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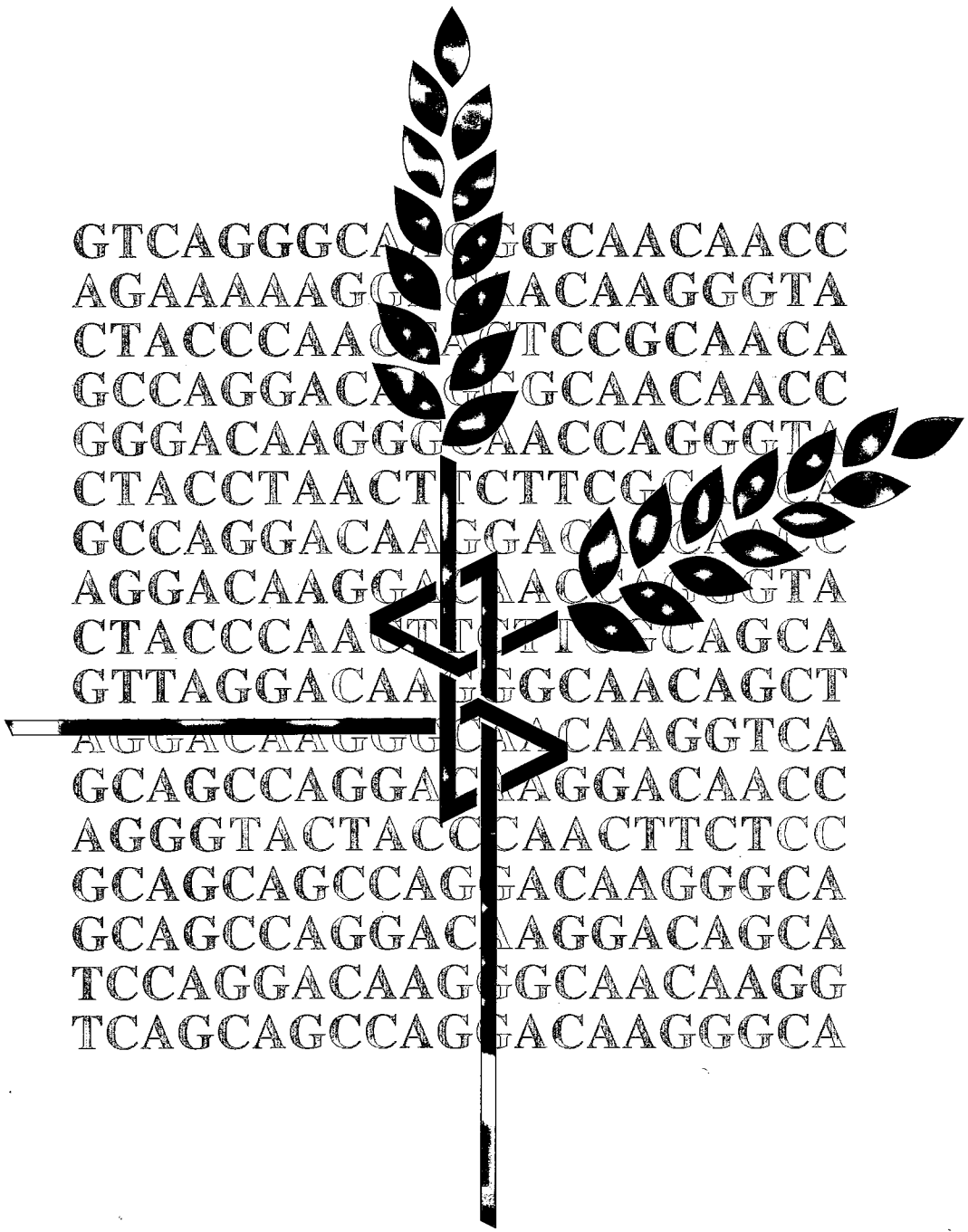

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Research article

Monosomic analysis of genic male-sterility in hexaploid wheat

Dalmir Singh and P.K. Biswas

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110012, India

Summary

Partial genic male-sterility (p-mst) caused by the conversion of anthers into ovaries, was isolated from F_3 population of a cross involving Sel.212 and variety HD 2009. The inheritance study has revealed its control by a single recessive gene. An attempt was made to locate the gene on specific chromosome using monosomic lines of cv. Chinese Spring. Detailed monosomic F_1 and F_2 analysis has pointed out the involvement of two independent genes located on chromosomes 4A and 6B, respectively.

Key words: genic male-sterility, monosomics, Chinese Spring, hexaploid wheat, gene location

Introduction

Genic male-sterility (g-mst) is controlled by nuclear gene whose action is not influenced by cytoplasmic factors. Therefore, the inheritance pattern and expression of the sterility are entirely Mendelian. It exhibits no reciprocal differences and is controlled by recessive genes in the majority of the cases.

Genic male-sterility (g-mst) has been reported in major crops (Kaul 1988). Generally g-mst is of spontaneous origin. In *Triticum aestivum* it has been reported by Pugsley and Oram (1959), Lupton and Bingham (1966-67), Athwal et al. (1967), Krupnov (1968), Lemekh et al. (1971), Jan (1974), Xiangmin and Herong (1981) and Deng and Gao (1982). Recently a novel genic male-sterility was reported by Singh (2002) where the male-sterility was incomplete, therefore, it was designated as p-mst (partial genic male sterility). The inheritance study was carried out which revealed its control by single recessive gene (Singh 2002).

In the present study, an attempt has been made to locate *ms* gene on specific chromosome of partial genic male sterile (p-mst) strain.

Material and methods

The partial genic male-sterility strain of *T. aestivum* (2n=42) from the Department of Genetics, IARI, New Delhi was considered appropriate for locating gene conditioning genic male-sterility. For this purpose monosomic analysis was employed. The 21 aneuploid lines of cv. Chinese Spring used were originally produced by Sears (1954).

The salient features of p-mst strain and cv. Chinese Spring: p-mst stock evolved from Selection 212 (monosomic 5B Chinese Spring / Rye // Sonalika) /// HD 2009. This strain is characterized by full awning, single gene dwarf, late maturing, resistant to stem and leaf rusts of wheat. It produces 10 to 12% selfed seeds which are sufficient for its maintenance. The seeds formed on p-mst plant are dented or notched on its sides. Cv. Chinese Spring an awnless and hooded spring wheat, susceptible to rusts.

Seeds of monosomic (2n=41) plants were planted in the field. At appropriate stage of meiosis, monosomic plants were identified cytologically at first meiotic metaphase. The monosomic plants were crossed with p-mst strain as female parents. A cross was also made with disomic parent. All the crossed seeds were planted in the field and monosomic F_1 hybrids were identified cytologically from all the 21 lines. F_2 seeds were harvested from all the monosomic F_1 hybrids and also from disomic cross and F_2 populations were raised. Data were recorded on agronomic traits from all the monosomic and disomic

F_1 hybrids and F_2 plants.

A chi-square test was applied to the segregation ratios of both the sterile and fertile F_2 plants of disomic cross and F_1 monosomic hybrids. The disomic cross provided the data of the conventional genetic analysis and among the F_2's derived from monosomic F_1's, only those lines which deviated from the expected ratios were considered to be the critical lines (chromosomes on which the fertility/fertility genes are located).

Results

The inheritance of sterility in p-mst strain was studied in crosses of cv. Chinese Spring monosomic lines and p-mst strain. The data recorded on seed set in parents, 21 monosomic and disomic F_1 hybrids are presented in Table 1. Considering the seed set per spikelet, cv. Chinese Spring produced 2.3 seeds, while the p-mst producded only 0.3 dented seeds per spikelet. F_1 hybrids involving cv. Chinese Spring and p-mst produced 0.1 more seeds than cv. Chinese Spring. All the 21 monosomic F_1 hybrids produced less number of seeds per spikelet than disomic F_1 hybrid. The degree of reduction varied from 1.7 seeds (4A x mst F_1) to 0.3 seeds per spikelet (3D x mst F_1). Two monosomic F_1 hybrids showed extremely high reduction in seed set, ie 1.7 in 4A x mst hybrid and 1.6 in 6B x mst hybrid. In appearance most of the seeds produced by monosomic F_1 hybrids of 4A and 6B were dented while in other cases the seeds were well filled.

The F_2 data showing the mode of segregation in different F_2 families including disomic cross, are presented in Table 2. A good fit to a ratio of 15 fertile : 1 sterile was obtained in the F_2's of the disomic cross (control) as well as in the 19 families of the monosomic F_2's. In crosses involving chromosomes 4A and 6B expected digenic segregation was not observed. 425 plants out of 576 from the progeny of monosomic 4A F_1 and 280 plants out of 381 from the progeny of

Table 1. Seed set in F_1 hybrids involving cv. Chinese Spring monosomics and genic male-sterility strain crosses.

Parents	No. of spikes	Spikelet number	No. of seeds	Seeds per spike	No. of seeds per spikelet
p-mst	11.3	26.5	87	7.7	0.3
CS disomic	11.0	25.6	638	58.0	2.3
CS disomic x mst	14.0	29.0	980	70.0	2.4
1A x mst	21	27	1170	55.7	2.1
1B x mst	19	25	971	51.1	2.0
1D x mst	22	29	1082	49.2	1.7
2A x mst	21	27	867	41.3	1.5
2B x mst	23	27	906	39.4	1.5
2D x mst	18	25	761	42.3	1.7
3A x mst	32	29	1443	45.1	1.6
3B x mst	10	27	396	39.6	1.5
3D x mst	27	29	1685	62.4	2.1
4A x mst	27	29	586	21.6	0.7†
4B x mst	21	25	770	36.6	1.5
4D x mst	17	29	581	34.7	1.2
5A x mst	14	27	753	53.7	2.0
5B x mst	20	25	964	48.2	1.9
5D x mst	19	25	827	43.5	1.7
6A x mst	26	27	1200	46.1	1.7
6B x mst	17	27	386	22.7	0.8†
6D x mst	21	29	1148	54.6	1.9
7A x mst	10	25	501	50.1	2.0
7B x mst	15	25	668	44.5	1.4
7D x mst	23	29	1145	49.8	1.7

†Monosomic F_1 hybrids with low seeds per spikelet.

monosomic 6B F_1 showed full fertility, while 151 plants from the progeny of 4A F_1 and 101 plants from the progeny of 6B F_1 showed partial sterility. Segregation pattern of fertile and sterile deviated significantly from the expected ratio of 15 fertile : 1 sterile which is expected if the chromosomes 4A and 6B are involved in the regulation of fertility trait. Based on these results it is suggested that the p-mst is controlled by two genes located on chromosomes 4A and 6B, respectively.

Discussion

The parents involved in the pedigree of p-mst strain are Selection 212, a wheat-rye recombinant (derived from the crosses involving monosomic 5B of cv. Chinese Spring, rye and var. Sonalika) and HD 2009 (an Indian wheat). P-mst strain is an highly evolved strain in the background of hexaploid wheat (2n=42).

Compared to other major cereals like maize, rice and barley, the number of spontaneously arisen mst mutants in wheat is low mainly because of its hexaploid nature. Genic male-sterility reported by Pugsley and Oram (1959), Lupton and Bingham (1966-1967), Athwal et al. (1967) and Lemekh et al. (1971) was associated with pollen sterility. The p-mst under report is genic male-sterility which is caused by the modification of anthers into ovaries. Central portion of p-mst spike exhibit a greater degree of anther transformation than the upper and lower parts of the spikes. On an average 10 to 12% seeds are produced by the p-mst plant. Similar genic male-sterility was reported by Jan and Qualset (1977), showing high influence of environmental factors over *ms* gene action. In the present case the p-mst is least influenced by environment.

The control of genic male-sterility strain was reported by one recessive gene (Singh 2002). For inheritance study p-mst was crossed with a fully fertile hexaploid wheat cv. Kundan. The results of monosomic analysis revealed the involvement of two recessive genes for controlling male-sterility in p-mst

Table 2. Segregation of F_2's of monosomic and disomic hybrids involving Chinese Spring monosomics and p-mst crosses

Hybrids	Fully fertile		Partially sterile		Total	χ^2 (fertile : sterile)	
	Obs.	Exp.	Obs.	Exp.		15:1	3:1
1A x mst	1021	1023.75	71	68.25	1092	0.12	-
1B x mst	894	892.50	58	59.50	952	0.04	-
1D x mst	927	930.00	65	62.00	992	0.16	-
2A x mst	801	802.50	55	53.50	856	0.05	-
2B x mst	951	941.25	53	62.75	904	1.62	-
2D x mst	702	705.94	51	47.06	753	0.35	-
3A x mst	1258	1259.06	85	83.94	1343	0.01	-
3B x mst	364	366.56	27	24.44	391	0.21	-
3D x mst	1606	1596.56	97	106.44	1603	0.89	-
4A x mst	425	432.00	151	144.00	576	391.85**	0.45
4B x mst	696	697.50	48	46.50	744	0.05	-
4D x mst	514	518.44	39	34.56	553	0.61	-
5A x mst	678	679.69	47	45.31	725	0.07	-
5B x mst	869	873.75	63	58.25	932	0.41	-
5D x mst	750	751.88	52	50.12	802	0.08	-
6A x mst	1050	1052.81	73	70.29	1123	0.12	-
6B x mst	280	285.75	101	95.25	381	266.92**	0.46
6D x mst	1016	1013.44	65	67.56	1081	0.10	-
7A x mst	460	462.19	33	30.81	493	0.17	-
7B x mst	608	610.31	43	40.69	651	0.14	-
7D x mst	1013	1016.25	71	67.75	1084	0.17	-
CS disomic x mst	881	873.75	51	58.25	932	0.96	-

**: Significant at the 1% level

strain. The genes have been located on chromosomes 4A and 6B. The difference in the results thus could be due to the variable parents used in the studies. In the inheritance study (Singh 2002) the p-mst was crossed with a recently released Indian hexaploid wheat (cv. Kundan) while in the monosomic study cv. Chinese Spring and its aneuploid lines were utilized. It is, therefore, assumed that for normal anther development cv. Chinese Spring carries two genes (on 4A and 6B) while cv. Kundan carries only one gene (on 4A). The gene located on chromosome 6B in cv. Kundan may be in recessive form.

Location of gene for mst trait on chromosome 4A confirms the finding of Driscoll (1975) and Kleijer and Fossati (1976) where *ms* genes of Pugsley and Probus mutants were located on chromosome 4A. Location of another gene for mst trait on chromosome 6B, is in support of the findings reported by Sears (1954) where it was reported that in nullisomic X (later changed to chromosome 6B) the stamens get replaced by pistils leading to male-sterility.

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Research article

Genetic analysis of quantitative and quality traits under varying environmental conditions in bread wheat

S.K. Joshi, S.N. Sharma*, D.L. Singhania and R.S. Sain

Department of Plant Breeding and Genetics, Rajasthan Agriculture University, Agricultural Research Station, Durgapura, Jaipur 302 018, Rajasthan, India

Summary

Genetic analysis was undertaken in 10 x 10 half parental diallel progenies (F_1 and F_2) for quantitative and quality traits under varying environmental conditions in bread wheat (*Triticum aestivum* L.). Genotype x environment interaction was found significant for all the characters in both F_1 and F_2 generations, indicating existence of non-linear response of genotypes to the varying environments. Both additive and non-additive gene effects were present in the material under study. However, the ratio of additive/non-additive genetic variance revealed that there was preponderance of additive gene effect in the expression of yield per plant, protein content and other yielding contributing traits studied. Both the gene effects were highly influenced by the environments. The parents WH 157, HD 2329 and HD 2285 were the best general combiners for grain yield and also high to average general combiners for most of the important traits. The parents HD 2285, Raj 3077, Lok-1 and Raj 1972 were the best general combiners to breed for higher protein content. The best specific cross for grain yield and protein content was Sonalika x WH 157 and Durgapura 65 x HD 2329, respectively. Biparental mating and/or diallel selective mating systems under favorable environment are suggested for a more tangible advancement in bread wheat.

Key words: bread wheat, combining ability, gene action, quantitative traits

Introduction

Wheat today occupies a unique position among cereals in India and attained a record 75.75 million tones of wheat production and continued to remain as the second largest producer of wheat in world. This achievement will go a long way in boosting the confidence of India in food security and to establish itself as a competitor in the global market. With all these achievements, the issue ahead are even more challenging. By the year 2020 India's population will be 1.3 to 1.4 billion and we visualize that to make available 180 g of wheat per person per day, the country should produce 109 million tones of wheat by 2020 (Nagarajan 2001). In India wheat grain is used by human beings mainly in the form of chapatti hence wheat cultivars with high baking quality will be preferred. The gliadin protein (a constituent of gluten) probably accounts for much of the baking differences observed among cultivars. Hence, there is need to develop high yielding wheat varieties with high protein.

An efficient breeding program is needed to break down the present plateau of productivity of wheat varieties. Grain yield, the major concerned of most crop breeders, is a complex character and is the result of interaction of many direct and indirect component traits, influenced by environmental fluctuations. As such it is difficult to manipulate yield through

* Corresponding author

recording yield alone. Several workers have suggested use of component characters as selection criteria for yield improvement. However, the compensatory effects and negative correlations between these traits may nullify improvement based on individual components. The experimental evidences clearly indicated that major yield components in wheat are tillers per plant, grains per spike and 1000-grain weight (Sharma and Kaul 1986; Maloo et al. 1993). Improving these direct and some other indirect components, grain yield can be improved. For this, combining ability studies are frequently used by plant breeders to evaluate newly developed genotypes for their parental usefulness and to assess the gene action involved in various characters, so as to design an efficient plan for further genetic upgrading of the existing material. However, the combining ability studies in a single environment may not provide precise information as environmental effects play an important role and greatly influence the combining ability estimates (Singh et al. 1986; Menon and Sharma 1994). Such information on combining ability analysis of wheat under varying environmental conditions is scanty. It is, therefore, necessary to assess combining ability, components of variance and combining ability x environment interaction for grain yield and its components to ensure better production and gain under selection. Present study deals with such endeavors.

Materials and methods

Ten varieties of bread wheat, *Triticum aestivum* L. Thell, namely, Raj 3077, CPAN 3004, HD 2428, Lok-1, Durgapura 65, Raj 1972, Sonalika, HD 2329, HD 2285 and WH 157 were crossed in all possible combinations excluding reciprocals. The 10 parents and their resulting 45 F_1's and 45 F_2's were grown in a randomized block design with three replications under early (E_1: 25th October), normal (E_2: 20th November) and late (E_3: 20th December) sown conditions at Agricultural Research Sub-Station, Tabiji, Ajmer, Rajasthan, India. Plots of parents and F_1's consisted of four rows of 3 m length while each plot of F_2 consisted of eight rows with the spacing of 30 cm between rows and 15 cm between plants. Twenty competitive plants in parents and F_1's and 60 plants in F_2 progenies were selected randomly for recording observations on twelve characters viz, days to heading (75%), days to maturity (75%), plant height (cm), flag leaf area (cm^2), Tillers per plant, spike length (cm), grain yield per spike (g), grains per spike, 1000-grain weigh (g), harvest index (%), grain yield per plant (g) and protein content (%) under each environment, separately. Six random samples of seeds from each parent and from every cross in both the generations in all the three environments were ground and powder was taken for protein estimation. Nitrogen percent of grain was estimated by micro-Kjeldhal's method and percentage of protein was obtained by multiplying percent nitrogen by the factor 6.25.

The mean of each plot was used for statistical analysis. The data were first subjected to the usual analysis followed for a randomized block design for pooled environments as well as for individual environment (Panse and Sukhatme 1967). The combining ability analysis was done following Method 2, Model 1 of Griffing (1956).

Results and discussion

The mean values for grain yield per plant and protein content of the parents exhibited variability among the parents under all the three environments (Table 1). Similarly, yield contributing traits also exhibited variability over environments indicated that diverse parents were used for present study. The pooled analysis of variance data revealed that in both the F_1 and F_2 generations significant differences among the genotypes existed and the genotypes also interacted significantly with environments for all the characters studied (Table 2). Significant differences between the environments were also observed, indicating the differences in the effects of environments on the expression of characters in both the generations.

Table 1. Mean values of parents for grain yield per plant and protein content(%) in three environments

Parent	Grain yield per plant			Protein content		
	E_1	E_2	E_3	E_1	E_2	E_3
Raj 3077	11.0	15.6	11.0	11.4	12.1	11.1
CPAN 3004	8.7	10.7	9.7	9.7	10.4	10.3
HD 2428	9.0	11.3	10.6	8.0	9.5	9.0
Lok- 1	12.0	13.1	12.2	10.5	11.9	10.8
Durgapura 65	10.6	12.4	11.0	10.2	11.3	10.0
Raj 1972	11.1	14.2	11.0	11.0	12.0	10.6
Sonalika	8.1	10.1	8.0	8.7	9.0	8.1
HD 2329	10.1	14.1	12.0	10.0	10.5	10.0
HD 2285	11.5	13.2	13.1	10.9	12.1	10.9
WH 157	9.3	12.0	9.9	10.0	11.4	10.3

Genotype x environment interaction was significant for each of the character in both F_1 and F_2 generations, indicating existence of non-linear response of genotypes of the varying environments. This is in conformity with the earlier reports of Allard and Bradshow (1964). In view of significant genotype x environment interaction for all the characters, the analysis of variance for individual environment was done for all the characters in all the three environments. The environment wise analysis of variance data revealed that significant differences existed among the parents as well as F_1's and F_2's for all the characters in all the three environments (sowing dates). The mean squares for parents vs F_1's and parents vs F_2's were also significant for most of the traits in different environments.

Combining ability analysis depicted that both general combining ability (gca) and specific combining ability (sca) variances were significant for all the characters in both the generations indicating the importance of additive and non-additive gene effects on the character expression (Table 3). The ratio between gca and sca variances titled in favor of general combining ability indicating the preponderance of additive gene effects in the genetic control for all the characters, except for flag leaf area (F_1 E_3), number of tillers per plant (F_2 E_2), grains per spike (F_1 E_3), and 1000-grain weight (F_1 E_1; F_1 and F_2 E_2), which indicated that these characters were primarily controlled by non-additive components of genetic variance. Results further exhibited that both gca and sca effects were not very consistent in different environments for most of characters in both the generations. The findings of Singh and Rana (1987), Pokhrel et al. (1993), Menon and Sharma (1995), Bhavasar et al. (1996) and Menon and Sharma (1997) are in agreement with the present results.

Both gca and sca exhibited highly significant interaction with the environments for grain yield and its components in both non-segregating (F_1) and segregating (F_2) generations, indicating the role of environment in

Table 2. Pooled analysis of variance showing mean squares of the data for parents, F_1s and F_2s for different characters in wheat.

Source	d.f.	Days to heading	Days yo maturity	Plant height	Flag leaf area	Tillers per plant	Spike length	Grain yield per spike	Grains per spike	1000-grain wight	Harvest index	Grain yield per plant	Protein content
P vs F_1													
Environments(E)	2	868.2**	4056.2**	9670.0**	236.9**	12.9**	62.4**	10.8**	309.6**	5319.6**	2745.0**	808.0**	58.1**
Replications(R)	2	0.5	8.3	4.4	0.4	0.2	0.4	92.3	4.0	1.8	0.1	2.2	2.3
R x E	4	0.4	3.4**	1.2**	0.2	6.8	0.3	73.2	0.9	0.4	0.6	6.6	3.1
Genotypes(G)	54	405.2**	545.0**	489.0**	28.4**	5.2	8.8**	0.5**	251.2**	258.2**	287.9**	10.6**	7.5**
G x E	108	4.9**	46.9**	181.1**	42.1**	1.6	2.1**	0.2**	29.0**	65.9**	23.0**	2.9**	0.4**
Error	324	0.8	1.0	27.1	0.4	0.9	0.3	19.5	4.6	0.1	0.7	9.9	0.4
P vs F_2													
Environments(E)	2	1569.4**	280.6**	633.6**	599.0**	26.3**	49.8**	8.6**	607.1**	6694.7**	2012.2**	722.0**	84.1**
Replications(R)	2	2.2	11.7**	4.5	3.1**	0.5	2.4**	0.1	1.5	3.2**	0.4	1.9**	0.8**
R x E	4	0.2	4.4	0.3	0.7	0.1	0.3	0.2	0.3	0.1	0.5	0.2	0.1**
Genotypes(G)	54	355.4**	544.8**	652.9**	36.1**	4.6**	10.2**	0.4**	263.2**	199.3**	230.5**	11.6**	7.2**
G x E	108	32.1**	41.7**	136.1**	4.0**	1.4**	1.7**	8.2**	14.2**	73.9**	19.7**	3.3**	1.2**
Error	324	0.9	0.6	24.2	0.3	0.2	0.4	0.2	6.3	0.1	0.1	0.5	0.1

** Significant at the 1% level

influencing the gene effects, which further complicated the problem of identification of promising parents and crosses. Other studies (Dasgupta and Mandol 1988; Menon and Sharma 1994, 1997) substantiate this point. However, gca x environment interaction variances were higher than sca x environment variances for almost all the traits, further signifying the importance of additive genetic variance for yield components. Thus, it may be concluded that the variances due to gca is by and large more important in a crop like wheat.

A perusal of the general combining ability (gca) estimates over the environments showed that parents HD 2285, HD 2329 and Raj 1972 were good general combiner for grain yield per plant in both the generations under all the three planting dates (Table 4). The parent Durgapura 65 also emerged as good general combiner for grain yield per plant. Results further indicated that parents HD 2285, Raj 3077, Lok-1 and Raj 1972 were the best general combiners to breed for higher protein content (Table 4). The general combining ability analysis estimates of yield contributing traits over environments further depicted that WH 157 emerged as good general combiner for flag leaf area, tillers per plant, spike length, grain yield per spike and grains per spike. Similarly parent HD 2329 and HD 2285 were suitable for earliness, plant height, flag leaf area, grain yield per spike, 1000-grain weight and harvest index, and HD 2285 and Raj 3077 were also good combiner for grains per spike. Sonalika was observed good general combiner for 1000-grain weight and earliness. Apparently, therefore, it is still further scope for improving upon the combining ability for component traits as none of the combiners for grain yield was a high combiner or at least an average combiner for all the desirable traits. It seems feasible that the gca rank for grain yield is related to the gca for the useful yield components. It is therefore, recommended that the breeder should breed for superior combining ability for the components traits with an ultimate objective to improve the over all gca for grain yield in wheat. The parents HD 2285, HD 2329 and Raj 1972 could be utilized intensively in hybridization program to accelerate the pace of genetic improvement of grain yield in bread wheat. The parents HD 2285, Raj 3077, Lok-1 and Raj 1972 exhibited highly significant positive gca effects in all the environments both in F_1 and F_2 generations and hence, they were to be considered to breed for higher protein content. The parents HD 2285 and Raj 1972 can be intensively used in the hybridization program aimed at amelioration of grain yield and protein content through development of new plant type in bread wheat.

In order to synthesize a dynamic population with most of the favorable genes accumulated, it will be pertinent to make use of the aforesaid parents, which are good general combiner for several characters, in a multiple crossing program. Apart from conventional breeding methods resting slowly upon additive or additive x additive type of gene action, population improvement appears to be a hopeful alternative. Diallel selective mating system (Jensen 1970) sounds to be a good technique, which delays quick fixation of gene complexes, permits breakdown of linkage, general fostering of recombinations and concentration of favorable genes/gene complexes, into central gene pool, by a series of multiple crosses.

Normally the sca effects do not contribute tangibly in the improvement of self-fertilizing crops, except where commercial exploitation of heterosis is feasible. Breeder's interest, therefore, vests in obtaining transgressive segregants through crosses and producing more potent homozygous lines. Jinks and

Table 3. Analysis of variance showing mean squares for combining ability in individual environment for different characters in wheat

Character	E	Source							
		gca (9)†		sca (45)		error (108)		gca : sca	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Grain yield per plant	E_1	2.5**	2.4**	0.7**	0.7**	0.02	0.03	3.3:1	3.2:1
	E_2	4.3**	4.8**	2.6**	2.8**	0.04	0.04	1.5:1	1.6:1
	E_3	2.5**	2.3**	1.2**	1.8**	0.03	0.02	1.9:1	1.2:1
Protein content	E_1	3.2**	2.6**	0.5**	0.7**	0.02	0.01	6.0:1	3.5:1
	E_2	3.2**	2.8**	0.6**	1.0**	0.01	0.00	5.1:1	2.8:1
	E_3	1.7**	2.7**	0.5**	0.4**	0.02	0.01	2.8:1	5.7:1

** Significant at the 1% level, † Degrees of freedom is given in parentheses.

Jones (1958) emphasized that the superiority of the hybrids might not indicate their ability to yield transgressive segregants, rather sca would provide satisfactory criteria.

The analysis of specific combining ability effects revealed that in the present investigation none of the hybrids showed consistency for their high sca effect for all the characters in different environments. The desirable crosses (on the basis of per se performance, high sca effects and heterosis) for grain yield per plant were Sonalika x WH 157, Lok-1 x Durgapura 65, Sonalika x HD 2285, CPAN 3004 x Raj 1972, HD 2428 x WH 157, HD 2329 x WH 157, HD 2428 x Durgapura 65, CPAN 3004 x HD 2329 and Durgapura 65 x Sonalika for either one or two environments. These crosses were also found superior for one or more yield contributing characters ie CPAN 3004 x Durgapura 65 for spike length and HD 2428 x Sonalika for tiller per plant and 1000-grain weight; Sonalika x HD 2285 for grains per spike; Lok-1 x Durgapura 65 for harvest index, spike length and grains per spike; HD 2329 x WH 157 for tiller per plant and grains per spike and HD 2428 x WH 157 for flag leaf area. The best crosses for protein content were Durgapura 65 x HD 2329, CPAN 3004 x WH 157, HD 2428 x HD 2329, Raj 1972 x WH 157, HD 2428 x Raj 1972 and HD 2329 x HD 2285. This information of the above desirable crosses may be used in making an appropriate choice of the parents in a crossing program involving multiple parents for tangible advancement of grain yield in bread wheat.

In the present study, comparison of sca effects of these top crosses and gca effects of their parents indicated that such crosses in general involved one parent with good gca effect and the other with poor or average gca effects. Hence, the presence of at least one good general combiner appeared to be desirable for getting the better hybrids. The sca effects of the crosses under different environments were also considered for tangible advancement of various characters as well.

