A,B,D; Replace with '*Xpsr150(Hsp82)-7A,B,D* [140][b]. and add '[*Xpsr150-7A,B,D* (140)].' in second column.

Add:
Xpsp3001-7A.2 (9743). SP3001F/PSP3001R. (3B, 7AL).
Xpsp3050-7A (9741,9743). PSP3050F/PSP3050R.
Xpsp3113-7D (9741,9743). PSP3113F/PSP3113R.
Xpsp3114-7A (9741,9743). PSP3114F/PSP3114R.
*Xpsr479(Brz)-7A** [96119][3]. [*XBrz-7A (96119)*]. pBz.Hv8-3 (9752).
Xwms44-7D (9736). WMS44F/WMS44R.
Whether *Xwms44-7D* belongs to group 7S or group 7AS : 4AL : 7DS is unknown.
Xwms46-7B (9736). WMS46F/WMS46R.

Group 7AS : 4AL : 7DS

Revise:
Xpsr119-7A,4A,7D; Replace with '*Xpsr119(Fedr)-7A,4A,7D* [140][b].' and add '[*Xpsr119-7A,4A,7D* (140)].' to second column.

Add:
Xglk576-7A (594,9740). pTag576.
Xpsp3028-4A (9743). PSP3028F/PSP3028R.
Xpsp3119-4A (9741,9743). PSP3119F/PSP3119R. (7B).

Group 7L

Revise:
XksuG7; Add '(5A,D).' in the last column.
XksuG12; Add '5D' in the last column.
Xpsr56-7A,B,D; Replace with '*Xpsr56(Caa)-7A,B,D* [139,140,182][b].' and add '[*Xpsr56-7A,B,D* (139,140,182)].' in second column.
Xpsr121(Glb3)-7A,B,D; substitute '9547' for '344'.
Xpsr148-7A,B,D; Replace with '*Xpsr148(Cat0)-7A,B,D* [181][b].' and add '[*Xpsr148-7A,B,D* (181)].' in second column.
Xpsr165-7A,B,D; Replace with '*Xpsr165(Sdh)-7A,B,D* [139,140][b].' and add '[*Xpsr165-7A,B,D* (139,140)].' in second column.
Xpsr169-7A,B,D; Replace with '*Xpsr169(Caa)-7A,B,D* [139,140][b].' and add '[*Xpsr169-7A,B,D* (139,140)].' in second column.
Xwia484(Glb3)-7A,B,D; substitute '9547' for '344'.

Add:

Xpsp3001-7A.1 (9743).	PSP3001F/PSP3001R.	(3B, 7AS).
Xpsp3033-7B (9741).	PSP3033F/PSP3033R.	
Xpsp3078-7D (9743).	PSP3078F/PSP3078R.	(4D, 6B).
Xpsp3081-7B (9743).	PSP3081F/PSP3081R.	
Xpsp3094-7A.1 (9741,9743).	PSP3094F/PSP3094R.	(7DL).
Xpsp3094-7D.2 (9743).	PSP3094F/PSP3094R.	(7AL).
Xpsp3123-7D (9741,9743).	PSP3123F/PSP3123R.	
Xwms37-7D (9736).	WMS37F/WMS37R.	
Xwms43-7B (9736).	WMS43F/WMS43R.	

Group 7

Note:
Xglk576 moved to 7AS : 4AL : 7DS.

Add:

Xabgp58-7B (9744).	ABG058F/ABG058R.	(2B, 5B).
Xabgp618-7D (9744).	ABG618F/ABG618R.	(4A).
Xabgp701-7A,B (9744).	ABG701F/ABG701R.	
Xcdop213-7D (9744).	CDO213F/CDO213R.	(1A, 4B).
XksupD2-7A,B,D (9744).	KSUD2F/KSUD2R.	
XksupD15-7B,D (9744).	KSUD15F/KSUD15R.	(1D, 5B,D).
XksupE8-7D (9744).	KSUE8F/KSUE8R.	(2B, 4D, 6B).
XksupG49-7D (9744).	KSUG49F/KSUG49R.	(4A).
Xpsp3003-7D (9741).	PSP3003F/PSP3003R.	(1A).
Xpsp3013-7B (9741).	PSP3013F/PSP3013R.	
Xpsp3034-7B (9741).	PSP3034F/PSP3034R.	(2B).
Xpsp3035-7D (9741).	PSP3035F/PSP3035R.	(3B).
Xpsp3045-7D (9741).	PSP3045F/PSP3045R.	
Xpsp3063-7A (9741).	PSP3063F/PSP3063R.	
Xpsp3070-7D (9741).	PSP3070F/PSP3070R0.	(6A).
Xpsp3082-7A (9741).	PSP3082F/PSP3082R.	
Xpsp3119-7B (9741).	PSP3119F/PSP3119R.	(4A).
Xpsr172(Lhcb1)-7A,B,D (9754).	PSR172.	(1A, 5A,B,D).
Xwgp232-7A (9744).	WG232F/WG232R.	(4A,D, 6B).

Glume Colour

2. Black

Add at the end of the section:
'**ma:** Cosegregation was shown between *Bg* and the *Nor9* locus in *T. monococcum* (96119)[3].

6. Chocolate chaff

cc. 7BS (9701). **dv:** CBC-CDd1 (9701).

Grain Hardness/Endosperm Texture

Add after the Ha section:
'**ma:** *Ha* was found to be closely linked to *Xmta9(Pui1)-5D* (9759). Also, single-factor effects on hardness were found for 2A, 2D, 5B and 6D, and interactive effects were found for 5A, 6D and 7A.

Grain softness proteins (GSPs), or friabilins, are 15-kDa polypeptides that are associated with purified starch granules from soft-grained wheat.

