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Research article

Development of ditelosomic 7DL in Chinese Spring wheat

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Summary

The ditelosomic lines of common wheat are invaluable tools for mapping genes. They have been bred in a single cultivar Chinese Spring (CS), but CS ditelosomics 7DL has not yet been developed. We started to produce CS ditelosomic 7DL by backcrossing Canthatch ditelosomic 7DL to CS. After eight backcrosses, several ditelosomic lines were developed. These lines were examined with chromosome constitution, were test-crossed with ditelosomic 7DS and were also analyzed by electrophoresis for α-amylase isozymes. Three of the ditelosomic lines turned out to be truly ditelosomic for 7DL.

Key words: aneuploid, ditelosomics, 7DL

Introduction

Hexaploid bread wheat, *Triticum aestivum* (2n=6x=42), possesses an ability to tolerate the addition or deletion of chromosomes. An array of aneuploid series were produced in Chinese Spring (CS) wheat (Sears 1954; Sears 1966; Sears and Sears 1978). Up to date, 36 telocentric lines for 1AS, 1AL, 1BS, 1BL, 1DS, 1DL, 2AS, 2BS, 2BL, 2DS, 2DL, 3AS, 3AL, 3BS, 3BL, 3DS, 3DL, 4AS, 4AL, 4BS, 4DS, 4DL, 5AL, 5BL, 5DL, 6AS, 6AL, 6BS, 6BL, 6DS, 6DL, 7AS, 7AL, 7BS, 7BL and 7DS have been maintained as ditelosomics, and five lines for 2AL, 4BL, 5AS, 5BS and 5DS have been maintained as ditelomonotelosomics (Furuta and Nishikawa unpub). These lines are invaluable tools for allocating genes and markers to specific chromosomes and chromosome arms. However, one line CS ditelosomics 7DL, has not yet been developed (Friebe et al. 1996), although a ditelosomic line 7DL has been established in Canthatch(Can) wheat.

In order to produce CS ditelosomic 7DL, we performed successive backcrosses of Can ditelosomic 7DL to CS. From selfing the BC_8 plants, 20 ditelosomic lines were developed. We examined the obtained lines to know whether they possessed a pair of telocentric chromosome 7DL, by observing the somatic chromosome constitution and the meiotic chromosome pairing in the progeny from a cross with ditelosomic 7DS. We also conducted electrophoresis for α-amylase isozymes, some of whose gene loci are on the chromosome arm 7DL.

Materials and methods

Plant materials: Can 7DL was derived from the misdivision of chromosome 7D in Can monosomic 7D that had been produced by a cross between Can_8 and Stewart durum wheat. We performed eight-time successive backcrosses of Can ditelosomic 7DL to CS. Finally through crossing BC8 plants with nulli7D-tetra7B and selfing the resulting plants, 20 offspring with 40 normal chromosomes and a pair of 7DL were isolated. For cytologically identifying 7DL, BC plants were crossed to CS ditelo 7DS and the chromosome constitution (41+2t, 20''+1t1''') was confirmed in every BC generation.
Cytological analysis: Root tips were pretreated in ice water for 24 hours and fixed with fresh Farmer's fluid. Anthers at metaphase-I were fixed in Farmer's fluid.

Table 1. Meiotic chromosome pairing and α-amylase isozyme pattern of developed lines and parental lines in wheat

Line	Chromosome constitution	Chromosome pairing	No.PMCs examined	α-amylase isozyme pattern
CS	2n = 42	21"	41	7DL
4-10-1	2n = 40 + 2t	20" + t"	220	7DL
4-10-2	2n = 40 + 2t	20" + t"	95	7DL
4-10-5	2n = 40 + 2t	20" + t"	228	7DL
4-10-8	2n = 40 + 2t	_	_	7DL
4-14-4	2n = 40 + 2t	20" + t"	133	7DL
4-14-5	2n = 40 + 2t	20" + t"	209	7DL
4-14-6	2n = 40 + 2t	20" + t"	206	7DL
4-16-2	2n = 40 + 2t	20" + t"	159	7DS
4-16-3	2n = 40 + 2t	20" + t"	12	7DS
4-16-7	2n = 40 + 2t	20" + t"	114	7DS
22-3-5	2n = 40 + 2t	20" + t"	290	7DS
22-10-4	2n = 40 + 2t	20" + t"	198	7DL
22-10-5	2n = 40 + 2t	20" + t"	238	7DL
22-10-7	2n = 40 + 2t	_	_	7DL
22-10-9	2n = 40 + 2t	20" + t"	37	7DL
22-11-2	2n = 40 + 2t	20" + t"	287	7DL
22-11-4	2n = 40 + 2t	20" + t"	29	7DL
22-11-5	2n = 40 + 2t	_	_	7DL
22-11-6	2n = 40 + 2t	20" + t"	75	7DL
22-11-8	2n = 40 + 2t	20" + t"	32	7DL
Candt7DL	2n = 40 + 2t	20" + t"	38	7DL
Candt7DS	2n = 40 + 2t	20" + t"	57	7DS
Can	2n = 42	21"	27	7DL

Chromosome preparations were made by the acceto-carmine squash method.

α-amylase isozymes: The genes for several α-amylase isozymes are located on the respective long arms of six chromosomes belonging to homoeologous groups 6 and 7 of CS (Nishikawa and Nobuhara 1971). We used this isozyme as a genetic marker for the identification of ditelosomic 7DL. The same zymogram technique described by Nishikawa et al (1979) was used for α-amylase of germinating seeds in this study.

Test-crossing with ditelosomic 7DS: Plants with α-amylase isozyme pattern specific to ditelosomic 7DL were crossed to ditelosomic 7DS. If the plants are authentic ditelosomic 7DL, the chromosome pairing in the F_1 is 20"+2t'. If they are ditelosomic 7DS, the F_1 shows 20"+t". If they are neither ditelosomic 7DL nor 7DS, the F_1 shows 19"+2(1t").

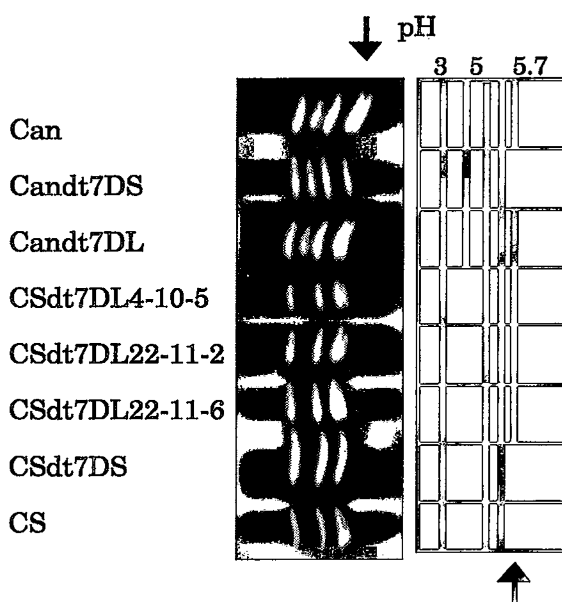

Fig.1. α-amylase zymogram in ditelosomic 7DL, ditelosomic 7DS and euploids. Arrow indicates 7DL specific band.

Results and discussion

In all 20 developed lines, somatic chromosome

Table 2. Meiotic chromosome pairing in F_1 test-crossed with ditelosomic 7DS wheat line

Line	Chromosome pairing	No.PMCs examined
F_1 4-10-5xCSdt7DS	20" + 2t'	195
	20" + t'	2
F_1 22-11-2xCSdt7DS	20" + 2t'	198
F_1 22-11-6xCSdt7DS	20" + 2t'	378
	20" + t'	1

constitution was 2n=40+2t in root tip cells and chromosome pairing was 20"+t" in pollen mother cells (Table 1). Considering the production process, the developed lines were either ditelosomic 7DL or 7DS. The difference in length between the long and short arms of chromosome 7D is small (Furuta et al. 1988, Endo and Gill 1996).

One of the genes for α-amylase isozymes is located on 7DL (Nishikawa and Nobuhara 1971). The zymogram of ditelosomic 7DL should be identical to that of euploid CS but that of ditelosomic 7DS lacks the band of 7DL (Fig. 1). Sixteen out of the 20 lines were ditelosomic for 7DL and four lines were ditelosomic for 7DS (Table 1). Of these 16 lines, three lines were randomly selected and crossed to ditelosomic 7DS. The F_1's all showed meiotic chromosome configuration 20"+2t' (Table 2, Fig. 2).

Height and seed fertility of these CS ditelosomic 7DL plants were intermediate between the euploid CS and ditelosomic 7DS (Table 3). The ditelosomic 7DL plants were cytologically stable, and their spike morphology was normal.

Fig.2. Chromosome pairing at the first metaphase cell of double-monotelosomic 7DL-7DS F1. Arrow indiccates telosomes.

CS is the most important variety among wheat lines to chromosome engineering. Since Sears (1954) established the monosomic series of CS, an array of aneuploid lines has been produced in this variety. Sears and Sears (1978) tried to produce ditelosomic 7DL using 2000 seeds but failed to recover the ditelosomic 7DL. Ditelosomic 7DL stock of CS is currently being extracted at John Innes Centre from the double ditelosomic 7D stock (Devos et al. 1999). The principal use of ditelosomic lines is to provide cytologically recognizable chromosomes in identifying aneuploids, locating and mapping genes, and determining degrees of meiotic pairing and somatic association. The CS ditelosomic 7DL stock developed by us in the present study will be useful for analyzing genes on chromosome 7D.

Table 3. Morphological data of ditelosomic 7DL, ditelosomic 7DS and disomic wheat lines

Line	No. plants analyzed	Height (cm)	Seed fertility (%)	Ear density
CS	13	124 ± 9.9	97.3 ± 2.3	32.0 ± 1.8
CSdt7DS	8	93 ± 1.8	82.6 ± 4.1	29.7 ± 2.1
dt7DS 4-16-3	7	89 ± 18.2	84.3 ± 5.6	29.3 ± 2.0
dt7DS 4-16-7	5	86 ± 16.8	84.5 ± 2.1	30.0 ± 2.5
dt7DS 22-3-5	7	94 ± 3.5	81.5 ± 3.1	30.2 ± 2.1
dt7DL 4-10-5	8	105 ± 3.2	92.8 ± 6.0	31.0 ± 2.8
dt7DL 22-11-2	8	103 ± 11.8	92.7 ± 3.6	31.6 ± 2.4
dt7DL 22-11-6	8	104 ± 4.1	93.8 ± 4.5	33.2 ± 2.2
Candt7DL	8	127 ± 7.9	91.4 ± 4.1	23.0 ± 1.1
Candt7DS	8	123 ± 6.4	61.3 ± 4.5	19.0 ± 1.3
Can	8	142 ± 2.8	89.7 ± 3.8	21.1 ± 1.1

References

Devos KK, Sorrells ME, Miller JA, Reader TE, Lukaszewski SM, Dubcovsky AJ, Sharp PJ, Faris J and Gale MD (1999) Chromosome aberrations in wheat nullisomic-tetrasomic and ditelosomic lines. Cereal Res Comm 27: 231-239.

Endo TR and Gill BS (1996) The deletion stocks of common wheat. Heredity 87: 295-307.

Friebe BR, Jellen EN and Gill BS (1996) Verification of the identity of the Chinese Spring ditelosomic stocks Dt7DS and Dt7DL. Wheat Inf Serv 83: 31-32.

Furuta Y, Nishikawa K and Shimokawa K (1988) Relative DNA content of the individual telocentric chromosomes in Chinese Spring wheat. Proc 5th Int Wheat Genet Symp: 281-286.

Nishikawa K and Nobuhara M (1971) Genetic studies of α-amylase isozymes in wheat.I Location of genes and variation in tetra- and hexaploid wheat. Japan J Genet 46: 345-353.

Nishikawa K, Furuta Y, Kudo S and Ujihara K (1979) Differentiation of tetraploid wheat in relation to DNA content of nucleus and α-amylase isozymes. Rep Plant Germ-plasm Inst Kyoto Univ 4: 30-38.

Sears ER (1954) The aneuploids of common wheat. Mo Agr Exp Sta Res Bull 572: 1-58.

Sears ER (1966) Nullisomic-tetrasomic combination in hexaploid wheat. Heredity 20: 29-45.

Sears ER and Sears MS (1978) The telocentric chromosome of common wheat. Proc 5th Int Wheat Genet Symp: 389-407.

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Research article

Influence of storage on seedling characters of var. Pb. C 591 monosomics

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Summary

Aneuploid lines of Var. Pb. C 591 are being maintained at the Division of Genetics, IARI. Seeds harvested during the year 1991, 1993 and 2000 were evaluated for their viability, root number, root length, coleoptile length and shoot length. Detailed study of these traits revealed that the germination percentage ranged from 86% to 100% in fresh seeds (2000), 82% to 100% in 1993 seeds and 66% to 100% in 1991 seeds. Means of root length were 12.96 cm in 2000 seeds, 11.50 cm in 1993 seeds and 10.55 cm in 1991 seeds. Means of root number were 5.09, 4.55 and 4.45 in the years 2000, 1993 and 1991 and the means of shoot length for the years 2000, 1993 and 1991 were 18.41 cm, 14.24 cm and 10.88 cm respectively. These observations clearly revealed that the seeds from 1991 showed high significant reduction in all the characters as compared to the fresh seeds (2000).