The sca effects for all the characters were in accordance with per se performance indicated by highly positive correlation between hybrid performance and sca effects calculated from both the generations (Table 5). However, the relative ranking of the best crosses on the basis of sca effects and per se performance exhibited slight differences. Thus, crosses which would give the highest sca effects would not necessarily give the highest mean values as later the realized value was good for all the characters, studied. Invariably the crosses showing high sca effects for grain yield revealed that higher sca effects would be observed for at least one or more of its component characters.

It is interesting to note that sca effects of top crosses in our study and gca effects of their parents indicated that majority of the good specific cross combinations was the result of good x good or poor x poor combinations. Thus, it was evident that good cross combination is not necessarily the result of good x good combination of parents, rather it might occur from poor x poor combinations as well. A number of studies also refer to such a situation (Chaudhary and

Table 4. Estimates of general combining ability effects for different characters in three environments

Parent	Grain yield per plant						Protein content					
	E_1		E_2		E_3		E_1		E_2		E_3	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Raj 3077	0.06**	–0.15**	–0.20**	–0.25**	–0.65**	–0.67**	0.57**	0.61**	0.38**	0.07**	0.24**	0.12**
CPAN 3004	–0.69**	–0.73**	–0.33**	–0.34**	–0.52**	–0.61**	–0.13**	–0.47**	–0.28**	0.11**	0.08**	0.29**
HD 2428	–0.02**	–0.15**	0.11**	0.05**	0.03**	0.03**	–0.51**	–0.29**	–0.44**	0.16**	–0.15**	–0.34**
Lok- 1	0.26**	0.45**	–0.08**	–0.42**	–0.07**	0.02**	0.34**	0.35**	0.49**	0.49**	0.22**	0.30**
Durgapura 65	0.58**	0.46**	–0.09**	0.86**	0.01**	0.01**	–0.01**	0.17**	0.01**	–0.04**	–0.30**	–0.11**
Raj 1972	0.30**	0.20**	0.98**	1.05**	0.42**	0.35**	0.38**	0.17**	0.45**	0.16**	0.17**	0.44**
Sonalika	–0.82**	–0.73**	–1.16**	–1.08**	–0.54**	–0.38**	–1.11**	–0.92**	–1.11**	–1.25**	–0.86**	–1.17**
HD 2329	0.12**	0.10**	0.85**	0.84**	0.67**	0.53**	–0.06**	–0.05**	–0.18**	–0.14**	0.00	–0.06**
HD 2285	0.44**	0.53**	0.06**	0.48**	0.50**	0.59**	0.75**	0.52**	0.61**	0.47**	0.54**	0.43**
WH 157	–0.04**	0.03**	–0.14**	–0.31**	0.14**	0.13**	–0.05**	–0.08**	–0.02**	–0.03**	0.05**	0.07**
SE (g_i) ±	0.018	0.002	0.032	0.003	0.023	0.002	0.016	0.000	0.050	0.000	0.012	0.001
SE (g_i-g_j)	0.040	0.004	0.071	0.008	0.052	0.004	0.036	0.002	0.000	0.000	0.027	0.002

*, ** Significant at the 5% and1% level, respectively

Table 5. Correlation between the parental mean and general combining effect in both F_1 and F_2 generations in wheat

Character	gca vs mean		sca vs mean	
	F_1	F_2	F_1	F_2
Days to heading	0.91**	0.88**	0.62**	0.65
Days to maturity	0.85**	0.80**	0.72**	0.75**
Plant height	0.84**	0.79**	0.77**	0.90**
Flag leaf area	0.83**	0.82**	0.89**	0.86**
Tillers per plant	0.84**	0.77**	0.81**	0.88**
Spike length	0.92**	0.91**	0.73**	0.80**
Grain yield per spike	0.41**	0.71**	0.75**	0.85**
Grains per spike	0.69**	0.87**	0.90**	0.87**
1000-grain weight	0.70**	0.65**	0.95**	0.89**
Harvest index	0.77**	0.85**	0.76**	0.77**
Grain yield per plant	0.79**	0.87**	0.84**	0.86**
Protein content	0.93**	0.86**	0.75**	0.76**

** Significant at the 1% level

Paroda 1979; Sheikh et al. 2000; Singh 2002). High sca effects of good x good combiners reflect additive x additive type of gene interaction and that superiority of favorable genes contributed by the parents. While those involving good x poor or poor x poor general combiners indicated the interaction of additive x dominance or dominance x dominance, respectively. Biparental progeny selection suggested by Andrus (1963) could be used to get some transgressive segregants from crosses good x good or good x average combinations for genetic improvement of the traits.

Present study confirmed that additive as well as non-additive gene effects controlled the expression of most of the characters under all the sowing dates. Hence, non-conventional breeding methods such as biparental mating (Joshi and Dhawan 1966) or diallel selective mating (Jensen 1970) in addition to conventional breeding methods were suggested for amelioration of grain yield through manipulating its component characters.

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Research article

Maximization of wheat yields with a unique variety in warmer areas

S.N. Sharma, V.K. Bhatnagar, M.S. Mann, U.S. Shekhawat and R.S. Sain

All India Coordinated Wheat and Barley Improvement Project, Rajasthan Agricultural University, Agricultural Research Station, Durgapura, Jaipur 302 018, Rajasthan, India

Summary

Breeding program for increasing wheat production in the warmer areas of India exhibited that wheat variety Raj 3765 has greater potential for sustaining the green revolution in new paradigms. It was developed from two genetically diverse cultivars (*Triticum aestivum* L.) through single cross (HD 2402/VL 639). This variety exhibited a higher level of productivity under both late sowing and very late sowing environments. Besides other desirable quality attributes, it possesses superior grain quality along with fairly high degree of resistance to rusts. Genetically, it is blessed with resistance to Lr23+10, Sr2+ rust races. It is a marvelous and reliable wheat variety that offers excellent degree of tolerance to initial and terminal heat under various sowing environments (normal, late and very late) in North Western Plains Zone (NWPZ) of India. Wheat Varietal Release Committee (AICWIP) recommended this variety for late sowing (1994) as well as for very late sowing (1998) in NWPZ of the country. Zonal Research and Extension Advisory Committee (ZREAC) recently recommend this variety for normal sown condition (2000) under mega environment of Rajasthan. The production of this variety can offer an exciting opportunity for overcoming the stagnating yield plateau of wheat in warmer areas of India and also to alleviate the socioeconomic status of the subsistent Indian farmers.

Key words: wheat, cultivars, rust resistance, terminal heat stress, grain yield

Introduction

Over 7 million hectares of wheat grown in approximately 50 countries are subjected to continual heat stressing environments with mean daily temperatures greater than 17.5°C in the coolest month of the year (Zhong-Hu and Rajaram 1994; Guha Sarkar et al. 2001). At least as great an area may experience heat stress at the end of the growth cycle, as occurs in the North Western Plains Zone (NWPZ) and North Eastern Plains Zone (NEPZ) of India. Hence, national program leaders identified improving heat tolerance of wheat as being a major research priority. Crop yield is determined by the interaction of genotype, management and environment. Water availability and temperature are the major environmental variables affecting crop yield. Howard (1924) while analyzing the factors controlling wheat production remarked, "wheat production in India is a gamble in temperature". This statement is valid even today. The cultivation of wheat is limited by temperature at both ends of the cropping season and high temperature stress has an adverse effect on wheat productivity. The present day rice-wheat cropping system, keeping in view of monsoonal irregularities, has compelled wheat crop to be subjected to rapidly ascending temperatures coupled with hot dry winds during the post anthesis stage, specially during grain development. These unfavorable environments terminate grain growth prematurely and reduces yield considerably. It has already been established that high temperature stress can be a significant factor in reducing yield and quality of wheat (Stone and Nicolas 1995). Wardlaw (1994) also reported that mean temperature greater than 15–18°C following anthesis can result in decrease in grain weight at maturity. Breeding program for heat

tolerance is an integral component of wheat breeding program at both national and international level (Acevedo et al. 1990). These programs will not only help in spreading wheat cultivation to nontraditional warmer areas besides, optimizing wheat yield in more tropical environments under the present situation of multiple-cropping system. Approximately, 3.0 million hectare area in northeastern and northwestern plains zone is exposed to terminal heat stress, which at grain filling stage blocks the synthesis and mobilization of photosynthates and results in shriveling of the grains. Hence there is an urgent need for the introduction of wheat varieties tolerant to terminal high temperature stress in India to meet the projected target of production of wheat ie, 105 million tones by 2020 AD.

Modern varieties of wheat are well adapted to control cultural practices, but they are generally not highly tolerant to extreme environmental stresses, such as high temperature. The varieties of one region are generally not suitable for the others, and separate breeding objectives will be needed for each situation (Rajaram 1988). Since plant tolerance to temperature stress is heritable, selection and breeding can be used to improve this trait. The objective of the present study was to establish a pure line for release as a commercial variety for warmer areas of India. Keeping this scenario in view, a specific breeding program was initiated for the development of high yielding and disease resistant varieties. A new wheat variety Raj 3765 has been developed in India, which has genetic potential for excellent performance under different environments (late and very late planting) in the major wheat-growing zone (NWPZ) of the India. Farmers can enjoy the rich harvest with Raj 3765 every year in warmer areas under different prevailing crop rotations particularly in rice-wheat farming system. This paper describes the development, performance, resistance to rusts and quality parameters of this new wheat variety.

Materials and methods

Wheat improvement for heat tolerance depends on intensive hybridization using heat tolerant donors and high yielding cultivars. For meeting immediate varietal needs, two genotypes (parents) namely, HD 2402 and VL 639 were selected from National Germplasm Screening Nursery on the basis of desirable developmental traits for heat tolerance. The parent HD 2402 was selected for earliness (perhaps favored the plant to escape the losses due to rise in temperature) and profuse tillering (contributor to grain yield). Whereas, the parent VL 639 was selected on the basis of higher grains per spike, biomass, harvest index and test weight. In the breeding program, attempts were made to incorporate genes for tolerance to heat and yield contributing traits along with resistance to various prevailing rust races. The varietal developmental program was initiated at Rajasthan Agricultural University, Agricultural Research Station, Durgapura, Jaipur, Rajasthan, India. Hybridization between the chosen parents (HD 2402/VL 639) was attempted. The expanded pedigree of this cross is BJ 66 SIB/NAD/63/LR 64 A/5/SL SIB/NP 852/4/PJ SIB/P14/KT 54 B/3/K 65/VL 639. Conventionally segregating generations of this cross were handled by pedigree selection program under late sown conditions (50th meteorological week) only. In this breeding method superior individual plants were selected in successive generations (F_2–F_5) under artificial epiphytotic conditions of rusts and a complete record of parent progeny relationship was maintained. For screening homozygous heat tolerant lines from advanced materials (F_6), sowing was done both in late and very late sown conditions to expose the crop to terminal heat stress. On the basis of various developmental traits for heat tolerance like earliness, high tillering, high number of spikelets per spike, high number of grains per spike, 1000-grain weight, grain yield per plant, reaction to important diseases and grain quality parameters, the most promising, homozygous line was screened out and named Raj 3765. Based on multi-location station trials in Rajasthan under late and very late sown conditions, this variety exhibited higher grain yield, resistance to rusts and desirable quality parameters. Hence, this variety was included into different varietal yield evaluation trials for normal sown (46th meteorological week), late sown (50th meteorological week) and very late sown (52nd meteorological week) conditions for three years at different locations of NWPZ of India under the All India Coordinated Wheat Improvement Project (AICWIP). In first year (Initial varietal trial) the trial was conducted in double lattice design and onwards (Advance varietal trial) in randomized block design was conducted under varietal testing programs at all locations across the zone (NWPZ). The mean averaged over locations for different traits has been given only for Raj 3765 and check varieties for interpretation of the results in this paper, although a number of other varieties were also tested in the coordinated trials.

To assess the adaptability in different date of sowings of this variety, the agronomical coordinated trials were planted under irrigated conditions at 46th (normal), 50th (late) and 52nd (very late) meteorological week. The experiment was laid out in

split plot design with four replications. The sowing was done in rows, 23 cm apart in normal sowing and 18 cm apart in late and very late sowings by drill method. Besides other recommended practices, six irrigations (at crown root initiation, late tillering, late jointing, flowering, milk stage and dough stage) were applied to raise the crop.

The resistance of Raj 3765 to rusts was tested with the help of AICWIP pathologists at several locations under epiphytotic conditions in the country. The standard inoculation and post-inoculation procedures and practices (Joshi et al. 1982; Nagarajan and Nayar 1986) were followed to generate comparable information. Host-pathogen interactions were scored into various grades following Stakman et al. (1962) for black rust, Johnston (1963) for brown rust and Jhonson et al. (1972) for yellow rust.

Quality laboratory under coordinated program assisted in screening varieties for different quality parameters required at the time of release of the variety. The evaluation of different quality parameters of the variety was made as suggested by Hanslas (1986).

Results and discussion

The high temperature prevailing during crop season hinders productivity of wheat. Various physio-chemical processes are responsible for heat tolerance in wheat varieties. To find out the genetic variation with regards to these parameters among certain varieties in wheat would be of great value to harvest higher yield in the warmer areas. Higher grain yield particularly under high temperature of late sown conditions, indicates presence of genes for heat tolerance. Raj 3765 was found suitable under late sown conditions for grain yield. This indicated that this variety has tolerance to the damage to the high temperature. This genetic resource can be used directly as a commercial variety for the warmer areas or may be useful for improvement of thermo tolerance in wheat. The main morphological characteristics of Raj 3765 are light green, non-waxy leaves, profuse tillering, intermediate and erected ears that turn dusty white at maturity and possess medium bold, amber and lustrous grains. The results obtained are enumerated below.

Late sown-irrigated condition : The analysis of varietal yield evaluation trials over 37 locations (1992–94) revealed that variety Raj 3765 significantly out yielded all check varieties in all the three years except in the third year, where it yielded as good as check PBW 226 (Table 1). The average mean yield of Raj 3765 under three years testing in trials across NWPZ was recorded 4.21 t/ha. This variety yielded 21.3%, 11.9%, 4.5%, 4.9% and 15.4% higher grain yield over Sonalika, HD 2285, PBW 226, Raj 3077 and UP 2338 check varieties, respectively.

The results of agronomic experiments of date of sowing and varieties under three environments (1993–

Table 1. Grain yield and rust reactions of Raj 3765 and check varieties in varietal yield evaluation trials under late and very late sown conditions in NWPZ of India

Variety	Zonal yield (t/ha)				Rust reaction †					
	1st year	2nd year	3rd year	Mean	Black	ACI	Brown	ACI	Yellow	ACI
Late sown-irrigated conditions (1992–94)										
Raj 3765	4.65	4.13	3.86	4.21	-	-	40 S	12.8	5 S	1.8
Sonalika	3.54	3.64	3.24	3.47	10 MS	-	100 S	72.9	60 S	34.0
HD 2285	4.10	3.60	3.60	3.77	-	-	100 S	81.4	40 S	10.2
PBW226	4.34	3.87	3.88	4.03	30 MR	-	80 S	38.6	30 S	7.5
Raj 3077	4.12	3.91	-	4.02	20 MR	-	80 S	62.1	10 S	3.0
UP2338	-	-	3.65	3.65	-	-	40 S	20.2	0	-
CD at 5%	0.17	0.10	0.10	-	-	-	-	-	-	-
Very late sown-irrigated condition (1996–98)										
Raj 3765	2.71	3.38	2.62	2.90	0	-	5 MS	0.4	5 S	2.6
Sonalika	2.48	3.02	2.05	2.52	0	-	60 S	33.6	60 S	-
HD 2285	2.56	3.41	2.29	2.75	0	-	100 S	52.8	60 S	30.1
C.D at 5%	0.21	0.11	0.12	-	-	-	-	-	-	-

† Maximum reaction and average coefficient of infection (ACI) during three years testing
S: susceptible, MS: moderately susceptible, MR: moderately resistant

94) at 6 locations of NWPZ of India exhibited that Raj 3765 variety yielded 3.98 t/ha under late sown conditions. However, mean yield over three environments was recorded 3.80 t/ha, which was numerically higher than all the three check varieties (Table 2). Raj 3765 also showed better performance under normal and very late sown conditions. Over all results of agronomical trials suggested that this variety is endowed with inherent mechanism of genetic homoeostasis. This enables a higher level of productivity both under optimum and suboptimum environments and permits stability and sustainability of production in NWPZ of India. The studies of morpho-physiological traits revealed that Raj 3765 showed high grain yield and high values of other yield contributing traits like shorter grain filling period (32.9 days), tillers per plant (5.8), flag leaf area (19.9 cm^2), spike length (10.6 cm), spike area (33.3 cm^2), grains per spike (43.2), grain yield per spike (1.7 g), harvest index (43.6%) and grain yield per plant (9.3 g) under warm condition. Hence, it gave higher grain yield and sustained productivity as compared to the widely cultivated late sown varieties (HD 2285, PBW 226 and UP 2338) under hotter environment. These results confirmed that Raj 3765 is the most stable among the check varieties for warm conditions therefore, it was recommended by AICWIP for late sown condition in 1994.

Very late sown-irrigated condition : The results of varietal yield evaluation trials over 28 locations (1996–98) revealed superiority of Raj 3765 in grain yield over check variety Sonalika during all the three years. However, it yielded as good as checks HD 2285 (Table 1). Over the years Raj 3765 gave maximum yield (2.90 t/ha) as compared to the checks. This variety produced 13.1% and 5.2% grain yield over Sonalika and HD 2285 check varieties, respectively. Results clearly exhibited superiority of Raj 3765 over widely cultivated current varieties under very late sown conditions, which were used as checks during experimentation in the trials of NWPZ.

The results of agronomic trials (1997–98) of NWPZ of India indicated that Raj 3765 variety gave significantly higher grain yield over all the checks in both the late and very late sowing conditions (Table 3). This variety gave 20.4% and 13.7% higher yield over Sonalika and HD 2285, respectively, under very late sown condition. The results of yield components exhibited that Raj 3765 had maximum number of tillers per m^2 (362.9), grains per spike (41.4) and 1000-grain weight (34.7 g) as compared to the check varieties (Sonalika and HD 2285) under warm

Table 2. Effect of date of sowing on grain yield (t/ha) of Raj 3765 and check varieties suitable to late sown condition during 1993–94 in NWPZ of India

	Sowing condition	Raj 3765	HD 228	PBW 226	UP 2338
Yield (t/ha)	Late sown	3.98	4.13	3.85	3.84
Percent gain or loss	Normal sown	+8.8	–8.7	+9.1	+11.1
	Very late sown	–22.2	–32.7	–16.1	–24.5
Mean yield (t/ha) over environments		3.80	3.56	3.76	3.71
C.D. at 5%					
Date of sowing (A) 0.15	Varieties (B) 0.29	B within (A) NS	A within (B) NS		

Table 3. Effect of date of sowing on grain yield (t/ha) of Raj 3765 and check varieties suitable to very late sown condition during 1997–98 in NWPZ of India

Variety	Time of sowing		Mean	Tillers per m^2	Grains per spike	1000-grain weight (g)
	Late	Very late				
Raj 3765	3.64	2.83	3.23	362.9	41.4	34.7
Sonalika (C)	3.07	2.35	2.71	340.6	35.6	35.5
HD 2285 (C)	3.31	2.49	2.90	352.4	39.0	33.6
C.D. at 5%						
Date of sowing (A) 0.08	Varieties (B) 0.26	B within (A) NS	A within (B) NS			

conditions indicated that this variety had better stability through these yield contributing traits to sustain productivity under heat stress environment (Table 3). Mean yield performance of wheat variety Raj 3765 in very late sown trials (1996–98) conducted at different locations of NWPZ and NEPZ of India revealed that this variety gave 15.4% and 8.6% higher grain yield over Sonalika and HD 2285 check varieties, respectively (Table 4). Results further exhibited that out of 28 locations, Raj 3765 was qualified in top group at 14 locations. Thus, these results clearly established that Raj 3765 is an excellent wheat variety, which offered persistent good response under late and very late sown conditions. Physiological studies in AICWIP revealed that the variety remained plastic to changes in climatic factors and found more tolerant to heat with minimum membrane injury, confirming its inbuilt mechanism for stresses. Hence, it was further recommended by AICWIP for very late sown situation in 1998.

This variety is also preferred by the farmers of Rajasthan for cultivation under normal sowing due to higher yield along with excellent grain quality, which provided them high premium in domestic market. This variety gave yield as good as Raj 3077 (4.0–5.0 t/ha). Raj 3077 is being occupied more than 50 percent area in the state but for the last 3–4 years it was observed susceptible to rusts under natural condition. In recognition of higher stability along with better productivity and resistance to rusts under mega environment of Rajasthan, this wheat variety was also recommended for normal sown irrigated condition for the whole state by the Zonal Research and Extension Advisory Committee (2000). Hence, recently this multifaceted wheat variety was further included in the package of practices for normal sown condition. Excellent performance of Raj 3765 to harvest higher yields along with better premium of produce in the domestic market, it has recently been attracted the farmers of Rajasthan to grow on more areas in normal sown condition too.

The most commonly grown wheat variety Sonalika and HD 2285 developed for such late sown situation have become low yielder in recent years due to susceptibility to brown and yellow rusts under field conditions. Similarly, a multifaceted wheat variety Raj 3077, promising varieties PBW 226 and UP 2338 have also become susceptible to rusts under natural conditions. Therefore, the need of another early maturing wheat variety coupled with high yield, heat

Table 4. Mean yield (t/ha) performance of Raj 3765 in very late sown trials conducted during 1996–98 at different locations of NWPZ and NEPZ wheat zones of India

	1995–96	1996–97	1997–98	Mean	Percent increase †	Frequency in the top group
Raj 3765	2.71	3.38	2.62	2.90		14 / 28
Sonalika	2.48	3.02	2.05	2.51	+15.4	5 / 28
HD 2285	2.56	3.41	2.05	2.67	+8.6	10 / 28
C.D. at 5%	0.21	0.17	0.12			

† Raj 3765 yield over Sonalika and HD 2285, respectively

Table 5. Agronomic and qualitative attributes of Raj 3765 and check varieties in varietal yield evaluation trials under late and very late sown conditions in NWPZ of India

Variety	Days to heading	Days to maturity	Plant height (cm)	1000-grain weight (g)	Protein (%)	Hectrolitre weight (kg)	Chapatti making score (1-10)
Late sown- irrigated condition (1992–94)							
Raj 3765	81	120	92	39	12.1	76.5	8.1
HD 2285	79	119	93	36	11.6	76.8	8.1
PBW 226	79	118	94	37	11.9	77.4	7.7
UP 2338	87	121	88	28	12.5	73.3	8.1
Very late sown -irrigated condition (1996–98)							
Raj 3765	68	101	78	35	12.5	75.7	8.2
Sonalika	63	99	84	37	12.2	74.2	8.6
HD 2285	67	100	77	34	11.9	75.9	7.7

tolerance and rust resistance was considered imperative for wheat breeders to meet the challenges of environmental constraints. The results of plant pathological screening nursery (1992–94; 1996–98) revealed that Raj 3765 variety has fairly high degree of resistance to rusts as compared to check varieties under different situations in the major wheat growing mega environment of NWPZ of India (Table 1). The research carried out on this aspect shows that Raj 3765 variety combining more than one gene (L r 23 + 10, Sr2 +) for resistance to maintain long lasting resistance (Nayar et al. 1994). Characterization of adult plant resistant genes (APR) studies repeated over years at Flowerdale, Shimla has shown the presence of race specific APR in Raj 3765 (Nayar 2001).

Quality attributes of the grains are decisive for the success of variety and also to fetch the remunerative price in domestic as well as in international market. Assessment of quality characteristics of Raj 3765 in different sowing environments of NWPZ showed that this variety has desirable quality parameters viz, mean protein value (11.8–12.5%), good chapatti score (8.0–8.2), good hectoliter weight (75.7–77.3 kg) and 1000-grain weight (36–41 g) which is preferred by the Indian consumers (Table 5). Besides this, Raj 3765 possesses superior grain quality comparable with desi wheat, preferred in local market on higher prices.

In built mechanism of this variety for higher yield along with heat tolerance and rust resistance, it is considered imperative to meet the challenges of environment constraints. Hence, Raj 3765 has potential to open up new vistas of boosting wheat production under mega environment of NWPZ, where new cropping sequences are emerging to produce more food for extra mouths and to earn more profitability from per unit area.

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Research article

Variation in genotypic responses of Indian hexaploid wheats for haploid production in crosses with maize

G. Najafian* and T.B. Singh

Department of Genetics and Plant Breeding, College of Agriculture, G.B. Pant University of Agriculture & Technology, Pantnagar 263 145, Uttaranchal, India

Summary

To study genotypic effects of wheat plant on haploid production through wheat x maize crossing, five F_1 hybrids of wheat (W_1–W_5) obtained from crossing of different hexaploid wheat varieties were pollinated with pollen from a composite variety of maize Kanchan in outdoor conditions. Cut glume method was used for emasculation. Hormonal treatment was 75 ppm solution of 2,4-D for two days after pollination and 300 ppm solution of gibberellic acid on the 3rd day. Seed set, rates of embryo formation, embryo germination and plantlet recovery were studied. Seed set was not directly affected by wheat genotypes. Response of wheat genotypes was different for embryo formation rate. The best genotype was W_1 with 12.8% embryo formation, while the poorest genotype W_2 showed 2.5% embryo formation. The pollen tube growth measurements inside the stigma conducted on W_1 and W_5 crosses showed a significant difference; W_1 had a higher mean of pollen tube length than W_5, which was in agreement with their embryo production percentage. It was suggested that growth of maize pollen tube inside the stigma of wheat genotypes followed by embryo production might be under control by some unknown crossability systems different from that by *Kr* genes. No genotypic effect was observed for embryo germination and plantlet recovery.

Key words: genotypic effects, haploid production, *Triticum aestivum*, wheat x maize crosses.

Introduction

Haploid breeding has potential of integration in wheat breeding programs, because of the production of homozygous lines from F_1 generation of a particular cross within a short period of time compared with other traditional methods. To be used successfully and cost-effectively in a breeding program any particular doubled haploid (DH) system should fulfil the following three criteria (Snape et al. 1986). These are 1) easy and consistent production of large number of DHs of all genotypes. 2) DHs should be genetically normal and stable and 3) DHs should contain a random sample of the parental gametes.

Production of wheat haploid plants through wheat x maize crossing, which at first was performed by Laurie and Bennett (1988), appears to fulfil above three criteria. This method has been suggested as a more perfect procedure of haploid induction in hexaploid wheats compared to the earlier procedures including anther/microspore culture and *bulbosum* system. So far several studies have reported the genotypic effect of wheat parent for percentage of embryo formation (eg Suenaga et al. 1991; Riera and Mujeeb-Kazi 1993; Giura 1994; Sadasivaiah et al. 1999). Some of these studies have shown the ineffectiveness or less effect of *Kr* crossability genes

*Corresponding author: Agricultural Research Centre, Blvd. Keshavarz, Sepah square, Kermanshah, Iran, Post code 67154 - 41769 e-mail: gnajafian@yahoo.co.uk

in wheat x maize crosses but still it is not fairly clear whether these genotypic effects are output of a crossability system (Laurie and Bennett 1987). The *Kr* crossability genes are effective through preventing or reducing the growth rate of male parent pollen tube inside the style or ovary of wheat flowers in case of wheat x *Secale cereale* and wheat x *Hordeum bulbosum* crosses. In consequence, there would be no or less number of embryos in such crosses (Falk and Kasha 1981, 1983; Sitch and Snape 1987).

In this study, through crossing of Indian hexaploid wheat genotypes with maize, the genotypic effect of wheat parent was studied on some characteristics of wheat x maize crosses including pollen tube growth.

Materials and methods

Plant materials : Five F_1 hybrids of hexaploid wheat were used as female parents in crosses with maize. These F_1 wheats referred to as W_1–W_5 were produced from crossing of different parents (Table 1). Maize genotype Kanchan, which is a composite cultivar, was used as a pollen parent in the wheat x maize crosses. Planting conditions, wheat x maize crossing, embryo rescue and regeneration of plantlets: Wheat genotypes (W_1–W_5) were planted under field conditions of Pantnagar University at two planting dates in November. Maize plants were planted in pots at two planting dates in glasshouse under natural temperature and light conditions. Eight more plantings of maize were done under outdoor conditions at weekly intervals during October to December to ensure availability of pollen. Wheat spikes of W_1–W_5 were emasculated manually using cut glume method two days before anthesis and pollinated with fresh pollen of maize cultivar two days after emasculation. Viability of collected pollen was checked by KI treatment, which led to black appearance in viable pollen grains and light color for inviable pollen grains. The pollinated spikes were treated with 75 ppm solution of 2,4-D for two days and 300 ppm gibberellic acid solution on the 3rd day after pollination, each day with one spraying on each side of spike. Embryos were excised 14–16 days after pollination and cultured on half strength basal MS medium (Murashige and Skoog 1962) supplemented with 0.5 mg/l nicotinic acid, 0.1 mg/l thiamine HCl, 0.5 mg/l pyridoxine HCl, 2 mg/l glycine and 30 g/l sucrose in aseptic conditions. The cultured embryos were kept at 4°C for 5–6 days in darkness and then transferred to incubation room with approximately 25°C with 16/8 hours light/darkness. When the plantlets of 5–15 cm were obtained they were potted in an off-season nursery in glasshouse to obtain haploid plants.

Verification of haploidy : The squashed root tips of the regenerated plantlets were prepared according to Love and Love (1975) by staining with 2% carmine and mitotic metaphase chromosome complement was counted and photographed.