Gsp-A1 (9755).	[GSP (9755)].	5A (9755).	**v:**	CS (9755).
Gsp-B1 (9755).	[GSP (9755)].	5B (9755).	**v:**	CS (9755).
Gsp-D1 (9755).	[GSP (9755)].	5DS (9755).	**v:**	CS (9755).

ma: Co-segregation of *Gsp-D1* and *Ha* was reported (9755).'

Height

Reduced height.

(See notes at end of section concerning a proposal for renaming loci with set nomenclature).

Add at the end of the *Rht1* section:
'**ma:** Linkage was shown between *Gai1 - Xpsr622* with a genetic distance of 1.8 cM in a tetraploid cross (9739)[2].'

'Temporary designation

Rht1(B-dw) (9745). **v:** Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezostaya 1 (9745).'

Add at the end of the *Rht10* section:

'***RhtAi-bian1a*** (9749). **v:** Ai-bian1a (a spontaneous mutant of Ai-bian1) (9749).'

Note to add at end of *Rht* section

'Proposed new symbols (9748).' (This section will be reviewed next year).

Rht-B1A	=	*rht* (tall allele on 4BS)
Rht-B1b	=	*Rht1*
Rht-B1c	=	*Rht3*
Rht-B1d	=	*Rht1S*
Rht-B1e	=	*Rht(B.dw)*
Rht-B1f	=	*Rht T. aethiopicum*
Rht-D1a	=	*rht* (tall allele in 4DS)

Rht-D1b = *Rht2*
Rht-D1c = *Rht10*
Rht-D1d = *Rht Ai-bian1a*

These symbols were employed in 9750. To date there has been no report of a break in the linkage of the *Rht* and *Gai* phenotypes at *Rht-B1* and *Rht-D1*. *Rht-D1* genes map 6 cM distal to *Xucb821(PhyA)* and 4 cM proximal to *Xpsr1871(Pki)* (9547).

Osmoregulation

or (733). 7A (733), 7AS (9740). etc

ma: *Or* was mapped to the short arm of 7AS, 13 cM proximal to *Xpsr119* (9740).

Proteins

1. Grain Protein Content (previously 'Seed Protein')

QGpc.ndsu-6B (9751). 6BS (9751). **tv:** Langdon (9751).
QGpc.ndsu-6Ba (9751). **tv:** Langdon (9751).
QGpc.ndsu-6Bb (9751). **tvs:** Langdon-*T. dicoccoides* 6B (9751).

Quantitative trait loci (QTL) mapped include the following:
ma:
QGpc.ndsu-6B associated (LOD score = 18.9) with the interval between *Xmwg79-6B* and *Xabg387-6B*. These loci were mapped in 6BS as follows: *Xmwg79-6B* - 5.9 cM - *Xabg387-6B* - 9.0 cM - centromere (9751).
QPro.mgb-4B associated at $P \le 0.001$ with *Gai1* and *Xpsr622* (9739)[2].
QPro.mgb-5A associated at $P \le 0.05$ with *Xpsr911* (9739)[2].
QPro.mgb-6A.1 associated at $P \le 0.01$ with *Xpsr167* and *XksuG8* (9739)[2].
QPro.mgb-6A.2 associated at $P \le 0.05$ with *Xmgb56* (9739)[2].
QPro.mgb-6B associated at $P \le 0.05$ with *Gli-B2* (9739)[2].
QPro.mgb-7B associated at $P \le 0.01$ with *Xpsr490(Ss1)* and *Pc* (9739)[2].

2. Enzymes

VIII. Glucosephosphatase isomerase

Gpi-S^{l}1 (9746). 1S^{l} (364), 1S^{l}S (9746). **ma:** *Ae. longissima 2* x *Ae. longissima 10* (9746). (For linkage information, see comment below).

Gpi-S^{l}1 , two glutein loci, and three gliadin loci were mapped relative to one another in *Ae. longissima* as (9746) as follows: *Glu-S^{l}1* - 15.9 cM - *Gpi-S^{l}1* - 38 cM - *Gli-S^{l}4* - 7.1 cM- *Glu-S^{l}3* - 0.9 cM - *Gli-S^{l}1* - 5.6 cM - *Gli-S^{l}5*. *Glu-S^{l}1* is located in 1S^{l}L and the other loci are in 1S^{l}S.

XV. Phosphogluconate dehydrogenase

Add:
'Pgd-A3. 7A^{m}S (96119).'

3. Endosperm Storage Proteins

I. Glutenins

Glu-S^{l}1 (9746). 1S^{l}L (9746). **ma:** *Ae. longissima 2* x *Ae. longissima 10.* (For linkage information, see comment below).

Glu-S^{l}3 (9746). 1S^{l}S (9746). **ma:** *Ae. longissima 2* x *Ae. longissima 10.* (For linkage information, see comment below).

Glu-S^{l}1, Glu-S^{l}3 , one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one another in *Ae. longissima* as (9746) as follows: *Glu-S^{l}1* - 15.9 cM - *Gpi-S^{l}1* - 38 cM - *Gli-S^{l}4* - 7.1 cM- *Glu-S^{l}3* - 0.9 cM - *Gli-S^{l}1* - 5.6 cM - *Gli-S^{l}5*. *Glu-S^{l}1* is located in 1S^{l}L and the other loci are in 1S^{l}S.

II. Gliadins

Gli-S^{l}3 (9746). 1S^{l}S (9746). **ma:** *Ae. longissima 2* x *Ae. longissima 10.* (For linkage information, see comment below).

Three gliadin loci, one glucose phosphate isomerase locus, and two glutein loci and were mapped relative to one another in *Ae. longissima* (9746) as follows: *Glu-S^{l}1* - 15.9 cM - *Gpi-S^{l}1* - 38 cM - *Gli-S^{l}4* - 7.1 cM- *Glu-S^{l}3* - 0.9 cM - *Gli-S^{l}1* - 5.6 cM - *Gli-S^{l}5*. *Glu-S^{l}1* is located in 1S^{l}L and the other loci are in 1S^{l}S. It is not clear how *Gli-S^{l}4* and *Gli-S^{l}5* relate to the *Gli-4* and *Gli-5* sets described above.