Introduction

Monosomics of the aneuploid lines of variety Pb. C 591 were reported by Swaminathan et al. (1968). These lines have been used for locating genes on specific chromosomes and are being maintained at the Division of Genetics, IARI, New Delhi. It is known that frequent planting and identification of monosomic lines enhances the chances for the occurrence of univalent shift which means that we should not expose the monosomic lines for frequent meiotic analysis. It is advantageous to make use of the stored seeds as long as seeds do not loose their viability. With this objective in mind a study was undertaken to evaluate the monosomic seeds harvested from cytologically identified plants from the years 1991, 1993 and 2000, respectively.

Materials and methods

To study the effect of storage on seed germination and other seedling characters seeds of all the monosomic lines of variety Pb.C591 of three different years 1991, 1993 and 2000 were taken. Seeds were wrapped in aluminium foil and covered with polythene and kept in refrigerator to avoid the effect of atmospheric humidity. The outside humidity was maintained at 4–5%. Seeds were taken from the cytologically identified monosomic plants which were stored in the refrigerator at 8±1°C. Twenty five seeds from each monosomic were kept for germination in two different petridishes and enough moisture was provided. Data were recorded on root number, root length, shoot length and coleoptile length on the 10th day of seed imbibition. Seed germination percentage and means of root length, root number, coleoptile length and seedling height were calculated. Statistical analysis of these traits was carried out (Gomez and Gomez 1984).

Results and discussion

Observations recorded on seed germination are presented in Table 1 and for other seedling traits in Tables 2 and 3 and ANOVA was performed (Table 4). The observations revealed the facts listed below.
Seed germination: Calculated percentages of seed germination (Table. 1) revealed that the fresh seeds (2000) varied from 86% to 100%. Higher reduction in seed germination was seen in the seeds stored for ten

years (1991), the range being 66% to 100%. While the range of seed germination in eight-year-old seeds (1993) was 82% to 100%. In the ten-year-old seeds the low percentage of 66% was observed in monosomic line (2B) and the highest 100% was observed in monosomic 4D. The seed germination percentage in fresh seeds (2000) was above 90% in all the lines except monosomic 6D where it was only 86%. These low percentage of seed germination did not show any relationship with monosomic lines over the years. It is, therefore, evident that the trait seed germination was greatly influenced by the environmental conditions.

Root length: The mean values of fresh seeds (2000) of all the monosomic lines were 12.96 cm and variations being 9.55 cm (3A) to 14.74 cm (2A). The F values for difference of root length amongst different years were found to be significant at 1% level (Table 4).

Root number: The mean values of 1991 seeds ranged from 3.46 (5A) to 5.06 (3D). The range of root number in 1993 seeds was 4.14 (5D) to 5.04 (2A). The mean values of 2000 seeds ranged from 4.33 (6B) to 6.06 (6D). The difference in root number of all the monosomics over the years were significant at 1% level (Table 4).

Coleoptile length: Mean values of coleoptile length

Table 1. Seed germination of cv. Pb.C591 monosomics.

Monosomics	1991	1993	2000
1A	45 (90)	49 (98)	49 (98)
1B	43 (86)	50 (100)	49 (98)
1D	40 (80)	44 (88)	46 (92)
2A	38 (76)	50 (100)	50 (100)
2B	33 (66)	48 (96)	47 (94)
2D	37 (74)	49 (98)	49 (98)
3A	47 (94)	48 (96)	50 (100)
3B	48 (96)	48 (96)	46 (92)
3D	48 (96)	48 (96)	49 (98)
4A	47 (94)	49 (98)	49 (98)
4B	44 (88)	50 (100)	48 (96)
4D	50 (100)	48 (96)	47 (94)
5A	47 (94)	50 (100)	49 (98)
5B†	—	—	—
5D	45 (90)	50 (100)	47 (94)
6A	35 (70)	42 (84)	48 (96)
6B	40 (80)	50 (100)	50 (100)
6D	43 (86)	49 (98)	43 (86)
7A	41 (82)	48 (96)	47 (94)
7B	41 (82)	43 (86)	45 (90)
7D	40 (80)	41 (82)	48 (96)

Figure in the parenthesis indicate percentage.
† Monosomic 5B was not there in all the years.

Table 2. Root length and root number of cv. Pb.C591 monosomics.

Monosomics	Root length (cm)			Root number		
	1991	1993	2000	1991	1993	2000
1A	12.61	9.76	13.75	4.93	4.32	5.26
1B	12.11	12.59	14.38	4.90	4.35	5.13
1D	17.16	11.76	14.62	4.75	4.58	4.88
2A	12.20	11.71	14.74	4.64	5.04	4.86
2B	10.34	12.23	12.46	4.56	4.59	4.75
2D	12.06	13.00	14.55	4.83	4.79	5.54
3A	7.27	11.68	9.55	1.81	4.26	4.66
3B	9.92	10.04	12.32	4.22	4.30	4.43
3D	9.64	9.02	13.01	5.06	4.71	4.49
4A	10.36	12.85	14.13	4.77	4.73	5.20
4B	11.12	12.81	13.53	4.28	4.88	4.72
4D	10.47	12.81	13.05	4.83	4.57	5.26
5A	9.33	8.68	11.79	3.46	4.22	5.24
5B	—	—	—	—	—	—
5D	9.64	11.31	12.30	4.18	4.14	5.47
6A	9.75	12.64	12.68	4.72	4.60	5.40
6B	10.33	9.45	13.73	4.24	4.67	4.33
6D	10.74	15.91	13.31	4.71	4.58	6.06
7A	10.94	12.71	13.04	3.85	4.38	5.43
7B	11.42	11.17	12.24	3.98	4.60	5.63
7D	8.67	8.04	10.16	4.00	4.85	5.20
Mean	10.55	11.50	12.96	4.45	4.55	5.09

Table 3. Colleoptile length and shoot length of cv. Pb.C591 monosomics.

Monosomics	Coleoptile length (cm)			Shoot length (cm)		
	1991	1993	2000	1991	1993	2000
1A	3.67	3.92	5.58	11.83	13.47	18.20
1B	4.07	3.92	5.36	12.16	14.63	19.95
1D	3.79	4.13	5.42	12.74	13.70	17.76
2A	3.64	3.49	4.03	11.56	13.72	16.26
2B	3.79	4.14	4.47	12.00	14.77	20.87
2D	4.07	4.14	4.68	12.04	16.33	19.01
3A	3.59	3.59	3.71	8.68	11.78	15.98
3B	3.40	3.52	3.84	10.53	13.99	16.06
3D	3.69	4.08	3.99	9.88	14.23	16.27
4A	3.97	4.00	3.95	10.81	15.88	21.98
4B	3.85	4.15	4.18	11.12	14.95	18.05
4D	3.98	4.02	4.14	10.97	17.01	20.57
5A	3.93	3.94	4.25	9.98	14.07	19.61
5B	–	–	–	–	–	–
5D	3.74	3.85	4.64	10.75	13.33	17.70
6A	4.22	4.12	4.68	12.15	16.20	19.94
6B	3.88	3.85	4.99	10.41	14.74	20.69
6D	4.07	4.14	3.96	9.33	11.40	18.00
7A	4.04	4.24	4.26	9.73	13.41	17.80
7B	4.44	3.82	4.64	11.50	13.86	16.71
7D	3.75	4.02	4.17	9.61	13.52	17.12
Mean	3.87	3.95	4.44	10.88	14.24	18.41

indicated that in fresh seeds (2000) the range was 3.71 cm (3A) to 5.58 cm (1A), in 1993 seeds the range was 3.49 cm (2A) to 4.24 (7A) while 1991 seed showed 3.40 cm (3B) to 4.44 cm (7B). The mean values showed variation over the years and the differences were found to be significant at 1% level. (Table 4).

Shoot length: The mean values of shoot length ranged from 8.68 cm (3A) to 12.74 cm (1D) in 1991 seeds, 11.40 cm (6D) to 17.01cm (4D) in 1993 seeds and 15.98 (3A) and 21.98 cm (4A) in 2000 seeds. Statistical analysis showed significant difference in the mean shoot length over the years (Table 4).

The process of ageing in stored seeds largely depends on the chemical composition of the seeds (Kataki et al. 1997; Mayer and Poljakoff-Mayber 1982), storage temperature, humidity and gaseous exchange (Roos and Manalo 1971). Ageing causes stress on seeds which leads to differential germination and loss in seedling vigor (Purkar et al. 1980). Genetic variation for seed ageing among the wheat genotypes has been demonstrated (Madan et al. 1989). Evaluation of wheat genotypes for seeds ageing under storage conditions would provide guidelines to ensure appropriate storage of germplasm of specific genotypes and commercial seed lot. Experiment conducted in the present study revealed significant differences in seed germination, root length, root number, coleoptile length, and seedling height over the years of ageing (Table 4). These observations corroborates with the earlier reports of Odimah (1986) and Madan et al. (1989). However, percentages of viability over the years are in the normal range. Slight reduction in viability percentage can be compensated by storing a larger number of seeds where available. Since fully viable and normal plants at maturity were obtained, it is inferred that seeds stored up to 11-12 years can still be used for cytological analysis. It will help the cytogeneticist to make use of the stored seeds for cytogenetical investigations for prolonged period without having to plant and identify monosomics every year.

References

Gomez KA and Gomez AA (1984) Statistical procedures for agricultural research. John Wiley & Sons, New York. pp.635.

Kataki PK, Horbowicz M, Taylor AG, Obendorf RL, Ellis

Table 4. Analysis of variance for root length, root number, coleoptile length and shoot length

Source	df	Root length			Root number			Coleoptile length			Shoot length			F
		Sum of squares	Mean squares	F cal value	Sum of squares	Mean squares	F cal value	Sum of squares	Mean squares	F cal value	Sum of squares	Mean squares	F cal value	tab value (1%)
Age (A)	2	119.546	59.773	116.6402	11.081	5.540	64.8269	7.219	3.609	68.3303	1126.099	563.050	572.8515	4.98
Line (B)	19	192.968	10.156	19.8186	6.499	0.342	4.0021	6.523	0.343	6.4997	117.610	6.190	6.2978	
A x B	38	72.626	1.911	3.7295	11.556	0.304	3.5583	8.012	0.211	3.9917	79.875	2.102	2.1386	
Error	60	30.747	0.512		5.128	0.085		3.169	0.053		58.973	0.983		
Total	119	415.887			34.263			24.923			1382.557			

RH, Black M, Murdoch J and Hong TD (1997) Changes in sucrose, cyclitols and their galactosyl derivatives with seed aging. Proc 5th Int Workshop on Seed (Basic and applied aspects of seed biology). In Ellis et al. (ed) Current Plant Sci and Biotechnol in Agric 3: 515-522.

Madan S, Talway G, Behl RK and Verma U (1989) Effect of accelerated ageing on germination. Seedling vigour and beta-amylase activity in wheat. Res & Dev Reporter 6: 48-54.

Mayer AM and Polijakoff-Mayber A(1982) The germination of seed. 3rd Ed, Pergamon Press Ltd: 10-37.

Odiemah M (1986) Germinability and vigour of wheat seed comportment at different periods of storage. 21st ISTA Congress, Preprint No. 6.

Purkar JK, Mehra RB and Banerjee SK (1980) Seed ageing induced variability in quantitative characters of pea and wheat. 19th ISTA Cong, Preprint No. 60.

Roos EE and Manalo JR (1971) Testing vigour of beans following unfavourable storage conditions. Hort Sci 6: 347-248.

Swaminathan MS, Chopra VL, Joshi BC and Singh D (1968) Development of a monosomic series in an Indian wheat and isolation of nullisomics lines. Wheat Inf Serv 27: 19-20.

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Research article

Genetic diversity in Chinese endemic wheats based on STS and SSR markers

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Summary

The genetic diversity and genetic relationships among 40 accessions of Chinese endemic wheats, including 9 Xingjiang rice wheat (XR), 9 Tibetan weedrace (TW), 14 Yunnan hulled wheat (YH) and 8 Sichuan White Wheat (SWW), were evaluated by STS and SSR markers. In STS analysis, 11 out of 14 markers (78.6%) and 16 out of 28 marker/enzyme combinations (57.1%) revealed polymorphisms. A total of 121 bands were observed in 28 marker/enzyme combinations, with 4.3 bands per marker/enzyme combination. Thirty-nine out of 121 bands (32.2%) were polymorphic, among which 1 to 8 polymorphic bands were generated by each informative marker/enzyme combination. Among 40 Chinese endemic wheat accessions, the STS-based genetic similarity (STS-GS) ranged from 0.645 to 0.989, with the mean of 0.822. In SSR analysis, 21 out of 24 SSR makers (87.5%) showed polymorphism. A total of 83 alleles were detected. The number of alleles ranged from 1 to 7, with an average of 3.5 alleles per SSR locus. The SSR-derived genetic similarities (SSR-GS) ranged from 0.540 to 0.941, with the mean of 0.717. The cluster analysis indicated that all 40 Chinese endemic wheat accessions could be distinguished by both STS and SSR markers. The XR wheat group was genetically distinct from other three Chinese endemic wheat groups, while SWW wheat group was genetically related to the YH group. The TW wheat group is more diverse than the SWW and YH groups, with some accessions more related to the YH group.

Key words: genetic diversity, genetic relationship, wheat landrace, SSR markers, STS markers

Introduction

Advances in DNA technology have greatly increased the number and type of molecular markers available for plant genetic diversity studies. The advent of the polymerase chain reaction (PCR) favored the development of different molecular techniques such as random amplification of polymorphic DNA (RAPD), simple sequence repeats (SSR or microsatellite), sequence tagged sites (STS) and inter-simple sequence repeat polymorphic DNA (ISSR) etc. (Saiki et al. 1988; Welsh and McCleland 1990; Williams et al. 1990; Akkaya et al. 1992; Tragoonrung et al. 1992; Zietkiewicz et al. 1994; Nagaoka and Ogihara 1997). All these molecular markers have been used in wheat for detecting genetic diversity, genotype identification, genetic mapping or gene tagging (Devos and Gale 1992; He et al. 1992; Chen et al. 1994; Talbert et al. 1994; Plaschke et al. 1995; Röder et al. 1995, 1998; Roy et al. 1999; Prasad et al. 2000). In comparison, SSRs are more abundant, ubiquitous in presence, hypervariable in nature and have high polymorphism information content (Röder et al. 1995; Gupta et al. 1996). It has been shown that the use of limited number of SSR markers is adequate to discriminate even the most closely related wheat genotypes (Plaschke et al. 1995).