Pollen tube growth study: Pollen tube growth was studied using spikes of W_1 and W_5 crosses which were fixed 30 minutes after pollination according to D'Souza (1972). For this, wheat pistils which were fixed in 1:2 lactic acid: ethyl alcohol solution, were first treated with 1N HCl for 10 minutes and then stained for 1–2.5 minutes with a solution of 1% cotton blue containing lactic acid, phenol, glycerol and distilled water with 1:1:1:1 ratio. The samples were destained with a solution of 40% acetic acid, orthophosphoric acid and distilled water in 1:1:1 ratio for 15–20 minutes. Stigma of these pistils was cut and one drop of lactic acid was added on slide for microscopy. The length of pollen tube was measured in W_1 and W_5

Table 1. Parentage of wheat hybrids W_1–W_5

Code	Parentage
W_1	UP 2003 x UP 262
W_2	UP 2003 x HP 1731
W_3	UP 2003 x Raj 3991
W_4	UP 262 x UP 2425
W_5	Raj 3991 x UP 2425

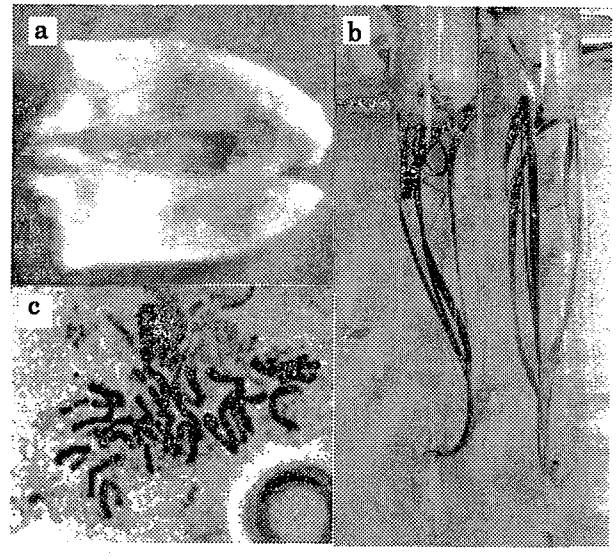

Fig. 1. a) A typical seed of wheat x maize crosses, b) regenerated haploid plantlets, c) chromosome complement of a haploid plant with 21, the gametophytic chromosome number of hexaploid wheat (2n=42).

crosses with an ocular micrometer.

Statistical methods : Since five wheat parents (W_1–W_5) were crossed by maize in different number of replications the completely randomized design with unequal number of replications was used to analyze variance for difference among genotypes according to Gomez and Gomez (1984). The analyzed traits included seed set (percentage of seed containing florets) and percentage of embryo formation (number of embryo containing seeds/total number of obtained seeds). In case of two other characteristics, ie, percentage of embryo germination (number of germinated embryos/number of cultured embryos) and plantlet recovery rate (number of plnatlets obtained /number of cultured embryos), three wheat parents, W_1, W_3 and W_5, were included in the analysis. Data were transformed to arc sin $(x)^{1/2}$ and $(x+0.5)^{1/2}$ before analysis of variance accordingly for each character. To compare means of pollen tube length between W_1 and W_5, Student's-t distribution was used according to Steel and Torie (1960).

Results

Seed Set: After crossing wheat x maize, so called seed-like structures (here we call seed) were formed, which showed embryo formation (Fig. 1a). For seed set, analysis of variance among the wheat genotypes W_1–W_5 showed a significant F-value (Table 2). Comparison of means showed that among these five genotypes, W_1–W_4 fell in the same class, while W_5 had a significantly smaller mean (Table 3). The smaller mean response of W_5 might have arisen from insufficient reception of hormone (probably 2,4-D), which is crucial for enlargement of ovary or seed set.

Percentage of embryo formation: There was a highly significant F-value for genotypes suggesting that at least two wheat parents significantly differed in haploid embryo production rate (Table 2). For this trait, mean comparison showed that W_1 with an average of 12.8% was the most superior genotype followed by W_3 (9.7%) and three other genotypes (Table 3). W_2 with 2.5% embryo formation rate was the poorest genotype.

The range of embryo formation was 5.1–17.5% for W_1, 1.2–4.1% for W_2, 6.2–12.6% for W_3, 0.0–9.7% for W_4 and 2.2–9.0% for W_5. The overall average across the five genotypes was 9.2%.

Embryo germination rate: Out of 366 cultured embryos, 227 (62%) germinated and started development of shoots and roots (Table 3). Three wheat genotypes W_1, W_3 and W_5 were more successful in embryo production than the other two, therefore they were used for study of the genotypic influence on embryo germination rate and plantlet recovery. According to ANOVA result for embryo germination rate, there was no significant difference among the genotypes, suggesting that germination of the cultured embryos was not directly affected by their wheat parents. But the means of these three genotypes (Table 3) show a smaller value for W_5, which showed also a lower percentage of embryo formation in comparison to W_1 and W_3.

Plantlet recovery: From 227 germinated embryos only 104 produced plantlets of 5–15 cm in length suitable for transplanting in pots (Fig. 1b). The rest of embryos showed a slow development of plantlets and mostly they stopped growth later. Plantlet recovery also showed no significant F-value for variation among genotypes (Table 3). It was observed that some embryos germinated but did not develop to green plantlets. Chromosome counting of the mitotic root cells confirmed haploidy of the regenerated plantlets (Fig. 1c). The average percentage of plantlet recovery over the five genotypes was 28.4% of cultured embryos.

Pollen tube studies: Pollen tube studies showed that within 30 minutes of pollination, maize pollen tube has already penetrated the lateral branches of wheat stigma and 1 hour after pollination the longest maize pollen tubes have entered the main axis of stigma. For the measurement of the length of pollen tube, only

Table 2. Analysis of variance for seed set and embryo formation rate among wheat genotypes W_1–W_5

Source of variation	Degrees of freedom	Seed set		Embryo formation	
		Sum of square	Mean square	Sum of square	Mean square
Genotypes	4	1.48	0.370**	13.55	3.338**
Error	18	1.28	0.071	7.88	0.438
Total	22	2.76		21.43	
Coefficient of variation		2.8%		23.2%	

**Significant at the 1% level

samples of 30 minutes after pollination were used because the more developed pollen tubes (after 30 minutes) were not suitable due to their entering to the main axis of stigma wings and ovary.

Result of t-analysis for pollen tube length of W_1 and W_5 crosses showed a highly significant difference between their means showing that the growth speed of maize pollen tube was not equal in stigma of these two wheat genotypes. The mean of pollen tube length in crosses of W_1 was greater (faster growth) than that of W_5 crosses (Table 4). This was in agreement with their performance for percentage of embryo formation suggesting that the genotype of W_5 is responsible for slower growth of maize pollen tube and less percentage of embryo formation.

Discussion

A significant F-value of genotypes for seed set suggested that at least two genotypes differed significantly in the rate of seed set (Table 2). Mean comparison showed that W_5 had a lower rate of seed set than the others (Table 3). Seed set in wheat x maize crosses is highly affected by 2,4-D. We observed that florets which received the hormone treatment produced seeds, but in those which did not, ovaries remained shrunken and no seed was produced (data not shown). The lower seed set in W_5 crosses might have been caused by factors affecting the level of hormone reception. Thinner spikes and more closed glumes of W_5 than the others appear to affect the reception of hormone in the spraying method employed. We suggest that seed set is not directly affected by genotypes of wheat parents.

In case of embryo formation rate, the highly significant F-value of genotypes suggested that the variation in response of different wheat parents resulted from different genotypes (Table 2). This was clearly due to the superiority of W_1 and W_3 over the other three genotypes (Table 3). Since pollen tube studies also showed a significant difference between the length of maize pollen tube growing inside the stigma of W_1 and W_5 (Table 4), it can be inferred that there may be some unknown crossability system different from that under *Kr* genes in hexaploid wheat. This system appears to be not strong enough to completely inhibit growth of maize pollen tube (like *bulbosum* system) but it reduces the speed of pollen tube growth and thus affects the percentage of embryo formation. In this study W_1 showed a mean performance of 12.8% for embryo formation while W_5 mean was 5.3% (Table 3). This was consistent with the higher mean of pollen tube growth in W_1 crosses than that of W_5. Genotypic variation of hexaploid wheats for embryo production in wheat x maize crosses has already been reported by others (Laurie and Bennett 1987; Suenaga et al. 1991; Oury et al. 1993;

Table 3. Response of different wheat genotypes in crossing with maize

Wheat genotype	Pollinated florets	Seed set†	Induced embryos‡	Cultured embryos	Germinated embryos§	Recovered plantlets¶
W_1	3772	3426 (90.8) a	439 (12.8) a	301	191 (63.5)a	86 (28.6)a
W_2	1091	973 (89.1)a	24 (2.5)c	-	-	-
W_3	726	641 (88.3)a	62 (9.7)ab	36	22 (61.1)a	11 (30.6)a
W_4	446	434 (97.3)a	15 (3.4)bc	-	-	-
W_5	1255	990 (78.9)b	53 (5.3)bc	29	14 (48.3)a	7 (24.1)a
Total	7290	6464	593	366	227	104
Mean	-	1292.8 (88.7)	118.6 (9.2)	-	75.7 (62.0)	34.7 (28.4)

Figures in parentheses are percentages. Different letters show significant differences at the 5 % level.
†Number of seeds/number of pollinated florets, ‡Number of embryos/number of seeds, §Number of germinated embryos/number of cultured embryos, ¶Number of plantlets/number of cultured embryos

Table 4. t-analysis for maize pollen tube growth in crosses with W_1 and W_5

		W_1 cross	W_5 cross
Mean of pollen tube length (micron)		259.156	215.192
Variance		5803.996	2916.316
Standard deviation		76.184	54.003
t-value for difference of means	2.8248		
Effective df	63		
Probability of t	0.0062		

Giura 1994; Lefebvre and Devaux 1996; Suenaga et al. 1997; Sadasivahiah et al. 1999).

In case of embryo germination rate there was no significant difference among the wheat genotypes (Table 3). The mean of W_1, W_3 and W_5 for this trait was 63.5%, 61.1% and 48.3%, respectively. The mean of W_5 is appeared to be lower than the other two genotypes though the difference was not statistically significant. The morphology of W_5 spikes might have affected the level of hormone reception, and this in turn might have reduced the seed set and even the development of embryos. If hormone is not trapped by wheat spikes sufficiently, the haploid embryos may not develop well, thus causing lower germination rate. The clear effect of hormone concentration on development and size of induced embryos in wheat x maize crosses has been documented by others (Sun et al. 1995; Zhang et al. 1996). Some reports (Bitsch et al. 1998; Suenaga and Nakajima 1989) referred to the effect of embryo size on its germination, ie failure of small embryos in germination. In case of W_5 lower seed set and less percentage of embryo germination might also have been due to its smaller embryo size.

Plantlet formation was also independent from genotypic effect of wheat parents. It appears that once an embryo germinates some factors might affect its development to a plantlet, eg conditions of nutritive medium and incubation temperature and light.

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Research article

Study of interspecific SSR polymorphism among 14 species from *Triticum-Aegilops* group

S. Sharma, H.S. Balyan, P.L. Kulwal, N. Kumar, R.K. Varshney[1], M. Prasad[1] and P.K. Gupta*

Molecular Biology Laboratory, Department of Agricultural Botany, Ch. Charan Singh University, Meerut-250 004 (U.P.), India
[1]Present address: Institute for Plant Genetics and Crop Plant Research, Correnssst. 3, D06466, Gatersleben, Germany

Summary

In the present study, using in-gel hybridization and PCR based approaches, interspecific SSR polymorphism was studied among 14 species of *Triticum-Aegilops* group. The material represented seven different genomes and three ploidy levels (2x, 4x, 6x). In-gel hybridization involved 13 probe-enzyme combinations (four SSR oligonucleotide probes in combination with 2–4 enzymes) and resolved 5 to 20 bands (0.40kb to >23kb) in each of the 14 individual species. This suggested ubiquitous distribution and interspecific polymorphism of SSRs among different species of *Triticum-Aegilops* group. The available polymorphism also proved helpful in discriminating not only the species with different ploidy levels and possessing different genomes, but also those possessing similar or very closely related genomes. The amplification of SSR loci using 15 primer pairs derived from hexaploid wheat was also carried out in all the 14 species. The primer pairs, each amplified SSR loci not only in species containing A, B and D genomes, but also in 2 to10 of the remaining species that contained other genomes. This suggested that wheat SSRs might have been derived from the corresponding SSRs in an ancestral genome and are conserved across a number of species in the *Triticum-Aegilops* group. Also, two pairs of SSRs (one consisting of WMC243 and WMC415 and the other consisting of WMC35 and WMC404) each discriminated all the 14 species examined during the present study. Therefore, one can infer from the present study that SSR primers can be used in studies on DNA polymorphism, genetic diversity, gene mapping and synteny conservation across different species of *Triticum-Aegilops* group.

Key words: in-gel hybridization, microsatellite, polymorphism, *Triticum, Aegilops*

Introduction

Molecular markers have been extensively utilized for the study of genetic diversity and genomic constitutions in a number of species of the tribe Triticeae. Genome-specific molecular markers have also been identified in several crops including wheat (Roder et al. 1998; Pestsova et al. 2000; Gupta et al. 2002). Among the different types of molecular markers, microsatellites or simple sequence repeats (SSRs)/simple tandem repeats (STRs) have become the markers of choice due to their abundance and ubiquitous distribution in both the nuclear and organellar genomes. It has also been shown that SSRs are frequent in both repetitive and unique sequences of the nuclear genome (for a review, see Gupta and Varshney 2000; Morgante et al. 2002).

SSR markers can also be used for distinguishing related genomes, since often homoeoloci in related

* Corresponding author: pkgupta@ndf.vsnl.net.in

genomes that are characteristic of RFLPs are infrequent among SSR loci. Wheat SSRs, therefore, facilitated a variety of studies that involved mapping and gene tagging (for review see Gupta et al. 1999; Varshney et al. 2000b; Varshney et al. 2001; Gupta et al. 2002), genetic diversity (Plaschke et al. 1995; Roder et al. 1995; Prasad et al. 2000), in-gel hybridization (Varshney et al. 1998) and in-situ hybridization (Cuadrado and Schwararchzer 1998). They have also been used for studying the role of natural selection in differentiation (Li et al. 1999, 2000). A proportion of SSRs derived from wheat and *Ae. tauschii* have also been used in related species containing A, B and D genomes (Sourdille et al. 2001; Guyomarc'h et al. 2002). In the present study, we examined the distribution and organization of SSRs in 14 different diploid and polyploid species of *Triticum-Aegilops* group through in-gel hybridization and PCR based amplification of SSR loci. This facilitated an assessment of the potential of SSR oligonucleotide probes and SSR primers for a study of molecular marker-based studies in the tribe Triticeae.

Materials and methods

Plant material: Seed of 19 accessions belonging to 14 species from *Triticum-Aegilops* group was procured from PAU, Ludhiana (India) and used for the present study (see Table 1).

SSR probes: Four synthetic SSR oligonucleotide probes including three tri-nucleotide repeats {$(CAC)_5$, $(CAG)_5$, $(TCC)_5$} and one di-nucleotide repeat {$(GA)_8$} were used for in-gel hybridization.

SSR primers: For 13 of the 15 SSR primers, the details on sequences, repeat motifs, locus designations and the expected product sizes are published elsewhere (Prasad et al. 2000; Varshney et al. 2000a). The remaining two primer pairs belonging to WMC404 and WMC415 were developed by Romestant (RAGT, France) and are proprietary in nature (mromestant@ragt.fr).

DNA isolation, digestion, electrophoresis, in-gel hybridization and PCR: The details of methods for DNA isolation, restriction digestion (using *Alu*I and *Hin*fI, *Hin*dIII, *Dra*I and *Eco*RI), electrophoresis, in-gel hybridization, PCR, and PAGE (polyacrylamide

Table 1. Summary of the results of amplification of DNA by 15 wheat microsatellite primers in 14 different species from *Triticum-Aegilops* group. Accession numbers of different species used are given in parentheses against the names of the species in the footnote.

Primer designation	Species and their genome constitution													
	Ae.ta (D)	*Ae.sp* (S)	*Ae.bi* (S^b)	*Ae.lo* (S^l)	*Ae.sh* (S^{sh})	*T. ur* (A)	*T. bo* (A)	*Ae.ko* (US)	*Ae.ov* (UM)	*Ae.ti* (UC)	*Ae.cy* (CD)	*Ae.cr* (DM)	*T. di* (AB)	*T. ae* (ABD)
WMC243	+	+	-	+	+	+	-	+	-	-	+	+	+	+
WMC 415	+	+	+	+	+	+	+	+	+	-	+	+	+	+
WMC 35	+	+	+	+	+	-	-	+	-	-	+	+	+	+
WMC 404	+	+	+	+	+	-	-	+	-	+	+	+	+	+
WMC 120	-	-	-	+	-	+	+	-	-	-	-	+	+	+
WMC 256	+	+	-	-	-	+	+	+	+	+	+	+	+	+
WMC 25	+	+	+	+	+	+	+	+	+	+	+	+	+	+
WMC 254	-	+	+	+	+	+	-	-	-	-	-	-	+	+
WMC 245	+	+	-	-	-	-	-	-	+	-	+	+	-	+
WMC 44	-	-	+	+	+	-	-	-	-	-	-	-	+	+
WMC 250	-	-	-	-	-	+	-	+	+	+	+	-	-	+
WMC 263	-	+	+	+	-	+	-	+	+	+	+	+	+	+
WMC 265	+	-	+	+	-	+	+	+	+	+	+	+	+	+
WMC 149	-	+	+	+	+	+	+	+	+	+	+	+	+	+
WMC 284	+	+	-	-	-	+	-	-	-	+	+	-	+	+

Ae. ta= Ae. tauschii (3727), *Ae. sp= Ae. speltoides* (743), *Ae. bi= Ae. bicornis* (3997), *Ae. lo= Ae longissima* (3506, 3770), *Ae. sh= Ae. sharonensis* (3513), *T. ur= T. urartu* (5324, 5338), *T. bo=T. boeoticum* (4856, 4866), *Ae. ko= Ae. kotschyi* (753), *Ae. ov= Ae. ovata* (3548), *Ae. ti= Ae. triuncialis* (750), *Ae. cy= Ae. cylindrica* (3472, 3486), *Ae. cr= Ae. crassa* (3509), *T. di= T. dicoccoides* (4634, 4640), *T. ae= T. aestivum* (anonymous)

+: Successful amplification, -: No amplification

gel electrophoresis) are described elsewhere (Varshney et al. 1998; Prasad et al. 2000).

Statistical analysis: Polymorphic information content (PIC) for each SSR locus was calculated using the formula: $PIC = 1-\Sigma(P_i)^2$, where P_i is the frequency of i^{th} allele at a locus (Botstein et al. 1980).

Results and discussion

In-gel hybridization using synthetic oligonucleotide (SSR) probes: Thirteen (13) probe-enzyme combinations (involving four synthetic SSR probes each in combination with 2–4 enzymes) were used for in-gel hybridization. SSR sequences, homologous to each of the four synthetic probes, were available in all the 19 accessions belonging to 14 different species from *Triticum-Aegilops* group. This is in agreement with earlier reports suggesting ubiquitous distribution of SSRs in different plant and animal species (for a review, see Gupta et al. 1996). No intraspecific polymorphism was detected in the present study. Even in an earlier study, we found that such intraspecific polymorphism was rather rare (Varshney et al. 1998). This suggested that in-gel hybridization involving synthetic SSRs as probes may not be a suitable technique for detection of intraspecific polymorphism in members of the tribe Triticeae; however, in several other plant species, a high level of intraspecific polymorphism was actually observed (see Weising et al. 1995).

In the present study, 12 of the 13 probe-enzyme combinations hybridized with 1–4 bands against a clear background while the remaining solitary probe-enzyme combination {(GA)$_8$-*Eco*RI} gave bands on in-lane smear background. In our earlier study on bread wheat also, out of the 142 probe-enzyme combinations, bands were available in 107 cases and a smear with high in-lane background was observed in 35 cases (Varshney et al. 1998). Using 12 different probe-enzyme combinations, a total of 20 bands were visualized (1–4 fragments per probe-enzyme combination) in 14 species. Only hexaploid wheat (*T. aestivum*, ABD genomes) and no other species gave all the bands, so that there was no unique fragment which was absent in wheat and present in another species, although as many as four additional genomes occurred in these alien species. In the remaining 13 individual species, a total of 5 to 15 bands were visualized with all the probe-enzyme combinations considered together. In 9 of the above 12 probe-enzyme combinations, a solitary band of >23 kb was observed in 9 of the 14 species examined; in the five remaining species (*Ae. kotschyii, Ae. sharonensis, Ae. cylindrica, T. boeoticum* and *T. urartu*), this band was not observed in a few of these 9 probe-enzyme combinations, but other bands were available. In the remaining three of the 12 probe-enzyme combinations {*Hin*dIII-(CAC)$_5$, *Alu*I-(CAC)$_5$, *Alu*I-(CAG)$_5$}, in accessions of several species, this characteristic band of >23 kb was observed in association with other bands ranging in size from 7 kb to 0.4 kb; in few species, however, one or more bands of smaller size were present. Similar high molecular weight bands (>21 kb to 30 kb) were also reported in earlier studies on barley, sugar beet and wheat (Beyermann et al. 1992; Schmidt and Heslop-Harrison 1996; Varshney et al. 1998). The high molecular weight band (>23kb) that was visualized with different probe-enzyme combinations, may represent same or different repeat sequences of >23 kb harboring SSRs. In a recent study in barley, characterization of clones harboring dinucleotide SSR repeats revealed that a high percentage of such clones are associated with retrotransposon-like and other dispersed repetitive elements (Ramsay et al. 1999). SSRs are, however, now known to be frequent in unique DNA sequences also (Morgante et al. 2002).

The above interspecific polymorphism among the 14 species of *Triticum-Aegilops* group proved helpful in discriminating not only species with different ploidy levels and possessing different genomes, but also those possessing similar or very closely related genomes. For instance, the patterns due to different probe-enzyme combinations discriminated among hexaploid wheat (ABD genomes), tetraploid wheat (AB genomes) and the two diploid species, *T. urartu* (A genome) and *Ae. tauschii* (D genome), which are the progenitors of hexaploid wheat. It was also noticed that three bands that were always present in hexaploid wheat (ABD genomes) were absent in *Ae. tauschii* (D genome) and one of these fragments was also absent in several other species including tetraploid wheat (AB genomes). Similarly, the trinucleotide probes (CAC)$_5$ and (CAG)$_5$ in combination with *Hin*dIII detected three bands that were common in *T. urartu* (A genome), the tetraploid wheat (AB genomes) and the hexaploid wheat (ABD genomes) suggesting that these bands could be specific to the A genome. However, these bands were not available in another A genome diploid species *T. boeoticum*, suggesting differentiation even within A genome during the course of evolution. Sometimes, a single probe-enzyme combination {(CAC)$_5$-*Hin*dIII} also proved adequate to discriminate between the three tetraploid species including *Ae. kotschyii* (US), *Ae. ovata* (UM) and *Ae. triuncialis* (UC) sharing U genome. Further, the trinucleotide probe (CAC)$_5$ in combination with four

restriction enzymes (*Hin*dIII, *Eco*RI, *Hin*fI and *Alu*I) gave characteristic banding patterns that were adequate to discriminate the four S-genome containing species (*Ae. speltoides*, *Ae. bicornis*, *Ae. longissima* and *Ae. sharonensis*).

PCR amplification using SSR primers: The results of PCR amplification with 15 wheat SSR primers are summarized in Table 1 and a representative amplification profile is shown in Fig. 1. In hexaploid wheat, 12 of these primer pairs amplified each a single locus, while each of the three remaining primer pairs amplified two different loci located on two different chromosomes. The chromosomes carrying the above 18 different loci were distributed in all the three genomes of hexaploid wheat (Prasad et al. 2000; Varshney et al. 2000a).

It may be noted that an individual wheat SSR primer pair amplified loci in 2 to 10 of the 14 species, which also included species containing genomes other than those present in bread wheat (A, B and D). Therefore, each of the wheat SSR seems to be derived from a corresponding SSR in the presumed ancestral Triticeae genome and is conserved in several diploid and tetraploid species of Triticeae having varied genomic constitutions. In the past, a high proportion of SSRs developed from *T. aestivum* and *Ae. tauschii* were also shown to be functional in related diploid species containing either A or B or D genome confirming their transferability and conservation across Triticeae species (Sourdille et al. 2001; Guyomarc'h et al. 2002). Such conserved wheat SSRs may be used in studies on polymorphism, genetic diversity, gene mapping and synteny conservation across different species of Triticeae.

The cases of failures of amplification of microsatellite loci in some of the species examined during the present study were classified as null alleles. It was assumed that such null alleles might have resulted either due to modification of the primer-binding site or to the loss of corresponding SSR during the course of evolution. Fourteen of the 15 microsatellite primer pairs detected null alleles in one or more (1 to 10) different species containing different genomes. Interestingly, some of the primer pairs that amplified loci on chromosomes of A/B genomes of bread wheat, were found to amplify loci in *Ae. tauschii*, which is the diploid progenitor of D genome. Similarly, there were SSR loci that belonged to the D genome of bread wheat, but were amplified in diploid species with an A genome (*T. urartu*) (Tables 1 and 2). This

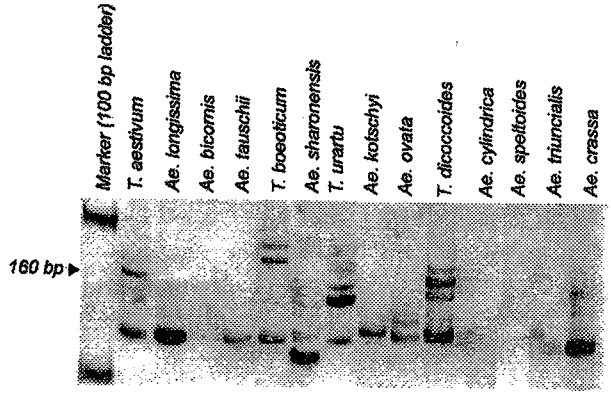

Fig. 1. DNA amplification patterns in accessions of 14 species of *Triticum-Aegilops* group using a microsatellite primer pair WMC 120 derived from hexaploid wheat. The arrowhead indicates the expected fragment size in hexaploid wheat (*T. aestivum*). Fragments in the expected size range were available in only six (*T. aestivum, Ae. longissima, T. boeoticum, T. urartu, T. dicoccoides and Ae. crassa*) of the 14 species. No fragment in the expected size range was available in the remaining eight species. Additional nonspecific fragments of varying sizes were observed in each of the 14 species.

Table 2. Microsatellite primers used along with locus designation, number of alleles and PIC values

Primer designation	Locus designation	No. of alleles	PIC
WMC25	*Xwmc25-2D*	11	0.616
WMC35	*Xwmc35-4B*	6	0.528
WMC44	*Xwmc44-1B*	4	0.386
WMC120	*Xwmc120-1A*	7	0.562
WMC149	*Xwmc149-2B*	10	0.780
WMC243	*Xwmc243-3A*	10	0.576
WMC245	*Xwmc245-2D*	8	0.466
WMC250	*Xwmc250-6D*	3	0.406
WMC254	*Xwmc254-4B*	7	0.614
WMC256	*Xwmc256-6A*	4	0.556†
	Xwmc256-6D	6	
WMC263	*Xwmc263-6B*	4	0.752
WMC264	*Xwmc264-3A*	10	0.615
WMC265	*Xwmc265-7D*	4	0.650
WMC404	*Xwmc404-1B*	7	0.562†
	Xwmc404-1D	4	
WMC415	*Xwmc415-5A*	8	0.643†
	Xwmc415-5B	5	

† PIC was estimated using alleles from both the loci

means that during the evolution of bread wheat, some of the SSR loci found in a particular genome of a diploid progenitor species were either lost, or carried a mutation in the primer binding site leading to the origin of a null allele. In several recent studies involving artificially synthesized and naturally occurring allopolyploids of Triticeae, it was shown that allopolyploidization either induced elimination or caused cytosine methylation of certain unique and repetitive DNA sequences (Ozkan et al. 2001; Shaked et al. 2001). However, in studies conducted in hexaploid wheat and related species, Southern hybridization with probes carrying sequences corresponding to SSR primers gave a positive signal in related species having null alleles. This suggested that the locus specificity of SSRs in bread wheat probably originated due to mutations in primer binding sites rather than due to loss of SSRs themselves in related genomes during polyploidization (Guyomarc'h et al. 2002).

The average number of alleles per locus in 14 species was 6.6 with a range of 4 to 11 (Table 2). The maximum number of 11 alleles (120 bp to 177 bp) was observed at *Xwmc25-2D* carrying $(GT)_n$. The polymorphic information content (PIC) varied from 0.386 for WMC44 to 0.780 for WMC149 (Table 2). The average number of alleles in the present study was slightly lower than an average of 7.5 alleles per locus reported by us within bread wheat in an earlier study, where 20 WMC SSRs were tried on 55 genotypes (Prasad et al. 2000). We believe that fewer alleles per locus in the present study could be due to small sample, so that a bigger sample having many more species each represented by several accessions should resolve many more alleles on each SSR locus.

In the present study no single primer pair was adequate to discriminate all the 14 species studied. However, two different pairs of SSRs, one consisting of WMC243 and WMC415, and the other consisting of WMC35 and WMC404, each discriminated all the 14 species. In our earlier study on bread wheat it was shown that 12 microsatellite markers discriminated 48 genotypes out of 55 genotypes studied (Prasad et al. 2000). The present study thus suggested that in addition to their use in discriminating accessions belonging to a particular species like bread wheat, SSR markers can also be used for discriminating different species of Triticeae.

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Research article

Cultivar identification and pedigree assessment of common wheat based on RAPD analysis

Wenguang Cao[1*], P. Hucl[2], G. Scoles[2], R. N. Chibbar[3], P. N. Fox[4] and B. Skovmand[4]

[1]Eastern Cereal and Oilseed Research Center, Agriculture and Agri-Food Canada, Building 50, 930 Carling Ave. Ottawa, ON K1A 0C6, Canada
[2]Dept. of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Sask., S7N 5A8, Canada
[3]Plant Biotechnology Institute, National Research Council, Saskatoon, Sask., S7N 0W9, Canada
[4]CIMMYT, Apartado Postal 6-641, CP. 06000, Mexico, D.F., Mexico

Summary

Knowledge of cultivar genetic relationships helps breeders make decision on the cross-combination in breeding programs, and cultivar identification is important for protection of breeders' right. Twenty-nine common wheat cultivars (*Triticum aestivum* L. em Thell) were used to evaluate randomly amplified polymorphic DNA (RAPD) analysis in identifying common wheat cultivars and assessing their pedigree relationships. Thirty-one primers produced polymorphisms were used in this study, generating a total of 214 reproducible amplified DNA fragments. The number of the DNA fragments for each primer varied from 3 to 12 with an average of 6.9 bands per primer. The sizes of DNA fragments ranged from 280 bp to 2800 bp. Out of 214 amplified products, 54.7% were monomorphic, and 45.3% were polymorphic, averaging 3.1 polymorphisms per primer. The marker $RC37_{700}$, specific to AC Domain, was found after evaluating 74 wheat cultivars. The RAPD data were analyzed using the unweighted pair-group method with arithmetical averages (UPGMA). A dendrogram based on Jaccard coefficients generally grouped cultivars with similar pedigrees closer together than those known to be unrelated. The results from this study suggest that RAPD analysis can be used for pedigree assessment in common wheat and identification of some wheat cultivars.