5. Other Proteins

V. Salt soluble globulins

ma: The *Glo-1* loci were mapped distally in the short arms of the group 1 chromosomes. *Glo-A1* maps 5.2 cM distal to *Gli-A1* in 1A and *Glo-D1* maps 2.9 cM distal to *Gli-D1* in 1D (9747).

VI. Starch granule proteins

Sgp-A1 (9758). 7AS (9758). **v:** CS.
  Sgp-A1a (9758). **v:** CS.
  Sgp-A1b (9758). **v:** Chosen 30, Chosen 57 (null).
  Sgp-A1c (9758). **v:** Hua Non 9.
Sgp-B1 (9758). 7BS (9758). **v:** CS.
  Sgp-B1a (9758) **v:** CS.

Sgp-B1b (9758).		v:	K79 (null).
Sgp-B1c (9758).		v:	Gnatruche.
Sgp-B1d (9758).		v:	Waratah.
Sgp-D1 (9758).	7DS (9758).	v:	CS.
Sgp-D1a (9758).		v:	CS
Sgp-D1b (9758).		v:	T116 (null).
Sgp-D1c (9758).		v:	Nobeokabouzu.
Sgp-D1d (9758).		v:	Chinsanwase.
Sgp-D1e (9758).		v:	Hosogara.
Sgp-A2 (9758).		v:	CS.
Sgp-B2 (9758).		v:	CS.
Sgp-D2 (9758).		v:	CS.
Sgp-A3 (9758).	7AS (9758).	v:	CS.
Sgp-A3a (9758).		v:	CS
Sgp-A3b (9758).		v:	Norin 61 (null).
Sgp-B3 (9758).	7BS (9758).	v:	CS.
Sgp-B3a (9758).		v:	CS.
Sgp-B3b (9758).		v:	Crest (null).
Sgp-B3c (9758).		v:	Spica.
Sgp-D3 (9758).	7DS (9758).	v:	CS.

Deletion mapping indicates that the order of the *Sgp* genes on the 7S arms is 'centromere - *Sgp-1* - *Sgp-3* - *Wx* (9758).

Response to Salinity

K^+/Na^+ discrimination

Kna1 (96128). 4DL (96128). **s:** *T. turgidum* cv. Langdon 4D(4B).

ma: *Kna1* co-segregates with *Xwg199-4D, Xabc305-4D, Xbcd402-4D, Xpsr567-4D* and *Xpsr375-4D.*

Reaction to Pests and Diseases

Reaction to BYDV

Several wheat lines with BYDV resistance derived from *Agropyrum intermedium* (9717) were cytologically characterized by Hohmann et al (9718).

Bdv2 (9719). **su:** TAF 2 (9717); Lines 5395 & 5395-243AA (9518).
Tr: TC14 = T7DS.7DL-7Ai#1L (9518). TC5, TC6, TC8, TC9, TC10 = T7DS-7Ai#1S.7Ai#1L (9518). TC7 = T1BS-7Ai#1S.7Ai#1L (9518).

Reaction to *Erysiphe graminis*

Pm3a.	**v:**	Norin 3 (9642); Norin 29 (9642).
Pm4b.	**v:**	Others (9708).
Pm8.	**v:**	ST1-25 (9708).

Hanusová (9728) reported expression of *Pm8* in 111 of 127 wheats identified to have 1BL.1RS.

Suppressor of *Pm8*

Zeller & Hsam (9723) located a suppressor of *Pm8* and *Pm17* in chromosome 7D of Caribo. Mildew resistance was suppressed in Florida, Ikarus and Sabina, which are derivatives of Caribo with 1BL.1RS. According to Ren et al. (9651), *SuPm8* does not suppress *Pm17*. Hanusová et al. (9728) listed 16 wheats that carry a suppressor of *Pm8*.

Pm17

Suppressor of *Pm17*

A suppressor of *Pm17* as well as of *Pm8* was located in chromosome 7D of Caribo (9723). Gene *SuPm8* identified by Ren et al (9651) did not suppress *Pm17*.

Pm22. **v:** Elia (9642); Est Mottin (9642); Ovest (9642); Tudest (9642).

Pm23 (9703). 5A (9703). **v:** Line 81-7241 *Pm8* (9703).
Although Line 81-7241 carries *Pm8*, evidence was presented to indicate that it was suppressed in Line 81-7241 and, by inference, also in Chinese Spring.

Temporary designation

mlre (9714). **v:** RE714 (9714).

Reaction to *Phaeosphaeria nodorum*

SnbTm (9706). 3A (9706). **tv:** S3-6 (9706); S9-10 (9706); S12-1 (9706).

Reaction to *Puccinia graminis*

Sr10. **v:** Hazen (9716).

Reaction to *Puccinia recondita*

Lr9. **v:** Clemson 201 (9715).
Lr11. **v:** Hazen (9716).
Lr26. Hanusová et al (9728) identified 127 wheats with *Lr26*, but only 16 of them were listed.
Lr31. Correction: 4BL.

Genotype lists: 9711 (Indian cultivars).

Reaction to *P. striiformis*

Yr2.	7B (9712).	**v:**	Yamhill Yr3a Yr4a (141, 9713).
Yr15 (9720).	1BS (9720).	**v:**	V763-2312 (9720); V763-254 (9720).
Yr25 (9725).	1D (9725).	**v:**	TP1295, TP981 (9725).

This gene is likely to be present in Strubes Dickkopf, Heines VII *Yr2*, Heines Peko *Yr2 Yr6*, Reichersberg 42 *Yr7* and Clement *Yr9* (9725).

Yr3a.	**v:**	Stephens Druchamp*Yr4a;* Nord Desprez*Yr4a* (9713). Yamhill *Yr2Yr4a* (9713).