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Wheat has been cultivated in China for several thousands of years, and China is rich in wheat genetic resources (Yen et al. 1988). Chinese endemic wheats include the Sichuan White Wheat complex (*T. aestivum* L.), the Tibetan weedrace (*T. aestivum* ssp. *tibetanum* Shao), the Xingjiang rice wheat (*T. petropavlovskyi* Udacz. et Migusch.) and the Yunnan hulled wheat (*T. aestivum* ssp. *yunnanese* King) (Shao et al. 1980; Dong et al. 1981; Yen et al. 1988). Several morphological and cytogenetic studies indicated that these Chinese endemic wheats have a primitive chromosomal constitution (Riley et al. 1967; Shao et al. 1980; Chen et al. 1985, 1988; Yen et al. 1988; Yang et al. 1992). Chinese endemic wheats exhibited less RFLP diversity and low variability for both HMW-glutenins and gliadins (Dvorák et al. 1998; Ward et al. 1998; Wei et al. 2000, 2002). The objective of this paper is to evaluate the level of SSR and STS-based genetic diversity among Chinese endemic wheats.

Materials and methods

Wheat genetic resources: A total of 40 accessions, which include 9 Tibetan weedrace (TW), 9 Xingjiang rice wheat (XR), 14 Yunnan hulled wheat (YH) and 8 Sichuan White Wheat (SWW) were employed in this study (Table 1).

DNA extraction: Genomic DNA was extracted from a bulk sampling of a minimum of ten individual plants for each accession following the procedure described by Sharp et al. (1988).

STS analysis: Fourteen STS markers, located on all 7 homoeologous chromosome groups of wheat, were used in this study (Table 2). All these STS-PCR markers were from RFLP clones of the wheat or barely mapping projects (Chen et al. 1994; Talbert et al. 1994). STS-PCR was conducted following the procedure described by Talbert et al. (1994). Amplified products were subsequently digested with approximately 1 U of *Hinf*I and *Hha*I (MBI) per reaction mixture for 1 h at 37°C, and then analyzed by electrophoresis in 2.0% agarose gels and stained with ethidium bromide.

SSR analysis: Twenty-four SSR markers, which located on 21 chromosomes (Devos et al. 1995; Röder et al. 1998), were used in this study (Table 2). PCR amplifications were carried out under the conditions described by Röder et al. (1998). The products were separated on 3.0% agarose gel and visualized by ethidium bromide staining.

Data scoring and analysis: Images for STS and SSR analysis were photographed, captured using ImageMaster VDS (Amersham Pharmacia Biotech). The size of each DNA band was automatically estimated using ImageMaster 1D Elite Software (Amersham Pharmacia Biotech). For each accession X marker combination, the presence (1) or absence (0) of an amplified band or allele was treated as an independent character without consideration of the quantitative aspects of the results, i.e. band intensity. The data matrix was then used to calculate genetic similarity index (GS) (Nei and Li 1979):

$$GS = 2N_{ij}/(N_i + N_j)$$

where N_{ij} is the number of bands (alleles) in common between genotypes i and j, and N_i and N_j are the total

Table 1. Chinese endemic wheat accessions used in the present study

No.	Accession	Group	No.	Accession	Group	No.	Accession	Group
1	AS329	TW	15	AS336	YH	29	AS363	XR
2	AS330	TW	16	AS337	YH	30	AS364	XR
3	AS907	TW	17	AS338	YH	31	Daomai-1	XR
4	AS908	TW	18	AS339	YH	32	Daomai-2	XR
5	AS1025	TW	19	AS340	YH	33	Chinese Spring (CS)	SWW
6	AS1026	TW	20	AS341	YH	34	Chendu-guangtou (CDGT)	SWW
7	AS1027	TW	21	AS342	YH	35	J-11	SWW
8	AS1028	TW	22	AS343	YH	36	AS1563	SWW
9	9053	TW	23	AS344	YH	37	AS1580	SWW
10	AS331	YH	24	AS356	XR	38	AS1582	SWW
11	AS332	YH	25	AS358	XR	39	AS1673	SWW
12	AS333	YH	26	AS359	XR	40	AS1697	SWW
13	AS334	YH	27	AS360	XR			
14	AS335	YH	28	AS362	XR			

number of bands (alleles) observed for genotypes i and j, respectively. Based on the (1–GS) matrix, a dendrogram showing the genetic relationships between genotypes was constructed using the unweighted pair-group method with arithmetic average (UPGMA) (Sneath and Sokal 1973) through the computer software NTSYS-pc Version 1.80 (Rohlf 1993).

Results

STS variations: The 14 STS markers (Table 2) were used to reveal genetic difference among 40 Chinese endemic wheat accessions. Upon digestion with *Hinf*I and *Hha*I, 11 out of 14 markers (78.6%) and 16 out of 28 marker/enzyme combinations (57.1%) revealed polymorphisms. The G36/*Hha*I combination generated more bands than any other marker/enzyme

Table 2. Chromosome location, numbers of enzyme-digested bands for the STS markers used

No.	Marker†	Location	Enzyme	Bands	Poly-morphic	No.	Marker	Location	Enzyme	Bands	Poly-morphic
1	E8	1	*Hha*I	6	+	8	F8	4	*Hha*I	4	+
			*Hinf*I	3	+				*Hinf*I	4	–
2	Hor2	1	*Hha*I	5	+	9	D16	5	*Hha*I	6	+
			*Hinf*I	3	–				*Hinf*I	8	+
3	D18	2	*Hha*I	1	–	10	I26	5	*Hha*I	7	+
			*Hinf*I	3	+				*Hinf*I	5	–
4	E16	2	*Hha*I	3	–	11	G8	6	*Hha*I	7	+
			*Hinf*I	1	–				*Hinf*I	4	+
5	G36	3	*Hha*I	9	+	12	F19	6	*Hha*I	3	–
			*Hinf*I	5	–				*Hinf*I	4	+
6	WG110.1	3	*Hha*I	2	–	13	A1	7	*Hha*I	6	+
			*Hinf*I	3	–				*Hinf*I	4	+
7	B5	4	*Hha*I	2	–	14	D2	7	*Hha*I	4	+
			*Hinf*I	1	–				*Hinf*I	8	+

† Primer sequences of STS markers are in Chen et al. (1994) and Talbert et al. (1994).

Table 3. Chromosomal location, annealing temperature and numbers of detected alleles for the microsatellite markers used

No.	Marker†	Location	An. temp.	Alleles	No.	Marker	Location	An. temp.	Alleles
1	γ-gliadin	1BS	65°C	7	13	GWM111	7DS	55°C	6
2	LMW-Glu	1BS	65°C	6	14	GWM120	2BL	60°C	4
3	GWM5	3AS	55°C	4	15	GWM157	2DL	60°C	2
4	GWM18	4BS	55°C	3	16	GWM160	4AS	60°C	4
5	GWM24	1BL	60°C	2	17	GWM164	1AS	55°C	3
6	GWM43	7BL	60°C	1	18	GWM174	5DL	55°C	4
7	GWM46	7BS	60°C	3	19	GWM186	5AL	60°C	4
8	GWM52	3DL	60°C	4	20	GWM194	4DL	55°C	4
9	GWM60	7AS	60°C	4	21	GWM325	6DS	60°C	2
10	GWM82	6AL	60°C	1	22	GWM328	2AL	55°C	1
11	GWM106	1DS	60°C	4	23	GWM408	5BL	55°C	4
12	GWM108	3BL	60°C	3	24	GWM518	6BS	55°C	3

† Primer sequences of microsatellite markers are in Devos et al. (1995) and Röder et al (1998).

Table 4. Genentic similarity values among 4 Chinese endemic wheat groups based on STS and SSR markers

	Group	SWW	YH	TW	XR	All
STS	Mean	0.921	0.907	0.849	0.842	0.822
	Variation	0.864~0.979	0.822~0.989	0.760~0.958	0.739~0.906	0.645~0.989
SSR	Mean	0.815	0.841	0.747	0.750	0.717
	Variation	0.725~0.892	0.755~0.941	0.637~0.902	0.647~0.901	0.540~0.941

combination, while the B5/*Hinf*I, D18/*Hha*I and E16/*Hinf*I combinations could only generate one band. Among 40 Chinese endemic wheats, a total of 121 bands were observed in 28 marker/enzyme combinations, with 4.3 bands per marker/enzyme combination. Thirty-nine out of 121 bands (32.2%) were polymorphic, among which 1 to 8 polymorphic bands were generated by each informative marker/enzyme combination.

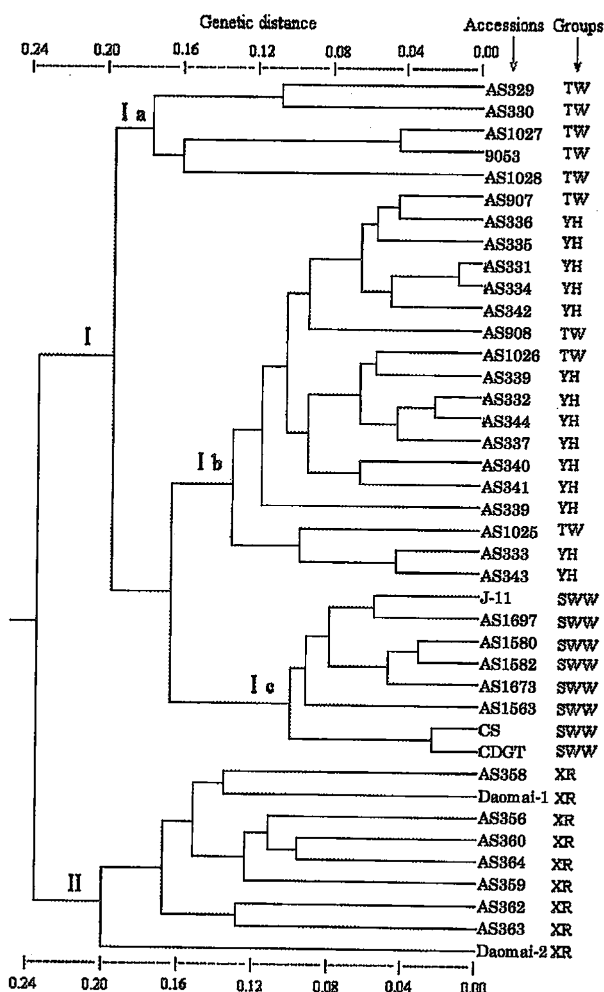

Fig. 1. Dendrogram resulting from cluster analysis of the STS-based genetic distance (1–GS) matrix among 40 Chinese endemic wheat accessions.

All the 121 bands, generated from 28 STS marker/enzyme combinations, were used to calculated genetic similarity index (GS) among 40 landraces (Table 4). Among 40 Chinese endemic wheat accessions, the GS value ranged from 0.645 to 0.989, with the mean of 0.822. The mean GS values within SWW, YH, TW and XR groups were 0.921, 0.907, 0.849 and 0.842, respectively. It indicated that the mean GS values of SWW and YH wheat groups were relatively higher than those of the TW and XR groups.

The genetic relationships within and between groups were estimated by a UPGMA cluster analysis of (1–GS) matrix (Fig. 1). The results showed that all 40 landraces could be distinguished by STS-PCR markers. Two distinct groups were evident, with the second group (II) including all 9 accessions from the XR wheat group. Three subgroups (Ia, Ib and Ic) were evident for the first group (I), with the subgroup Ib and Ic more closely related. The subgroup Ic was a cluster for the accessions from the SWW group. The subgroup Ib included all 14 YH wheat accessions and 4 TW wheat accessions. It indicated that the XR wheat group was genetically distinct from other three Chinese endemic wheat groups, while the SWW group was genetically related to the YH group. The TW wheat group is more diverse than the SWW and YH groups, with some accessions more related to the YH group.

SSR polymorphisms: Twenty-four SSR markers, located on 21 wheat chromosomes, were used for PCR amplification of the genomic DNA of 40 Chinese endemic wheat accessions, among which PCR products of 21 SSR makers (87.5%) showed polymorphism (Fig.2). A total of 83 alleles were detected among the 40 accessions. The number of alleles ranged from 1 to 7, with an average of 3.5 alleles per SSR locus. On 3 SSR loci (i.e. γ-gliadin, LMW-Glu and GWM111) more than 6 alleles could be detected.