Key words: RAPD markers, cultivar identification, pedigree assessment, *Triticum aestivum*

Introduction

The identification of crop cultivars or breeding lines is important to protect breeder's right. Phenological and morphological characteristics may not be able to distinguish cultivars unequivocally (Mailer et al. 1994). Protein and isozyme electrophoresis has facilitated the identification of cultivars. However, the level of polymorphism often is insufficient to distinguish cultivars, and isozyme markers can be dependent on growth conditions and developmental stage (Kuhns and Fretz 1978; Falkenhagen 1985). DNA-based markers have largely overcome these disadvantages and have been applied successfully to discriminate among genotypes in a wide range of agricultural crops (Weising et al. 1991; He et al. 1992; Nybon 1994; Jain et al. 1994). Restriction fragment length polymorphism (RFLP) is a powerful technique and has been used to generate genetic maps in crop species such as tomato (*Lycopersicon esculentum* L.), potato (*Solanum tuberosum* L.), maize (*Zea mays* L.) (Helentjaris et al. 1986; Tanksley et al. 1989); barley (*Hordeum vulgare* L.) (Tragoonrung et al. 1992;

* Corresponding author: caowen@em.agr.ca

Patrick et al. 1996); and wheat (*Triticum aestivum* L. em Thell) (Chao et al. 1989; Gill et al. 1991). The random amplified polymorphic DNA (RAPD) technique, however, is preferred to the RFLP technique because it is relatively easy, requires very little DNA and does not require radioactive probes (Marshall et al. 1994). The use of RAPD in distinguishing cultivars has been demonstrated in broccoli and cauliflower (*Brassica oleracea* L.) (Hu and Quiros 1991; Kresovich et al. 1992); celery (*Apium graveolens* L.) (Yang and Quiros 1993). The RAPD technique has also been used for taxonomic studies of the genus *Pellia* (Pacak et al. 1998), for parentage determination in hybrid rice (*Oryza sativa* L.) (Wang et al. 1994), for cultivar pedigree relationships in barley (*Hordeum vulgare*) (Tinker et al. 1993) and for cultivar identification in rye (*Secale cereale* L.) (Iqbal and Rayburn 1995). Common bread wheat (*Triticum aestivum* L. em Thell), a hexaploid species, has approximately 1.6×10^{10} bp DNA in the haploid nucleus, about 35–40 times more than rice, a diploid species (Joshi and Nguyen 1993). Eighty percent of the wheat genome is repetitive DNA (Peacock et al. 1981), limiting the number of polymorphisms detected in common wheat (Devos and Gale 1992). A high level of polymorphism, however, was found among 15 American bread wheat cultivars using 40 random primers (Joshi and Nguyen 1993). Recently, techniques of amplyfied fragment length polymorphism (AFLP) and simple sequence repeat (SSR) have been used in genetic mapping and cultivar fingerprinting. A disadvantage of SSR marker is that it is expensive and time-consuming to identify and map these marker loci (Mackiel et al. 1996), whereas AFLP markers are not efficient to be converted into sequence specific markers (Shan et al. 1999). The

Table 1. Common wheat cultivars used to study cultivar identification and pedigree assessment

No.	Name	Pedigree
1	Cutler	Cro/4/ Sonora 64/ Yaqui50E//Gto/3/ Inia
2	Roblin	RL4302/RL4356//RL4359/RL4353
3	Wildcat	Glenlea/Potam
4	CDC Merlin	RL4386//BW525/BW37
5	CDC Teal	BW514/Benito//BW38
6	Grandin	Len//Butte*2/ND507/3/ND593
7	Biggar	Tobari 66/Romany
8	Kenyon	Neepawa*5/Buck Manantial
9	Genesis	Tobari 66/Romany//Pitic 62/Gaines
10	Laura	Manitou/Tobari66/3/Carazinho/CT763//Atlas66/CT262
11	Leader	Fortuna/Chris
12	Oslo	Sonora64/Yaqui50E//Guajalote/3/Inia/4/Ciano// Elgan/Sonora64
13	AC Domain	BW83/ND585
14	Pasqua	BW63*2/Columbus
15	AC Michael	Park/Neepwa
16	Neepawa	RL4125/RL4008
17	Invader	Sinton/Stoa
18	AC Taber	HY320*3/BW553
19	CDC Makwa	Huelquen/Wisconsin261//Benito
20	Conway	Chris/Siete Cerros//Neepawa/Opal
21	AC Minto	Columbus/BW63//Katepwa/BW552
22	Katepwa	Neepawa*6/RL2938/3/Neepawa*6//CI8154/2*Frocor
23	AC Cora	Katepwa/RL4509
24	Columbus	Neepawa*6/RL4137
25	Crocus	Columbus*6/Chinese Spring
26	Chinese Spring	Unknown
27	Norstar	Winalta/Alabaskaya
28	Bezostaya 1	Lutescens 17/Skorospelka 2
29	Cook	Timgalen/Condor //Condor

objective of this study was to investigate the value of RAPD analysis in identifying registered Canadian hexaploid spring wheat cultivars and assessing their pedigree relationships.

Materials and methods

Plant materials: Twenty-nine cultivars of common wheat (Table 1) were investigated in this study. Two cultivars (Norstar and Bezostaya 1) are winter wheats, the other cultivars are spring wheat. Cook was developed in Australia, while Crocus was developed as an isogenic line of Columbus, with two crossability genes derived from cv. Chinese Spring. The remaining spring wheat cultivars were registered for production in western Canada.

DNA amplification and gel electrophoresis: DNA extraction was based on the methods described by Procunier et al. (1990). Oligonucleotide primers (10-mers) were purchased from the Biotechnology Laboratory, University of British Columbia, while 9-mer primers were synthesized on an Applied Biosystems Model 394 DNA synthesizer using beta-cyanoethyl phosphoramidite.

Data scoring and analysis: The presence of a amplified product was identified as "1" and the absence was designated as "0". Although a few faint bands were produced, only the bright ones were used in this study. The data were analyzed using the SIMQUAD (Similarity for Qualitative Data) to generate Jaccard similarity coefficients. These similarity coefficients were used to construct dendrograms using the unweighted pair group method with arithmetic averages (UPGMA) employing the SAHN (Sequential, Agglomerative, Hierarchied, and Nested clustering) from the NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System), version 1.80 (Applied Biostatistics) program.

Results and discussion

Two hundred and thirty-five random primers (10-mers and 9-mers) were screened against four cultivars (Columbus, Oslo, Biggar and Grandin) to detect RAPD polymorphisms. Forty-seven (20%) primers did not produce any amplified products. Twenty-five (10.6%) primers produced amplified DNA fragments, but the fragments were faint. One hundred and thirty-two (56.2%) primers produced fragments that were monomorphic across the four cultivars. Thirty-one (13.2%) primers produced polymorphisms. These primers and their sequences are listed in Table 2. A total of 214 reproducible amplified fragments were generated by these 31 primers against the 29 cultivars

Table 2. Thirty-one random primers (and their sequences) which produced polymorphisms across four common wheat cultivars.

Primer no.	Sequence	Primer no.	Sequence
UBC29†	CCG GCC TTA C	UBC251	CTT GAC GGG G
UBC39	TTA ACC GGG C	UBC253	CCG TGC AGT A
UBC59	TTC CGG GTG C	UBC256	TGC AGT CGA A
UBC80	GTG CTC TAG A	UBC257	CGT CAC CGT T
UBC142	ATC TGT TCG G	UBC265	CAG CTG TTC A
UBC211	GAA GCG CGA T	UBC268	AGG CCG CTT A
UBC215	TCA CAC GTG C	UBC293	TCG TGT TGC T
UBC223	GAT CCA TTG C	UBC295	CGC GTT CCT G
UBC225	CGA CTC ACA G	RC9‡	TCC GAT CCA
UBC226	GGG CCT CTA T	RC17	CCC AGC GTT
UBC227	CTA GAG GTC C	RC18	GCT CAC ATC
UBC229	CCA CCC GAG G	RC19	TAC GCA CGG
UBC238	CTG TCC AGC A	RC21	CAA ACG CCA
UBC247	TAC CGT CGG A	RC32	GTC ACC GGA
UBC248	GAC TAA GCG G	RC37	ACC GCC GTT
UBC250	CGA CAG TCC C		

†The UBC group primers were purchased from the University of British Columbia;
‡The RC group primers were synthesized on an Applied Biosystems Model 394 DNA synthesizer

of common wheat listed in Table 1. The number of fragments produced by each primer varied from 3 to 12 with an average of 6.9 per primer. The size of fragments ranged from 280 bp to 2800 bp. Of the 214 amplified fragments, 54.7% were monomorphic and 45.3% were polymorphic, with an average of 3.1 polymorphisms per primer. Polymorphisms produced among the 29 common wheat cultivars by one primer (UBC229) are shown in Fig. 1. Ninety-seven polymorphisms were detected among the 29 wheat cultivars with the 31 pre-selected random 9- or 10-base primers. This result is similar to that reported by Joshi and Nguyen (1993), demonstrating that RAPD polymorphisms among common wheat cultivars are sufficient to allow some of them to be distinguished. Common wheat is a hexaploid species (42 chromosomes) and has a large genome consisting of 80% repetitive sequences (Peacock et al. 1981). Devos and Gale (1992) detected only a few polymorphisms in hexaploid wheat, attributing this to the large portion of repetitive DNA in the common wheat genome. However, their conclusion was based on data from only six primers. Compared to rice, a diploid species, where 80% of amplified fragments were polymorphic (Yu and Nguyen 1994), a smaller percentage of fragments were polymorphic (45.3%) in common wheat in the current study. However, more polymorphic bands might be revealed by improving the RAPD technique. Silver staining of acrylamide gels or denatured gradient gel electrophoresis might separate minor polymorphic bands which are unresolvable by agarose gel electrophoresis.

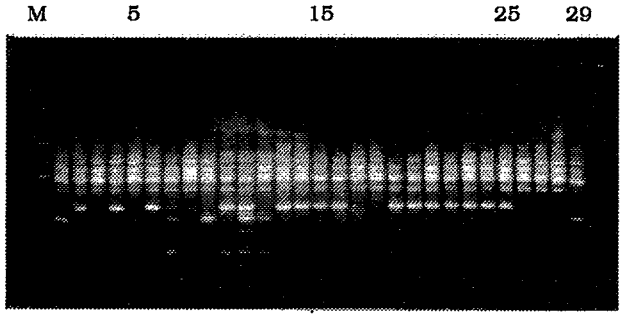

Fig. 1 RAPD polymorphisms revealded in 29 wheat cultivars by the primer UBC229. Lane numbers refer to the cultivars listed in Table 1. The molecular weight marker (1kb ladder) is shown in the left lane (M).

Cultivar fingerprinting with RAPD markers has been achieved in a number of plant species (Demeke et al. 1997). Wang et al. (1994) successfully identified inbred parents and their hybrids in rice using RAPD markers. Two random primers were sufficient to distinguish 14 cultivars of broccoli, whereas three primers distinguished 12 cultivars of cauliflower (Hu and Quiros 1991). In this study, a RAPD marker, RC37$_{700}$ specific for the cultivar AC Domain (Fig. 2), was found after screening the 31 primers against 29 cultivars. In order to confirm if this marker was unique to AC Domain, a further 45 registered Canadian and American wheat cultivars (Table 3) were screened with the primer RC37. With the exception of AC Domain, the RAPD marker RC37$_{700}$ was not produced when the DNA of the 45 additional common wheat cultivars listed in Table 3 was amplified in the presence of the primer RC37 (Fig. 3), confirming that RAPD marker RC37$_{700}$ was specific to the cultivar AC Domain.

In the current study, the cultivar pedigree relationships (Table 1) were in agreement with cultivar relationships obtained using cluster analysis based on RAPD polymorphism data (Fig.4). In the dendrogram, subgroup 1 consisted of the cultivars which share CIMMYT-based (Mexico) pedigrees. The cultivars sharing "North Dakota" germplasm in their pedigrees were clustered into subgroup 2. All cultivars in subgroup 3 had a Neepawa-involved pedigree. In

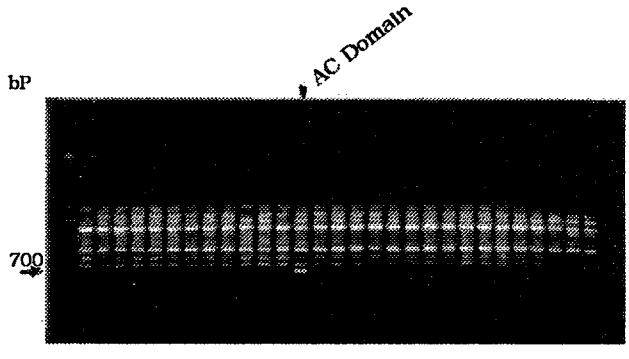

Fig. 2 The positive RAPD marker RC37$_{700}$ (arrow), specific for the cultivar AC Domain, was detected by the primer RC37.

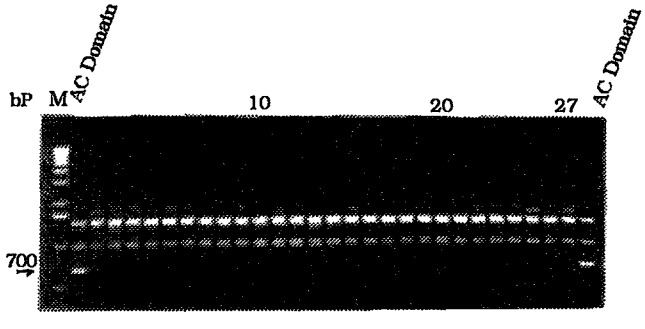

Fig. 3 The positive RAPD marker RC37$_{700}$ (arrow), specific for the cultivar AC Domain, was tested against 27 of the additional 45 cultivars. Lane numbers refer to the cultivars listed in Table 1. M: 1 kb DNA molecular weight marker.

Table 3. Forty-five common wheat cultivars used for evaluation of RAPD markers specific for the cultivars Grandin and AC Domain.

No.	Name of cultivar	Growth habit	No.	Name of cultivar	Growth habit
1	Fielder	Spring	24	Casavant	Spring
2	Bluesky	Spring	25	CDC Kestrel	Winter
3	Manitou	Spring	26	Norwin	Winter
4	AC Reed	Spring	27	Winalta	Winter
5	Park	Spring	28	AC Mimi	Spring
6	Benito	Spring	29	AC Pollet	Spring
7	AC Voyageur	Spring	30	McNeal	Spring
8	AC Foremost	Spring	31	Era	Spring
9	AC Barrie	Spring	32	Marshall	Spring
10	HY 320	spring	33	AC Readymade	Winter
11	Pitic 62	Spring	34	Yorkstar	Winter
12	Laval 19	Spring	35	Butte	Spring
13	Glenlea	Spring	36	Waldron	Spring
14	Messier	Spring	37	Len	Spring
15	Harus	Winter	38	AC Eatonia	Spring
16	Augusta	Winter	39	Sinton	Spring
17	Algot	Spring	40	Saunders	Spring
18	Consens	Spring	41	Pembina	Spring
19	Belvedere	Spring	42	Thatcher	Spring
20	AC Baltic	Spring	43	Marquis	Spring
21	Aquino	Spring	44	Garnet	Spring
22	Opal	Spring	45	Selkirk	Spring
23	Celtic	Spring			

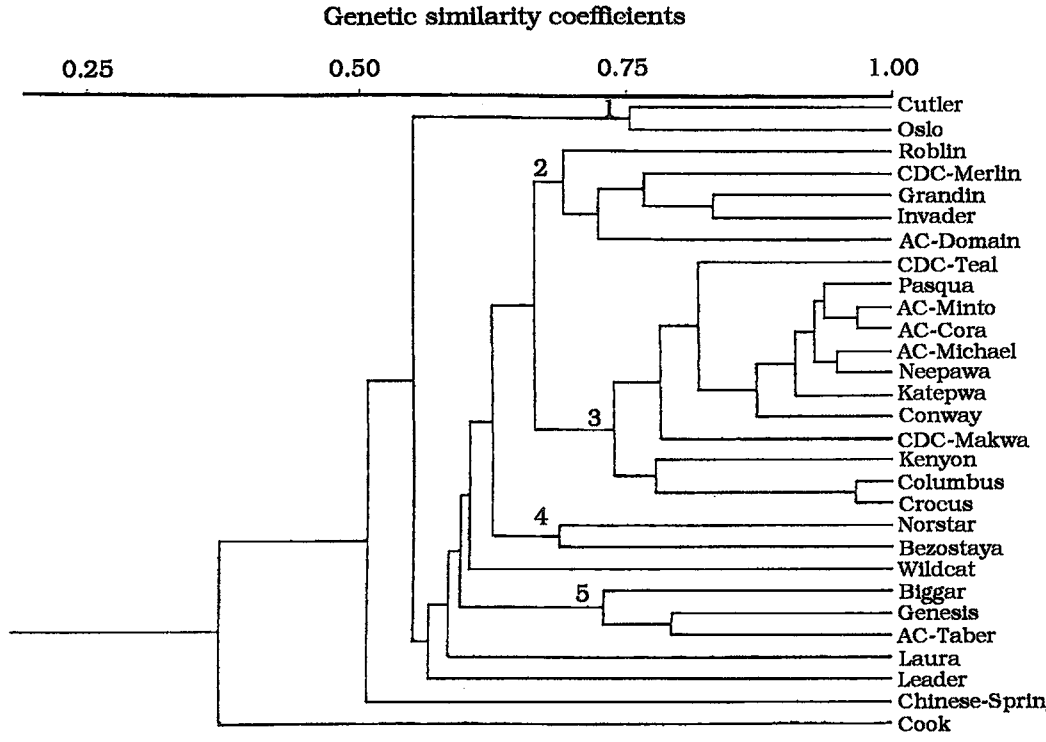

Fig. 4 Dendrogram of 29 common wheat cultivars based on Jaccard genetic similarity coefficients using 97 RAPD polymorphisms.

this subgroup, the cultivars Columbus and AC Minto were very close to the cultivars Crocus and AC Cora, respectively, with a genetic similarity coefficient of 0.97. The results are in agreement with the fact that Columbus and Crocus are near-isogenic for two crossability alleles (Zale 1993), and that AC Minto and AC Cora share more than 94% of their pedigrees with Neepawa. In subgroup 4, both cultivars are winter wheats of Russian origin. Bezostaya 1 is a Russian cultivar while Norstar, a Canadian cultivar, is partly of Russian origin since its parent cultivar Alabaskaya is a Russian land race. The apparent lack of divergence between spring and winter wheats is somewhat surprising since winter and spring wheats probably represent different gene pools. Three cultivars (Wildcat, Laura and Leader) did not fall within the five sub-groups and the pedigrees of these three cultivars were different from each other and from the cultivars in the five sub-groups. There was a significant correlation between coefficients based on Jaccard genetic similarity and the coefficients of parentage (r = 0.69, data not shown), indicating that the genetic similarity values appear to correctly reflect the genetic background of the samples analyzed. Halldén et al. (1994) compared RFLP and RAPD markers for their ability to determine genetic relationships in *B. napus* breeding lines. They confirmed that RAPD markers could estimate the relationship between closely related *B. Napus* genotypes. RAPD markers have also been used succesfully to determine cultivar relationship in broccoli and cauliflower (Hu and Quiros 1991), barley (Tinker et al. 1993) and celery (Yang and Quiros 1993). Previous studies and the present study indicate that RAPD analysis can be used to assess common wheat cultivar genetic relationships.

In conclusion, cultivar-specific markers were found to be stable and might be used to fingerprint spring wheat cultivars. A significant correlation between genetic coefficients based on RAPD markers and cultivar pedigrees was detected, indicating that the RAPD data provide a good indication of genetic relatedness. These results suggest that if such an analysis is extended to additional wheat cultivars with unknown pedigree, it would be possible to obtain information on their genetic relationships. The utilization of RAPD has been confirmed by Cao et al. (1999) for the reclassification of *Triticum* accessions, Qian et al. (2001) for the detection of genetic diversity in wild rice (*Oryza granulata* L.) and Fernández et al. (2002) for genotype identification among barley cultivars. Sharma et al. (1996) reported that AFLP technique can detect much higher levels of polymorphisms than the RAPD analysis. Recently, this technique has been used to analyze genetic similarity among genotypes of sugar cane (*Saccharum* spp.) (Lima et al. 2002) and to estimate genetic diversity in modern cultivars of durum wheat (*Triticum turgidum* L. subsp. *durum* Husn.) (Soleimani et al. 2002). AFLP technique may be more efficient than RAPD for study of genetic diversity and cultivar genetic relationships.

Acknowledgments

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Research article

The genetic system controlling number of spikelets per ear in macaroni wheat over environments

S. N. Sharma*, R. S. Sain and R. K. Sharma

All India Coordinated Wheat and Barley Improvement Project, Rajasthan Agricultural University, Agricultural Research Station, Durgapura, Jaipur 302 018, Rajasthan, India

Summary

The genetic system controlling spikelets per ear was studied from twelve generations of three intervarietal crosses of macaroni wheat (*Triticum durum* Desf.) in two separate environments. The results of joint scaling test indicated that non-allelic interactions had a major role to control this trait in almost all the cases in both the sowing environments. Additive (d) gene effects were frequently observed significant than dominance (h). Both the digenic and trigenic interactions played a significant role in the expression of this trait in the cross HI 8062 x JNK-4W-128. Whereas, in the cross Cocorit 71 x A- 9-30-1 and Raj 911 x DWL 5002 only trigenic interaction was involved, which indicated the major contribution of trigenic interactions to control the inheritance of spikelets per ear in durum wheat. Absolute totals of the non-fixable gene effects were higher than fixable gene effects, confirmed the major role of non-additive gene effects in almost all cases. Digenic and trigenic epistatic interactions cause significant and positive heterosis in the cross HI 8062 x JNK-4W-128 only. The dissipation of epistatic effects involving dominance in F_2 generation causes significant inbreeding depressions. Restricted recurrent selection or diallel selective mating method would be helpful in improving this trait in the material derived from the three crosses. Favorable and a suitable environment must be considered before finalizing the any breeding program for its simple inheritance to get desirable improvement for high grain yield.

Key words: durum wheat, genetic system, epistatic interactions, gene effects, heterosis.

Introduction

Durum or macaroni wheat, *Triticum durum*, (2n = 4x = 28, genomes AABB), is grown on about 30 million hectares and accounts for almost 8 percent of total world wheat production. It is the second important cultivated species of the genus *Triticum* in India, occupying about 2.5 million hectare and has a lot of potential both for domestic consumption and for export market since durum wheat is used for making special products. Despite its importance for the human diet little progress has been made in improving the yield and nutritional qualities on durum wheat. Historically durum wheat has received insufficient attention from plant breeder. Therefore, any efforts to increase yield in durum will be directly supportive to boost up the over all wheat production of the country and it could be helpful to meet out the food requirements for the burgeoning population. Secondly, the surplus durum wheat could be exported in the international market to earn foreign currency.

Information on the genetic parameters associated with the inheritance of a character is a prerequisite to plan a sound-breeding program for its improvement. Yield is a very complex character (Adams 1967), direct

*Corresponding author

improvement for which is not effective. Earlier, breeders suggested tangible advancement of yield components as a possible method for yield improvement. Number of spikelets per ear is one of the important yield contributing component. Some studies have already been conducted in the past revealed that grains per ear can be increased by increasing the number of grains per spikelet. Hence, genetic information concerning the nature of gene action for number of spikelets per ear would be a valuable tool for breeding higher yielding cultivars. The inheritance of this trait was already studied by a number of workers using second order statistics such as diallel analysis (Nanda et al. 1981; Singh and Anand 1971; Maloo 1978; Reddy unpub; Verma 1981). However, the use of first-degree statistics is too limited, which provide the information for nature and the magnitude of gene action (additive, dominance and epistatic) involving in controlling the inheritance of characters related to productivity. This would aid in the choice of effective and efficient breeding methods and thus, accelerate the pace of its genetic improvement of grain yield. Present study was therefore, undertaken to obtain precise information regarding the genetic system controlling the inheritance of spikelets per ear in macaroni wheat using generation means analysis. The information so obtained shall be useful in formulating a sound breeding program in this crop for its tangible advancement in the future.

Materials and methods

The experimental material generated from six diverse parents, comprised three crosses namely, Cocorit 71 x A-9-30-1, HI 8062 x JNK-4W-128 and Raj 911 x DWL 5002. One of the parents (A-9-30-1, JNK-4W-128 and Raj 911) in each cross had higher number of spikelets per ear. Twelve basic generations viz, two parents, F_1 and F_2, first backcross generations with both parents (BC_1 and BC_2), where BC_1 was the cross between F_1 x female parent and BC_2 was F_1 x male parent, their selfed progenies (BC_1F_2, BC_2F_2) and

Table 1. Results of joint scaling test and gene effects for number of spikelets per ear in durum wheat over environments

Effects	Cocorit 71 x A-9-30-1		HI 8062 x JNK-4W-128		Raj 911 x DWL 5002	
	Normal sown	Late sown	Normal sown	Late sown	Normal sown	Late sown
m	22.24**	18.82**	19.63**	18.93**	20.16**	16.91**
	±0.11	±0.64	±0.38	±0.60	±0.59	±0.58
(d)	–0.74**	0.66	–3.20**	–2.86**	0.80	0.72
	±0.10	±0.35	±0.35	±0.56	±0.42	±0.49
(h)	–0.21	–1.35	–0.92	–1.35	2.89**	0.94
	±0.24	±0.71	±0.75	±1.12	±0.85	±0.99
(i)		0.81	6.55**	5.40**	1.06	1.23
		±2.22	±0.64	±0.93	±1.64	±1.28
(j)		–3.21	0.37	1.04	2.29	1.02
		±1.95	±1.91	±2.30	±1.95	±2.19
(l)		6.64	13.35**	9.05	–10.75	–3.02
		±7.38	±2.92	±5.28	±6.17	±5.17
(w)		–5.98**	2.47*	2.02	1.49	1.54
		±1.47	±1.13	±2.23	±1.66	±1.81
(x)		6.58	19.47**	14.25**	–7.84	–3.98
		±9.30	±3.38	±5.83	±7.55	±6.23
(y)		10.24	2.13	4.69	–2.49	–5.28*
		±6.79	±5.20	±3.43	±5.21	±2.09
(z)		0.41	0.26	7.13	12.97	11.26
		±12.61	±6.99	±6.64	±9.76	±7.05
χ^2 for 10 parameter model		0.77 (2)†	3.81 (2)	5.27 (2)	37.71 (2)	6.02 (2)

*, ** Significant at the 5% and 1% level, respectively.

† Degrees of freedom for χ^2 is given in parentheses

second backcross generations ie the BC_1 and BC_2 plants again crossed with both original parents (BC_1 x female parent; BC_1 x male parent and BC_2 x female parent; BC_2 x male parent). All these populations were raised together in randomized block design with three replications at 30 cm x 15 cm spacing under normal and late sown environments in the same cropping seasons at research farm of Rajasthan Agricultural University, Agricultural Research Station, Durgapura, Jaipur. Each parent and F_1 generations were sown in 2 rows, each backcross generation in 4 rows and F_2 and the second cycle of backcrosses in 6 rows of 5 m length. Number of spikelets per ear was recorded on 15 random plants in each parent and F_1, 30 plants in each backcross generations and 60 plants in each F_2 and second backcross generations in both environments.

The data of each population in both environments were analyzed separately by joint scaling test of Cavalli (1952) to determine the nature of gene action. Components of heterosis in the presence of trigenic interactions were calculated as suggested by Hill (1966).

Results and discussion

Significant differences were observed among generation means for spikelets per ear in all the three crosses in both the sowing environments, which revealed the presence of genetic diversity for this attribute in the material. On the basis of different models fitted to data, the joint scaling tests revealed the presence of epistatic interaction in both the environments except in the cross Cocorit 71 x A-9-30-1 under normal sown, where additive-dominance model was fitted to the data. In all other cases, 10-parameter model was adequate to explain genetic variation in different generations in both the sowing environments except in the cross Raj 911 x DWL 5002 under normal sowing where even this model was not adequate, indicating the more complex genetic systems involved in controlling this trait. However, looking to the low value of chi-square and very low probability of 10-parameter model, the different gene effects were estimated according to this model (Table 1).

The analysis of gene effects revealed that the additive (d) effect was only significant in the first cross (Cocorit 71 x A-9-30-1) under normal sowing conditions, indicating that this character was simply inherited and can be improved by simple breeding method such as progeny selection. Additive (d) effects were also found significant in the second cross (HI 8062 x JNK-4W-128) in both the sowing environments only. However, dominance (h) was only found significant in the third cross (Raj 911 x DWL 5002) under normal sowing. Both digenic and trigenic interactions had important role in controlling the inheritance of this trait in the cross HI 8062 x JNK-4W-128. Whereas, in the first and third cross under late sowing only trigenic interaction additive x additive x additive (w) and additive x dominance x dominance (y) control the inheritance of trait studied, respectively. However, none of the digenic and trigenic interactions were found significant in the cross Raj 911 x DWL5002 under normal sowing, confirmed that more complex type of non-allelic interactions or linkages are involved to control spikelets per ear (Table 1). Magnitude and directions (signs) of epistatic interactions were depended upon the material and sowing environments.