Yr3b. Chen & Line (9713) found that a second gene in Hybrid 46 - presumably this gene - was not located at the *Yr3* locus.

Yr3c.	**v:**	Minister (9713).
Yr4a.	**v:**	Druchamp *Yr3a* (9713); Nord Desprez *Yr3a* (9713). Yamhill *Yr2 Yr3a* (9713).
Yr4b.	**v:**	Hybrid 46 *Yr3b* (618; 9713).

Temporary designations

YrHVII (9712).	4A (9712).	**v:**	Heines VII *Yr2* (9712).
YrCle (9712).	4B (9712).	**v:**	Clement *Yr9* (9712).
YrMor (9712).	4B (9712).	**v:**	Moro *Yr10* (9712).
YrTye (9712).	6D (9712).	**v:**	Tyee (9712).
YrTr1 (9712).	6D (9712).	**v:**	Tres *YrTr2* (9712).
YrTr2 (9712).	3A (9712).	**v:**	Tres *YrT1* (9712).
YrDa1 (9712).	1A (9712).	**v:**	Daws *YrDa2* (9712).
YrDa2 (9712).	5D (9712).	**v:**	Daws *YrDa1* (9712).

Reaction to *Pyrenophora tritici-repentis*

1. Insensitivity to tan spot toxin

Tsn1 should replace *Tsn.*

ma: *Xbcd1030* - 5.7 cM - *tsn1* -16.5 cM - *Xwg583* (9629).

2. Resistance to chlorosis induction

Tsc1 (9707).	1AS (9707).	**v:**	Synthetic W7984 (9707).
tsc1 (9707).		**v:**	Opata 85 (9707).

Tsc1 is the resistance allele which was mapped using a QTL approach. *Tsc1* was identified with marker *Gli-A1* (9707).

Reaction to *Schizaphis graminum*

Lazar et al. (9710) found that resistance in Largo and derivatives was controlled by multiallelic

complementary genes. On their conclusions, *Gb3* would be one of the loci concerned.

Genetic Linkages

Chromosome 1A

1AS		*Gli-A1*	-	*Glu-A3*	1.5 ± 0.3 cM (9726).

Chromosome 1B

1BS		*Yr10*	-	*Yr15*	34 ± 2 cM (9720).
		Yr15	-	centromere	7cM (9720).

Chromosome 2A

2AS.		*bh*	-	centromere	8.5 ± 2.1 cM (9701).
2AL.		*Yr1*	-	*Pm4a*	2.0 ± 0.6 cM (9721).

Chromosome 5A

		H10	-	*H17*	20 cM (9709).
		H17	-	*H16*	25 cM (9709).
		H16	-	*H12*	25 cM (9709).

Gene order: *H9/H15* - *H10* - *H17* - *H16* - *H12* (9709).

Chromosome 5B

5BL		*Xbcd103*	-	*tsn 1*	5.7 cM (9629).
		tsn1	-	*Xwg583*	16.5 cM (9629).

Chromosome 6B

6BS	**tv:**	*Nor2*	-	*Xpsr312*	24.8 cM (9722).
	tv:	*Xpsr312*	-	*Su1*	5.3 cM (9722).
	tv:	*Su1*	-	*Pgk 2*	6.8 cM (9722).

Chromosome 7A

7AL		centromere	-	*cn-A1d*	46.6 ± 3.8 cM (9701).
7AL		*Rc1*	-	*P*	20.3% (9537).
	tv:	*P*	-	*cn-A1d* (CDd6)	37.9 ± 3.2 CM (9727).

Chromosome 7B

7BS		*cc*	-	centromere	33.5 ± 4.1 cM (9701).
7BL		centromere	-	*cn-B1a*	42.6 ± 4.3 cM (9701).

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Amendments.

429. Change '(In Press)' to 'Theoretical and Applied Genetics 92: 559-565.
950. Replace with '949'.
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Number 85: 82–86 (1997)

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 eidor thanks CSA for authorizing WIS to publish the database.

1997

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(2)
ACCN:001765282 CTLN:4021893
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Shaughnessy, J.D.,Jr.;Jenkins, N.A.; Copeland, N.G.*
AFFN:Mammalian Genet. Lab., ABL-Basic Res. Prog., NCI-Frederick Cancer Res. and Dev. Cent., P.O. Box B, Frederick, MD 21702, USA
TITL:cDNA cloning, expression analysis, and chromosomal localization of a gene with high homology to wheat eIF-(iso)4F and mammalian eIF-4G
HTIL:GENOMICS
HSSN:0888-7543
HYER:1997
HCOL:vol. 39, no. 2, pp. 192-197

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(3)
ACCN:001765293 CTLN:4021904
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Feuillet, C.;Schachermayr, G.;Keller, B.
AFFN:Dep. Resistance and Quality Breeding, Swiss Federal Res. Stn. for Agroecology and Agric., Reckenholzstrasse 191, CH-8046 Zuerich, Switzerland
TITL:Molecular cloning of a new receptor-like kinase gene encoded at the Lr10 disease resistance locus of wheat
HTIL:PLANT J.
HSSN:0960-7412
HYER:1997
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(4)
ACCN:001788293 CTLN:4045037
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); V (Virology & AIDS Abstracts)
AUTH:Marcon, A.;Kaeppler, A.*;Jensen, S.G.
AFFN:Univ. Wisconsin, Dep. Agron., Madison, WI 53706-1597, USA
TITL:Genetic variability among maize inbred lines for resistance to the high plains virus-wheat streak mosaic virus complex
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:1997
HCOL:vol. 81, no. 2, pp. 195-198

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ACCN:001788489 CTLN:4045234
ABSJ:G (Genetics Abstracts)
AUTH:Lafiandra, D.; Tucci, G.F.; Pavoni, A.; Turchetta, T.;Margiotta, B.
AFFN:Dep. Agrobiology and Agrochemistry, Univ. Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:PCR analysis of x- and y-type genes present at the complex Glu-A1 locus in durum and bread wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1997
HCOL:vol. 94, no. 2, pp. 235-240