The SSR-derived data were used to calculate genetic similarities (GS) among 40 Chinese endemic wheat accessions. In these Chinese landraces, the GS values ranged from 0.540 to 0.941, with the mean

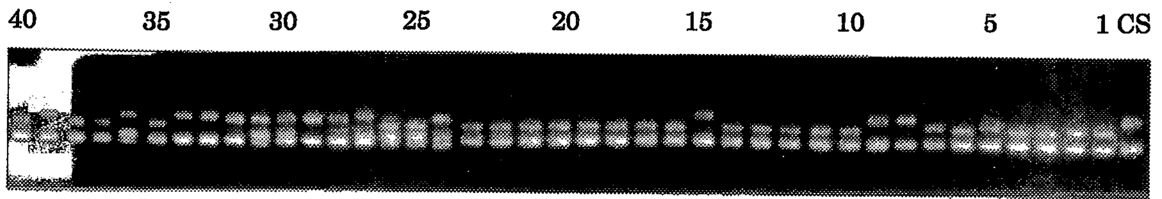

Fig. 2. PCR fragments amplified by GWM111 of Chinese endemic wheat accessions. Number 1 to 40 represent the accession numbers corresponding in Table 1.

of 0.717 (Table 4). The mean GS values within the SWW, YH, TW and XR wheat groups were 0.815, 0.841, 0.747 and 0.750, respectively. It indicated that the mean GS values of the SWW and YH wheat groups were relatively higher than those of the TW and XR groups.

The genetic relationships (Fig.3) among 40 Chinese endemic wheat accessions were estimated by a UPGMA cluster analysis of the genetic diversity (1–GS) matrix. The results showed that all 40 accessions could be discriminated by 24 SSR markers. All 9 XR accessions were less related with other accessions, and divergent from the other accessions. Three subgroups were evident in the remaining 31 accessions. Among them, the subgroup Ib more closely related to Ic. All 8 accessions belonging to the SWW wheat group were included in the subgroup Ic. The subgroup Ib included all 14 YH wheat accessions and 3 TW wheat accessions (i.e. AS907, AS908 and AS1026). These things indicated that the XR wheat group was genetically distinct from other three Chinese endemic wheat groups, while the SWW group was genetically related to the YH group. The TW wheat group is more diverse than the SWW and YH groups, with some accessions more related to the YH group.

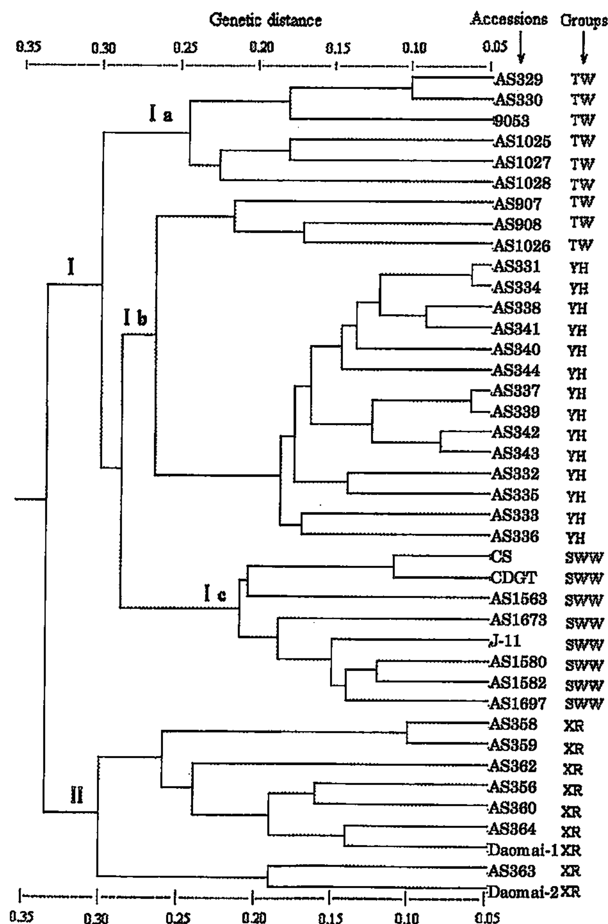

Fig. 3. Dendrogram resulting from cluster analysis of the SSR-based genetic distance (1–GS) matrix among 40 Chinese endemic wheat accessions.

Discussion

In wheat, SSR markers show a much higher level of polymorphism and informativeness than any other molecular marker (Röder et al. 1995; Plaschke et al. 1995; Prasad et al. 2000). The similar results were observed in this study. Among 40 Chinese endemic wheat accessions, the genetic similarity (GS) based on SSR markers ranged from 0.540 to 0.941, with the mean of 0.717, while the GS based on STS markers ranged from 0.645 to 0.989, with the mean of 0.822. In earlier study, the mean GS based on RFLP markers among Chinese endemic wheat accessions was 0.969 (Ward et al. 1998). It indicated that SSR markers had the relative superiority in detecting DNA polymorphism than STS and RFLP markers.

The average number of alleles per SSR locus and genetic similarity (GS) in present study was compared with those published earlier in wheat. The average number of alleles per locus in this study was relatively lower than those earlier reported, while the mean genetic similarity in this study was relatively higher than those earlier reported. Only 3.5 alleles per locus were detected among Chinese endemic wheats, while in three earlier studies on wheat the average number of alleles per locus were 4.6, 6.2 and 7.4 alleles per

locus reported by Röder et al. (1995), Plaschke et al. (1995) and Prasad et al. (2000), respectively. Among 40 Chinese endemic wheat accessions, the mean GS based on SSR markers was 0.717. In two earlier studies, the mean GS were 0.31 (Plaschke et al. 1995) and 0.23 (Prasad et al. 2000), respectively. It suggested that the 40 Chinese endemic wheat accessions were more closely related. It is agreement with the results obtained from isoenzyme (Yang et al. 1992), HMW-glutenins and gliadins (Wei et al. 2000, 2002), and RFLP markers (Dvorák et al. 1998; Ward et al. 1998).

From morphological (Yen et al. 1988), HMW-glutenins and gliadins (Wei et al. 2000, 2002), and RFLP (Dvorák et al. 1998; Ward et al. 1998) analyses, it is proposed that Chinese Spring is a strain of Sichuan landrace Chengdu-guangtou, a famous landrace of the Chengdu Plain, which is one of the Sichuan White Wheat. In this study, the cluster analysis based on SSR and STS-PCR markers showed that Chinese Spring was more closely related with Chengdu-guangtou than any other Chinese endemic wheat accession, providing further support to the proposal that Chinese Spring is a strain of Chengdu-guangtou.

From RFLP analysis, Ward et al. (1998) found that the XR wheat group was genetically distinct from the other three Chinese endemic wheat groups and the TW group was genetically similar to, but more diverse than, the SWW and YH groups. The similar results were obtained in this study. The genetic relationships within and between Chinese endemic wheat groups were estimated by a UPGMA cluster analysis of (1–GS) matrix (Fig. 1 and 3). The results indicated that the XR wheat group was genetically distinct from other three Chinese endemic wheat groups, while SWW wheat group was genetically related to the YH group. The TW wheat group is more diverse than the SWW and YH groups, with some accessions more related to the YH group.

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Referances

Akkaya MS, Bhagwast AA and Cregan PB (1992) Length polymorphisms of simple sequence repeat DNA in soybean. Genetics 132: 1131-1139.

Chen PD, Jiu DJ, Pei GZ, Qi LL and Huang L (1988) The chromosome constitution of three endemic hexaploid wheats in Western China. Proc 7th Int Wheat Genet Symp Vol 1: 75-80.

Chen HB, Martin JM, Lavin M and Talbert LE (1994) Genetic diversity in hard red spring wheat based on sequence -tagged-site PCR markers. Crop Sci 34: 1269-1632.

Chen Q, Sun Y and Dong Y (1985) Cytogenetic studies on interspecific hybrids of Xingjiang wheat. Acta Agron Sinica 11: 23-28.

Devos KM, Bryan GJ, Collins AJ, Stephenson P and Gale MD (1995) Application of two microsatellite sequences in wheat storage proteins as molecular markers. Theor Appl Genet 90: 247-252.

Devos KM and Gale MD (1992) The use of random amplified polymorphic DNA markers in wheat. Theor Appl Genet 84: 567-572.

Dong YS, Zheng DS, Qiao DY, Zeng XQ, En ZC and Chen XR (1981) Investigation and study on Yunnan wheat (*Triticum aestivum* ssp. *yunnanense* King). Acta Agron Sinica 7: 145-151.

Dvorák J, Luo MC, Yang ZL and Zhang HB (1998) The structure of the *Aegilops tauschii* genepool and the evolution of hexaploid wheat. Theor Appl Genet 97: 657-670.

Gupta PK, Balyan HS, Sharma PC, Ramesh B (1996) Microsatellites in plants: a new class of molecular markers. Curr Sci 70:45-54.

He S, Oham H and Machenzie S (1992) Detection of DNA sequence polymorphisms among wheat varieties. Theor Appl Genet 84: 573-578.

Nagaoka T and Ogihara Y (1997) Applicability of inter-simple sequence repeat polymorphisms in wheat for use as DNA markers in comparison to RFLP and RAPD markers. Theor Appl Genet 94: 597-602

Nei M and Li W (1979) Mathematical model for studying genetic variation in terms of restriction endonucleases. Proc Natl Acad Sci USA 76: 5269-5273.

Plaschke J, Genal MW and Röder MS (1995) Detection of genetic diversity in closely related bread wheats using microsatellite markers. Theor Appl Genet 91: 1001-1007.

Prasad M, Varshney PK, Roy JK, Balyan HS and Gupta PK (2000) The use of microsatellites for detecting DNA polymorphism genotype identification and genetic diversity in wheat. Theor Appl Genet 100: 584-592.

Riley R, Coucoli H and Chapman V (1967) Chromosomal interchanges and the phylogeny of wheat. Heredity 22: 233-248.

Röder MS, Korzun V, Wendehake K, Plaschke J, Tixier MH, Leroy P and Ganal MW (1998) A microsatellite map of wheat. Genetics 149: 2007-2023.

Röder MS, Plaschke J, Konig SU, Boener A, Sorrells ME, Tanksley SD and Ganal MW (1995) Abundance, variability and chromosomal location of microsatellites in wheat. Mol Gen Genet 246: 327-333.

Rohlf FJ (1993) NTSYS-pc version 1.80. Distribution by Exeter Software, Setauket, New York

Roy JK, Prasad M, Varshney RK, Balyan HS, Blake TK, Dhaliwal HS, Singh H, Edwards KJ and Gupta PK (1999) Identification of a microsatellite on chromosomes 6B and a STS on 7D of bread wheat showing an association with preharvest sprouting tolerance. Theor Appl Genet 99: 336-340.

Saiki RK, Gelfond DH, Stoffel S, Scharf SJ, Higuchi R, Horn BT, Mullis KB and Erlich HA (1988) Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 239: 487-491.

Shao QQ, Li CS and Basang CR (1980) Semi-wild wheat from Xizang (Tibet). Acta Genet Sinica 7: 150-156.
Sharp PJ, Kresis M, Shewry P and Gale MD (1988) Location of β-amylase sequences in wheat and its relatives. Theor Appl Genet 75: 286-290.
Sneath PHA and Sokal RR (1973) Numerical taxonomy. Freeman, San Francisco.
Talbert LE, Blake NK, Chee PW, Blake TK and Magyar GM (1994) Evaluation of "sequence-tgged-site" PCR products as molecular markers in wheat. Theor Appl Genet 87: 789-794.
Tragoonrung S, Kanazin V, Hayes PM and Blake TK (1992) Sequence-tagged-site facilitated PCR for barley genome mapping. Theor. Appl. Genet., 84: 1002-1008
Ward RW, Yang ZL, Kim HS and Yen C (1998) Comparative analyses of RFLP diversity in landraces of *Triticum aestivum* and collections of *T. tauschii* from China and Southwest Asia. Theor Appl Genet 96: 312-318.
Wei YM, Zheng YL, Liu DC, Zhou YH and Lan XJ (2000) Gliadin and HMW-glutenin variations in *Triticum turgidum* L. ssp. *turgidum* and *T. aestivum* L. landraces native to Sichuan, China. Wheat Inf Serv 90: 13-20.
Wei YM, Zheng YL, Liu DC, Zhou YH and Lan XJ (2002) HMW-glutenin and gliadin variations in Tibetan weedrace, Xinjiang rice wheat and Yunnan hulled wheat. Genet Resour Crop Evol 49: 327-330
Welsh J and McClelland J (1990) Fingerprinting genomes using PCR with arbitrary primers. Nucleic Acids Res 18: 7213-7218.
Williams JGK, Kubelik AR, Livak KJ, Rafalski JA and Tingey SV (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Acids Res 18: 6531-6535.
Yang WY, Yen C and Yang JL (1992) Cytogenetic study on the origin of some special Chinese landraces of common wheat. Wheat Inf Serv 75: 14-20.
Yang ZL, Luo MC and Yen C (1992) The study on esterase and peroxidase isozymes in landraces of wheat from Sichuan. J Sichuan Agric Univ 10: 105-112.
Yen C, Luo MC and Yang JL (1988) The origin of the Tibetan weedrace of hexaploid wheat, Chinese Spring, Chengdu-guang-tou and other landraces of White Wheat Complex from China. 7th Int Wheat Genet Symp. Vol 1: 175-179.
Zietkiewicz E, Rafalski A, Labuda D (1994) Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. Genomics 20: 176-183

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Yield potential and genetic gain in Indian and Mexican spring bread wheat

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Summary

Yield potential progress of 15 spring wheat (*Triticum aestivum* L.) genotypes (five of Indian and ten of Mexican origin) was studied under disease free, artificial lodging control by using mesh (20 x 20) and high N (300 kg/ha) application at CIMMYT (Centro Internacional de Mejoramiento de Maiz y Trigo), near Ciudad Obregon, Sonora, Mexico during 1997-98 and 1998-99. From pooled analysis, Super Seri, the latest variety named in 1999 produced significantly higher grain yield (9968 kg/ha) than other varieties and 23.7 % more grain yield than the lowest yielding variety Pavon 76 (8056 kg/ha) released in 1976. Even second highest yielding cultivar WH 542 produced 774 kg/ha less yield than Super Seri. Genetic progress, including both Indian and Mexican genotypes, showed that gain in grain yield was 48 kg/ha/year in absolute term and 0.54 % per year in relative term. Under real farm situation these genetic gains will be higher due to inability of farmers to control lodging and diseases. To quantify separately the effect of Indian and Mexican genotypes it was observed that Indian varieties, released during 1982 and 1995, gained grain yield @ 22.7 kg/ha/year or 0.25 % per year. On the other hand, Mexican cultivars released during 1976 and 1999 increased grain yield @ 57 kg/ha/year in absolute term or 0.63 % per year in relative term.