Results of the absolute totals of epistatic effects (Table 2) clearly indicated that second order interactions had higher value than the first order interactions and the main effects in all the cases in both the sowing environments except in the first cross where additive dominance model was fitted to the

Table 2. Absolute totals of epistatic effects, fixable and non-fixable gene effects for number of spikelets per ear in durum wheat over environments

Cross	Environment	Main effects		Epistatic effects		Total gene effects	
		(d)	(h)	I order†	II order‡	Fixable§	Non-fixable¶
Cocorit 71 x A-9-30-1	Normal	–0.74	–0.21	-	-	0.74	0.21
	Late	0.66	–1.35	10.66	23.21	7.46	28.43
HI 8062 x JNK-4W-128	Normal	–3.20	–0.92	20.28	24.33	12.22	36.51
	Late	–2.86	–1.35	15.48	28.08	10.28	37.49
Raj 911 x DWL 5002	Normal	0.80	2.89	14.10	24.79	3.35	39.23
	Late	0.72	0.94	5.27	22.06	3.49	25.49

† [(i), (j), (l)], ‡ [(w), (x), (y), (z)], § [(d), (i), (w)], ¶ [(h), (j), (l), (x), (y), (z)]

Table 3. Components of heterosis for number of spikelets per ear in durum wheat over environments

Effects	Cocorit 71 x A-9-30-1		HI 8062 x JNK-4W-128		Raj 911 x DWL 5002	
	Normal sown	Late sown	Normal sown	Late sown	Normal sown	Late sown
(h)	–0.21	–1.35	–0.92	–1.35	2.89	0.94
–(i)	-	–0.81	–6.55	–5.40	–1.06	–1.23
1/2(x)	-	3.29	9.34	7.12	–3.92	–1.99
1/4(z)	-	0.10	0.07	1.78	3.24	2.81
–(d)	0.74	–0.66	3.20	2.86	–0.80	–0.72
1/2(j)	-	–1.61	0.19	0.52	1.15	0.51
–(w)	-	5.98	–2.47	–2.02	–1.49	–1.54
–1/4(y)	-	–2.56	–0.53	–1.17	0.62	1.32
Heterosis (%)	–3.04	0.16	9.41**	9.61**	1.51	–0.16
Inbreeding depression(%)	3.09	5.17	13.26**	12.00**	2.35	6.05*

*, ** Significant at the 5% and 1% level, respectively.

data. Thus, it is clear that epistatic effects particularly trigenic effects contributed maximum to control the inheritance of this trait. Earlier Nanda et al. (1981) reported that additive-dominance model was sufficient to explain genetic variance among the generation means for this trait in *aestivum* wheat whereas additive x additive (i) and dominance x dominance (l) variance along with additive variance were reported by Singh and Anand (1971), which had significant role to control this trait. Type of the epistasis could not be ascertained as either (h) or (l) or both were non-significant in each case.

Furthermore, results indicated that the absolute totals of the non-fixable gene effects were higher than fixable in almost all cases except in the cross Cocorit 71 x A-9-30-1 (under normal sown), where fixable gene effect (additive) had important role. Dasgupta and Mondal (1988), Raghuvanshi et al. (1988) and Patil et al. (1997) also reported the predominant role of additive gene effects in the expression of this trait. Epistatic interactions shared a major portion of the non-fixable effects in both the environments. Earlier Maloo (1978), Reddy (unpub), Verma (1981), Saini (1987), Kathiria (1991), Mann et al. (1992) and Khedar (1998) also observed the significant role of non-additive gene effects to control this trait.

Analysis of components of heterosis over better parent revealed that both digenic and trigenic epistatic interactions had an important role to cause significant and positive heterosis in the cross HI 8062 x JNK-4W-128. Additive x additive x dominance (x) followed by additive x additive (i) and additive (d) frequently contributed to the expression of significant heterosis in this cross under both the environments (Table 3). Earlier Maloo (1978) and Verma (1981) also observed significant heterosis for this trait. Absence of heterosis in remaining two crosses could be attributed to internal cancellation of the components of heterosis. Significant inbreeding depression was also observed in the second and third cross (late sown) due to the dissipation of non-additive dominance effects or epistatic effects involving dominance in F_2 generation.

The results of the present study revealed that as a consequence of higher magnitude of digenic and trigenic interactions, non-fixable effects were higher than the fixable effects. Naturally, the successful breeding methods will be the ones, which can mop-up the genes to form superior gene constellations interacting in a favorable manner. The breeding methods suggested to achieve this objective are restricted to recurrent selection (Joshi 1979) and diallel selective mating (Jensen 1978). Furthermore, sowing environments should also be taken in consideration before finalizing the breeding method for its improvement. Favorable environment must be considered for taking advantage of its simple inheritance to achieve desirable improvement to get high grain yield in durum wheat in future.

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Research information

Post-anthesis stem reserve mobilization in new plant type wheat

P.C. Pandey, MRS Kaim, S.S. Singh[1], G.P. Singh[1], D.K. Joshi and A.P.S. Verma

[1]Nuclear Research Laboratory, Division of Genetics Indian Agricultural Research Institute New Delhi, India

Post-anthesis stem reserve mobilization is an important assimilate contributing source for grain filling in wheat under temperature stress conditions invariably encountered in major wheat growing regions of the world (Al-Khatib and Paulsen 1990; Blum et al. 1994). Quick screening of genetic variability in post-anthesis relative stem reserve mobilization therefore, assumes importance for developing improved wheat plant types. Post-anthesis changes in proton relaxation time T_1 of wheat stem were suggested to indicate the post-anthesis stem reserve mobilization (Pandey et al. 1998) and also genotypic differences in such mobilization under normal and one month late sown conditions (Pandey et al. 2001). It was also suggested by these authors that thick/hollow stem character, capable of superior storage and post-anthesis remobilization of assimilates may be studied for designing new plant type for increased yield potential. More recently new plant type of wheat with thick stem, improved grain weight and grain number per ear has been developed (Singh et al. 2001). It has been suggested that physiologically these new plant type genotypes have developed an improved translocation path up to the individual floret level and an improved pre-anthesis assimilate reserve and its post-anthesis mobilization to the grain. It is in this context, the post-anthesis changes in NMR T_1 and moisture percent in the peduncle region of one of the new plant type DL 1266-5 was studied.

The wheat genotype DL-1266-5 (Singh et al. 2001) was sown on 20th November 2001–02 in the field of Indian Agricultural Research Institute. Fertilizers NPK were applied in the form of urea, single super phosphate and muriate of potash @ of 120:60:40. Nitrogen was applied as basal dose (50%) and 50% at crown root initiation stage. Main shoots were tagged at the time of anthesis and were harvested for sampling on the day of anthesis and 2, 10, 16 and 25 days after anthesis (DAA) in moistened polythene bags to avoid moisture loss. Separated peduncle portion, were gently packed in NMR sample tubes (18 mm diam) upto sample height restricted to 20 mm within the homogeneous field of the magnet. T1 was measured by Saturation Recovery method-using software loaded in EDM 511 (supplied with the instrument), which gives a single component with three-parameter fit, by a 20 MHz Bruker minispec pc20 NMR system. The water content was measured in the same samples after measuring T1 by oven drying to constant weight at 85°C.

T1 parameter shows an increase after 10th day of anthesis in spite of a sharp decline in the moisture percentage (Fig.1) suggesting a rapid mobilization of stem reserves from stem in this genotype after 10th

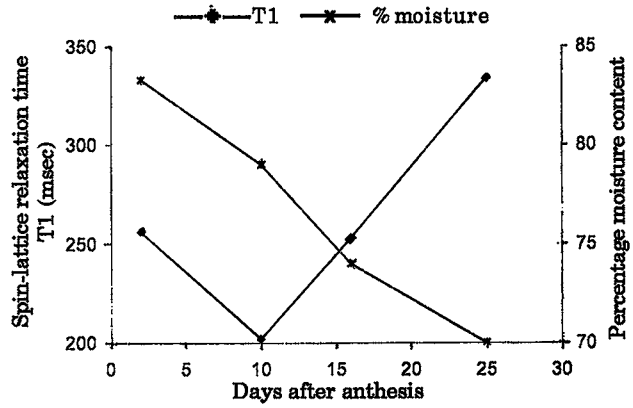

Fig.1. Post-anthesis changes in T1 and % moisture content of the peduncle in new wheat plant type DL-1266-5

E-mail: gpsingh@iari.ernet.in

day of anthesis under normal sown conditions. These observations tend to support the suggested efficient post-anthesis mobilization of stem reserve in the DL 1266-5.

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Efficacy of new chemicals/fungicides for the control of loose smut of wheat caused by *Ustilago segetum* var. *tritici*

Rajender Sing, S.S. Karwasra and M.S. Beniwal

Department of Plant Pathology, CCS-Haryana Agricultural University, Hisar, India

Loose smut of wheat caused by *Ustilago segetum (pers) Roussel* var. *tritici* is one of the important diseases of wheat in India. The disease causes 1–2 percent losses in wheat production. Losses caused by this disease may be upto 5–7% in cases where the farmers recycle their own seed (DWR 1992). Since cultivated varieties lack resistance to loose smut, so chemical control of gain is important. Hence there is need to identify some new molecules that are cheaper and effective against loose smut of wheat.

The experiment was conducted at wheat breeding research area of CSHAU-Hisar-India during 2000–2002 crop seasons. The seed of wheat var. WH 147 inoculated with 20% loose smut infection for testing. The plot size was of 6 lines and 2 m length in triplicate randomized block design. The treatment of tested molecules were Dividend 3%WS (difenoconazole) @ 1.0, 2.0, 2.5, 3.0 g/kg seed, Pulsor 2F (thifluzamide) @ 1.0, 1.5, 2.0, ml/kg seed, Vitavax 200FF (carboxin) @ 2.0, 3.0 ml/kg seed, Vitavax 200WP (carboxin) @ 2.0,3.0,4.0 g/kg seed, Raxil 2DS (tebuconazole)@ 0.5,1.25 g/kg seed, Vitavax 75WP (carboxin) and Bavistin 50WP (carbendazim) both @ 2 g/kg seed as presowing dry and slurry treatment of fungicide in comparison to check. The crop was raised as per recommended agronomic practices. The smutted and healthy tillers/plot were counted and percentage of smutted tillers was calculated on tillers basis.

All fungicides controlled loose smut incidence. Seed treatment of Raxil 2DS and Dividend eradicated the disease upto 99.5 and 83.9 percent, respectively in comparison to recommended fungicides Vitavax 75WP (2g/kg) controlled upto 91.6 percent. Pulsor 2F, Vitavax 200FF, Vitavax 200WP reduced the disease 48.9 to 83.3% depending upon the dose. There was no phytotoxicity observed in none of treatment. The present studies clearly indicated that Raxil 2DS can be used at lower dose ie @ 0.5 g/kg seed quite effectively. It is concluded that Raxil 2DS and Dividend 3%WS may be used in addition to carboxin and carbendazim for controlling the loose smut of wheat. The effectiveness of Raxi l2DS in controlling loose smut at the rate of 0.2% has been reported by Sinha and Singh (1996) and Goel et al. (2001).

Table.1 Relative efficacy of fungicides on control of loose smut of wheat.

Fungicide	Doses (–/kg seed)	Smutted tillers (%)†	Disease control (%)
Bavistin 50WP	2.0 g	5.8 (13.87)‡	67.0
Vitavax 75WP	2.0 g	1.5 (6.91)	91.6
Vitavax 200WP	2.0 g	7.2 (15.58)	58.6
Vitavax 200WP	3.0 g	4.1 (11.73)	76.3
Vitavax 200WP	4.0 g	1.7 (7.51)	90.2
Raxil 2DS	0.5 g	0.3 (6.49)	98.4
Raxil 2DS	1.25 g	0.1 (1.44)	99.5
Vitavax 200FF	2.0 ml	8.9 (17.36)	48.9
Vitavax 200FF	3.0 ml	6.7 (14.96)	61.8
Pulsor 2F	1.0 ml	11.0 (19.37)	36.9
Pulsor 2F	1.5 ml	5.2 (13.24)	69.9
Pulsor 2F	2.0 ml	2.9 (9.81)	83.3
Dividend 3%WS	1.0 g	4.6 (12.63)	73.4
Dividend 3%WS	2.0 g	1.1 (5.87)	83.9
Dividend 3%WS	2.5 g	0.8 (5.04)	95.5
Dividend 3%WS	3.0 g	0.4 (3.45)	97.9
Control		17.4 (24.68)	

†Average of three replicate
‡Figures in parenthesis are angular transformed value

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Research information

Influence of weed seed of sweet clover and NaCl on germination and seedling growth of wheat

S.M. Alam

Plant Physiology Division, Nuclear Institute of Agriculture, Tandojam, Pakistan.

Weed seed of sweet clover was evaluated alone or in combination with NaCl for its effect on germination and seedling growth of wheat. There was no effect of weed seed or NaCl salinity on the germination. It was observed that weed seed alone and with 0.2 % NaCl had significant effect on shoot length. Similarly, 0.4 % NaCl alone or in combination with weed seed reduced the shoot length. The root length was reduced by weed seed alone and in combination with NaCl. It was also observed that root length was affected more than the shoot.

Plants influence each others growth by means of exudates (Rice 1984), leachates from residues incorporated in the growing medium (Cotton and Einhellig 1980) or residues in natural undisturbed condition. It is commonly assumed that economical reduction in main crops from weed seeds are the direct result of competition or of the both acting together. Literature reveals that allelopathic interference by weed extracts has been established as one of the several factors that regulate the growth of plants (Alam 1993; Alam et al. 1997; Rice 1984). A variety of organic compounds have been implicated as the possible agents responsible for growth reduction and it has been assumed that in most cases, it is the collective action of several compounds, which cause the growth depression (Rice 1984).

In the process of competition, weed seeds frequently absorb nutrients much more than the crop plant. Evenari (1949) reviewed the various studies conducted and concluded that most weed seeds contain essential oils, alkaloids, or glycosides, which inhibit germination and seedling growth of other crops present in their immediate vicinity. The findings of McCalla and Duley (1948) revealed that soaking corn seeds in aqueous extract of sweet clover for 24 hours reduced germination and growth of tops and roots in petri dishes. Saraswat (1987) reported that sweet clover exhibited allelopathic effect on the growth of rice seedlings. It was also observed that leachates from fresh material of sweet clover produced high inhibition of radicle growth of corn, bean and squash and a reduction of 68 % in the growth of corn has been reported (Anaya et al. 1987). They further reported that reduction is due to allelopathic potential of this weed. In another experiment, they found similar effect of sweet clover.

Coumarin compound and phenolic derivatives of benzoic and cinnamic acids are some of the frequently reported water-soluble allelochemicals. These chemicals may alter several aspects of plant metabolism. These include mitochondrial respiration, photosynthesis rate and chlorophyll content. Some authors have reported coumarin, o-coumaric acid and melilotic acid as the major active compounds in sweet clover (Langer and Hill 1982; Nicollier et al. 1985). Putnam and Weston (1986) reported that corn plant performed poorly, when planted into stubble mulch of white sweet clover.

Gressel and Holm (1964) reported that seed of barnyard grass reduced the germination of alfalfa and turnip by 41 and 43 %, respectively, when compared with the water control. Contrary to this Bhatia et al. (1982) found that stem and roots of *Melilotus indica* promoted the growth of wheat seedlings. This study was therefore, carried out to see the effect of weed seed of sweet clover on the seedling growth of wheat (cv. Pavon). Some of growth characteristics of cv. Pavon are as: plant height (86.6); growth habit (seedling) (erect); flag leaf attitude (semi-erect); auricle anthocyanin (absent); head shape and color (tapering, light red); head awnness (awned); stem (stiff); seed

color and shape (amber, ovate); 1000 grain weight (42.1 g); No. of grains/spike (80); protein content (11.3 %); fat (2.1 %); ash (2.0%); days to heading (77); days to maturity (135); yield potential (5075 kg/ha); average yield (4765 kg/ha); spike length (9.0 cm); spikelets per spike (17.8); harvest index (36.1%); resistance to stem and leaf rust.

Weed seeds of sweet clover were collected from matured weed plant growing in wheat field. The seeds were cleaned and then sun dried. The experiment was carried out in glass bowls of 250 ml capacity. A 0.8 percent agar-jel was prepared and the agar-media was incorporated with sodium chloride solution to get 0.0, 0.2 and 0.4 percent salinity levels. Fifty ml of each salinized agar-media was poured into sterilized glass bowls of 250 ml capacity for seed planting. Seeds of wheat (cv. Pavon) and weed seed of sweet clover were surface sterilized by 1% sodium hypochlorite solution for three minutes and then rinsed with distilled water. Ten healthy wheat seeds were placed in a circle on the surface of each bowl containing weed seed and agar-media salinized solution. A set containing no weed seed and no NaCl was also kept and treated as control. All the bowls were then covered with sterilized petri dishes and incubated at 28°C. The treatments were kept in a randomized design with four replication. The experiment was terminated after 5 days. The germinated seeds were noted and their shoot and root lengths were measured. The data has been analyzed and presented in Table 1.

The weed seed of sweet clover and NaCl levels had no effect on seed germination (Table 1). Weed seed alone, and in combination with 0.2 % NaCl and 0.4 % NaCl alone had similar decreasing effects on shoot length, and reduced the shoot lengths by 57.5, 56.3 and 61.0 %, respectively compared to control. The NaCl level of 0.4 % in combination with weed seed had significantly reduced the shoot length by 74.4 % compared to control. The weed seed alone and in combination with 0.2 % and 0.4 % NaCl significantly reduced the root lengths by 85.8, 86.0 and 87.8 %,

Table 1. Effect of seed of sweet clover (*Melilotus indica* L.) weed and NaCl on germination and seedling growth of wheat

Variance analysis

Source	df	Germination (%)	Shoot length (cm)	Root length (cm)
		variance	variance	varianace
between	5	0.32	7.54**	37.58**
within	12	2.5	0.15	0.31

**Significant at 1% level

Mean ± SD and percent increase (+) or decrease (–) over control

Treatments	Germinatio(%)	Shoot length(cm)	Root length(cm)
Control (no weed seed, no NaCl)	90±1.0 a	6.18±0.11 a	9.80±0.09 a
weed seed	90±0.00 a	2.63±0.26 c (–57.5)†	1.39±0.22 d (–85.8)
0.2% NaCl	83±2.89 a	3.87±0.27 b (–37.4)	6.72±0.44 b (–31.4)
0.2% NaCl+weed seed	87±1.53 a	2.70±0.23 c (–56.3)	1.37±0.15 d (–86.0)
0.4% NaCl	83±1.53 a	2.41±0.73 c (–61.0)	3.88±1.26 c (–60.4)
0.4% NaCl+weed seed	90±1.00 a	1.58±0.37 d (–74.4)	1.19±0.07 d (–87.9)

† Values in parenthesis indicate percent increase (+) or decrease(–) over control

respectively over to control and the salinity levels alone (0.2 and 0.4 % NaCl) reduced the root length by 31.4 and 60.4 %, respectively when compared to control (Table 1).

Sweet clover seed in the present study, did not show any effect on seed germination, but it has significant decreasing effect on both shoot and root lengths of wheat. This shows that for germination phenomenon, there was a tolerance behavior in wheat seed to bear the effects negative of two stresses, and thus there was no harmful effect of the treatments on seed germination. Seed germination is considered to be the most critical stage, especially under stress conditions. The first requirement of seed germination of any crop is water for hydrolysis of reserves, as a medium of translocation, hydration of enzymes, for operational conformation of cell membranes and organelles and finally to provide the driving force for cell expansion induced by germination. The findings of Hadas (1977) suggest that the germination rate and the final seed germination decrease with the decrease of the water movement into the seeds during imbibition. It is also known that during germination, rapid biochemical changes take place which provides the basic frame work for subsequent growth and development. The initial metabolic changes that occur immediately after the imbibition of water are the increase in the hydrolytic enzymes such as alpha amylase and protease.

In the present experiment, the root length was affected more than the shoot. Although, we did not determine the biochemical parameters, but it is obvious that the seed of sweet clover contains leachable allelochemicals, which have more profound effect on roots than shoot. Unfortunately, there is no report on the effect of seed extracts of sweet clover. Literature suggests that different parts of sweet clover contain large amount of coumarin, o-coumarin, melilotic acid as the major active compounds (Langer and Hill 1982, Nicollier et al. 1985) and is considered to be highly effective in reducing plant growth. Sweet clover extract has been shown to reduce germination, shoot and root length of corn (McCalla and Duley 1948). It exhibited high inhibition of radicle growth in corn, bean and squash (Anaya et al. 1987). Saraswat (1987) found adverse allelopathic effect on rice growth. It was concluded from this study, that seeds of sweet clover had no inhibitory effect on seed germination, but it had depressive effects on shoot and root lengths of wheat crop

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Genetic stock

Utilization of genetic stocks in National Genetic Stock Nursery — a "suggested crossing block"

Vinay Mahajan[1], NVPR Ganga Rao and Jag Shoran

Division of Crop Improvement, Directorate of Wheat Research, Karnal 132 001, Haryana, India

The success of wheat breeding program primarily depends upon the availability of reliable genetic stocks for key characters. The National Genetic Stock Nursery (NGSN) initiated in 1964–65 was re-constituted into a "Suggested Crossing Block" in 1996–97 at Directorate of Wheat Research, Karnal, wherein confirmed genetic sources from different nurseries are included to assist the plant breeder in making their crossing block more vibrant. Normally the new confirmed genetic stocks are added every year by different programs after years of evaluation. The primary aim of this nursery is to provide confirmed genetic stocks to the wheat breeders of the India as well as to provide the opportunity for evaluation of genetic stocks for agronomic superiority, biotic and abiotic stress tolerance in various wheat growing zones through 35 centers spread throughout the country. The data so generated was compiled and published in the form of Progress Report, Vol II, Genetic Resources every year (Mahajan 1997, 1998, 1999; Mahajan and Ganga Rao 2000, 2001).

Among various other NGSN components, the Latest Agronomic Base (LAB) and Exotic Material (EMAT) are two important components of "Suggested Crossing Block" since 1996–97. The LAB includes the entries from 2nd year of "Advanced Varietal Trial" of bread and durum wheat grown in all the six agro-climatic zones of India. These were among the best performers but lack in some essential agronomic or disease component necessary for a genotype to qualify as variety for release and general cultivation. The supply of these entries to cooperators ranged from 7 (1998–99) to 16 (2000–01)(Table 1) and their exploitation ranged from 12.0 (1998–99) to 19.0 percent (1997–98). The utilization of genetic stock was computed as:

$$\text{Overall Genetic Stock Utilization (\%)} = \frac{\text{Number of entries selected}}{\text{Number of centers x Total entries}} \times 100$$

Table 1. Utilization status of NGSN components (Latest Agronomic base and Exotic Materials) of "Suggested Crossing Block"

Crop Season	Latest agronomic base		Exotic materials		Number of reporting centers	Overall utilization (NGSN) (%)
	Entries supplied	Utilization (%)	Entries supplied	Utilization (%)		
1996–97	14	13.5	14	23.5	17	19.5
1997–98	14	19.0	12	29.2	24	19.2
1998–99	7	12.0	9	15.0	27	15.0
1999–00	11	15.4	10	19.7	30	14.5
2000–01	16	13.9	9	19.4	31	15.6

[1]Corresponding author, email: vimahan@hotmail.com

Table 2. Mode of utilization in some NGSN components

Crop Season	Hybridization		Direct selection	
	Entries†	Percent	Entries†	Percent
Latest agronomic base				
1999-00	57	11.9	17	3.8
2000-01	60	12.1	9	1.9
Exotic materials				
1999-00	47	15.7	12	4.0
2000-01	37	12.9	17	5.9

†Number of times entries picked up over locations

The selections made on EMAT included genetic materials like synthetic wheat lines and large spike buitre material. These materials were not so good in many characters like threshability, seed filling, quality, susceptible to disease resistance (especially buitre material) etc, but were important sources of biotic and abiotic stress tolerance (synthetic wheat) and very large spike and more grains per spike (buitre material). The genetic material was provided to cooperators primarily for their pre-breeding activities or crossing block. Since 1996–97, 9 (1998–99) to 14 (1996–97) EMAT were supplied to cooperators in India (Table 1) and their exploitation by cooperators ranged from 15.0 (1998–99) to 29.2 per cent (1997–98).

On understanding the mode of utilization of genetic stocks the two years (1999–2000 and 2000–01) of data revealed that use of genotypes was primarily through hybridization in their breeding programs and in very few cases it was utilized as direct selection in less explored agro-climatic areas. The entries of LAB utilized through hybridization were 11.9 and 12.1 percent during 1999–2000 and 2000–01, respectively (Table 2). However through direct selection the exploitation of LAB genotypes was meager. Similarly the EMAT was primarily used in hybridization with exploitation of 15.7 and 12.9 percent in crop seasons 1999–2000 and 2000–01, respectively.

Hence over the years both the components ie LAB and EMAT, of "Suggested Crossing Block" contributed effectively in enriching the breeding programs of the cooperating centers of India.

Acknowledgments

The authors are grateful to the Project Director, Wheat for guidance and help in execution and transformation of NGSN into a "Suggested Crossing Block". The authors are also grateful to all the cooperators for providing information on the use of genotypes. We are thankful to all the contributors and staff members for their active cooperation in synthesis of an active "Suggested Crossing Block".

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Gene symbol

CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2002 Supplement

R.A. McIntosh[1], K.M. Devos[2], J. Dubcovsky[3] and W.J. Rogers[4]

[1]Plant Breeding Institute, The University of Sydney, 107 Cobbitty Road, Cobbitty, N.S.W., Australia, 2570.
[2]John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk, NR4 7UH, U.K.
[3]Department of Agronomy and Range Science, University of California, Davis, 95616 CA, U.S.A.
[4]Catedra de Genetica y Fitotecnia, Universidad Nacional del Centro de la Provincia de Buenos Aires, 7300 Azul, Argentina

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Revisions

10. Laboratory Designators for DNA markers

barc	Cregan, P. USDA-ARS Beltsville, MA	*uaz*	
cn		*ucg*	
gdm	Röder, M.S. (Gatersleben D-genome microsatellite*) Institut fuer Pflanzengenetik und Kulturpflanzenforschung (IPK) Corrensstr. 3 06466 Gatersleben Germany		
unl	Gill, K. kgill@unl.edu Department of Agronomy 362H Plant Science P.O. Box 830915 University of Nebraska, Lincoln Lincoln NE68583-0915 USA		

Gross Morphology: Spike characteristics

5. Elongated glume

P1. Revise:

P1. [*P* {911}; *Eg* {922}; *P-A^{pol}1* 7AL {922,1547}, 7A or 7B (based on linkage of 0.2 with a gene for red coleoptile {922}. {0254}; *P-A^{pet}1* {0254}].

i: Saratovskaya 29*8//Novsibirskaya 67*2/*T. polonicum* {922}.

itv: P-LD222 = LD222*11/*T. turgidum* var *polonicum* {1546,1547}.

tv: *T. polonicum* {0254}; *T. petropavlovskyi* {0254}.

ma: *Xgwm260-7A* (S) - 2.3 cM - *P1* - 5.6 cM - *Xgwm1083-7A* (L) {0254}; *Xgwm890-7A* - 2.1 cM - *P1* {0254}.

Add at the end of the 'Elongated glume' section:

Note: The loci determining elongated glumes in the *T. turanicum* and *T. durum* conv. *falcatum* are not homoeologous to the *P* loci in the centromeric region of the group 7 chromosomes {0254}.

Alkylresosocinals Content in Grain

Ar1 {0281}.	5AL {0281}.		High alkylresocinols content is dominant {0281}.
		tv:	Langdon {0281}.
ar1 {0281}.		tv:	Ardente {0281}. This cultivar has a low content compared to all tested durum and common wheats {0281}

Aluminium Tolerance

Alt2. **ma:** Add: '*Alt2* cosegregated with *Xbcd1230-4D* and fell within the interval *Xgdm125-4D* – 4.8cM – *Alt2* – 1.1cM – *Xpsr914-4D* {0248}.'.

Anthocyanin Pigmentation

3. Red/purple coleoptiles

Replace the previous entries with:

There is an orthologous gene series on the short arms of homoeologous group 7. The 'a' alleles confer red coleoptiles.

Rc-A1a {0250}.	[*Rc1, R* {401}].	7A {769,1293}, 7AS {0250}.	**s:** CS*6/Hope 7A {1293}.
	v: Hope *Rc-B1*		
	ma: *Rc-A1* (distal) - 11.9 cM - *Xgwm913-7A* {0250}.		
Rc-B1a {0250}.	[*Rc2, R2* {401}].	7B {742}, 7BS {401, 769, 0250}	**s:** CS*6/Hope 7B {769}.
	v: Hope *Rc-A1*.		
	ma: *Xgwm263-7B* - 26.1 cM - *Rc-B1* - 11.0 cM - *Xgwm1184* {0250}.		
Rc-D1a {0250}.	[*Rc3*].	7D {596}, 7DS {1241, 1444, 0250}.	
	v: Mironovskaya 808 {1444}; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404 {1240}; Tetra Canthatch/*Ae. squarrosa* var. *meyeri* RL 5289, RL 5406 {1240}; Sears' *T. dicoccoides/Ae. squarrosa* = Sears' Synthetic {596}.		
	ma: *Rc-D1* (distal) - 3 cM - *Xpsr108-7D* {180}; *Xgwm44-7D* - 6.4 cM - *Rc-D1* - 13.7 cM - *Xgwm111-7D* {0250}.		

Tahir & Tsunewaki {1453} reported that *T. spelta* var. *duhamelianum* carries genes promoting pigmentation on chromosomes 7A and 7D and genes suppressing pigmentation on 2A, 2B, 2D, 3B and 6A. Sutka {1444} reported a fourth factor in chromosome 6B and suppressors in 2A, 2B, 2D, 4B and 6A.

Awnedness

1. Dominant Inhibitors

1.2. Tipped 1

B1 Revise '5AL {1293}.' to '5AL {1293,0242}.'.

DNA Markers

Group 1S

Amendments:

Xabg500-1A. Revise the first column to '*Xabg500-1A* {280}[5], *1B,D* {0252}[1].'.

Xbcd446-1A. Add '(1BL).' in the last column.

Xbcd1124-1A,B. Revise the first column to '*Xbcd1124-1A* {280}[5], *1B* {1529}[1], *1D* {0252}[1].'.

Xbcd1706-1A,B. Revise the first column to '*Xbcd1796-1A* {280}[5], *1B* {1529}[1], *1D* {0252}[1].'.

Xcdo99-1B,D. Revise the first column to '*Xcdo99-1A* {0252}[1], *1B* {154}[1], *1D* {1529}[4].'.

Xcdo388-1B,D. Revise the first column to '*Xcdo388-1B.1* [{1529,0252}]^{1}, *1D* {1529}^{4}.', add '[*Xcdo388-1B* {1529}, *Xcdo388a-1B* {0252}].' in the second column and revise the last column to '(1BL, 2B, 3D, 4A,D, 5A,B, 6A,D).'.

Xcdo534-1B. Revise the last column to '(3A, 6A,B,D, 7A).'.

Xcdo580-1A. Revise the first column to '*Xcdo580-1A* {280}^{1,3,5},{1529}^{1}, *1D* {0242}.

Xcdo658-1A,B,D. Revise the first column to '*Xcdo658-1A* {280}^{3,5},{0252}^{1}, *1B,D* {445}^{1}.'.

Xcdo1173-1A,B,D. Revise the first column to '*Xcdo1173-1A* {280}^{3,5},{0252}^{1}, *1B* {1529}^{1},*1D* {445}^{1}.'.