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(6)
ACCN:001788557 CTLN:4045324
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Schachermayr, G.;Feuillet, C.;Keller, B.*
AFFN:Dep. Resistance and Quality Breeding, Swiss Federal Res. Stn. for Agroecology and Agric. (FAL), Reckenholzstrasse 191, CH-8046 Zuerich,

Switzerland
TITL:Molecular markers for the detection of the wheat leaf rust resistance gene Lr10 in diverse genetic backgrounds
HTIL:MOL. BREED.
HSSN:1380-3743
HYER:1997
HCOL:vol. 3, no. 1, pp. 65-74

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ACCN:001794387 CTLN:4052329
ABSJ:G (Genetics Abstracts)
AUTH:Tsujimoto, H.;Yamada, T.;Sasakuma, T.
AFFN:Kihara Inst. for Biol. Res., Yokohama City Univ., 641-12 Maioka-cho, Totsuka-ku, Yokohama 244, Japan
TITL:Molecular structure of a wheat chromosome end healed after gametocidal gene-induced breakage
HTIL:PROC. NATL. ACAD. SCI. USA
HSSN:0027-8424
HYER:1997
HCOL:vol. 94, no. 7, pp. 3140-3144

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(8)
ACCN:001794653 CTLN:4052701
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology,Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Kolmer, J.A.
AFFN:Agric. and Agri-Food Canada, Cereal Res. Cent., 195 Dafoe Rd.,Winnipeg, Manitoba, Canada, R3T 2M9
TITL:Virulence in Puccinia recondita f. sp. tritici isolates from Canada to genes for adult-plant resistance to wheat leaf rust
HTIL:PLANT DIS.
HSSN:0191-2917
HYER:1997
HCOL:vol. 81, no. 3, pp. 267-271

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(9)
ACCN:001798829 CTLN:4057344
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Krugman, T.;Levy, O.;Snape, J.W.;Rubin, B.; Korol, A.;Nevo, E.
AFFN:Institute of Evolution, Haifa University, Mt. Carmel, Haifa 31905, Israel
TITL:Comparative RFLP mapping of the chlorotoluron resistance gene (Su1) in cultivated wheat (Triticum aestivum) and wild wheat (Triticum dicoccoides)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1997
HCOL:vol. 94, no. 1, pp. 46-51

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(10)
ACCN:001798835 CTLN:4057350
ABSJ:G (Genetics Abstracts)
AUTH:Ciaffi, M.;Dominici, L.;Lafiandra, D.
AFFN:Dipartimento di Agrobiologia ed Agrochimica, Universita della Tuscia, 01100 Viterbo, Italy
TITL:Gliadin polymorphism in wild and cultivated einkorn wheats
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1997
HCOL:vol. 94, no. 1, pp. 68-74

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(11)
ACCN:001798838 CTLN:4057353
ABSJ:G (Genetics Abstracts)
AUTH:Schwarzacher, T.;Wang, M.L.;Leitch, A.R.; Miller, N.;Moore, G.;Heslop-Harrison, J.S.
AFFN:John Innes Centre, Colney Lane, Norwich NR4 7UH, UK
TITL:Flow cytometric analysis of the chromosomes and stability of a wheat cell-culture line
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1997
HCOL:vol. 94, no. 1, pp. 91-97

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(12)
ACCN:001798839 CTLN:4057354
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology,Mycology & Protozoology)
AUTH:Faris, J.D.;Anderson, J.A.;Francl, L.J.; Jordahl, J.G.
AFFN:Department of Plant Pathology, Throckmorton Plant Sciences Center, Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:RFLP mapping of resistance to chlorosis induction by Pyrenophora tritici-repentis in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1997
HCOL:vol. 94, no. 1, pp. 98-103

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(13)
ACCN:001807260 CTLN:4065616
ABSJ:G (Genetics Abstracts)
AUTH:Lukaszewski, A.J.

AFFN:Dep. Botany and Plant Sci., Univ. California, Riverside, CA 92521, USA
TITL:The development and meiotic behavior of asymmetrical isochromosomes in wheat
HTIL:GENETICS
HSSN:0016-6731
HYER:1997
HCOL:vol. 145, no. 4, pp. 1155-1160

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(14)
ACCN:001810472 CTLN:4069100
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Holappa, L.D.;Walker-Simmons, M.K.*
AFFN:U.S. Dep. Agric., Agric. Res. Serv., Wheat Genet., Quality, Physiol. and Dis. Res., Washington State Univ., Pullman, WA 99164-6420, USA
TITL:The wheat protein kinase gene, TaPK3, of the PKABA1 subfamily is differentially regulated in greening wheat seedlings
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1997
HCOL:vol. 33, no. 5, pp. 935-941

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(15)
ACCN:001811692 CTLN:4070577
ABSJ:G (Genetics Abstracts)
AUTH:Sadhu, D.;De, D.K.;Ghimiray, T.S.;Sarkar, K.K.
AFFN:Department of Genetics & Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur 741252, India
TITL:Inheritance of seminal root numbers in wheat
HTIL:ENVIRON. ECOL.
HSSN:0970-0420
HYER:1997
HCOL:vol. 15, no. 1, pp. 9-11

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(16)
ACCN:001815349 CTLN:4073455
ABSJ:G (Genetics Abstracts)
AUTH:Limin, A.E.;Danyluk, J.;Chauvin, L.-P.; Fowler, D.B.;Sarhan, F.
AFFN:Crop Dev. Cent., Univ. Saskatchewan, 51 Campus Dr., Saskatoon, Saskatchewan, S7N 5A8, Canada
TITL:Chromosome mapping of low-temperature induced Wcs120 family genes and regulation of cold-tolerance expression in wheat
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1997
HCOL:vol. 253, no. 6, pp. 720-727