Key words: spring bread wheat, yield potential, genetic gain

Introduction

The advent of Norin 10 dwarfing genes opened up era of semi-dwarf wheat, which dramatically increased the yield potential during mid 1960s. Maximum possible yield can be achieved where there are no biotic and abiotic constraints and crop is free from lodging. This yield will be close to the physiological yield potential, which is generally calculated from solar radiation and temperature and genetic ability of the plant to convert light energy into dry matter and subsequently partition this dry matter into economic grain yield (Hobbs et al. 1998). Genetic progress in the yield of spring bread wheat was 0.7 to 1.3 % per year (Byerlee and Moya 1993) and 0.88 % per year or 67 kg/ha/year (Sayre et al. 1997). Former study included the tall wheat whereas the latter involved from Pitic 62 released in 1962 to Bacanora 88 released in 1988. In both the studies, yield progress was associated with use of Norin 10 dwarfing genes, *Rht-1* or *Rht-2*, and with an increase in the harvest index. Whereas, Waddington et al. (1986) pointed out that the increase in grain yield (after 1975) was due to increased biomass rather than harvest index. In another study of 50 experiments, Bell et al. (1995) reported that genetic gain in yield was 0.7 % per year during 1968-1993, but it became slow down after 1980s. Yield potential progress of spring bread wheat

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during the last quarter of century (1975 to 2000) is not very well established. Therefore, present study was carried out under irrigated, high N application (300 kg/ha), disease free and artificial lodging control condition with use of 10 Mexican and 5 Indian high yielding spring wheat genotypes released during 1976 to 1999. This provided an opportunity to update the genetic progress made by Indian and Mexican spring bread wheat genotypes, all semi-dwarf wheat, developed during the last quarter of 20th century.

Materials and methods

A field experiment was conducted in 1997-98 and 1998-99 at CIMMYT (Centro Internacional de Mejoramiento de Maiz y Trigo), near Ciudad Obregon, Sonora, Mexico (lat. 27.33'N, long.109.09'W and 38 m above sea level). The soil type was coarse sandy clay, mixed montmorillonitic typic calciorthid, low in NO_3^- N (29.5 ppm) and NH_4^+N (6.1 ppm), medium in available P (7.7 ppm) and organic matter (0.89 %), high in K (557 ppm) and alkaline (pH = 8.0) in nature. The cation exchange capacity (CEC, meq/100g) and electrical conductivity (EC, mmhos/cm) were 29.4 and 1.07 in top 15 cm soil, respectively. The weather condition during winter and spring seasons was nearly normal except more rainfall after sowing in the first year, which did not affect the germination. Besides this, minimum temperature in November, December, January and March was lower (about 1°C) in 1998-99 as compared to 1997-98 (Table 1). So, the second crop cycle was more favorable for growth and development than the first one.

Table 1. Average monthly maximum and minimum temperature and rainfall during wheat growing season (1997-98 and 1998-99) at Obregon, Sonora, Mexico.

Months	Temperature (°C)				Rainfall (mm)	
	'97-98		'98-99		'97-98	'98-99
	max	min	max	min		
November	29.7	13.4	30.3	12.8	38.5	1.1
December	23.3	8.6	25.2	7.7	33.4	1.0
January	26.1	7.1	26.7	5.5	0.0	0.0
February	24.6	7.1	27.2	7.1	11.8	0.0
March	27.7	9.4	27.9	8.9	1.9	3.4
April	30.4	9.8	29.9	11.3	0.0	0.0

The study consists of 15 varieties (Table 2, 10 from Mexico and 5 from India), which were grown in randomized block design with three replications. Eight rows were planted in a plot size of 5.5 x 1.6 m^2 under flat condition. The crop was sown during the last week of November by plot drill into dry soil followed by irrigation to give about 300 viable seeds/ m^2 in rows, 20 cm apart. Prior to planting, a summer green manure crop (*Sesbania aculeata*) was incorporated by cultivation. At the time of planting, 100 kg N/ha was applied as Urea and 46 kg/ha phosphorous as Single Super Phosphate. Potash was not applied due to inherent high content of potassium

Table 2. List of varieties, their pedigree, year of release and source

Varieties	Pedigree	Year of release	Source
1. Pavon 76	VCM//CNO/7C/3/KAL/BB	1976	CIMMYT, Mexico
2. Seri 82	KVZ/BUHO//KAL/BB	1982	CIMMYT, Mexico
3. HD 2329	SLSib/NP852/4/PjSib/P14//Kt54B/3/K65/5/Ska/6/UP262	1982	India
4. Star	LFN/SDY//PVN	1985	CIMMYT, Mexico
5. Munia/Kauz	JUN/BOW//VEE#5/BUC	1987	CIMMYT, Mexico
6. Bacanora 88	JUP/BJY//URES	1988	CIMMYT, Mexico
7. Rayon 89	URES*2/PRL	1989	CIMMYT, Mexico
8. Weaver	HAHN*2/PRL	1991	CIMMYT, Mexico
9. CPAN 3004	GLL/AUSTII61.157//CNO/NO/3/VEE	1991	India
10. Baviacora 92	BOW/NAC//VEE/3/BJY/COC	1992	CIMMYT, Mexico
11. WH 542	JUP/BJY//URES	1992	India
12. Pastor	PFAU/SERI//BOW	1993	CIMMYT, Mexico
13. UP 2338	UP368/VL421//UP262	1994	India
14. PBW 343	ND/VG9144//KAL/BB/3/YACO/4/VEE#5	1995	India
15. Super Seri	Seri*5//Aga/6*Yr	1999	CIMMYT, Mexico

(557 ppm) in soil (0-15 cm depth). Top dressing of 200 kg N/ha through Urea was done at DC 31 stage (Zadoks et al. 1974) followed by irrigation.

Netting (20 x 20 mesh) was imposed after first irrigation to facilitate easy growing of young plants and its height was adjusted with the growth of crop. This was done to avoid the crop from lodging, which generally occurs after anthesis during or after irrigation, so as to ensure uninterrupted supply of nutrients and continuous interception of solar radiation to achieve maximum possible yield. Irrigation was applied as per need of the crop by flat method. Herbicides, like Topik (Clodinafop-propargyl) @ 250 ml/ha and Brominal (Bromixinil @ 1.5 l/ha) + Harmony (Thiofensulfuron @ 25 g /ha) were used by Knap Sack sprayer at two leaves weed stage for control of grassy and non-grassy weeds, respectively. Fungicides were applied at every 15 days interval after heading to prevent diseases, which facilitated proper estimation of yield potential.

Net plot of 3.6 m², excluding border rows and ends of the plot, was harvested manually after 7-10 days of physiological maturity. Dates of 75 % seedling emergence and 50 % anthesis, at which spikes extruded at least one anther, and physiological maturity was recorded. Duration from emergence to anthesis and maturity was considered as anthesis and maturity period of different varieties, respectively. At the time of harvest, a sub sample of 100 culms was taken, which were weighed, dried at 70°C and again weighed and used for adjustment of constant moisture in biomass and calculations of spikes/m². Remainder plot material was threshed after a week of sun drying and grain yield was recorded. Another sub sample of grain was taken, weighed (fresh and dry), for adjustment of grain yield at 12 % moisture, which was further used for determining thousand grain weight. All the yield and yield attributing characters were obtained by using methods as described by Bell and Fischer (1994).

The data of the experiment were analyzed on pooled basis by using MSTATC (Michigan State University), a statistical analysis package (Nissen 1983). Phenotypic correlation (r) between yield and other traits were calculated by using Pearsons Correlations. Calculation of genetic gain was done by regressing the mean grain yield and natural logarithm of yield with the year of release of varieties. The slope (b) in linear regression equation of grain yield and year gave an increase in grain yield in kg/ha/year (absolute term). Similarly, natural logarithm of grain yield with year resulted in per cent per year

Table 3. Differences in plant height, days to anthesis and maturity, yield and its attributes in Indian and Mexican spring varieties (pooled analysis of 1997-98 and 1998-99)

Variety	Height (cm)	Anthesis (days)	Maturity (days)	Yield (kg/ha)	Biomass (kg/ha)	HI	1000 grain weight (g)	Spikes/ m²	Grains/ m²	Grains/ spike
Pavon 76	97.1	87.5	131.2	8056	17412	0.408	40.21	559	17635	31.8
Seri 82	92.7	92.2	131.8	9028	18125	0.438	41.05	448	19404	43.4
HD 2329	89.1	74.8	124.3	8706	16457	0.469	45.67	513	16772	32.8
Star	85.1	94.7	137.2	8492	19177	0.390	38.73	582	19375	33.3
Munia/Kauz	90.3	87.3	126.3	8890	17421	0.449	36.05	455	21706	48.2
Bacanora 88	86.5	90.7	131.7	9067	18186	0.439	35.54	496	22457	45.3
Rayon 89	99.9	89.5	132.5	8256	17945	0.404	35.82	515	20321	39.5
Weaver	77.0	94.8	136.0	9083	18867	0.424	35.30	696	22708	32.7
CPAN 3004	95.8	87.2	128.3	8601	16620	0.456	44.22	397	17117	43.3
Baviacora 92	103.6	90.2	133.8	9143	18415	0.437	47.55	411	16919	41.2
WH 542	87.1	90.8	132.8	9194	18309	0.441	35.36	532	22960	43.2
Pastor	104.0	90.2	132.7	8357	18707	0.393	44.40	477	16555	34.8
UP 2338	91.4	87.2	132.2	9102	18383	0.436	45.70	422	17537	41.7
PBW 343	93.7	91.5	131.2	8846	17569	0.441	47.13	460	16608	36.0
Super Seri	94.2	93.0	133.8	9968	18976	0.462	40.84	456	21512	47.3
LSD at 5 %	2.5	0.8	1.2	408	1042	0.02	1.24	41	1076	3.1
Correlation (r) with yield	–0.28	0.25	0.16	1.0	0.36	0.62*	–0.01	0.19	0.44	0.60*

* Significant at the 5% level

(relative term) increase when b was multiplied by 100 (Ortiz Monasterio et al. 1997).

Results and discussion

From combined analysis over the years, it was observed that varietal difference in plant height, days to anthesis and maturity, biomass, grain yield, HI, thousand grain weight, spikes/m^2, number of grains/m^2 and grains/spike were significant (Table 3). A variety Weaver was shortest (77 cm) and Pastor and Baviacora 92 (104 cm) were tallest followed by Rayon 89 (100 cm). Plant height of other varieties was around 90 ± 5 cm. Among the varieties under study, HD 2329 was early in nature and took 75 days till anthesis, whereas others extruded their anthers in approximately 90 ± 2 days after emergence. Similarly, varieties HD 2329 and Munia/Kauz matured in 124 and 126 days, respectively whereas others showed their physiological maturity in 132 to 135 days after emergence. Therefore, it can be considered that varieties under investigation were of similar maturity group except HD 2329 and Munia/Kauz.

From pooled analysis, variety advanced line, Super Seri named in 1999 recorded significantly higher grain yield (9968 kg/ha) than other varieties and this genotype also yielded 774 kg/ha more in absolute term, which comes to be 8.4 % higher, as compared to second highest yielding cultivar WH 542 (9194 kg/ha). Super Seri also exhibited 23.7 % higher grain yield than the lowest yielding variety Pavon 76 (8056 kg/ha) released in 1976. Varieties like Seri 82, Munia/Kauz, Bacanora 88, Weaver, Baviacora 92, WH 542, UP 2338 and PBW 343 displayed non-significant difference in grain yield, which was in the range of 8800 to 9200 kg/ha. At CIMMYT, in a historic set of 8 cultivars was studied for six years by Sayre et al. (1997) and they reported about 27 % increase in grain yield from Pitic 62 (6680 kg/ha) released in 1962 to Bacanora 88 (8475 kg/ha) released in 1988. While, in the present investigation, yield potential approached to 10 tonne/ha. Even Super Seri gave 9.9 % higher grain yield than Bacanora 88. The estimation of yield potential without netting is a complex phenomenon. It is limited by lodging if irrigation is given during late milk stage, and if not then yield is reduced due to reduction in grain weight (Hobbs et al. 1998). Super Seri (containing *Lr19* and *Lr26*) recorded 10.4 % higher grain yield over Seri 82 (*Lr26* gene). This finding was in corroboration with Singh et al. (1998) who have conducted experiments at CIMMYT with the use of near isogenic lines and reported 8.2 % increase in grain yield due to *Lr19* gene.

Super Seri also exhibited the second highest biomass (18976 kg/ha) and HI (0.462) after Star (19177 kg/ha) and HD 2329 (0.469). The lowest biomass was exhibited by Indian variety HD 2329 (16457 kg/ha), which probably lead to higher HI. In contrast, lowest HI (0.390) was exhibited by Star despite highest biomass production. Varieties Baviacora 92 (47.55 g) and PBW 343 (47.13 g) recorded significantly higher thousand grain weight as compared to other genotypes. The difference between these two varieties is not significant. On the other hand, variety Weaver and WH 542 weighed lowest thousand grain weight (35.3 g). Among the varieties under study, it was observed that genotypes possessing lower thousand grain weight have shown higher number of spikes/m^2 and vice versa. The number of productive tillers/m^2 was lowest in CPAN 3004 (397) and highest in Weaver (696), which was significantly higher than other varieties. The number of grains/m^2 was product of numbers of spikes/m^2 and grains/spike, and it ranged from 16555 (Pastor) to 22960 (WH 542). The latter variety showed highest grains/m^2 due to lowest thousand grain weight.