Xcdo1188-1A.1,B.1,D. Revise the first column to '*Xcdo1188-1A.1* [{280}]^{3,5},[{0252}]^{1}, *1B.1* [{1529}]^{1}, *1D* {445}^{1}.', add '[*Xcdo1188-1A.*{280}^{3,5},{0252}^{1}, *1B* {1529}^{1}].' in the second column , and add '(1AL,BL).' in the last column.

Xcdo1340-1B. Revise the first column to '*Xcdo1340-1A* {0252}, *1B* {1529}, *1D* {0252}.' and add '(1BL).' to the last column.

Xcmwg645-1A.2. Revise the first column to '*Xcmwg645-1A.1* {280}^{3,5},[{0252}]^{1}, *1B.1, D.1* [{0252}]^{1}.' and add '[*Xcmwg645a-1A,B,D* {0252}^{1}].' in the second column.

Xgwm18-1B. Add '(4B).' in the last column.

Xgwm33-1A. Revise the first column to '*Xgwm33-1A* {1226}^{1}, *1B* {0270}^{2}.' and add '(1BL).' in the last column.

Xgwm136-1A. Revise the first column to '*Xgwm136-1A* {9929},{0269}^{2}.'.

Xgwm273-1B. Revise the first column to '*Xgwm273-1B* {9929},{0270}^{2}.'.

Xgwm413-1B. Revise the first column to '*Xgwm413-1B* {9929},{0270}^{2}.'.

XksuE19-1A,B,D. Revise the last column to '(6D, 7B).'.

XksuF43-1B.1,.2. Revise the first column to '*XksuF43-1A* {252}, *1B.1,.2* {1529}, *1D* {0252}.'.

Xmwg60-1A. Revise the first column to '*Xmwg60-1A* {280}^{1,5}, *1B,D* {0250}^{1}.'.

Xmwg68-1A,B. Revise the first column to '*Xmwg68-1A* {280}^{5},{0252}^{1}, *1B* {1529}^{1}, *1D* {0252}.'.

Xmwg837-1B.1,D. Revise the first column to '*Xmwg837-1A* [{0252}], *1B.1,D* {1529}.' and add '[*Xmwg837a-1A* {0252}].' in the second column.

Xmwg938-1B,D. Revise the first column to '*Xmwg938-1A* [{0252}], *1B.1* [{1529,0252}], *1D* {1529}.', add '[*Xmwg938a-1A,B* {0252}, *Xmwg938-1B* {1529}].' in the second column and revise the last column to '(1BL, 7A).'

Xmwg2021-1A.2,.2. Revise the first column to '*Xmwg2021-1A.1* {280}^{3,5}, *1A.2* {280}^{1}, *1B.1,D* [{0252}].', add '[*Xmwg2021a-1B,D* {0252}].' in the second column and revise the last column to '(1BL, 2A, 3A).'.

Xmwg2048-1A. Revise the first column to '*Xmwg2048-1A* {282}^{3},{0252}^{1}, *1B,D* {0252}^{1}.'.

Xmwg2083-1A. Revise the first column to '*Xmwg2083-1A* {280}^{5}, [{0250}]^{1}, *1B.1,D* [{0252}]^{1}.', add '[*Xmwg2083a-1B,D* {0252}].' in the second column and add '(1BL).' in the last column.

Xmwg2245-1D. Revise the first column to '*Xmwg2245-1A,B* {0252}, *1D* {0135}.'.

Xpsr596-1A,B,D. Add '(2B, 3A).' in the last column.

Xrz244-1A. Revise the first column to '*Xrz244-1A* {1529}, *1B,D* {0252}.'.

Xsfr2(Lrk10)-1A. Revise the first column to '*Xsfr2(Lrk10)-1A* [{356,0252}], *1B,D* [{0252}].' and revise the second column to '[*Lrk10* {356}, *XLrk10-1A,B,D* {0252}].'.

Xutv1391-1: Revise the first column to '*Xutv1391-1A* {9959}^{2}, *1B* {0269}^{2}.'

Add:

Xabg53-1A,B,D {0252}.		ABG53.	
Xabg59-1B,D {0252}.		ABG59.	
Xabg74-1A,B,D {0252}.		ABG74.	
Xabg494-1A,B,D {0252}.		ABG494.	
Xbcd368-1A {0242}.		BCD368.	
Xbcd371-1B {0275}.		BCD371.	
Xbcd762-1A.2,B.2,D [{0252}].	[*Xbcd762a-1A,B,D* {0252}].	BCD762.	(1AL,BL)
Xbcd1340-1A,B,D {0252}.		BCD1340.	
Xcdo127-1A,B.1,D [{0252}].	[*Xcdo127a-1A,B,D* {0252}].	CDO127.	(1B, 3A).
Xcdo127-1B.2 [{0252}].	[*Xcdo127b-1B* {0252}].	CDO127.	(1A,B,D, 3A).
Xcdo580-1A,B.1,D [{0252}].	[*Xcdo580a-1A,B,D* {0252}].	CDO580.	(1B).
Xcdo580-1B.2 [{0252}].	[*Xcdo580b-1B* {0252}].	CDO580.	(1A,B,D).
Xcdo618-1B {0269}^{2}.		CDO618.	(1A,B,D).
Xcdo1373-1B {0269}^{2}.		CDO1373.	(1BL).
Xcdo1423-1A,B,D {0252}.		CDO1423.	

Xmwg835-1A,B.1,D [{0252}].	[*Xmwg835a-1A,B,D* {0252}.	MWG835.	(1BL, 2A, 5A).
Xmwg913-1B.1 [{0252}].	[*Xmwg913a-1B* {0252}].	MWG913.	(1BS).
Xmwg913-1B.2 [{0252}].	[*Xmwg913b-1B* {0252}].	MWG913.	(1BS).
Xmwg2056-1A,B,D [{0252}].	[*Xmwg2056a-1A,B,D* {0252}].	MWG2056.	(1BL).
Xmwg2148-1A,B.1,D [{0252}].	[*Xmwg2148a-1A,B,D* {0252}].	MWG2148.	(1BL).
Xmwg2197-1A,B {0252}.		MWG2197.	
Xsun18-1B {0256}.		SUN 18F/SUN18R.	
Xuaz299-1B {0269}[2].		PROBE?	
Xutv1366-1A.1 {0269}.[2]	[*Xutv1366d-1A* {0269}[2]].	UTV1366.	
Xutv1366-1A.2 {0269}[2].	[*Xutv1366c-1A* {0269}[2]].	UTV1366.	
Xwmc24-1A [{0242}].	[*Xwmc024-1A* {0242}].	WMC 24F/WMC 24R.	(2A).
Xwmc147-1D {0242}.		WMC 147F/WMC 147R.	
Xwmc336-1D {0242}.		WMC 336F/WMC 336R.	
Xwmc432-1D {0242}.		WMC 432F/WMC 432R.	

Group 1L
Amendments:

Xabc151. Revise the first column to '*Xabc151-1B* {0252}[1], *1D* {1529}[4].'.
Xabg452. Revise the first column to '*Xabg452-1A* {1529}[1],{280}[1,3,5], *1B,D* {0252}[1].'.
Xbcd22-1A. Revise the first column to '*Xbcd22-1A* {280}[5], *1B* {0242,0252}[1], *1D* {0252}[1].' and revise the last column to '(3A,D)'.
Xbcd207-1A. Revise the first column to '*Xbcd207-1A* {280}[5], *1B* {0274}[1].'
Xbcd310-1B. Revise the first column to '*Xbcd310-1A* {0242}, *1B* {445}.'.
Xbcd265-1A,B,D. Revise the last column to '(2B, 4B,D, 5A).'.
Xbcd762-1A,B. Revise the first column to '*Xbcd762-1A.1* [{280}][5], *1B.1* [{1529,0252}][1].', add '[*Xbcd762-1A* {280}[5], *Xbcd762-1B* {1529}[1], *Xbcd762b-1B* {0252}[1]].' in the second column and add '(1AS,BS,DS).' in the last column.
Xbcd808-1A.1, .2. Revise the first column to '*Xbcd808-1A.1* {1529}[1],{280}[1,3,5], *1A.2* {1529}, *1B* {0242}.'.
Xbcd921-1A,D. Revise the first column to '*Xbcd921-1A* {280}[5], *1B* {0252}[1], *1D* {445}[1].'
Xcdo105-1A. Revise the first column to '*Xcdo105-1A* {280}[1,5], *1B* {0275}[1].'.
Xcdo393-1A,B. Revise the first column to '*Xcdo393-1A* {1529}[1], {280}[3], *1B* {154}, *1D* {0242}.'.
Xcdo346-1B. Revise the last column to '(2B, 5D).'.
Xcdo473-1A. Revise the first column to '*Xcdo473-1A* {1529}, *1B* {0242}.'.
Xcdo1160-1A. Revise the first column to '*Xcdo1160-1A* {1529}, *1B* {0275}.'.
Xcdo1396-1A. Revise the first column to '*Xcdo1396-1A* {280}[5], *1B* {0275}[1].'.
Xcmwg645-1A.2. Revise the first column to '*Xcmwg645-1A.2* {280}[5], *1B.2* [{1529,0250}][1].', add [*Xmwg645* {280,1529}, *Xcmwg645b-1B* {0252}].' in the second column and revise the last column to '(1AS,BS,DS, 5A).'.
Xcmwg758-1A,B. Revise the first column to '*Xcmwg758-1A* {280}[1,3,5], *1B* {1529}[1], *1D* {0252}.'.
Xgwm124-1B. Revise the first column to '*Xgwm124-1B* {9929}[1],{0270}[2].'.
Xgwm153-1B. Revise the first column to '*Xgwm153-1B* {9929}[1],{0270}[2].'.
Xgwm268-1B. Revise the first column to '*Xgwm268-1B* {9929}[1],{0270}[2].'.
Xgwm403-1B. Revise the first column to '*Xgwm403-1B* {9929}[1],{0270}[2].'.
Xgwm498-1B. Revise the first column to '*Xgwm498-1B* {9929},{0270}[2].'.
XksuA1-1B. Revise the last column to '(2D, 3B, 5B, 7D).'.
XksuD49-1B,D. Revise the first column to '*XksuD49-1A* {0242}, *1B* {728}, *1D* {448}[1,4], {1529}[1].'.
Xmwg837-1B.2. Add '(1AS,BS,DS).' in the last column.
Xwg180-1A. Revise the last column to '(4B, 7BS,L).'.

Add:

Xbcd372-1B,D {0252}.		BCD372.	(3A,D).
Xbcd402-1D {0242}.		BCD402.	(4A, 5A,4B,D).
Xbcd446-1B {0275}.		BCD446.	(1AS).
Xbcd1495-1B {0269}[2].		BCD1495.	(6B).
Xcdo388-1B.2 [{0252}].	[*Xcdo388b-1B* {0252}].	CDO388.	(1BS,DS, 2B, 3D, 4A,D, 5A,B,

			6A,D).
Xcdo583-1B [{0242}].	[*Xcdo583a-1B* {0242}].	CDO583	(3B).
Xcdo1340-1B {0269}[2].		CDO1340.	(1AS,BS,DS).
Xcdo1373-1B {0269}[2].		CDO1373.	(1BS).
Xmwg539-1A,B,D {0252}.		MWG539.	(7D).
Xmwg584-1A,,B,D {0252}.		MWG584.	(3A, 4A[m], 5D).
Xmwg835-1B.2 [{0252}].	[*Xmwg835b-1B* {0252}].	MWG835.	(1AS,BS,DS, 2A, 5A).
Xmwg896-1A,B,D {0252}.		MWG896.	
Xmwg938-1B.2 [{0252}].	[*Xmwg938b-1B* {0252}].	MWG938.	(1AS,BS,DS, 7A).
Xmwg2021-1B.2 [{0252}].	[*Xmwg2021b-1B* {0252}].	MWG2021.	(1AS,BS,DS, 2A, 3A).
Xmwg2056-1B.2 [{0252}].	[*Xmwg2056b-1B* {0252}].	MWG2056.	(1AS,BS,DS).
Xmwg2083-1B.2 [{0252}].	[*Xmwg2083b-1B* {0252}].	MWG2083.	(1AS,BS,DS).
Xmwg2148-1B.2 [{0252}].	[*Xmwg2148b-1B* {0252}].	MWG2148.	(1AS,BS,DS, 1BL).
Xmwg2148-1B.3 [{0252}].	[*Xmwg2148c-1B* {0252}].	MWG2148.	(1AS,BS,DS, 1BL)
Xpsr305-1B {0242}.		PSR305.	(3A,B,D).
Xuaz243-1B {0269}[2].		PROBE?	
Xutv135-1A {0269}[2].		UTV135.	(3BS, 4B).
Xutv1441-1A {0269}[2].		UTV1441.	(3BL, 4B).
Xwmc304-1A {0242}.		WMC 304F/WMC 304R.	
Xwmc312-1A {0242}.		WMC 312F/WMC 312R.	
Xwmc373-1B [{0242}].	[*Xwmc373-1-1B* {0242}].	WMC 373F/WMC 373R.	
Xwmc429-1D {0242}.		WMC 429F/WMC 429R.	

Group 1
Amendments:
Xcmwg758-1D. Revise the last column to '(1AL,BL,DL).'.
Xwg232-1A. Revise the last column to '(4A,B, 5A,B,D, 6B, 7A,B).'.
Xwpg501(Pdi)-1B. Add reference 0263 in the first column, i.e. '{0064,0263}'.

Add:

Xbcd175-1A {0242}.		BCD175.
Xbcd1072-1A,B,D {0252}.		BCD1072.
Xsun19-1B {0156}.		SUN 19F/SUN 19R.
Xwmc84-1A [{0242}].	[*Xwmc084-1A* {0242}].	WMC 84F/WMC 84R.
Xwmc406-1B {0242}.		WMC 406F/WMC 406R.

Group 2S
Amendments:

Xabg378-2A. Revise the last column to '(6A,D, 7A,4A).'.
Xbcd152-2A,B. Add '(6B).' to the last column.
Xbcd348-2A.1,.2,B,D. Add '(4A).' to the last column.
Xbcd718-2A,D. Revise the first column to '*Xbcd718-2A* {1060}[1], *2B* {0269}[2], *1D* {1060}[1]. '.
Xcdo1090-2A. Revise the first column to '*Xcdo1090-2A* {1060}, *2B* {0269}[2].'.
Xfba38-2D. Revise the first column to '*Xfba38-2B* {0242}, *2D* {1060}.'.
Xfbb185-2B. Revise the last column to '(3B, 6B).'.
Xfba349-2D. Add '(7A).' to the last column.

Xgwm129-2B. Revise the last column to '(4D, 5A).'.
Xpsr801(Rbcs)-2A,B,D. To the note added to this listing in the 2001 Supplement add the reference 0271, i.e. '{0149,0271}'.

Add:

Xbcd175-2D {0242}.		BCD175.	
Xbcd221-2B {0269}[2].		BCD221.	(4B, 6B).
Xcn19(Pdc)-2B [{0269}][2].	[*Pdc-2B* {0269}[2]].	PROBE?	
Xpsr596-2B {0242}.		PSR596.	(1A,B,D, 3A).
Xsun17-2D {0256}.		SUN 17F/SUN 17R.	
Xwmc25-2B [{0242}].	[*Xwmc025.2-2B* {0242}].	WMC 25F/WMC 25R.	(2D).
Xwmc111-2D {0242}.		WMC 111F/WMC 111R.	
Xwmc112-2D {0242}.		WMC 112F/WMC 112R.	
Xwmc154-2B {0242}.		WMC 154F/WMC 154R.	
Xwmc314-2B {0242}.		WMC 314F/WMC 314R.	

Group 2L
Amendments:
Xabc451-2A. Revise the first column to '*Xabc451-2A* **{282}**[3], *2B* **[{0242}]**, *2D* **{0242}**.' and add '[*Xabc451a-2B* **{0242}**].' in the second column.
Xbcd135-2B,D. Add '(4A, 5D).' in the last column.
Xbcd266-2D. Revise the first column to '*Xbcd266-2A* {0242}, *2B* {0164}, *2D* {864}.'.
Xbcd292-2A,D. Revise the first column to '*Xbcd292-2A* {1060}, *2B* {0242}[1],{0269}[2], *2D* {864}[1].'.
Xbcd410-2A,D. Revise the first column to '*Xbcd410-2A* {1060}, *2B* [{0242}], *2D* {1060}.' and add '[*Xbcd410d-2B* {0242}].' in the second column.
Xgwm526-2B. Add '(2A).' in the last column.
XksuF43-2D. Revise the last column to '(1A,B,D, 4D, 5D, 6D).'.
Xmwg835-2A. Revise the last column to '(1A,B,D, 5A).'.
Xmwg950-2B. Revise the first column to '*Xmwg950-2B* {1060}, *2D* {0242}.'.
Xmwg2021-2A. Revise the last column to '(1A,B,D, 3A).'.
Xutv861-2B. Revise the first column to '*Xutv861-2A* {0269}[2], *2B* {9959}[2].'.
Xwg184-2D. Revise the last column to '(3D, 4D, 5A).'.

Add:

Xabc165-2D.2 [{0242}].	[*Xabc165b-2D* {0242}]	ABC165.	(2D).
Xbcd265-2B [{0242}].	[*Xbcd265c-2B* {0242}].	BCD265.	(1A,B,D, 4B,D, 5A).
Xbcd512-2B {0242}.		BCD512.	
Xcdo346-2A {0269}[2].		CDO346.	(1B, 5D).
Xcdo365-2B {0269}[2].		CDO365.	(6B).
Xcdo669-2B [{0242}].	[*Xcdo669a-2B* {0242}].	CDO669.	(4A,B,D, 7A).
Xgwm526-2A [{0253}].	[*Xgwm526-2A.2* {0253}].	WMS F526/WMS R526.	(2B).
XksuA1-2D [{0242}].	[*XksuA1b-2D* {0242}].	pTtksuA1.	(1B, 3B, 5B, 7D).
XksuF37-2B {0242}.		pTtksuF37.	(6A,B,D).
Xksu931(Chi4)-2D [{0266}][4].	[*Xksu931(Chi4)* {0266}].	SM383.	
Xksu932(Chi7)-2D [{0266}][4].	[*Xksu932(Chi7)* {0266}].	SM194.	
Xpsp3045-2A {0253}.		PSP3045F/PSP3045R.	(5B, 7D).
Xpsr370-2B,D [{0242}].	[*Xpsr370b-2B*, *Xpsr370a-2D* {0242}].	PSR370.	(5A,B,D).
Xsun11-2B {0256},[{0242}].	[*Xsunm11-2B* {0242}].	SUN 11F/SUN 11R.	
Xsun21-2B {0256}.		SUN 21F/SUN 21R.	
Xsun22-2B {0256}.		SUN 22F/SUN 22R.	
Xwmc339-2B {0242}.		WMC 339F/WMC 339R.	
Xwmc360-2B {0242}.		WMC 360F/WMC 360R.	

Group 2
Amendments:

Xabg356-2D. Revise the first column to '*Xabg356-2B* {0242}, *2D* {9926}[4].'.
Xwmc24-2A. Add '(1A).' in the last column.
Xwmc25-2D. Add '(2B).' in the last column.
Xwmc149-2B. Add '(5B).' in the last column.

Add:

Xabc162-2A {0242}.		ABC162.	
Xabc165-2D.1 [{0242}].	[*Xabc165a-2D* {0242}].	ABC165.	(2DL).
Xcdo366-2B,D {0242}.		CDO366.	
Xcdo665-2A {0242}.		CDO665.	(4A).
Xgwm271-2B [{0242}].	[*Xgwm271a-2B* {0242}].	WMS F271/WMS R271.	(5B, 5D).
XksuE7-2B {0242}.		pTtksuE7	(7D).
Xstm773-2B {0242}.		STM 773F/STM 773R.	
Xwmc18-2D [{0242}].	[*Xwmc018-2D* {0242}].	WMC 18F/WMC 18R.	
Xwmc35-2B [{0242}].	[*Xwmc035a-2B* {0242}].	WMC 35F/WMC 35R.	(4B).
Xwmc190-2D {0242}.		WMC 190F/WMC 190R.	
Xwmc198-2A {0242}.		WMC 198F/WMC 198R.	
Xwmc445-2B {0242}.		WMC 445F/WMC 445R.	

Group 3S
Amendments:
Xabg471-3A,B. Add '(6B).' to the last column.
Xcdo395-3A,D. Revise the first column to '*Xcdo395-3A* {1061}[1], *3B* {0242}[1], *3D* {9926}[4].'.
Xfbb185-3B. Revise the last column to '(2B, 6B).'.
Xgwm369-3A. Revise the first column to '*Xgwm369-3A* {9929}[1],{0269}[2].'.
Xgwm389-3B. Revise the first column to '*Xgwm389-3B* {9929}[1],{0269}[2].'.
XksuA1-3B. Revise the last column to '(1B, 2D, 5B, 7D).'.
XksuB8-3D. Revise the first column to '*XksuB8-3A,B* {0242}, *3D* {448}.'.
Xmwg584-3A. Revise the last column to '(1A,B,D, $4A^m$, 5D).'.
Xmwg2021-3A. Revise the last column to '(1A,B,D, 2A).'.
Xpsr305-3A,B,D. Add '(1B).' to the last column.
Xsfr2(Lrk10)-3B,D. Revise the last column to '(1A,B,D).'.

Add:

Xpsr311-3A {0242}.		PSR311.	(7A,B,D).
Xutv135-3B {0269}[2].		UTV135.	(1A, 4B).
Xwmc11-3A [{0242}].	[*Xwmc011-3A* {0242}].	WMC 11F/WMC 11R.	
Xwmc43-3B [{0242}].	[*Xwmc043-3B* {0242}].	WMC 43F/WMC 43R.	

Group 3L
Amendments:
Xbcd115-3A,D. Revise the first column to '*Xbcd115-3A* {1061}, *3B* {0269}[2], *3D* [{862}].
Xbcd22-3D. Revise the first column to '*Xbcd22-3A* {0242}, *3D* {1061}.' and revise the last column to '(1A,B,D).'.
Xbcd195-3B. Revise the first column to '*Xbcd195-3A* {0269}[2], *3B* {0078}[1].'.
Xbcd372-3A,D. Add '(1B,D).' to the last column.
Xbcd451-3A,D. Revise the first column to '*Xbcd451-3A* {1061}, *3B* {0242}, *3D* [{862}].'.
Xcdo105-3B. Revise the last column to '(1A,B).'.
Xcdo482-3A,D. Revise the first column to '*Xcdo482-3A* {1061},*3B* {0242}, *3D* {862}.'.
Xcdo583-3B. Add '(1B).' to the last column.
Xcdo718-3B. Revise the first column to '*Xcdo718-3A* {0242}, *3B* {1061}.'.
Xfba175-3A. Add '(6B).' in the last column.
Xgwm155-3A. Revise the first column to '*Xgwm155-3A* {9929}[1],{0269}[2].'.
Xgwm299-3B. Revise the first column to '*Xgwm299-3B* {9929}[1],{0269}[2].'.

XksuG59-3A,D. Revise the first column to '*XksuG59-3A* {282}[3], *3B* {0242}[1], *3D* {448}[4], {1061}[1].'.
Xutv416-3A. Revise the first column to '*Xutv416-3A* {9959}[2], *3B* {0269}[2].'.
Xutv560-3A. Revise the first column to '*Xutv560-3A* {9959}[2], *3B.1,.2* [{0269}][2].' and add '[*Xutv560a,b-3B* {0269}].' in the second column.

Add:

Xabg75-3B {0242}.		ABG75.	
Xbcd941-3A {0175}.		BCD941.	
Xcdo534-3A {0269}[2].		CDO534.	(1B, 6A,B,D, 7A).
Xksu933(Glb3)-3B,D {0266}.		SM289.	
Xksu934(Glb3)-3D {0266}.		SM638.	
Xmwg2153-3A {0269}[2].		MWG2153.	
Xpsr596-3A,B [{0242}].	[*Xpsr596b-3A*, *Xpsr596a-3B* {0242}].	PSR596.	(1A,B,D, 2B).
Xpsr604-3B [{0242}].	[*Xpsr604-3B* {0242}].	PSR604.	(7A,4A,7D).
Xsun23-3A {0256}.		SUN 23F/SUN 23R.	
Xucg2(Acc-2)-3A,B,D [{0265}].	[*Xucg2-3A,B,D* {0265}].	UCG2.	(5D).
Xutv601-3A {0269}[2].		UTV601.	
Xutv920-3A {0269}[2].		UTV920.	
Xutv1151-3A {0269}[2].		UTV1151.	(6A).
Xutv1371-3B {0269}[2].		UTV1371.	(1AL, 4B).
Xutv1441-3B {0269}[2].		UTV1441.	
Xutv1474-3A {0269}[2].		UTV1474.	
Xwmc169-3A {153,0238}.		WMC 169F/WMC 169R.	
Xwmc236-3B {0242}.		WMC 236F/WMC 236R.	
Xwmc334-3B {0242}.		WMC 334F/WMC 334R.	
Xwmc428-3A {0242}.		WMC 428F/WMC 428R.	

Group 3
Amendments:
Xwg184-3D. Revise the last column to '(2D, 4D, 5A).'.
Xwmc169-3A. Delete (moved to 3L).

Add:

Xwmc50-3A [{0242}].	[*Xwmc050-3A* {0242}].	WMC 50F/WMC 50R.	
Xwmc375-3D {0242}.		WMC 375F/WMC 375R.	
Xwmc379-3A {0238}.		WMC 379F/WMC 379R.	

Group 4S (4AL:4BS:4DS)
Amendments:
Xbcd265-4B,D. Revise the last column to '(1A,B,D, 2B, 5A).'.
Xbcd583-4A. Revise the last column to '(1A,B).'.
Xbcd402-4A. Revise the last column to '(1D, 5A,4B,D).'.
Xcdo669-4A,B,D. Add '(2B, $4A^m$).' in the last column.
Xcdo795-4B. Revise the first column to '*Xcdo795-4A* {0242}, *4B* {1059}.'.
Xgwm18-4B. Add '(1B).' in the last column.
Xwg184-4D. Revise the last column to '(2D, 3D, 5A).'.

Add:

Xcdo949-4B {0269}[2].		CDO949.	(4DL).
Xcn110(Lpx-B1)-4B [{0269}][2].	[Loxmjt].	LOXMJT.	
Xfba363-4B {0242}.		FBA363.	(7A).
Xutv434.1-4A.1,.2 [{0269}][2].	[*Xutv434a,b-4A* {0269}[2]].	UTV434.	(4A).

Xwg232-4B {0269}[2].		WG232.	(1A, 4A, 5A,B,D, 6B, 7A,B).
Xwmc141-4B {0242}.		WMC 141F/WMC 141R.	

4A^{m}S
Amendments:

Xcdo66-4A. Revise the last column to '(2B, 4A,B,D).'.
Xmwg584-4A.1. Revise the last column to (1A,B,D, 3A, 4A^{m}L, 5D).'.
Xwg622-4A. Revise the last column to '(4AL,BS,DS, 6A).'.

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

Xcdo1395-4B. Revise the first column to '*Xcdo1395-4B* {1008}, *4D* {0248}.'.
Xwg622-4A,B,D. Add '(6A).' in the last column.

Add:

Xbcd1230-4D {0248}.	BCD1230.	

4A^{m}L
Amendments:
Xabg463-4A. Revise the last column to '(4D, 5A, 5B).
Xmwg584-4A.2. Revise the last column to '(1A,B,D, 3A, 4A^{m}S, 5D).

Group 5AL:4BL:4DL
Amendments:

Xbcd402-5A,4B,D. Revise the last column to '(1D, 4A).'.
Xcdo949-4D. Add '(7B).' in the last column.
Xutv434-4A.1. Revise the last column to '(4AS, 4AL).'.

Group 4
Amendments:

Xabg397-4D. Add '(5A).' in the last column.
Xabg463-4D. Revise the last column to '(4A, 5B, 5D).'.
XksuF43-4D.1. Revise the last column to '(1AB,D, 2D, 4D, 5D, 6D).'.
XksuF43-4D.2. Revise the last column to '(1A,B,D, 2D, 4D, 5D, 6D).'.
Xwg232-4A. Revise the last column to '(1A, 4B, 5A,B,D, 6B, 7A,B).'.
Xwmc35-4B. Add '(2B).' in the last column.
Xwpg501(Pdi)-4A,B,D. Add reference 0263 in the first column, i.e. '{0064,0263}'.

Add:

Xbcd221-4B {0269}[2].		BCD221.	(2B, 6B).
Xbcd1975-4A {0269}[2].		BCD1975.	(7D).
Xbcd348-4A {0269}[2].		BCD348.	(2A,B,D).
Xcdo414-4A {0269}[2].		CDO414.	(7B).
Xcdo949-4A [{0242}].	[*Xcdo949b-4A* {0242}].	CDO949.	(4D).
Xgwm129-4D {0242}.		WMS F129/WMS R129.	(2B, 5A).
Xgwm613-4A {0269}[2].		WMS F613/WMS R613.	(6B).
Xstm91-4D {0242}.		STM 91F/STM 91R.	
Xutv135-4B {0269}[2].		UTV135.	(1A, 3B).
Xutv434-4A.3 [{0269}][2].	[*Xutv434d-4A* {0269}[2]].	UTV434.	(4AL).
Xutv1136-4A.1,.2 [{0269}][2].	[*Xutv1136a,c-4A* {0269}[2]].	UTV1136.	
Xutv1441-4B {0269}[2].		UTV1441.	(1A, 3B).

Xwg180-4B [{0242}].	[*Xwg180a-4B* {0242}].	WG180.	(1A, 7BS,L).
Xwmc47-4B [{0242}].	[*Xwmc047-4B* {0242}].	WMC 47F/WMC 47R.	(7A).
Xwmc48-4A,B,D [{0242}].	[*Xwmc048a-4A* , *Xwmc048c-4B, Xwmc048b-4D* {0242}].	WMC 48F/WMC 48R.	

Group 5S

Amendments:

Xabg873-5B. Revise the first column to '*Xbcd873-5B* {1059}, *5D* {0242}.' and add '(7A,D).' in the last column.
Xbcd207-5A. Revise the last column to '(1A,B).'.
Xgwm129-5A. Revise the last column to '(2B, 4D).'.
Xgwm443-5B. Add '(5A).' in the last column.
Xmwg835-5A. Revise the last column to '(1A,B,D, 2A).'.