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(17)
ACCN:001815358 CTLN:4073464
ABSJ:G (Genetics Abstracts)
AUTH:Belay, G.;Merker, A.
AFFN:Swedish Univ. Agric. Sci., Dep. Plant Breeding Res., Box 7003, S-750 07 Uppsala, Sweden
TITL:Cytogenetic studies in Ethiopian landraces of tetraploid wheat (Triticum turgidum L.). II. Spontaneous chromosome translocations and fertility
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1997
HCOL:vol. 126, no. 1, pp. 35-43

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(18)
ACCN:001815360 CTLN:4073466
ABSJ:G (Genetics Abstracts)
AUTH:Linde-Laursen, I.;Heslop-Harrison, J.S.; Shepherd, K.W.;Taketa, S.
AFFN:Botanical Sect., Dep. Botany, Dendrology and Forest Genet.,Royal Veterinary and Agric. Univ., Rolighedsvej 21, DK-1958 Frederiksberg C (Copenhagen), Denmark
TITL:The barley genome and its relationship with the wheat genomes. A survey with an internationally agreed recommendation for barley chromosome nomenclature
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1997
HCOL:vol. 126, no. 1, pp. 1-6

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(19)
ACCN:001815569 CTLN:4073677
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Keller, S.M.;McDermott, J.M.;Pettway, R.E.;Wolfe, M.S.;McDonald, B.A.
AFFN:Dep. Plant Pathol. and Microbiol., Texas A&M Univ., College Station, TX 77845-2123, USA
TITL:Gene flow and sexual reproduction in the wheat glume blotch pathogen Phaeosphaeria nodorum (anamorph Stagonospora nodorum)
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X

HYER:1997
HCOL:vol. 87, no. 3, pp. 353-358

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(20)
ACCN:001818471 CTLN:4077074
ABSJ:G (Genetics Abstracts)
AUTH:Damania, A.B.;Pecetti, L.*;Qualset, C.O.; Humeid, B.O.
AFFN:Istituto Sperimentale per le Colture Foraggere, viale Piacenza 29, 20075 Lodi, Italy
TITL:Diversity and geographic distribution of stem solidness and environmental stress tolerance in a collection of durum wheat landraces from Turkey
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:1997
HCOL:vol. 44, no. 2, pp. 101-108

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(21)
ACCN:001818472 CTLN:4077075
ABSJ:G (Genetics Abstracts)
AUTH:Jaaska, V.
AFFN:Dep. Botany, Inst. Zool. and Botany, Tartu, Estonia
TITL:Isoenzyme differences between the wild diploid and tetraploid wheats
HTIL:GENET. RES. CROP EVOL.
HSSN:0925-9864
HYER:1997
HCOL:vol. 44, no. 2, pp. 137-146

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(22)
ACCN:001821693 CTLN:4080521
ABSJ:G (Genetics Abstracts)
AUTH:Ribeiro-Carvalho, C.;Guedes-Pinto, H.; Harrison, G.;Heslop-Harrison, J.S.
AFFN:Dep. Genet. and Biotechnol., Univ. Tras-os-Montes and Alto Douro, 5000 Vila Real, Portugal
TITL:Wheat-rye chromosome translocations involving small terminal and intercalary rye chromosome segments in the Portuguese wheat landrac Barbela
HTIL:HEREDITY
HSSN:0018-067X
HYER:1997
HCOL:vol. 78, no. 5, pp. 539-546

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(23)
ACCN:001825678 CTLN:4084980
ABSJ:G (Genetics Abstracts)
AUTH:Procunier, J.D.;Knox, R.E.;Bernier, A.M.; Gray, M.A.;Howes, N.K.
AFFN:Agriculture and Agri-Food Canada, Cereal Research Centre, 195 Dafoe Road, Winnipeg, MB R3T 2M9, Canada
TITL:DNA markers linked to a T10 loose smut resistance gene in wheat (Triticum aestivum L.)
HTIL:GENOME
HSSN:0831-2796
HYER:1997
HCOL:vol. 40, no. 2, pp. 176-179

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(24)
ACCN:001825682 CTLN:4084984
ABSJ:G (Genetics Abstracts)
AUTH:Asakura, N.;Nakamura, C.*;Ohtsuka, I.
AFFN:Graduate School of Science and Technology and Laboratory of Plant Genetics, Department of Biological and Environmental Science, Faculty of Agriculture, Kobe University, 1 Rokkodai-cho, Nada-ku, Kobe 657, Japan
TITL:RAPD markers linked to the nuclear gene from Triticum timopheevii that confers compatibility with Aegilops squarrosa cytoplasm on alloplasmic durum wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1997
HCOL:vol. 40, no. 2, pp. 201-210

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(25)
ACCN:001825686 CTLN:4084988
ABSJ:G (Genetics Abstracts)
AUTH:William, H.M.;Hoisington, D.;Singh, R.P.; Gonzalez-De-Leon, D.*
AFFN:Centro Internacional de Mejoramiento de Maiz y Trigo, Lisboa 27, Apartado Postal 6-641, 06600 Mexico D.F., Mexico
TITL:Detection of quantitative trait loci associated with leaf rust resistance in bread wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1997
HCOL:vol. 40, no. 2, pp. 253-260

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(26)
ACCN:001825687 CTLN:4084989
ABSJ:G (Genetics Abstracts)
AUTH:de la Pena, R.C.;Murray, T.D.*;Jones, S.S.
AFFN:Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA
TITL:Identification of an RFLP interval containing Pch2 on chromosome 7AL in wheat
HTIL:GENOME
HSSN:0831-2796