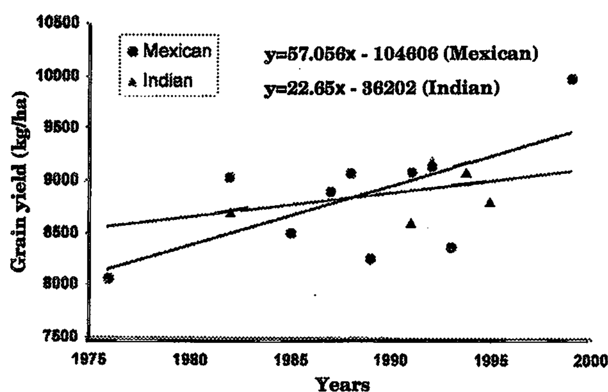

Fig. 1. Genetic gain in grain yield in absolute term

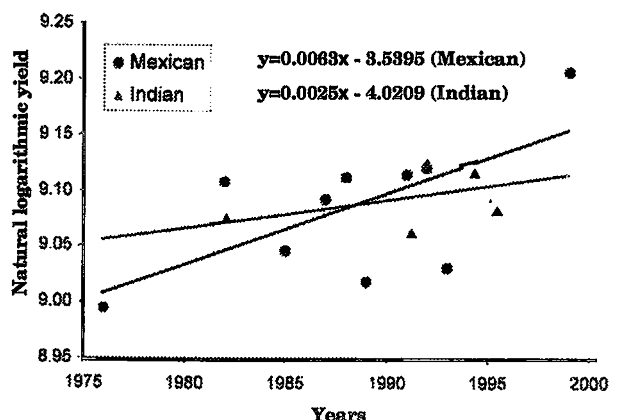

Fig. 2. Genetic gain in grain yield in relative term

Variety Munia/Kauz recorded maximum grains/spike (48.2) followed by Super Seri (47.3) and Bacanora 88. On the other hand, Pavon 76 recorded lowest number of grains/spike (31.8).

The effect of cultivation year was significant for biomass, grain yield, HI, number of grains/m^2 and grains/spike, and 1998-99 crop cycle performed higher grain yield as compared to 1997-98. This was possible due to favorable condition during subsequent crop cycle than previous one. From mean of two years, grain yield correlated maximum with HI ($r = 0.62$, $P<0.05$) and number of grains/spike ($r = 0.60$, $P<0.05$). Therefore, it could be said that increase in grain yield was cumulative effect of the yield attributing parameters.

Genetic progress in grain yield: Genetic progress in grain yield of 10 Mexican and 5 Indian varieties was calculated from mean of two years data. Combined effect, including both released in India and Mexico, showed that progress in grain yield was 48 kg/ha/year or 0.54 % per year, and that absolute yield ranged from 8056 kg/ha by Pavon 76 (released in 1976) to 9968 kg/ha by Super Seri (named in 1999). Indian varieties released during 1982 and 1995 enhanced grain yield @ 22.7 kg/ha/year or 0.25 %, and Mexican cultivars released during 1976 and 1999 increased grain yield @ 57 kg/ha/year in absolute term or 0.63 % per year in relative term (Fig. 1 and 2). Yield potential progress (1982 to 1995) by Indian varieties was slower, probably due to inclusion of Indian varieties released during 13 years period only, as compared to CIMMYT, Mexico genotypes released during last 25 years. Our finding was in corroboration with observation of Bell et al. (1995) who have mentioned that genetic gain was 0.7 % per year during 1968 to 1993 (study of 50 experiments). At CIMMYT, Ortiz Monasterio et al. (1997) also calculated genetic gain @ 89 kg/ha/year or 1.9 % per year at 300 kg N/ha application by using varieties released between 1950 and 1985. This was higher due to inclusion of tall varieties like Yaqui 50 and Nainary 60 and crop was not prevented from lodging. Lodging susceptibility of tall varieties at such higher N rates (300 kg/ha) was another factor for higher genetic gain. In another study at the same place, genetic gain in grain yield was 67 kg/ha/year in absolute term and 0.88 % per year in relative term, where eight semi-dwarf varieties included, the earliest from Pitic 62, released in 1962 to Bacanora 88 released in 1988 (Sayre et al. 1997). In this case also genetic gain was a little higher than our findings, because the oldest variety was Pitic 62, which was released just after advent of Norin 10 dwarfing genes.

Therefore, it can be considered that yield potential progress in spring wheat genotypes under irrigated, high N use, disease free and lodging control condition was raised substantially during the last quarter of 20th century. So, it will be futile to preclude that genetic progress was stagnated but certainly slowed down as compared to green revolution era. Furthermore, this gain in grain yield will be undoubtedly higher under farmer's field condition due to development of higher disease resistant and lodging tolerant varieties.

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References

Bell MA and Fischer RA (1994) Guide to plant and crop sampling: Measurements and observations for agronomic and physiological research in small grain cereals. Wheat Special Report No. 32. CIMMYT, Mexico, D.F.

Bell MA, Fischer RA, Byerlee D and Sayre KD (1995) Genetic and agronomic contributions to yield gains. A case study for wheat. Field Crops Res. 45:55-65.

Byerlee D and Moya P (1993) Impact of international wheat breeding research in the developing world. 1966-90. CIMMYT, Mexico, D.F.

Hobbs P, Sayre KD and Ortiz Monasterio RJI (1998) Increasing wheat yield through agronomic means. NRG paper 98-01. Mexico, D.F., Mexico.

Ortiz Monasterio RJI, Sayre KD, Rajaram S and Mcmahon M (1997) Genetic progress in wheat yield and nitrogen use efficiency under four nitrogen rates. Crop Sci. 37: 898-904.

Nissen O (1983) MSTATC – A microcomputer programme for the design, management and analysis of agronomic research experiments. Version I. Agric Univ, Norway.

Sayre KD, Rajaram S and Fischer RA (1997) Yield potential progress in short bread wheat in Northwest Mexico. Crop Sci. 37: 36-42.

Singh RP, Espino JH, Rajaram S and Crossa J (1998) Agronomic effects from chromosome translocations 7DL.7Ag and 1BL.1RS in spring wheat. Crop Sci. 38: 27-33

Waddington SR, Ransom JK, Osmanzai M and Saunders DA (1986) Improvement in yield potential of bread wheat adapted to northwest Mexico. Crop Sci. 26:698-703.

Zadoks JC, Chang TT and Konzak CF (1974) A decimal code for growth stages of cereals. Weed Res. 14:415-421.

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Research information

WIS

Seedling reaction of Thatcher (*Triticum aestivum* L.) near isogenic lines with adult plant leaf rust resistance genes *Lr34* and *Lr37*

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Leaf rust caused by *Puccinia triticina* is an important disease of wheat causing yield losses world over. Use of adult plant resistance genes in development of leaf rust resistant cultivars is gaining in importance because such genes often provide long lasting resistance. The adult plant resistance gene *Lr34* is frequently identified from wheats having proven record of durable resistance to leaf rust (McIntosh 1992). Another adult plant resistance gene *Lr37* is also effective against many races from India (Saini et al. 1998). Thus, the gene *Lr37* also has potential for use in the Indian subcontinent. The nursery test to detect adult plant resistance genes at seedling stage can be helpful to the breeders because this saves time and resources. The present report describes seedling reaction of the adult plant resistance genes *Lr34* and *Lr37* against three Indian leaf rust races at two temperatures which may be useful in selection of these genes at seedling stage.

Two Thatcher near isogenic lines RL6058 (6*Thatcher/PI58548) and RL6061 (6*Thatcher/PI208316) both carrying *Lr34*, and RL6081 (VPM1/6*Thatcher) carrying the other adult plant resistance gene *Lr37*, were tested for seedling infection types along with a susceptible cultivar Agra Local against leaf rust races 11, 63 and 106 at 14.5°C and 20°C. Five rows each containing 15–20 seeds of wheat accessions to be tested were planted in 8.5" X 4.5" sized bread boxes. Agra Local was sown as a control in every 6th row. First leaf of seven-day-old seedlings was inoculated separately with races 11, 63 and 106. These were incubated for 16 hours at 100% relative humidity at 20 ±1°C and then transferred to glass houses maintained at 14.5°C and 20°C. The observations on infection types on seedlings kept at 14.5°C and 20°C were recorded 21 and 14 days after inoculation respectively, according to Stakman et al. (1962). The result of observations are given in Table 1. RL6058 carrying *Lr34* showed low reaction against races 11, 63 and 106 at 14.5°C but at 20°C this line was resistant only to race 106. The line RL6061 also showed resistance at 14.5°C against the races 11, 63 and 106 but at 20°C this line showed resistance against races 63 and 106 only. These results indicate that the gene *Lr34* in RL6058 and RL6061 expresses at 14.5°C against races 11, 63 and 106. The low reaction of RL6058 against race 106 and of RL6061 against races 63 and 106 at 20°C was assumed to be caused by additional gene (s). The line RL6081 having *Lr37* showed low reaction against races 11 and 106 and it was susceptible to race 63 both at 14.5°C and 20°C. This indicates that *Lr37* can also be detected at

Table 1. Infection types on the Thatcher near isogenic lines carrying the adult plant resistance genes *Lr34* or *Lr37* against races 11, 63 and 106 at two temperatures

Accession	*Lr* gene	Incubated temperature	Infection type/races		
			11	63	106
RL6058	*Lr34*	14.5°C	0;	;	0;
		20°C	3	3	0;
RL6061	*Lr34*	14.5°C	0;	0;	0;
		20°C	3	0;	0;
RL6081	*Lr37*	14.5°C	0;	3	0;
		20°C	0;	3	0;
Agra Local	None	14.5°C	33^+	33^+	33^+
		20°C	33^+	33^+	33^+

seedling stage similar to *Lr34*. Because the reaction pattern of RL6081 is different than that of the lines RL6058 and RL6061 both carrying the gene *Lr34*, the accessions carrying the genes *Lr34* and *Lr37* can be distinguished using seedling reaction against races 11 and 63 at 14.5°C and 20°C.

Variation in expression of the gene *Lr34* in different genetic backgrounds, growth stages and environments is reported to exists. Shiwani et al. (1990) reported two adult plant genes for leaf rust resistance from the line RL6058 which is considered as reference line for the gene *Lr34*. The present results also suggest that the differential expression of the gene *Lr34* in RL6058 and RL6061 may be due to additional gene (s) carried by these accessions.

References

McIntosh RA (1992) Close genetic linkage of genes conferring adult-plant resistance to leaf rust and stripe rust in wheat. Pl Path 41: 523-527.

Saini RG, Kaur L and Kaur M (1998) Adult plant leaf rust (*Puccinia recondita tritici*) resistance of known *Lr* genes against three virulence variants of race 77 from Indian sub-continent. Indian J Agri Sci 68: 776-779.

Shiwani, Saini RG and Gupta AK (1990) Additional resistance in some derivatives with known adult plant leaf rust resistance genes. Cereal Rusts and Powdery Mildew Bull 18: 45-51.

Stakman EC, Stewart DM and Loegering WQ (1962) Indentification of physiologic races of *Puccinia graminis* var. *tritici*. USDA Agric Res Serv Bull E-617 (rev): 1-53.

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Research information

Identification of chromosome translocations in the Bulgarian wheat variety Gladiator 113

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The Bulgarian variety Gladiator 113 is of breeding interest owing to its long multispikelet spike, complex disease resistance and high grain protein content. It has been isolated through crosses (Skorospelka 35 x Mexipac) x Siete Ceros, combined with radiation treatments of parents and hybrids (Savov 1987). The variety was expected to carry translocations from its close or more distantly related ancestors: a 1BL.1RS translocation from Skorospelka 35 (Mettin et al. 1973), and a 2A.2D translocation from the Brazilian variety Fronteira (Berzonsky 1996) through Mexipac or Siete Cerros. Additional structural rearrangements were likely to have been induced by the radiation treatments.

To identify the chromosome interchanges in Gladiator 113, chromosome N-banding technique (Gill et al. 1991) was applied on mitotic chromosomes in Gladiator 113 and on meiotic chromosomes in F_1 hybrids of Gladiator 113 with varieties Chinese Spring, Rusalka and Rannaya 12.

In all hybrids, multivalents were recorded in the majority of cells (Table 1). The most frequently observed polyvalent configurations were 1'''' or 2'''', 1''', 1''' + 1''''. This indicates that at least four chromosomes in the hybrids participate in translocations. Penta- and hexavalents were also observed, but with lower frequency.

A 5A.6B translocation was identified in all hybrids (Fig.1a, b, c). The translocated chromosomes formed ring or chain quadrivalents (in 40 % of the examined cells), heterologous rod bivalents (47 %), a trivalent plus univalent (6 %), or four univalents (7 %). The aberration, however, does not alter the N-banding pattern of the two chromosomes (Fig. 2). To our knowledge, a 5A.6B translocation has not been reported earlier, although both chromosomes were known to be involved in exchanges with other chromosomes (Schlegel 1996). This translocation is supposed to be a newly induced structural aberration as a result of radiation treatments.