Add:

Xabg397-5A {0242}.		ABG397.	(4D).
Xcdo465-5A {0269}[2].		CDO465.	(5AL,BL,DL).
Xgdm68-5D {0242}.		DMS 68F/DMS 68R.	(5A,B, 5DL).
Xgwm443-5A {0242}.		WMS F443/WMS R443.	(5B).
Xpsp3045-5B [{0253}].	[*Xpsp3045-5B.2* {0253}.	PSP3045F/PSP3045R.	(2A, 7D).
Xwg184-5A {0242}.		WG184.	(2D, 3D, 4D).
Xwmc149-5B {0242}.		WMC 149F/WMC 149R.	(2B).
Xwmc159-5A {0242}.		WMC 159F/WMC 159R.	
Xwmc233-5D {0242}.		WMC 233F/WMC 233R.	

Group 5L

Amendments:

Xabg473-5A,B,D. Revise the last column to '(6A,B).
Xbcd265-5A. Revise the last column to '(1A,B,D, 2B, 4B,D).'.
Xcdo346-5D. Revise the last column to '(1B, 2B).'.
Xcdo465-5A,B,D. Add '(5AS).' to the last column.
Xcdo1090-5A. Revise the last column to '(1A,B).'.
Xgdm68-5D. Revise the last column to '(5A,B, 5DS).
XksuA1-5B. Revise the last column to '(1B, 2D, 3B, 7D).'.
Xgwm271-5D. Add '(2B, 5B).' in the last column.
Xpsr370-5A,B,D. Add '(2B).' to the last column.
Xwg232-5A,B,D. Revise the last column to '(1A, 4A,B, 6B, 7A,B).'.

Add:

Xabg463-5B {0242}.		ABG463.	(4A,D, 5D).
Xcdo775-5B {0269}[2].		CDO775.	(7A,B,D).
Xcn111(Lpx-B2)-5B [{0269}][2].	[*Lox11-1* {0269}[2]].	LOX11-1.	
Xgwm271-5B [{0242}].		WMS F271/WMS R271.	(2B, 5D).
Xstm652-5B {0242}.		STM 652F/STM 652R.	
XsunG5-5B [{0242}].	[*XsunG5B-5B* {0242}].	SUN G5F/SUN G5R.	
Xucg2(Acc-2)-5D [{0265}].	[*Xucg2-5D* {0265}].	UCG2.	(3A,B,D).
Xunl1-5B {0247}.		UNL1.	
Xunl2-5B {0247}.		UNL2	
Xunl3-5B {0247}.		UNL3.	
Xutv497-5A {0269}[2].		UTV497.	
Xutv1435-5A {0269}[2].		UTV1435.	
Xwmc28-5B [{0242}].	[*Xwmc028-5B* {0242}].	WMC 28F/WMC 28R.	
Xwmc235-5B {0242}.		WMC 235F/WMC 235R.	
Xwmc376-5B {0242}.		WMC 376F/WMC 376R.	

4AL:5BL:5DL
Amendments:

Add:
Xcdo506-4A {0242}. CDO506.
A *Xcdo506-5D* locus has been reported in {1059} in the 7BS:5BL:5DL category. It is possible that this is a misclassification and that *Xcdo506-4A* and *Xcdo506-5D* are homoeologous.
Xwmc161-4A [{0242}]. [*Xwmc161a-4A* {0242}]. WMC 161F/WMC 161R.
Xwmc258-4A {0242}. WMC 258F/WMC 258R.

7BS:5BL:5DL
Amendments:

Group 5
Amendments:

Xabg463-5D.1, .2. Revise the last column to '(4A,D, 5B).'.
Xcmwg645-5A. Revise the last column to '(1A,B,D).'.
Xgdm68-5A,B. Revise the last column to '(5DS, 5DL).'.
XksuF43-5D.1, .2. Revise the last column to '(1A,B,D, 2D, 4D, 6D).'.
Xmwg584-5D. Revise the last column to '(1A,B,D, 3A, 4A).
Xwg232-5A.1,B. Revise the last column to '(1A, 4A,B, 6B, 7A,B).'.
Xwg232-5A.2. Revise the last column to '(1A, 4A,B, 6B, 7A,B).'.
Xwg420-5D.1,.2. Revise the last column to '(7A,B,D).'.

Add:
Xabg3-5A,D [{0242}]. [*Xabg3b-5A* {0242}]. ABG3.
Xbcd135-5D {0242}. BCD135. (2B,D, 4A).
Xgwm304-5A {0242}. WMS F304/WMS R304.
Xstm286-5B {0242}. STM 286F/STM 286R.
Xstm337-5A [{0242}]. [*Xstm337a-5A* {0242}]. STM 337F/STM 337R. (7B).
Xwmc96-5A [{0242}]. [*Xwmc096-5A* {0242}]. WMC 96F/WMC 96R.
Xwmc110-5A {0242}. WMC 110F/WMC 110R.

Group 6S
Amendments:
Xabg378-6A,D. Revise the last column to '(2A, 7A,4A).'.
Xbcd1398-6D. Revise the first column to '*Xbcd1398-6B* {0242}, *6D* {900}.'.
Xbcd1821-6A,D. Revise the first column to '*Xbcd1821-6A* {900}, *6B* {0244}, *6D* {900}.'.
Xcdo270-6A,D. Revise the first column to '*Xcdo270-6A* {900}[1], *6B* {0269}[2], *6D* {900}[1].'.
Xcdo365-6B. Add '(2B).' to the last column.
Xcdo534-6A,B,D. Revise the last column to '(1B, 3A, 7A).'.
Xfba307-6A,D. Revise the first column to '*Xfba307-6A* {900}, *6B* {0244}, 6*D* {900}.'.
Xfba381-6B,D.2. Revise the first column to '*Xfba381-6B.2,D.2* [{0081}]', add '[*Xfba381-6B* {0081}]' in the second column and revise the last column to '(6BL,DL)'.
Xfbb194-6A. Add '(4A).' to the last column.
Xgwm132-6B. Add '(6D).' to the last column.
Xgwm613-6B. Add '(4A).' to the last column.
Xgwm644-6B. Revise the first column to '*Xgwm644-6B* {9929}[1],{0269}[2].'
XksuF43-6D. Revise the last column to '(1A,B,D, 2D, 4D, 5D).'.
Xmwg573-6A.2,B,D. Revise the last column to '(6AL, 6BL).'.
Xpsr546-6A. Revise the first column to '*Xpsr546-6A.1* [{9927}][2].', add [*Xpsr546-6A* {9927}[2]].' in the second column and revise the third column to '(6AL, 6BL,DL).'.

Add:
Xabg471-6B {0269}[2]. ABG471. (3A,B).
Xbarc101-6B {0175}. BARC F101/BARC R101

		{0239}.	
Xbcd152-6B {0269}^{2}.		BCD152.	(2A,B).
Xbcd1299-6B {0269}^{2}.		BCD1299.	
Xfba175-6B.1 [{0244}].	[*Xfba175a-6B* {0244}].	FBA175.	(3A, 6BL).
Xgwm132-6D {0242}.		WMS F132/WMS R132.	(6B).
Xpsr119-6A [{0242}].	[*Xpsr119a-6A* {0242}].	PSR119.	(7A,4A,7D).
Xutv1151-6A.1,.2 [{0269}]^2.	[*Xutv1151a,b-6A* {0269}^{2}].	UTV1151.	(3A).

Group 6L
Amendments:

Xabc175-6A,D. Revise the first column to '*Xabc175-6A* {9927}^{2},{0081}^{1}, *6B* [{0242}]^1, *6D* {900}^{1}.' and add '[*Xabc175a-6B* {0242}].' in the second column.
Xabg473-6B. Revise the first column to '*Xabg473-6A* {0242}, *6B* {900}.'.
Xabg652-6A. Add '(7A).' in the last column.
Xfba381-6D. Revise the first column to '*Xfba381-6B.1* [{0244}], *6D.1* [{900}]', revise the second column to '[*Xfba381-6B* {0244}, *6D* {900}]', and add '(6BS,DS)' in the last column.
Xgwm427-6A. Revise the first column to '*Xgwm427-6B* {9929}^{1},{0269}^{2}.'.
XksuF37-6A,B. Add '(2B, 6D).' in the last column.
Xmwg573-6A.1. Revise the last column to '(6AS,BS,DS, 6BL).'.
Xpsr546-6B,D. Revise the last column to '(6AS, 6AL).'.

Add:

Xbcd279-6B {0269}^{2}.		BCD279.	
Xcdo686-6B {0269}^{2}.		CDO686.	(7B).
Xfba175-6B.2 [{0244}].	[*Xfba175b-6B* {0244}].	FBA175.	(3A, 6BS).
Xfbb185-6B [{0242}].	[*Xfbb185c-6B* {0242}].	FBB185.	(2B, 3B).
Xmwg573-6B {0242}.		MWG573.	(6AS,BS,DS, 6AL).
Xpsr546-6A.2 [{0242}].	[*Xpsr546a-6A* {0242}].	PSR546.	(6AS, 6BL,DL).
Xsun5-6D [{0242}].	[*XsunM5b-6D* {0242}].	SUN 5F/SUN 5R.	
Xutv1136-6A {0269}^{2}.		UTV1136.	
Xwg622-6A {0242}.		WG622.	(4A,B,D).
Xwmc163-6A {0242}.		WMC 163F/WMC 163R.	

Group 6
Amendments:

Xabc451-6D. Revise the last column to '(2A,B,D).'.
Xbcd221-6B. Add '(2B, 4B).' to the last column.
Xbcd1299-6B. Add '(6B).' to the last column.
Xbcd1495-6B. Add '(1B).' to the last column.
XksuE19-6D. Revise the last column to '(1A,B,D, 7B).'.
XksuF37-6D. Add '(2B, 6A,B).' to the last column.
Xwmc76-6B. Add '(7B).' to the last column.
Xwmg573-6D. Revise the last column to '(6AS,BS,DS, 6AL, 6BL).'.

Add:

Xwg232-6B [{0242}].	[*Xwg232b-6B* {0242}].	WG232.	(1A, 4A,B, 5A,B,D, 7A,B).
Xwmc416-6D {0242}.		WMC 416F/WMC 416R.	

Group 7S
Amendments:

Xabc158-7A. Revise the first column to '*Xabc158-7A* {1059}, *7B* {0242}.'.

Xabc465-7A,D. Revise the first column to '*Xabc465-7A* {282}[3], *7B* [{0242}][1], *7D* {9926}[4].', add '[*Xabc465a-7B* {0242}].' in the second column and add '(4A).' in the last column.
Xbcd310-7B. Revise the last column to '(1A,B).'.
Xcdo534-7A. Revise the last column to '(1B, 3A, 6A,B,D).'.
Xcdo1395-7A. Revise the last column to '(4B,D).'.
Xfba363-7A. Add '(4B).' in the last column.
Xgwm60-7A. Delete (entry moved to 7AS:4AL:7DS).
Xgwm537-7B. Revise the first column to '*Xgwm537-7B* {9929},{0242}.' and remove the sentence 'Whether *Xgwm537-7B* belongs to the 7S arm group or the 7BS:5BL:5DL arm group is uncertain.'.
Xgwm631-7A. Delete (entry moved to 7L).
Xwg180-7B. Revise the last column to '(1A, 4B, 7BL).'.

Add:

Xgwm111-7D {9929,0211}.		WMS F111/WMS R111.	(4A, 7BL).
Xgwm255-7B {0250}.		WMS F255/WMS R255.	
Xgwm263-7B {0250}.		WMS F263/WMS R263.	
Xgwm332-7A.1 [{0269}][2].	[*Xgwm332a-7A* {0269}[2]].	WMS F332/WMS R332.	(7AS, 7AL).
Xgwm332-7A.2 [{0269}][2].	[*Xgwm332b-7A* {0269}[2]].	WMS F332/WMS R332.	(7AS, 7AL).
Xgwm890-7A {0254}.		WMS F890/WMS R890.	
Xgwm913-7A {0254}.		WMS F913/WMS R913.	
Xgwm1002-7D {0250}.		WMS F1002/WMS R1002.	
Xgwm1065-7A {0254}.		WMS F1065/ WMS R1065.	
Xgwm1173-7B {0250}.		WMS F1173/WMS R1173.	
Xgwm1184-7B {0250}.		WMS F1184/WMS R1184.	
Xgwm1220-7D {0250}.		WMS F1220/WMS R1220.	

It is not known whether *Xwmc1220-7A* belongs to group 7S or 7AS:4AL:7DS.

Xsun16-7B {0256},[{0242}].	[*XsunM16-7B* {0242}].	SUN 16F/SUN 16R.	
Xutv1521-7A {0269}[2].		UTV1521.	
Xwmc17-7A [{0242}].	[*Xwmc017-7A* {0242}].	WMC 17F/WMC 17R.	

It is not known whether *Xwmc17-7A* belongs to group 7S or 7AS:4AL:7DS.

Xwmc76-7B [{0242}].	[*Xwmc076-7B* {0242}].	WMC 76F/WMC 76R.	(6B).
Xwmc83-7A {0153},[{0242}].		WMC 83F/WMC 83R {0161}.	
Xwmc283-7A {0242}.		WMC 283F/WMC 283R.	
Xwmc338-7B {0242}.		WMC 338F/WMC 338R.	

It is not known whether *Xwmc338-7B* belongs to group 7S or 7BS:5BL:5DL.

Xwmc405-7A,D [{0242}].	[*Xwmc405a-7A* {0242}].	WMC 450F/WMC 405R.	

7AS:4AL:7DS
Amendments:

Xabg378-7A. Revise the first column to '*Xabg378-7A* {282}[3], *4A* [{0242}][1].' and add '[*Xabg378b-4A* {0242}].' in the second column.
Xabg704-7A. Revise the first column to '*Xabg704-7A* {282}[3], *4A* {0242}[1], *7D* {[0242}][1].' and add '[*Xabg704c-7D* {0242}].' in the second column.
Xbcd129-7D. Revise the first column to '*Xbcd129-7A* {0242}, *7D* [{1059}] {1057}.'
Xbcd1975-7D. Add '(4A).' in the last column.
Xcdo665-4A. Add '(2A).' in the last column.
Xpsr604-7A,4A,7D. Add '(3B).' in the last column.
Xutv434-4A.2. Revise the last column to '(4AS, 4AL).'.

Add:

Xabc465-4A [{0242}].	[*Xabc465b-4A* {0242}].	ABC465.	(7A,B,D).
Xabg75-7A,D [{0242}].	[*Xabg75b-7A, Xabg75a-7D* {0242}].	ABG75.	
Xbcd135-7A, 4A [{0242}].	[*Xbcd135a-7A, Xbcd135b-4A* {0242}].	BCD135.	(2B,D, 5D).
Xbcd873-7A,D [{0242}].	[*Xbcd873a-7A, Xbcd873b-7D* {0242}].	BCD873.	(5B,D).
Xfbb194-4A {0242}.		FBB194.	(6A).
Xgwm60-7A {724,0250}.		WMS F60/WMS R60.	
Xstm271-7A {0242}.		STM 271F/STM 271R.	

It is not known whether *Xstm271-7A* belongs to group 7AS:4AL:7DS or 7S.

Xwmc262-4A {0242}.		WMC 262F/WMC 262R.	
Xwmc313-4A {0242}.		WMC 313F/WMC 313R.	

Group 7L

Amendments:

Xcdo414-7B. Add '(4A).' to the last column.

Xcdo686-7B. Add '(6B).' to the last column.

Xcdo775-7A,B,D. Add '(5B).' to the last column.

Xgwm111-7B,D. Revise the first column to '*Xgwm111-7B* [{0031}].' and revise the last column to '(4A, 7DS).'.

Xgwm332-7A. Revise the first column to '*Xgwm332-7A.3* [{9929}].', add '[*Xgwm332-7A* {9929}].' in the second column and add '(7AS).' to the last column.

XksuA1-7D. Revise the last column to '(1B, 2D, 3B, 5B).'.

Xmwg938-7A. Revise the last column to '(1A,B,D).'.

Xpsr311-7A,B,D. Add '(3A).' to the last column.

Xrz508-7B. Add '(7AS).' to the last column.

Xwg180-7B. Revise the last column to '(1A, 4B, 7BS).'.

Xwg232-7A. Revise the first column to *Xwg232-7A* [{154}], *7B* [{0242}], add '[*Xwg232a-7B* {0242}]' in the second column and revise the last column to '(1A, 4A,B, 5A,B,D, 6B).'.

Xwg420-7A,D. Revise the first column to '*Xwg420-7A* {282}[3], *7B* {0242}[1], *7D* {1059}[1].

Add:

Xabg652-7A {0242}.		ABG652.	(6A).
Xfba349-7A {0242}.		FBA349.	(2D).
Xgwm631-7A.{0178,0254}.		WMS F631/WMS R631.	
Xgwm698-7A {0254}.		WMS F698/WMS R698.	
Xgwm748-7A {0254}.		WMS F748/WMS R748.	
Xgwm767-7B {0250}.		WMS F767/WMS R767.	
Xgwm870-7A {0254}.		WMS F870/WMS R870.	
Xgwm871-7B {0250}.		WMS F871/WMS R871.	
Xgwm897-7B {0250}.		WMS F897/WMS R897.	
Xgwm963-7B {0250}.		WMS F963/WMS R963.	
Xgwm1044-7D {0250}.		WMS F1044/WMS R1044.	
Xgwm1061-7A {0254}.		WMS F1061/WMS R1061.	
Xgwm1066-7A {0254}.		WMS F1066/WMS R1066.	
Xgwm1085-7B {0250}.		WMS F1085/WMS R1085.	
Xgwm1083-7A {0254}.		WMS F1083/WMS R1083.	
XksuE19-7B {0242}.		pTtksuE19.	(1A,B,D, 6D).
Xutv507-7B {0269}[2].		UTV507.	
Xutv621-7B {0269}[2].		UTV621.	
Xwmc14-7D [{0242}].	[*Xwmc014-7D* {0242}].	WMC 14F/WMC 14R.	
Xwmc116-7A {0242}.		WMC 116F/WMC 116R.	

Xwmc157-7D {0242}.		WMC 157F/WMC 157R.
Xwmc247-7A {0242}.		WMC 247F/WMC 247R.
Xwmc346-7A {0242}.		WMC 346F/WMC 346R.

Group 7
Amendments:
Xbcd410-7D. Revise the last column to '(2A,B,D).'.
Xbcd707-7D. Revise the first column to '*Xbcd707-7B* {0242}, *7D* {1059}.'.
XksuE7-7D. Add '(2B).' in the last column.
Xmwg539-7D. Add '(1A,B,D).' in the last column.
Xpsp3045-7D. Add '(2A, 5B).' in the last column.
Xwg232-7A.1. Revise the last column to '(1A, 4A,B, 5A,B,D, 6B, 7B).'.
Xwg232-7A.2. Revise the last column to '(1A, 4A,B, 5A,B,D, 6B, 7B).'.
Xwmc47-7A. Add '(4B).' in the last column.
Xwmc83-7A. Delete (the entry has been moved to group 7S).

Add:

Xcdo949-7B {0242}.		CDO949.	(4D).
Xstm337-7B [{0242}].	[*Xstm337b-7B* {0242}].	STM 337F/STM 337R.	(5A).
Xstm764-7A [{0242}].	[*Xstm764a-7A* {0242}].	STM 764F/STM 764R.	
Xwmc94-7D {0242}.	[*Xwmc094-7D* {0242}].	WMC 94F/WMC 94R.	
Xwmc121-7D {0242}.		WMC 121F/WMC 121R.	
Xwmc364-7B {0242}.		WMC 364F/WMC 364R.	
Xwmc402-7B {0242}.		WMC 402F/WMC 402R.	

Dormancy (Seed)
Cross AC Domain/Haryutaka: one major QTL in chromosome 4AL and two lesser possibly homoeologous QTLS in 4BL and 4DL {0226}.

Ear emergence

QEet.ipk-2D 2DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Lateness was contributed by W-7984 {0255}.
ma: Associated with *Xfba400-2D* and *Xcdo1379* {0255}.
QEet.ipk-2D coincides with a QTL for flowering time, *QFlt.ipk-2D*. Both QTLs are likely to correspond to *Ppd-D1* {0255}

QEet.ipk-5D 5DL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Lateness was {0255}. contributed by W-7984 {0255}.
ma: Associated with *Xbcd450-5D* {0255}.
QEet.ipk-5D coincides with a QTL for flowering time, *QFlt.ipk-5D*. Both QTLs are likely to correspond to *Vrn-D1* {0255}.

Flowering time

QFlt.ipk-3A 3AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Lateness was {0255}. contributed by W-7984 {0255}.
ma: Associated with *Xbcd451* {0255}.

Frost Resistance
Responses to cold exposure and their genetics are reviewed in {0020,0274}.

Fr1. **ma:** *Fr1* mapped 2 cM proximal to *Xwg644-5A* and *Vrn-A1* {0291} and was flanked by deletion points 0.67 and 0.68 {0292}.
Fr2 {0291}. 5DL {0291}. **s:** CS*7/Cheyenne 5D {0291}. **ma:** *Fr2* mapped 10 cM proximal to *Vrn-D1* {0291}.

QWin.ipk-6A 6AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Winter hardiness was contributed by W-7984 {0255}.
ma: Associated with *Xfba85* and *Xpsr10(Gli-2)* {0255}.

Glume Colour

1. Red (brown/bronze)

Rg2.

QRg.ipk-1D 1DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The glume colour was contributed by W-7984 {0255}. {0255}.

ma: Associated with *Gli-D1* {0255}.

This QTL coincides with a QTL for awn colour, *QRaw.ipk-1D* {0255}.

7. Awn colour

QRaw.ipk-1A 1AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The awn colour was contributed by W-7984 {0255}. {0255}.

ma: Associated with *Gli-A1* {0255}.

QRaw.ipk-1D 1DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The awn colour was contributed by W-7984 {0255}. {0255}.

ma: Associated with *Gli-D1* {0255}.

Grain Hardness / Endosperm Texture

Add at end of section:

QTL: Ten QTLs for kernel hardness (54 % of the variation) were mapped in a cross 'Forno'/ 'Oberkulmer' spelt {0280}.

Grain Quality Parameters

1. Sedimentation value

QTL : QTL associated with *Glu-1*on chromosome arms 1AL and 1DL and *Gli-1/Glu-3* on 1BS were detected in RSLs from the cross Cheyenne (high quality) x CS (low quality) {0251}. Cultivar Cheyenne contributed the higher SDS sedimentation values {0251}. The QTL on 1AL coincided with a QTL for bread loaf volume {0251}. The QTL on 1DL and 1BS coincided with QTL for bread mixing time {0251}.

4. Milling yield

QTL : A QTL associated with *Pinb* on chromosome arm 5DS was detected in RILs from the cross NY6432-18 x Clark's Cream {0241}. Cultivar Clark's Cream contributed the higher flour yield allele {0241}. This QTL coincided with QTL for hardness, hydration traits (dough water absorption, damaged starch and alkaline water retention capacity (AWRC), and baked product traits (cookie diameter and cookie top grain) {0241}.

5. Alveograph dough strength W

Add at the end of section:

QTL: Ten QTLs for W (39 % of the variation), nine QTLs for P (48% of the variation) and seven QTLs for P:L (38% of the variation) were mapped in 'Forno'/'Oberkulmer' spelt {0280}.

6. Mixograph peak time (new category)

QTL : A QTL associated with *Glu-Dy1* on chromosome arm 1DL was detected in RILs from the cross NY6432-18 x Clark's Cream {0241}. Cultivar Clark's Cream contributed the higher mixograph peak time allele {0241}. This QTL coincided with a QTL for bread mixing time {0241}.

Height

Reduced Height

Rht-B1. Add at end of section: The line XN004, earlier considered to have *Rht21* {0230}, was shown to carry an allele at the *Rht-B1* locus {0231}.

Rht-D1. Add at end of section: The line XN004, earlier considered to have *Rht21* {0230}, was shown to carry an allele at the *Rht-D1* locus {0231}.

Various common wheat and durum NIL pairs differing at the *Rht-A1* or *Rht-D1 loci* are listed in {02102}.

Rht8a. Integrate alphabetically in the **v:** section:

Hope {0243}; Marquis {0243}; Michigan Amber {0243}.

Rht8b. Integrate alphabetically in the **v:** section:

Arthur {0243}; Carsten V {0243}; Diakovchanka {0243}; Odom {0243}; Oasis {0243}; Purdue Abe {0243}; Salzmünder Bartweizen 14/44 {0243}; Tp114/65 {0243}; Wiskonsin 245 C/11226 {0243};

Rht8c Integrate alphabetically in the **v:** section:
Al'batros odesskii {0243}; Arthur 71 {0243}; Donskaya polukarlikovaya {0243}; Erythrospermum 127 {0243}; Erythrospermum 1072 {0243}; Erythrospermum 272-87 {0243}; Erythrospermum 949-38 {0243}; Fakir {0243}; Fedorovka {0243}; Kaloyan {0243}; Khar'kovskaya 50 {0243}; Khar'kovskaya 93 {0243}; Khersonskaya 86 {0243}; Mv 03-89 {0243}; Mv 06-88 {0243}; Mv 17{0243}; Obrii {0243}; Odesskaya 51 {0243}; Odesskaya 117 {0243}; Odesskaya 132 {0243}; Odesskaya krasnokolosaya {0243}; Odesskaya polukarlikovaya {0243}; Roazon {0243}; Simvol odesskii {0243}; Sivka {0243}; Strumok {0243; Tira {0243}; Ukrainka odesskaya {0243}; Vympel {0243}; Yubileinaya 75 {0243}; Zolotava {0243}.

At the end of the list {1999 Suppl.} add: 'Although CS carries a 192 bp fragment, sequencing showed it was a different allele than other genotypes with *Rht8c* {02103}.'.

Rht8g. Associated with a 196-bp fragment of WMS 261 [{0243}]. **v:** Mirleben {0243}.

Rht8h. Associated with a 206-bp fragment of WMS 261 [{0243}]. **v:** Weihenstephan M1 {0243}.

Rht21 {0230}. 2DL {0230}. **v:** XN004 {0230}. The existence of this gene could not be confirmed {0231}.

QHt.ipk-4A 4AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The height is {0255}. contributed by Opata {0255}.
ma: Associated with *Xmwg549, Xabg390* and *Xbcd1670* {0255}.
QHt.ipk-4A coincides with QTLs for ear length (*QEl.ipk-4A*), grain number (*QGnu.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.
QHt.ipk-6A 6A {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The height is {0255}. contributed by W-7984 {0255}.
ma: Associated with *Xcdo29* and *Xfba234* {0255}.
QHt.ipk-6A coincides with QTLs for peduncle length (*QPdl.ipk-6A*) and ear length (*QEl.ipk-6A*) {0255}

Leaf erectness (new category)
QLer.ipk-2A 2AS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. The erect leave {0255}. phenotype was contributed by Opata {0255}.
ma: Associated with *Xbcd348* {0255}.
Note: Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants {0255}.

Male Sterility
ms1d {0290}. **v:** Mutant FS2 {0290}.

ms1e {0290}. **v:** Mutant FS3 {0290}.

ms1f {0290}. **v:** Mutant FS24 {0290}.

ms3. **ma:** *Xwg341-5A* – 0.8cM – *ms3*... .....cent {0289}. *Xcdo-677-5A* and *Xbcd1130-5A* also cosegregated with *Xwg341-5A* but were located in a different region in the physical map {0289}.

ms4 {0293}. 4DS {0293}. Dominant allele for sterility, distinguished from *ms2* on the basis of different degrees of recombination with the 4D centromere. **v:** Konzak's male sterile.

ms5 {0290}. 3A {0290}. **v:** Mutant FS20 {0290}.

Meiotic Characters
2. Pairing homoeologous
Ph1.
On a new line following the *ph1c* entry add: 'Several *ph1* mutants are described in {0219}.'.

ma: Add: PCR-based assays for presence and absence of *Ph1* have been described {0214,0217,9965}. The *Ph1* factor(s) was restricted to a region flanked by *Xrgc846-5B* and *Xpsr150-5B* {0219}.

Nucleolus Organiser Regions
Add at the end of descriptive paragraph and before allele descriptions:
'Deletion mapping divided the *Nor-B1* in a proximal subregion *Nor-B1p* (short repeat) and a distal subregion *Nor-B1d* (long repeat) {0275}'.

Proteins
1. Grain protein content
QTL: Nine QTLs (51 % of the variation) were mapped in cross 'Forno'/ 'Oberkulmer' spelt {0280}.

QGpc.ndsu-6Bb. Add at the end of the **ma:** section: {0244} reports the location of this QTL in the 4 cM interval flanked by *Xmwg79-6B* and *Xcdo365-6B.*

QTL A QTL for grain and flour protein content, contributed by CS, was associated with *XTri-1D*/Centromere in a RSL population from the cross Cheyenne (high quality wheat) x CS (low quality wheat) {0251}.

3. Endosperm Storage Proteins
3.1 Glutenins
Add at the end of the sentence 'The *Glu-3* loci are defined as the cluster of LMW glutenin genes previously considered a component of the compound *Gli-1* loci.'
'More than 30 LMW glutenin complete genes, partial genes or pseudogenes have been sequenced from *Triticum* species (reviewed in {0245}).

5. Other proteins
5.6 Waxy proteins
At end of preamble add: 'Partial genomic clones of various diploid, tetraploid, and hexaploid wheats have been sequenced {0278,0279}.'

Wx-d1e {0234}. **v:** Tanikei A6599-4 {0234}. Relative to Kanto 107, Tanikei A6599-4 carries an alanine to threonine substitution at position 258 in the mature protein {0234}.

5.8. Puroindolines
Revised section: Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). Hard wheats result from unique changes in the puroindoline amino acid sequence or, currently, four null forms {0295} of the completely linked genes (max. map distance 4.3 cM) {452}.