HYER:1997
HCOL:vol. 40, no. 2, pp. 249-252

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(27)
ACCN:001825703 CTLN:4085005
ABSJ:G (Genetics Abstracts)
AUTH:Sreeramulu, G.;Singh, N.K.*
AFFN:Department of Molecular Biology and Genetic Engineering, G.B. Pant University of Agriculture and Technology, Pantnagar 263 145, India
TITL:Genetic and biochemical characterization of novel low molecular weight glutenin subunits in wheat (Triticum aestivum L.)
HTIL:GENOME
HSSN:0831-2796
HYER:1997
HCOL:vol. 40, no. 1, pp. 41-48

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(28)
ACCN:001827986 CTLN:4086522
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); W2(Agricultural and Environmental Biotechnology Abstracts); G (Genetics Abstracts); D (Ecology Abstracts)
AUTH:Van Overbeek, L.S.;Van Veen, J.A.;Van Elsas, J.D.
AFFN:Res. Inst. for Plant Prot. (IPO-DLO), P.O. Box 9060, 6700GW Wageningen, The Netherlands
TITL:Induced reporter gene activity, enhanced stress resistance, and competitive ability of a genetically modified Pseudomonas fluorescens strata released into a field plot planted with wheat
HTIL:APPL. ENVIRON. MICROBIOL.
HSSN:0099-2240
HYER:1997
HCOL:vol. 63, no. 5, pp. 1965-1973

Wheat Information Service
Number 85: 87–91 (1997)

Information

1. 9th International Wheat Genetics Symposium

August 2-7, 1998
University of Saskatchewan, Saskatoon, Saskatchewan, Canada
Internet homepage:http://www.usask.ca/agriculture/cropsci/winter_wheat/9th_iwgs/

See in the previous issue of WIS (no. 84, p. 86).

2. 18th International Congress of Genetics

Beijing, China
August 10-15, 1998

Scientific program: Food supply shortages are increasingly threatening the rapidly growing populations of the world, especially in the countries of the developing world. New theories of genetics and techniques of genetic engineering are beginning to offer new approaches to these global challenges. In recognition of these exciting possibilities for genetics, the scientific session of the congress is being organized to emphasize the most recent developments in genetics in relation to agriculture, medicine, population, resources and the environment. The congress will consist of an opening session, plenary sessions, symposia, workshops and posters. All participants are invited to present their research in poster form at the Congress. Deadline for the receipt of abstracts is March 31, 1998, and that for registration is May 1st, 1998. Detailed information on the Congress are available in the Second announcement from;

Secretariat of the XVIIIth IGC
Institute of Genetics, Chinese Academy of Sciences
Datun Road., Andingmenwai, Beijing 100101, CHINA
Internet homepage: http://www.ihep.ac.cn/ins/IHEP/div10/icg/index.html

3. 13th International Chromosome Conference

Ancona and Numana, Italy
September 8-12, 1998

The scientific program of the Conference will consist of plenary lectures, contributed papers in poster format and workshops. The official language of the conference is English. The deadline for receipt of both regular registration and abstract is March 31st, 1998. Second announcement is now available from;

Prof. Ettore Olmo
Secretary General, Instituto di Biologia e Genetica, Università di Ancona
via Brecce Bianche, 60131 Ancona, ITALY
Tel:+39-71-2204615/619/614
Fax:+39-71-2204609

4. KOMUGI Database——Wheat Genetic Resources Database

Yukiko Yamazaki[1], Hisashi Tsujimoto[2] and Taihachi Kawahara[3]

[1] Center for Genetic Resource Information, National Institute of Genetics, Mishima, 411 Japan
[2]Kihara Institute for Biological Research, Yokohama City University, Totsuka-ku, 244 Japan
[3]Plant Germ-plasm Institute, Faculty of Agriculture, Kyoto University, Muko, 617 Japan

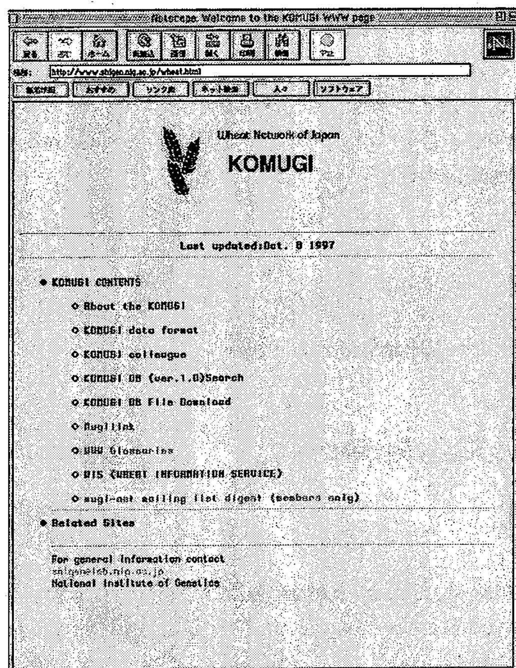

Fig. 1. KOMUGI WWW home page.

Introduction

KOMUGI, meaning wheat in Japanese, was established in 1995 as a wheat network of Japan to ensure the long term conservation of genetic resources and guarantee the availability and distribution of the information for benefit of researchers. At present nineteen institutions are members of KOMUGI. As a product of database working group of KOMUGI, we have constructed the database, "KOMUGI DB", that combines information of wheat genetic resources developed by and maintained in these institutions. KOMUGI DB is the first exhaustive public database which covers most wheat stocks in Japan. The Release 1.0 contains over 13000 accessions and is available from the KOMUGI WWW home page (Fig. 1). The next version will be released early 1998 with new format and some images.

KOMUGI Database Release 1.0

Database Contents

The collaboration with 16 institutions and 24 colleagues resulted in the assemblage of 13763 accessions including wild species (3293 accessions), landrace and cultivars (7111), testers and breeding lines (226), mutants (130), isogenic lines (52), chromosome lines (1547), artificial polyploids (171) and cytoplasmic substitution lines (1233). Table 1 shows a sample entry form which consists of 10 categories and 60 items with unique record number. New items shown in the different column of Table 1 will appear in the next release as well as image files of phenotype. An asterisk indicates the items with controlled vocabularies and syntax.