A 2A.2D translocation was not identified with certainty. Chromosome 2D rarely formed polyvalent associations with 2A, and paired more frequently with other A or D genome chromosomes (Fig. 1c). In hybrids Rannaya 12 x Gladiator 113 more complex chromosome associations, involving chromosome 1B, were expected to be formed, as variety Rannaya 12 was reported to carry a 1B.2D translocation (Schlegel 1996). Chromosome 2D, however, was not observed in configurations with 1B.

The wheat-rye translocation 1BL.1RS was observed in meiosis in all F_1-hybrids forming rod bivalents with chromosome 1B (Fig. 1a, b), and in mitosis in Gladiator 113 (Fig. 2). This translocation is supposed to have been transmitted to Gladiator 113 from Skorospelka 35, thus contributing important

Table 1. Meiotic pairing configurations in pollen mother cells in F_1- hybrids of Gladiator 113 (G113) with varieties Chinese Spring (CS), Rusalka (RUS), and Rannaya 12 (R12).

Genotype	Configurations per cell					
	I	II	III	IV	V	VI
Gladiator 113	0.40	20.46	-	0.17	-	-
Rusalka	-	21.00	-	-	-	-
Rannaya 12	-	21.00	-	-	-	-
F_1: CS x G113	0.21	19.46	0.05	0.68	-	-
F_1: RUS x G113	0.51	18.43	0.13	1.03	-	0.02
F_1: R12 x G113	0.80	18.00	0.19	1.10	0.01	0.03

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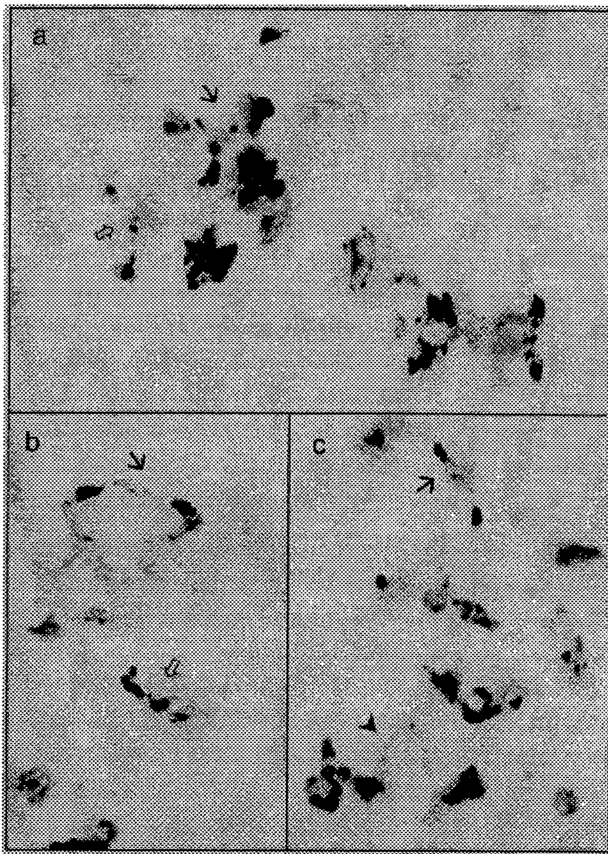

Fig. 1. Representative metaphase I meiotic configurations in pollen mother cells. a. Chinese Spring x Gladiator 113, b. Rusalka x Gladiator 113, c. Rannaya 12 x Gladiator 113 after chromosome N-banding. (Black arrows: 5A.6B configurations, white arrows: 1B.1R bivalents and arrowhead: a configuration involving chromosome 2D).

genes.

The present study shows that variety Gladiator 113 carries translocations, involving chromosomes, which control plant morphogenesis and development, adaptability, yield quantity and quality. This knowledge is of importance when utilizing this variety and its hybrids in wheat breeding.

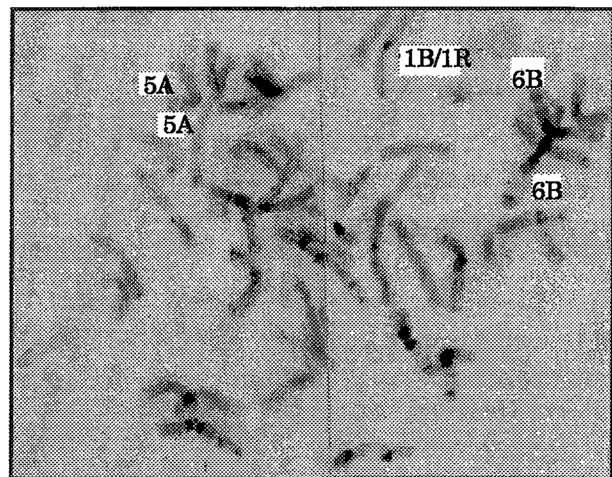

Fig. 2. N-banded mitotic chromosomes of Gladiator 113.

Acknowledgments

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References

Berzonsky W (1996) Brazilian origin and inheritance of a heterozygous reciprocal chromosome translocation in wheat (*Triticum aestivum* L.). Cytologia 61: 253-258.

Gill BS, Friebe B and Endo TR (1991) Standard karyotype and nomenclature system for description of chromosome bands and structural aberrations in wheat (*Triticum aestivum* L.). Genome 34: 830-839.

Mettin D, Blüthner WD and Schlegel R (1973) Additional evidence on spontaneous 1B/1R wheat-rye substitutions and translocations. Proc 4th Int Wheat Genet Symp : 179-184.

Savov P (1987) A contribution to the gene pool of wheat. Genetics and Breeding (Sofia) 20 (5): 375-380. (in Bulgarian, with English summary).

Schlegel R (1996) A compendium of reciprocal translocations in wheat. 2nd Edition. Wheat Inf Serv 83: 35-46.

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Research information

Seedling and adult plant response of some hexaploid wheat lines to different variants of leaf rust pathotype

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Vertical resistance (VR) genes provide hypersensitive type of reaction and confer a high level of resistance throughout the life cycle of the plant. However, this type of resistance exerts a high level of selection pressure on the pathogen population which then mutates and evolves resistant strains ultimately rendering the resistant gene ineffective in the long run. Horizontal resistance (HR) genes or what are commonly known as adult plant resistance (APR) genes, on the other hand, provide race nonspecific, moderate level of resistance to the carrier genotypes. Such genes do not exert a strong selection pressure on the pathogen population and let pathogens coexist but at a much lower population density level and thereby ensuring that the pathogen does not cause serious economic losses. This also confers a long lasting durable resistance. The study under report was conducted to assess the seedling and adult plant response of some newly developed bread wheat lines against an array of leaf rust pathotypes so as to identify the potential donors of adult plant leaf rust resistance for use by breeders.

The study made use of a collection of 28 elite wheat lines developed through pedigree breeding method for yield improvement. These lines were screened in seedling stage (Stakman et al. 1962) against selected leaf rust pathotypes (77-5, 77-6, 77-7, 77-2 and 12-2) under glass house conditions. The same set of genotypes was also screened under field conditions at adult plant stage (Loegering 1959) after creating field epidemic with the mixture of test pathotypes. Based on the data recorded in seedling and adult stage the

Table 1. Seedling and adult plant response of some wheat genotypes to a range of leaf rust pathotypes

Genotype	Seedling reaction to leaf rust pathotypes					Adult plant response
	77-5 1231R63-1	77-6 121R55-1	77-2 109R31-1	77-7 121R127	12-2 1R5	
DW1232	3	3	3	3	3	40MS–S (L)[†]
DW1237	3	3	3	3	3	20R–MR(VL)
DW1239	3c	33+	2–3	3	0	0 (VL)
DW1240	3	3	3	3	3	0 (VL)
DW1229	3	3	3	3	:1n	20MS–S (L)
DW1234	33+	3	X±	X	0	20MS (L)
DW1242	3c	3	3	3	X+	10S (L)
DW1243	3c	3	3	3	0	20MS (L)
DW1246	3	3+	3+	3	0	10MS (L)
Agra Local	33+	3–4	4	33+	33+	80S (H)

[†] VL: very low response (0 – 20MR), L: low response (20MS–60MS–S), H: high response (60–80S)

Table 2. Parentage of promising wheat lines

Genotype	Parentage
DW1232	Vee's'/CPAN2407//HD2329/3/DL788-3
DW1237	HD2674/DL788-3/Minivit/HD2680
DW1239	GS532/CPAN3083
DW1240	CDWR9549/HD2347//HD2402
DW1229	WL711/HD2624
DW1234	CPAN2009//HD2628/HD2380
DW1242	PF10354/ALD'S'/MES/3/SERI
DW1243	CPAN4067/PBW277/HD2681
DW1246	CHILL/UP2338/HD2652

lines DW1237, DW1239, DW1240, DW1229, DW1234, DW1242, DW1243, DW1246 and DW1232 were categorized into low (L) and very low (VL) field response to leaf rust as against seedling susceptibility to most of the pathotypes (Sawhney et al. 1996). Results revealed a high degree of APR in these lines which can serve as donors for this trait in wheat breeding program (Table 1). Out of the 28 lines screened, nine have exhibited (parentage in Table 2) desirable adult plant resistance. However, these lines seem to have diverse genetic bases as is indicated by their differential reaction to the individual pathotypes as well as to a mixture of the latter. Among the known APR genes, *Lr22a* and *Lr34* have been shown to exhibit very low (resistant) and low (moderately resistant) response under field conditions (Sawhney and Sharma 1992). It is likely that some of these lines carry *Lr34* since most materials originating from CIMMYT carry this gene. The resistant lines identified carrying APR genes will serve as important source to introgress the APR genes into future breeding program.

References:

Logering WQ (1959) Method of recording cereal rust data. USDA, Int Spring Wheat Nursery, USA.

Sawhney RN, Sharma JB and SharmaDN (1992) Genetic diversity for adult plant resistance to leaf rust in near isogenic lines used in Indian wheat. Pl Breed 109: 248-254.

Sawhney RN, Sharma JB, Sharma DN and Nagarajan S (1996) Adult plant resistance sources for breeding wheat with durable resistance to leaf rust. Cereal Rust and Powdery Mildew Bull 24 : 29-34.

Stakman EC, Stewart DM and Loegering WQ (1962) Identification of physiologic races of *Puccinia graminis* var. *tritici*. USDA Agric Res Ser No E 617 (Rev.) 53.

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Gene symbol

Catalogue of gene symbols for wheat

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PREFACE

It is with much gratitude to Professor Y. Yamazaki and her colleagues at the National Institute of Genetics, Mishima, Japan, that this issue of the Catalogue of Gene Symbols for Wheat was prepared from a database. Despite discussions of a database on numerous occasions, it has taken 35 years from my appointment as Coordinator of the Catalogue at the Third IWGS in Canberra in 1968. At that time the main reference to gene symbols in wheat ({047}, Ausemus et al. 1946) was 17 pages in length. The catalogue is now a large volume listing more than 11,500 genes/markers and 2,100. Clearly, that number will continue to increase quite rapidly. With a functioning database it will be possible to update on a regular basis, probably annually. A likely model is that annual supplements will be generated and published on a similar basis to the recent past so that people can see what is new. These updates will then be added to the database. Currently we do not have a mechanism for updating reference numbers so separate chronological and alphabetical lists will be available. It is expected that the database and Word output files will be available from a number of websites, and possibly by CD on request.

The objective of this Catalogue is to have a document that is helpful to a wide range of people, from 'coal-face' researchers to extension workers, and even farmers. Different sections of the Catalogue were prepared in different ways and a major challenge for our Japanese colleagues was to develop a common system. Various modifications were made to achieve this. In addition, we are attempting to expand the DNA section to include genetic mapping information and, in future, bin groupings. This has necessitated separate chromosome listings in the database. Genes on a particular chromosome can be displayed in alphabetical order or, when mapped, in linkage order. The consensus maps were generated by Professor R. Appels and colleagues, but while the genes on the maps are listed, they are still to be crated fully into the database. While we have to adapt to the increasing universality of genetics across species, we must not lose track of our agricultural background and the fact that our organism is wheat. Farmers grow wheat!

The curator panel for the Catalogue continues to expand. It is only appropriate that Yukiko Yamazaki be recognized for her role in this project, following an initial discussion with a group of Japanese scientists in Tokyo in 2000. Since the 9 IWGS, Gary Hart and Mike Gale have retired and Jorge Dubcovsky was co-opted. Rudi Appels will be helping to incorporate mapping information. With the increasing cloning, sequencing and transformation, Olin Anderson will join the team to assist in those areas. Despite her recent move to the USA, Katrien Devos will continue her significant role in preparation of the annual supplements. Some recent revisions in the protein section were conducted by Craig Morris. From time to time I seek help and advice from various colleagues in revising particular sections of the Catalogue and I express my gratitude to all those named as well as unnamed. Over the past years I have been assisted by a number of people with aspects of the Catalogue, Supplements and records, and I especially recognize assistance from Catherine Cupitt and Fran Siemon. Until my retirement in 2000 my position and research within the University of Sydney was supported by the Grains Research and Development Corporation. I thank the University and the Director of the Plant Breeding Institute, Professor Peter Sharp, for allowing me to continue to work in an honorary capacity.

I record our thanks to the editorial committees and editors of Wheat Information Service and Annual Wheat Newsletter for publishing annual supplements and the managers of GrainGenes for displaying the Catalogue and Supplements on their website.

My usual request for advice on the catalogue (your catalogue!) is more imperative than ever before. Please advise us of omissions, errors, typos so we can fix them and your suggestions on better ways to provide and display wheat genetics information are always welcome.

The Japanese Connection: In 1996 Dr. Yamazaki joined the 'Wheat network of Japan' whose objective was to construct a wheat resource database for Japanese scientists. The 1998 catalogue was seen as a basis for that resource. Whereas it was recognized that a database of the 1998 catalogue would be relatively easy to produce, it was quickly realized that maintenance would be very difficult. The most recent of many versions of MacGene now includes an ever expanding range of tools that permit user-friendly revisions and additions of new information. The MacGene project team included: T. Yamakawa, K. Watanabe, E. Koi, Y. Abe, S. Yano and Y. Yamazaki.