Pina-A^{m}1 {0083} 5A^{m}S {0083}. **dv:** *T. monococcum* DV92, G3116 {0083}
In *T. momococcum Pina-A^{m}1* is completely linked to *Gsp-A^{m}1* {0083}.
Pina-D1 5DS {452}. **v:** CS
Pina-D1a {452}.
v: Aurelio *Pinb-D1a* {0249}; Bellevue {0249}; Bezostaja *Pinb-D1b* {0249}; Bilancia *Pinb-D1a* {0249}; Bolero *Pinb-D1a* {0249}; Brasilia *Pinb-D1b* {0249}; Centauro *Pinb-D1a* {0249}; Cerere *Pinb-D1b* {0249}; Chinese Spring *Pinb-D1a* {452,0249}; Colfiorito *Pinb-D1b* {0249}; Cologna 21 *Pinb-D1b* {0249}; Courtot {0249}; David *Pinb-D1b* {0249}; Democrat *Pinb-D1b* {0249}; Etruria *Pinb-D1b* {0249}; Fortuna {0249}; Francia *Pinb-D1b* {0249}; Galaxie 0249}; Gemini *Pinb-D1b* {0249}; Genio *Pinb-D1b* {0249}; Gladio *Pinb-D1b* {0249}; Heron {1035}; Lampo *Pinb-D1a* {0249}; Leone *Pinb-D1a* {0249}; Leopardo *Pinb-D1a* {0249}; Libero *Pinb-D1a* {0249}; Livio *Pinb-D1a* {0249}; Marberg *Pinb-D1b* {0249}; Mentana *Pinb-D1a* {0249}; Mieti *Pinb-D1b* {0249}; Mosè *Pinb-D1a* {0249}; Neviana *Pinb-D1a* {0249}; Newana *Pinb-D1b* {0249}; Oscar *Pinb-D1a* {0249}; Pandas *Pinb-D1b* {0249}; Pascal *Pinb-D1b* {0249}; Sagittario *Pinb-D1b* {0249}; Salgemma *Pinb-D1b* {0249}; Saliente *Pinb-D1b* {0249}; Salmone *Pinb-D1b* {0249}; Serena *Pinb-D1a* {0249}; Serio *Pinb-D1b* {0249}; Soissons {0249}; Veda *Pinb-D1b* {0249}; Zena *Pinb-D1b* {0249}.'
Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying a hardness mutation in puroindoline b {452,1035,0082, 0204}.
Pina-D1b {1035}. Null allele
v: Amidon *Pinb-D1a* {0249}; Barra *Pinb-D1a* {0249}; Butte 86 {1035}; Ciano *Pinb-D1a* {0249}; Dorico *Pinb-D1a* {0249}; Eridano {0249}; Falcon {1035}; Fortuna (USA) *Pinb-D1a* {0249}; Glenman *Pinb-D1a* {0249}; Golia *Pinb-D1a* {0249}; Guadalupe *Pinb-D1a* {0249}; Inia 66 *Pinb-D1a* {0249}; Jecora *Pinb-*

D1a {0249}; Indice *Pinb-D1a* {0249}; Kalyansona {0249}; Manital *Pinb-D1a* {0249}; Mendos *Pinb-D1a* {0249}; Padus *Pinb-D1a* {0249}; Prinqual *Pinb-D1a* {0249}; Sibilia *Pinb-D1a* {0249}; Super X {0249}; Yecora Rojo {0204}.
i: Gamenya sel. {0298,0203}; Heron/7*Falcon sel.{0298,0203}.

Present only in some hard hexaploid wheats. *Pina-D1b* is associated with harder texture than *Pinb-D1b* {0177,0206}.

Pinb-A^{m}1 {0083}.m 5A^{m}S {0083}. **dv:** *T. monococcum* DV92, G3116 {0083}.
In *T. momococccum Pinb-A^{m}1* is 0.1 cM proximal to *Pina-A^{m}1* and both loci are less than 36 kb apart.

Pinb-D1 5DS {452} **v:** CS.

Pinb-D1a {452}.
v: Amidon *Pina-D1b* {0249}; Aurelio *Pina-D1a* {0249}; Barra *Pina-D1b* {0249}; Bilancia *Pina-D1a* {0249}; Bolero *Pina-D1a* {0249}; Centauro *Pina-D1a* {0249}; Chinese Spring *Pina-D1a* {452,0249}; Ciano *Pina-D1b* {0249}; Dorico *Pina-D1b* {0249}; Fortuna (USA) *Pina-D1b* {0249}; Glenman *Pina-D1b* {0249}; Golia *Pina-D1b* {0249}; Guadalupe *Pina-D1b* {0249}; Hill 81 {452}; Inia 66 *Pina-D1b* {0249}; Jecora *Pina-D1b* {0249}; Idice *Pina-D1b* {0249}; Lampo *Pina-D1a* {0249}; Leone *Pina-D1a* {0249}; Leopardo *Pina-D1a* {0249}; Libero *Pina-D1a* {0249}; Livio *Pina-D1a* {0249}; Manital *Pina-D1b* {0249}; Mendos *Pina-D1b* {0249}; Mentana *Pina-D1a* {0249};Mosè *Pina-D1a* {0249}; Neviano *Pina-D1a* {0249}; Oscar *Pina-D1a* {0249}; Padus *Pina-D1b* {0249}; Prinqual *Pina-D1b* {0249}; Serena *Pina-D1a* {0249}; Sibilia *Pina-D1b* {0249}.
Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pina-D1b* mutation {452,1035,0082,0204}.

Pinb-D1b {452}. 5DS {452}.
i: Paha*2//Early Blackhull/5*Paha {02111,0203}; Early Blackhull der./5*Nugaines sel. {0298,0203}.
s: CS*7/Cheyenne 5D {452}.
v: Bezostaya *Pina-D1a* {0249}; Brasilia *Pina-D1a* {0249}; Cerere *Pina-D1a* {0249}; Colfiorito *Pina-D1a* {0249}; Cologna 21 *Pina-D1a* {0249}; David *Pina-D1a* {0249}; Democrat *Pina-D1a* {0249}; Etruria *Pina-D1a* {0249}; Francia *Pina-D1a* {0249}; Gemini *Pina-D1a* {0249}; Genio *Pina-D1a* {0249}; Gladio *Pina-D1a* {0249}; Marberg *Pina-D1a* {0249}; Mieti *Pina-D1a* {0249}; Newana *Pina-D1a* {0249}; Pandas *Pina-D1a* {0249}; Pascal *Pina-D1a* {0249}; Sagittario *Pina-D1a* {0249}; Salgemma *Pina-D1a* {0249}; Saliente *Pina-D1a* {0249}; Salmone *Pina-D1a* {0249}; Serio *Pina-D1a* {0249}; Thatcher {0204}; Veda *Pina-D1a* {0249}; Wanser {452}; Zena *Pina-D1a* {0249}; hard component of Turkey {0204}.

Pinb-D1b is a "loss-of-function" mutation resulting from the replacement of a glycine by a serine at position 46 {452}.

Pinb-D1c {0082} **v:** Avle {0082}; Reno {0082}; Tjalve {0082}; Bjorke {0082}; Portal {0082}.
Pinb-D1c is a "loss-of-function" mutation resulting from the replacement of a leucine by a proline at position 60 {0082}.

Pinb-D1d {0082}. **v:** Bercy {0082}; Mjolner {0082}.
Pinb-D1d is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a arginine at position 44 {0082}.

Pinb-D1e {0204}. **v:** Gehun {0204}; Canadian Red {0204}; Chiefkan {0204}.
Pinb-D1e is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 39 {0204}.

Pinb-D1f {0204}. **v:** the hard component of Utac {0204}.
Pinb-D1f is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 44 {0204}.

Pinb-D1g {0204}. **v:** Andrews {0204}.
Pinb-D1g is a "loss-of-function" mutation resulting from the replacement of a cysteine by a stop codon at position 56 {0204}.

Pinb-D1b, Pinb-D1c, Pinb-D1d, Pinb-D1e, Pinb-D1f, or *Pinb-D1g* are present in hard hexaploid wheats not carrying the *Pina-D1b* (null) mutation {452,1035,0082,0204}.

Wheats with *Pinb-D1b* were slightly softer and a little superior to those with *Pina-D1b* in milling and bread-making characteristics although there was considerable overlap {0206}. Transgenic rice with the *Pina-D1a* and *Pinb-D1a* alleles possessed softer grain {0207}.

Genotypes for a selection of North American wheats are given in {0204}.

5.9. Histone H1 Proteins

HstH1-A1 {0215}.	5AL {0215}.	**v:**	CS {0215}.
HstH1-B1 {0215}.	5BL {0215}.	**v:**	CS {0215}.
HstH1-D1 {0215}.	5DL {0215}.	**v:**	CS {0215}.
HstH1-D1a {0215}.		**v:**	CS {0215}; 18 others {0215}.
HstH1-D1b {0215}.		**v:**	Grekum 114 {0215}; Kirgizsky Karlik {0215}.
HstH1-A2 {0215}.	5AL {0215}.	**v:**	CS {0215}.
HstH1-A2a {0215}.		**v:**	CS {0215}.
HstH1-A2b {0215}.	Null allele {0215}.	**v:**	Mara {0215}; 10 others {0215}.
HstH1-B2 {0215}.	5BL {0215}.	**v:**	CS {0215}.
HstH1-B2a {0215}.		**v:**	CS {0215}; 19 others {0215}.
HstH1-B2b {0215}.		**v:**	Excelsior {0215}.
HstH1-D2 {0215}.	5DL {0215}.	**v:**	CS {0215].

The relationship of this gene series with a *Hst-A1, Hst-B1, Hst-D1* series in group 5 chromosomes {0216} based on DNA hybridization studies was not established.

Response to Tissue Culture

Add at the end of the section:

QGpp.kvl-2A {0253}.	2AL {0253}.	**v:**	Ciano/Walter DH mapping population {0253}. The green plant percentage was contributed by Ciano {0253}.
	ma:	Associated with *Xpsp3045-2A* {0253}.	
QGpp.kvl-2B.1 {0253}.	2BL {0253}.	**v:**	Ciano/Walter DH mapping population {0253}. The green plant percentage was contributed by Ciano {0253}.
	ma:	Associated with *Xgwm388-2B* {0253}.	
QGpp.kvl-2B.2 {0253}.	2BL {0253}.	**v:**	Ciano/Walter DH mapping population {0253}. The green plant percentage was contributed by Ciano {0253}.
	ma:	Associated with AFLP markers {0253}.	
QGpp.kvl-2A {0253}.	2AL {0253}.	**v:**	Ciano/Walter DH mapping population {0253}. The green plant percentage was contributed by Ciano {0253}.
	ma:	Associated with *Xpsp3045-2A* {0253}.	

Response to Vernalization

Vrn-B1. Vm2. 5BL or 7BL. Add to reference {635}, i.e. {635,0282}.

In the final paragraph include reference 0202 with the first reference, i.e. {1173,0202}.

Yellow berry tolerance

QTL : A QTL for yellow berry tolerance, contributed by RS111, was associated with *Xgwm190* and *Xgwm174* on chromosome 5D in a RIL population from RS111/CS {0237}. A tolerance QTL contributed by CS, the susceptible parent, was detected on 6B {0237}.

Yield Components

1000-grain weight

QTgw.ipk-5A {0255}.	5AL {0255}.	**v:**	Opata/W-7984 (ITMI) RI mapping population {0255}. The higher yielding allele is contributed by W-7984 {0255}.
	ma:	Associated with *Xfba351* and *Xcdo1312* {0255}.	

QTL : QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL in a RIL population from RS111/CS {0236}.

QTL Eight QTLs for 1,000-kernel weight (54 % of the variation) were mapped in 'Forno'/ 'Oberkulmer'

spelt {0280}.

Kernel number per spike

QGnu.ipk-4A 4AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Higher kernel number was contributed by Opata {0255}.
ma: Associated with *Xmwg549, Xabg390* and *Xbcd1670* {0255}.
QGnu.ipk-4A coincides with QTL for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.

Spike length

QEl.ipk-1B 1BL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Longer ear was contributed by Opata {0255}.
ma: Associated with *Xbcd388* and *Xwg605* {0255}.

QEl.ipk-4A 4AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Longer ear was contributed by Opata {0255}.
ma: Associated with *Xmwg549, Xabg390* and *Xbcd1670* {0255}.
This QTL is likely to be a pleiotropic effect of the gene underlying the height QTL, *QHt.ipk-4A* {0255}.

QEl.ipk-5A 5AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Longer ear was contributed by W-7984 {0255}.
ma: Associated with *Xmwg522* {0255}.

Grain weight/ear

QGwe.ipk-2D 2DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Higher grain weight was contributed by Opata {0255}.
ma: Associated with *Xcdo1379* and *Xbcd1970* {0255}.

QGwe.ipk-4A 4AL {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Higher grain weight was contributed by Opata {0255}.
ma: Associated with *Xmwg549, Xabg390* and *Xbcd1670* {0255}.
QGwe.ipk-4A coincides with QTL for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain number (*QGnu.ipk-4A*) {0255}.

Reaction to Diseases and Pests

Reaction to Barley Yellow Dwarf Virus

Bdv2. **tr:** TC14 {059,0201}.
v: TC14*2/Hartog {0225}; TC14/2*Spear {0201}; TC14/2*Tatiara {0225}.
ma: Complete association with *Xpsr129-7D, Xpsr548-7D, XksuD2-7D, XcslH81-7D,* and *Xgwm37-7D* selected as a diagnostic marker {0225}.

Reaction to *Diuaphis noxia*

Dn1. 7DS {0211}. **i:** Betta-Dn1 {0211}; Karee-Dn1 {0211}; Tugela-Dn1 {0211}.
ma: *Xgwm111-7D*$_{210}$ - 3.20 ± 0.20 cM - *Dn1* (0211}.

Dn2. 7DS {0211}. **i:** Betta-Dn2 (0211}; Karee-Dn2 {0211}; Tugela-Dn2 {0211}.
ma: *Xgwm111-7D*$_{200}$ – 3.05 ± 0.18 cM - *Dn2* {0211}.

Dn4. **v:** Halt {0209}.

Dn5. 7DS {0211}. **i:** Betta-Dn1 {0211}.
ma: *Xgwm111-7D*$_{220}$ - <3.20 cM – *Dn5* {0211}.

Dn8 {0211}. 7DS {0211}. **i:** Karee-Dn8.
v: PI 294994 *Dn5Dn9* {0211}.
ma: *Xgwm635-7D*$_{100}$ - <3.20 cM – *Dn8* {0211}.

Dn9 {0211}. 1DL {0211}. **i:** Betta-Dn9.
v: PI 294994 *Dn5Dn8* {0211}.
ma: *Xgwm642-7D*$_{180}$ - <3.20 cM - *Dn9* {0211}.

Dnx {0211}. 7DS {0211}. **v:** PI 220127 {0211}.
ma: *Xgwm111-7D*$_{210}$ – 1.52 ± 0.15 cM – *Dnx* {0211].
Dnx was considered to be located at a locus different from *Dn1*, *Dn2* or *Dn5* {0211}, which were likely to be identical or allelic.

Reaction to *Erysiphe graminis*

Pm4b. ma: Pm4b - 4.8cM - Xgbx3119b {0272}.

Pm5a {0257}. Pm5{787}. v: Add: Galaxie {0257}; Kutulukskaya {0257}; Lambros {0257}; Navid {0257}; Pagode {0257}; Regina {0257}; Sicco (0257}; Tarasque {0257}; Zolotistaya {0257}.

Pm5b {0257}. Mli {540,558}. v: Add: Cucurova {0257}; Fruhprobst {0257}; Kirkpinar-79 {0257}; Kontrast {0257}; Ilona {0257}; Nadadores {0257}; Siete Cerros {0257}; Una {0257}; Wettiness {0257};

Pm5c {0257}. 7B {0257}. v: T. sphaerococcum cv. Kolandi {0257}.

Pm5d {0257}. 7B {0257}. i: IGV 1-455 = CI 10904/7*Prins {0257}; CI 10904/7*Starke {0257}.

Pm5e {0258}. mlfz {0259}. v: Fuzhuang 30 {0258}. ma: Xgwm1267-7B - 6.6cM – Pm5e – 12.6cM - Xubc405-628 {0258}.

Pm8. ma: A STS marker distinguishes Pm17 from Pm8 {0286}.

Pm17. 1BL.1RS.
ma: A STS marker distinguishes Pm17 from Pm8 {0286}.

Pm30. ma: Pm30 – 5.6 cM – Xgwm159-5B {0163}.

Mlxbd {0259}. 7B {0259]. Xiaobaidong {0258}.

Add to genotype list: '{02104} (Hungarian wheats).'.

QTL: Several QTLs were detected in two RE714/Hardi populations when tested at two growth stages and with different cultures over three years. The most persistent band effective QTL was located in the vicinity of *Xgwm174-5D* {0272}. Three QTLs, *QPm.vt-1B*, *QPm.vt-2A* and *QPm.vt-2B*, with additive gene action, accounted for 50% of the variation in a population developed from Becker/Massey {0284}.

QPm.ipk-2B {0255}. 2BS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Resistance was contributed by Opata {0255}.
ma: Associated with *Xcdo405* and *Xmwg950* {0255}.

QPm.ipk-4B {0255}. 4B {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Resistance was contributed by W-7984 {0255}.
ma: Associated with *Xcdo795* and *Xbcd1262* {0255}.

QPm.ipk-7D {0255}. 7DS {0255}. **v:** Opata/W-7984 (ITMI) RI mapping population {0255}. Resistance was contributed by Opata {0255}.
ma: Associated with *Xwg834* and *Xbcd1872* {0255}.

Reaction to *Fusarium graminearum*

QFhs.ndsu-3B {9925,0175}. 3BS {9925}. **v:** Sumai 3 {9925,0175}.

ma: Associated with *Xbcd907-3B.2* (LOD>3) {9925} and microsatellite markers *Xgwm533* and *Xgwm493* {0175}. This QTL explained 41.6 % of the variation in the cross Sumai3/Stoa {0175}.

QTL: Two additional QTL for resistance to *Fusarium graminearum* were identified in the cross Sumai3/Stoa {0175}. The QTL on 4BS was associated with *Xwg909* and the QTL on 6BS was associated with *Xbarc101* and *Xbcd1383* {0175}. The QTL associated with markers *Xgwm493/Xgwm533* (explaining 24.8 % of the variation), and *Xbarc101/Xbcd1383* were also identified in a RIL population from the cross ND2603/Butte 86 {0175}. In addition, one QTL on chromosome 3AL associated with *Xbcd941* and one on chromosome 6AS associated with *XksuH4* were identified in RILs from the cross ND2603/Butte 86 {0175}.
The resistance QTL on chromosome 3BS associated with *Xgwm493* and *Xgwm533* was also identified in a DH population of the cross CM-82036 (a Sumai 3 derivative) x Remus {0240}. Additional QTL in this cross were detected on chromosome 5A, associated with *Xgwm293* and *Xgwm304*, and possibly on 1B, associated with *Glu-B1* {0240}.

For review see {0283}.

Reaction to *Heterodera avenae*

Cre8 {0220}. *CreF* {0012,0138}. 6B {0220}. [On basis of linkage with *Xbcd1* and *Xcdo347*].

v: Barunga {0220}; Festiguay {0012,0220}; Frame {0138,0220}; Molineaux {0220}. **ma:** Associated with a unique allele when probed with CDO347 which hybridizes to group 6 and group 7L {1059}.

Reaction to *Mayetiola destructor*

H21. ma: An STS primer set SJ07 was developed to identify 2RL, and hence H21 {0233}.

H30 {0256}.	Derived from Ae triuncialis {0256}.	v: TR-3531 {0256}.	al: *Ae. Triuncialis* {0256}.

Reaction to *Mycosphaella graminicola*

Stb5. **ma:** *Rc3* - 6.6cM- *Stb5* - 7.2cM - *Xgwm44*/Centromere {0186}.

Reaction to *Phaeosphaeria nodorum*

SnbTM. **ma:** $UBC521_{650}$ - 15 cM – *SnbTM* – 13.1 cM – $RC37_{510}$ {0212}. $UBC521_{650}$ was converted to a SCAR marker {0212}.

Reaction to *Pseudocercosporella herpotrichoides*

Pch1. 7A {0224}. **tv:** Five recombinant lines {0224}.

Reaction to *Puccinia graminis tritici*

Sr22. ma: Add: See also {0158}.

Sr26. ma: Can be detected with several RFLP probes {0138}.

Sr31. 1BL.1RS: Cougar {0267}; Rawhide (heterogeneous) {0267}.

Sr36. v: GK Kincs_ {0235}.

Sr38 {062}. Derived from Ae. ventricosa. See Reaction to *P. recondita tritici* Lr37 and P. striiformis tritici Yr17 for details.

Sr38 {062}. Derived from *Ae. ventricosa*. See Reaction to *P. recondita tritici Lr37* and *P. striiformis tritici Yr17* for details.

v: Moisson derivatives Mx12 and Mx22 also carry *Sr38* {0213}.

Reaction to *Puccinia recondita tritici*

Lr10. **v:** Scout 66 {02101}.

Lrk10. A receptor-like kinase. The locus *Xsfr1(Lrk10)-1A*, detected by the probe Lrk10, is completely linked with *Lr10* in chromosome 1AS {356}. Lrk10 encodes a receptor-like kinase with extracellular and kinase domains {0297}. Using probe pLrk10-A, developed from the extracellular domain, 6 homologues were found in chromosomes 1A (1), 1B (3) and 1D (2) as well as group 1 chromosomes of *T. monococcum*, *Ae. tauschii* and barley {0296,0294}. Probes based on the kinase domain identified further homologues in chromosomes 3AS and 3BS as well as the corresponding regions in rice and maize {0294}. Both orthologous and paralogous evolution were suggested.

Lr11. **v:** Karl 92 *Lr3 Lr10* {02101}.

Lr12. **v:** AC Domain *Lr10 Lr34*{0228}.

Lr13. **v:** Hereward {0288}; Moulin {0288}; Pastiche {0288}. BH1146 *Lr34* {0268}.

Lr16. **v:** Arapahoe {02101}; Brule {02101}; Millenium {02101}; Redland {02101}; Vista {02101}.

Lr17b. 2A {1350}. **v:** Brock {0260}; Tarso {0229}; Norman {1350}.

Lr19. 7BL. **v:** 4 further derivatives of 88M22-149 {0232}.
ma: An STS marker closely linked and distal to *Lr19* was developed from an AFLP {0273}.

Lr21. **v:** McKenzie {0228}; WGRC2 = TA1649/3* Wichita {0299}; WGRC7 = Wichita/TA1649//2*Wichita {0299}.
dv: *Aegilops squarrosa* accessions: RL5289 = TA1599 {1241}; TA1649 {0299}; TA1691 {0299}; TA2378 {0299}; TA2470 {0299}; TA2483 {0299}; TA2495 {0299}; TA2527 {0299}; TA2528 {0299}.
ma: All members of the *Lr21* family carry a STS derivative of *ksuD14-1D* that has a resistance gene analogue structure {0299}.

Lr23. **v:** Cranbrook {02119}.

Lr26. 1BL.1RS: Cougar {0267}; Rawhide (heterogeneous) {0267}.

Lr34. Westphal 12 {0268}. BH1146 Lr13 {0268}.

Lr37 {062}. 2AS {062}. Derived from *Ae. ventricosa* .
VPM1 and derivatives: 2AS {062} = 2AL.2AS-2N^{v}S {0213}.
i: Tc*8/VPM1 {316}; Various NILs listed in {0213}.
v: Hyak {021}; Madsen {020}; Rendezvous {062}; VPM1 {062}. See also Reaction to *P. striiformis tritici Yr17.*
Moisson derivatives: *Lr* {113}. 2AS = 2AL.2AS-2N^{v}S {113}.
ad: Moisson + 6N^{v} = 6N^{v}S.6N^{v}L-2N^{v}S or 6N^{v}L.6N^{v}S-2N^{v}S {0009}.
v: Mx12 {0213}; Mx22 {0213}.
ma: (relevant to both groups of derivatives). PCR primers designed from marker csVrga1D3' {0183} producing a 383 bp product allows detection of the 2N^{v}S segment {0213}. See also: Reaction to *P. striiformis tritici Yr17.*
Lr37 can be recognised in seedling tests at low temperatures (17C) and is effective in adult plants under field conditions.

Lr39 {02100}. 2DS {02100}. Derived from *Aegilops tauschii* {02100}.
v: TA4186 = TA1675*2/Wichita {02100}.
dv: *Aegilops tauschii* TA 1675 {02100}.

ma: 10.7 cM distal to *Xgwm210-2D* {02100}.

Lr41. **v:** Thunderbolt {02100}.

Lr50 {0221}. 2BL {0221} [Based on linkage with SSR markers].
v: WGR36 = TAM107*3/TA870//Wichita {0221}.
tv: *T. armeniacum* TA870 {0221}.

LrTm {0277}. **dv:** *T. monococcum.*
ma: Linked to microsatellite locus *Xgwm136* {0277}.

LrTr {0227]. **v:** *Aegilops triuncialis* derivatives {0227}.
ad: WL711 BC2F5 addition lines {0227}.
al: *Aegilops triuncalis* Acc. 3549 {0227|.
ma: Lines with *LtTr* possessed a homologue of *Xgwm368-4B* {0227}.

Genotype lists: Australian wheats {0288}, European wheats {0229,0260,0288}.

Reaction to *Puccinia striiformis tritici*

Yr9. 1BL.1RS: Cougar {0267}; Rawhide (heterogeneous) {0267}.

Yr10. YrVav {0262}. v: QLD709 = Janz*2/T. Vavilovii {0262}.
tv: T. vavilovii AUS 22498 {0262}.
ma: A SCAR marker was described in {0261}. QLD709 and T.spelta 415, both with white glumes, failed to amplify the SCAR sequence, but bot5h carried unique alleles at the Gli-B1 and XPsp3000 loci {0262}. These differed from the Moro source of Yr10} Yr10 –1.5+-0.9cM -Gli-B1- 1.1+-0.8cM – XPsp3000 {0262}.

Yr17 {062}. 2AS {062}. See reaction to *P. recondita tritici Lr37* for details.
v: Genotype list in {02105}.
v: Arche {0044}, Balthazar {0044}, Brigadier {0044}, Cordial {0044}, Eureka {0044}, Hussar {0044}, Lynx {0044}, Pernel {0044}, Renan {0044}.
ma: *Yr17* was closely linked to the SCAR marker SC-Y15, developed from RAPD marker OP-$Y15_{580}$, and to *Xpsr150-2N*^{v} {0044}.

Yr26. 1BS {0285}. The earlier reported location opf 6AL.6VS {617} is not correct.
v: Wheat-*Haynaldia villosa* lines R43, R55, R64 and R77 {0285}.
tv: *T. turgidum* Gamma 80-1.
ma: *Yr26* – 1.9cM – *Xgwm11-1B/Xgwm18-1B* {0285}.

Yr28. **ma:** Linkage with *Xmwg634-4D* {1377}.

YrH52.
QTL: In the ITMI mapping population, QTLs were found in 2BS, 7DS, and possibly 5A, 3D and 6D {0287}.
In Camp Remy/Michigan Amber, QTLS were found in 2AL and 2BL {0287}.

Reaction to *Pyrenophora tritici repentis*

2. Resistance to chlorosis induction

QTsc.ndsu-1A. Add {0040,0264}' to the references for QTL and the marker association.

QTsc.ndsu-4A. Add to: **v:** In W-7976/Trenton resistance was contributed by W-7976 {0264}. **ma:** Add: 'In W-7976/Trenton there was association with *Xwg622-4A*{0264} and minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants {0264}.

Reaction to *Sitodiplosis mosellana*

Insect pest: Orange blossum wheat midge, Wheat midge

Sm1 {0218}. 2B{0218}. **v:** Augusta {0218}; Blueboy {0218}; Caldwell {0218}; Clark {0218}; FL302{0218}; Howell {0218} Knox 62 {0218}; Mono {0218}; Seneca {0218}. **ma:** Linked to a SCAR marker {0223}.

Reaction to *Ustilago tritici*
Add: Resistance to race 19 was associated with chromosome 6A of Cadet, Kota, Thatcher and TD18 {0208}. In the case of Cadet, resistance was localized to 6AS {0208}.

Resistance to colonization by *Eriophyes tulipae*
Curl mite colonization

Cmc1.		**v:**	Norstar derivative {0222}.
Cmc3 {0222}.	1A = 1AL.1RS.	**v:**	Amigo; TAM107. KS96GRC40 *Cmc4* {0222}.
Cmc4 {0222}.	6DS {0222}.	**v:**	KS96WRC40 *Cmc3* {0222}.
		dv:	*Aeg. Tauschii* (accession no {0222}.

Genetic Linkages

To the references in the first paragraph in the 2001 Supplement, add: '187'.

Chromosome 4D
4DS

ms4	-	centromere	I	{0293}

Summary table 1
Add:

Ar	Alkylresocinols content of grain
Eet	Ear emergence time
El	Ear length
Flt	Flowering time
Gnu	Grain number
Gpp	Green plant percentage
Gwe	Grain weight/ear
Ler	Leaf erectness
Pdc	Pyruvate decarboxylase
Pdl	Peduncle length
Raw	Red awn colour
Tgw	1000-grain weight
Win	Winter hardiness

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Editorial remarks

The present issue of Wheat Information Service No. 95 includes "Catalogue of gene symbols for wheat: 2002 supplement" in addition to the articles of seven original papers, three information and one genetic stock. We wish to express special appreciation to the continuous efforts by the editors of the Gene Catalogue. Enormous information accumulated in the Catalogue is undoubtedly the basis of bioinformatics together with the information of DNA sequences.

In these years the media for exchanging information have been largely changed. Now Internet may be the most suitable medium in regard to reliability, speediness, and cost/performance. Nevertheless, a great volume of scientific journals has been still published as hard copies. We have started to consider the suitable medium for Wheat Information Service. We want to ask for your opinion.

This year, we have received manuscripts twice as many as those in these years, which caused delay of reviewing the manuscripts. The rate of acceptance is about 50%. We would like to ask the contributors to prepare the manuscript carefully following "Instruction to Authors" on the back of the cover page.

Editorial Office:
K. Nishikawa, T. Sasakuma, H. Tsujimoto and K. Furukawa

Kihara Memorial
Yokohama Foundation for the Advancement of Life Sciences

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

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

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

Kihara Memorial Foundation

641-12 Maioka-cho, Totsuka-ku, Yokohama 244-0813, Japan.
Phone: +81-45-825-3487, Fax: +81-45-825-3307
E-mail: yamabosi@yokohama-cu.ac.jp

Business Office

Wheat Information Service
c/o Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
641-12 Maioka-cho, Totsuka-ku, Yokohama 244-0813, Japan.
Phone: +81-45-825-3487. Fax: +81-45-825-3307, E-mail: yamabosi@yokohama-cu.ac.jp
Mr. K. Hasegawa (Managing director), Mr. K. Sugizaki (Chief officer), Ms. K. Furukawa (Publication secretary)

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発行所　木原記念横浜生命科学振興財団

〒244-0813 横浜市戸塚区舞岡町641-12
Tel : (045)825-3487
Fax: (045)825-3307
E-mail: yamabosi@yokohama-cu.ac.jp

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