How to access the Database

There are database files (FileMaker Pro) available from the anonymous FTP server. If you are interested in submitting your data, information is available by contacting the address for general information below. The most user-friendly way to browse the KOMUGI DB is to access the KOMUGI WWW home page provided by the SHIGEN (SHared Information of GENetic resources) server at the National Institute of Genetics, Mishima, Japan. Genetic resources databases for many other species are also available through the server.

Electronic Addresses

KOMUGI WWW home page..........http://www.shigen.nig.ac.jp/wheat.html
anonymous FTP server .... shigen.lab.nig.ac.jp
SHIGEN server .... http://www.shigen.nig.ac.jp
general information...................... shigen@lab.nig.ac.jp

Table 1. KOMUGI DB format (*controlled vocabulary)

Category	Item	Example	New Item
Accession	*Record No. Strain No. Strain name *Group name *Availability	12345 KMG0001 Sm1A Landrace & Cultivar Limited	*Record No. Strain No. Strain name *Group name *Availability
Institution	Institution name *Institution code Contact person	KOMUGI Univ. KMG H.Komugi	Institution name *Institution code Contact person
	*Genus *Species *ssp./cv./var./strain ssp./cv./var./strain name	Triticum aestivum cv. Shinchunaga	*Genus *Species Subspecies name Cultivar name Variety name
	*Gene donor genus	Aegilops	*Gene donor genus

(Table 1 continued)

Taxonomy	*Gene donor species *Gene donor ssp./cv./var./strain Gene donor ssp./cv./var./strain name	speltoides ssp. aucheri	*Gene donor species Gene donor subspecies name Gene donor cultivar name Gene donor variety name Gene donor strain name Gene donor strain No.
			*Chromosome donor genus *Chromosome donor species Chromosome donor subspecies name Chromosome donor cultivar name Chromosome donor variety name Chromosome donor strain name Chromosome donor strain No.
	*Cytoplasm donor genus *Cytoplasm donor species *Cytoplasm donor ssp./cv./var./strain Cytoplasm donor ssp./cv./var./strain name Cytoplasm type	Aegilops caudata var. polyathera C	*Cytoplasm donor genus *Cytoplasm donor species Cytoplasm donor subspecies name Cytoplasm donor cultivar name Cytoplasm donor variety name Cytoplasm donor strain name Cytoplasm donor strain No. Cytoplasm type
History	Old strain No. Locality Country Altitude Latitude Longitude Person established/collected Person acquired *Year established/collected *Year acquired	K0001 Rome Italy 1020 T.Komugi A.Komugi 1880 1960	Old strain No. Locality Country Altitude Altitude numerical Latitude Longitude Person established/collected Person acquired *Year established/collected *Year acquired
Phenotype	grain color cleoptile color leaf hairiness glaucousness awnedness awn color glume hairiness glume color fertility heading growth habit	red green glabrous glaucous awnless brown hairy yellow sterile early spring	grain color cleoptile color leaf hairiness glaucousness awnedness awn color glume hairiness glume color fertility heading growth habit
Genetics	genotype Chromosome/Arm Chromosome pairing Abbreviation Chromosome number Genome formula mutant gene symbol	Vrn1 4BS 20"+t" Dt1AL 40+2t ABD Ph	genotype Chromosome/Arm Chromosome pairing Abbreviation Chromosome number Genome formula mutant gene symbol

(Table 1 continued)

Category	Item	Example	New Item
	mutant gene name marker gene symbol marker gene name transgene vector *copy number	pairing homoeologous Hp1 hairy peduncle pUC18 2	mutant gene name marker gene symbol marker gene name transgene vector *copy number
Method	Pedigree/Production method Purpose *Maintenance	Backcrossing Inbred line open pollination	Pedigree/Production method Purpose *Maintenance
Reference	Reference	Authors Title Journal Vol. Page Year	Authors Title *Journal Vol. Page *Year
Comment	Comment	free text	Comment
Image		KOMUGI.gif	Image file name

Future plan

The development of the direct data management system through each researcher can submit and/or update their own data by connecting to the remote computer running the database is ongoing. Integration with relevant databases such as wheat DNA clones DB and barley genetic resources DB is planed to be implemented in the near future.

ACKNOWLEDGMENTS

This work is supported in part by a Grant-in-Aid from the Ministry of Education, Science, Sport and Culture of Japan. We would like to thank all of KOMUGI colleagues and wheat researchers who continue to support this activity.

Wheat Information Service
Number 85: 92 (1997)

Editorial remarks

1998 is the year of 9th International Wheat Genetics Symposium. Everybody must look for meeting each other at Saskatoon under Canadian blue sky. Please be careful for the registration described in detail in Information of this volume.

The editorial board is proud of issuing the present volume, because the contents is ideal for the original aim of WIS with a variety of information, including seven research articles, four research information, an opinion on the discussing issue, a gene catalog, a literature list, as well as an announcement of a database construction. Especially, the database, KOMUGI, should be one of achievement of international cooperation by wheat researchers, because it contains various genetic stocks historically established by the pioneers worldwide. Although KOMUGI itself, meaning wheat in a Japanese word is for Japanese domestic conservation, we hope the scientific achievement should be commonwealth of the world.

The next issue of WIS will be under review by new members of the editorial board. It should be more attractive and informative, if you contributors decide to open research results and information you have already accumulated in your laboratory to the world.

Season's greeting and a happy new year for 1998.

Editor, T. S.

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* Editor in chief, **Secretary

WIS No. 85

編　集　西　川　浩　三
発行所　木原記念横浜生命科学振興財団
〒244　横浜市戸塚区舞岡町 641-12
Tel (045)825-3487
Fax(045)825-3307
発行日　1 9 9 7 年 1 2 月 2 4 日

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