R.A. McIntosh July, 2003

1. Recommended Rules for Gene Symbolization in Wheat

(Adapted from the International Rules of Genetic Nomenclature)

1. In naming hereditary factors, the use of languages of higher internationality should be given preference.
2. Symbols of hereditary factors, derived from their original names, should be written in italics, or in Roman letters of distinctive type.
3. Whenever unambiguous, the name and symbol of a dominant should begin with a capital letter and those of a recessive with a small letter (see also special rules for symbolizing biochemical and DNA loci and host:pathogen/pest systems).
4. All letters and numbers used in symbolization should be written on one line; as far as possible no superscripts or subscripts should be used.
5. The plus sign (+) will not be used in symbolization of hereditary factors in wheat.
6. Two or more genes having phenotypically similar effects should be designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) will be designated in accordance with two procedures:
(i) in sequential polymeric series where an Arabic numeral immediately follows the gene symbol; e.g., *Sr9*.
(ii) in orthologous sets where the basic symbol is followed by a hyphen ("-") followed by the locus designation taking the form of the accepted genome symbol and a homoeologous set number represented by an Arabic numeral; e.g., *Adh-A1* designates the A-genome member of the first *Adh* set. Different alleles, or alleles of independent mutational origin, are designated by a lower-case Roman letter following the locus number designation; e.g., *Sr9a*, *Adh-A1a*. (See also guidelines for nomenclature of biochemical and DNA loci).

6.1 Temporary symbol designations: Where linkage data are not available, provision has been made for temporary symbols. These shall consist of the basic symbol followed by an abbreviation for the line or stock and an Arabic number referring to the gene; e.g., *SrFr1*, *SrFr2*, etc., refer to two genes for reaction to *Puccinia graminis* in cultivar Federation. It is recommended that official records of temporary

designations be kept, but it is not essential that subsequent numbers from other laboratories (e.g., *SrFr3*) be checked against earlier numbers either phenotypically or genetically.

7. Inhibitors, suppressors, and enhancers are designated by the symbols *I, Su*, and *En*, or by *i, su*, and *en* if they are recessive, followed by a space and the symbol of the allele affected.
8. In wheat and related species, linkage groups and corresponding chromosomes are designated by an Arabic numeral (1-7) followed by genome designated by a capital Roman letter; i.e., for hexaploid wheat of group *aestivum* (Morris and Sears {1038}), 1A-7D. This system supersedes the original designations using Roman numerals; i.e., I-XXI. The designations for homoeologous group 4 chromosomes of wheat are as agreed at Workshop I, 7th International Wheat Genetics Symposium, Cambridge, UK (see Proceedings, Miller TE & Koebner RMD eds. pp. 1205-1211); that is, the previously designated chromosome 4A was redesignated 4B and the previous 4B was redesignated 4A. Consequently, the former 4AS became 4BS and the former 4AL is 4BL. Likewise, the former 4BS and 4BL were redesignated 4AS and 4AL, respectively. Chinese Spring is accepted as having the standard chromosome arrangement. Chromosome arms (or telocentric chromosome derivatives) are designated S (short), L (long), on the basis of relative arm length within the chromosome. In the case of equal arms they are arbitrarily designated S or L on the basis of homoeology with the short or long arms of the other chromosomes of their homoeologous group (see Workshop I Proceedings of the 7th International Wheat Genetics Symposium).
9. Genetic formulae may be written as fractions, with the maternal alleles given first or above. Each fraction corresponds to a single linkage group.
10. Chromosomal aberrations should be indicated by the abbreviations Df for deficiency, Dp for duplication, In for inversion, T for translocation, and Tp for transposition. In wheat there are a number of genes derived from related species by introgression. Such genes in different instances reside at different locations. One location may be taken as standard. Other locations will be considered as transpositions relative to a designated standard. When a gene does not reside in its standard chromosome position, the new chromosome designation may be given in brackets following the gene designation; e.g., *Hp* (Tp 6D) refers to a line carrying the introgressed "hairy neck" gene on chromosome 6D instead of 4B which is taken as standard. Alternatively, the chromosome involved may be described as a translocation. Guidelines for the description of translocated chromosomes both within wheat, and between wheat and alien chromosomes are provided in {705}.
11. The zygotic number of chromosomes is indicated by 2n, the gametic number by n and the basic number by x.
12. Symbols for extra-chromosomal factors should be enclosed within brackets and precede the genetic formula.

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

2.1 Biochemical nomenclature: Biochemical nomenclature should be in accordance with the rules of the Joint Commission of Biochemical Nomenclature (JCBN) of the International Union of Pure and Applied Chemistry. The nomenclature recommended by the JCBN is published periodically in major international biochemical journals, such as the Journal of Biological Chemistry and the European Journal of Biochemistry. Also, for enzymes, the publication Enzyme Nomenclature {035,036} may be consulted. Enzymes and other macromolecules have both formal and trivial names. The formal name should be given the first time a macromolecule is mentioned in a publication; the trivial name or an abbreviated name may be used subsequently. For example, ADH is the commonly used abbreviation for aliphatic alcohol dehydrogenase (E.C.1.1.1.1; Alcohol: NAD+ oxidoreductase).

2.2 Basic symbol: The basic symbol for a gene locus should consist of a two-, three-, or four-letter abbreviation of the trivial name of the enzyme, protein, or other macromolecule affected. The initial letter should be a capital and all characters in the symbol should be italicized.

2.3 Loci specifying the structure of similar macromolecules: Non-allelic gene loci that specify the structure of similar non-enzymatic proteins, of enzymes that catalyze the same or similar reactions, or of similar RNA molecules should be assigned the same basic symbol. The remainder of the symbol for each such locus should be formulated in accordance with one or the other of two procedures, depending upon whether or not evidence is available to assign the locus to an homologous set.

2.3.1 *Loci that are members of an orthologous set.* The basic symbol should be followed by a hyphen (-), the accepted symbol for the genome to which the locus belongs and an homologous set number in the form of an Arabic numeral. For example, *Adh-A1, Adh-B1, Adh-D1* and *Adh-E1* designate the A-, B-, D-,

and E- genome members, respectively, of the first-designated homologous set of aliphatic alcohol dehydrogenase structural gene loci. Identification of a minimum of two members of a set is required to use this nomenclature.

2.3.2 *Other loci*: In the absence of evidence to assign loci to an homologous set, they should be designated in sequential series by a common basic symbol followed immediately by an Arabic numeral. If evidence to assign the loci to an homologous set is obtained subsequently, the loci should be redesignated in accordance with the procedures in section 2.2.1.

Rye loci should be designated in accordance with these procedures (see {1448}). For barley loci, the procedures described in section 2.2.1 should be used when designation of a locus as a member of an homologous set of Triticeae loci is desired; otherwise, barley genetic nomenclature should be employed. Thus, for example, *Adh-H1* and *Adh-R1* designate the H- and R- genome members, respectively, of the *Adh-1* set of loci.

Evidence regarding phylogenetic relationships among structural genes may be obtained by comparative studies of (1) nucleotide sequences and other molecular properties of genes, (2) physical and/or biochemical properties of gene products, and (3) intra-chromosomal map positions and/or physical locations of genes in homoeologous chromosomes or segments. Criteria for determining whether or not gene loci that encode isozymes are homologous and, for homologous gene loci, whether they belong to the same or different homologous sets, are described in {512}. Most of the criteria are also applicable to non-enzymatic proteins. The evidence that is the basis for designating gene loci as members of an homologous set should be stated in the publication in which symbols for the loci are proposed.

2.4 Alleles: Different alleles are designated by a lower case italic letter following the locus designation. For example, *a-Amy-A1a* and *a-Amy-A1b* are two alleles of the A genome *a-Amy-1* locus. One strain should be designated the prototype strain for each allele discovered, since variation that has not been detected by the methods used may be present within each allelic class. Currently, Chinese Spring should be the prototype for allele 'a'. If an apparently identical allele in other strains is found by new methods to be different from that in the prototype strain, it should be assigned a new lower case italic letter and a prototype strain designated. This system allows the orderly assignment of symbols to newly-identified alleles and allows ready comparisons of new variants with previously reported variants.

3. Gene complexes

Gene complexes, also called compound loci, consist of a number of functionally related genes that are genetically closely linked. Whether composed of a few or many genes, a gene complex should be assigned one symbol, in accordance with the procedures described in section 2. The individual genes that compose gene complexes may be designated by adding a hyphen (-) and an Arabic numeral to the locus designation. For example, *Glu-A1-1* and *Glu-B1-1* designate, respectively, the A- and B- genome genes that encode the x-type glutenin-1 proteins while *Glu-A1-2* and *Glu-B1-2* designate, respectively, the A- and B-genome genes that encode the y-type glutenin-1 proteins. Different alleles of genes that are components of gene complexes may be designated following the system described in section 2.3 but with the lower-case italic letter following the gene designation rather than the locus designation. For example, *Glu-A1-1a* designates the Chinese Spring A genome allele that encodes the x-type glutenin-1 protein.

Triticeae enzyme and protein gene loci are commonly initially identified and assigned designations based on studies of aneuploid strains that lack and/or contain extra copies of whole chromosomes or telosomes. Consequently, evidence may be obtained for the production of two or more similar enzyme or protein promoters by one chromosome arm without genetic evidence as to whether or not the promoters are the products of one gene, of different genes that are members of a gene complex, or of two or more genes that are not members of one gene complex. In these situations, only one locus designation for similar proteins or enzymes should be assigned to a chromosome arm until recombination evidence indicates otherwise.

4. Phenotype Symbols

The basic symbol for a macromolecule should be identical to the basic symbol for the locus or loci that encode the macromolecule (see Section 2.1) except that each letter in the symbol should be a capital Roman letter. For a macromolecule encoded by the members of a homologous set of loci, the phenotype symbol should consist of the basic symbol followed by a hyphen (-) and the same Arabic numeral as is contained in the genotype symbol. For example, the products of the *Adh-1* set of gene loci are designated ADH-1.

5. Symbols for DNA Markers and Alleles

This section describes nomenclature for genetic markers that are detected at the DNA level,

including those detected by hybridization with DNA probes [e.g., RFLPs (restriction-fragment-length polymorphisms)] and by amplification with primers [e.g. RAPDs (random-amplified-polymorphic DNAs) and STSs (sequence tagged sites, including loci detected with sequenced RFLP clones, sequenced RAPDs and clones containing micro- and mini-satellites).

5.1 Basic symbol: The basic symbol for DNA markers of unknown function should be 'X'

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

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

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

5.3 Duplicate DNA-marker loci: DNA markers located in the same chromosome that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the addition of a period and an Arabic numeral immediately after the chromosome designation. For example, *Xpsr933-2A.1* and *Xpsr933-2A.2* designate duplicate loci located in 2A that are detected with probe PSR933. As when two or more enzyme or protein promoters are produced by one chromosome arm, multiple DNA fragments from one chromosome arm that hybridize to one probe or that are amplified by one pair of primers (or by one primer) should be assigned to only one locus until recombination evidence indicates otherwise. As noted in Section 5.1, DNA markers located in different chromosomes that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the chromosome designation.

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

normally should be stated in the first publication describing an allele.

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

Finally, *Xbgl485(Ger)-4D.2* may be abbreviated on a map of 4D by omission of the hyphen, the chromosome designation and the period, i.e. as *Xbgl485(Ger)2*. In some contexts it will also be possible to abbreviate the symbols for alleles as, for example, *BamH1b*, or even simply *b*.

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

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

6. Symbols for loci and alleles controlling quantitative characters

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

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

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

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

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

7. AFLP amplified fragment length

polymorphism

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format '*XxyzAN1N2N3*, where '*X*' is the usual symbol for a DNA marker of unknown function; 'xyz' is the usual laboratory designator (e.g., *kg* for Keygene); A is a single upper-case letter denoting the rare-cutter enzyme used, e.g., P for *PstI*, etc.; N1 and N2 are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N3 is a three-digit number corresponding to the molecular weight of the fragment.

The foregoing should be considered only as a proposal at this time as no AFLPs are listed in the catalogue. Comments regarding the proposal are welcomed and should be sent to the authors.

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

1. All genes for resistance (low reaction) will be designated with a capital letter, even though they behave as recessive alleles. Moreover, the dominance of individual alleles may vary with the environment, the genetic background and the particular culture of the pathogen. Symbols for disease/pest-reaction genes are used by people of many disciplines, and since they are frequently communicated verbally, dominance relationships are not clear. Those alleles initially designated with a lower-case letter have tended to be miswritten with a capital. For example, the usually recessive resistance allele *Sr17* was initially designated *sr17* but its presentation in some reports was confusing.
2. Where no recombination occurs between genes conferring resistance to more than one pathogen, the gene(s) segment shall be designated separately for each disease; e.g. *Pm1*, *Sr15* and *Lr20*.
3. Where recombination occurs between two closely linked factors for reaction to a pathogen, the recombined 'allele' may be designated as a combination of the separate alleles; e.g. the recombined 'allele' obtained by combining *Lr14a* and *Lr14b* was designated as *Lr14ab*. The decision as to whether a designation should be as a combination or as separate genes shall be at the discretion of particular workers. A maximum value of 1 crossover unit for designation as an 'allele' is suggested. Although the need to consider uniform symbolization of corresponding genes in pathogens is recognized, no recommendations are proposed.

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* In part indicates basis for name.

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10. Organization of the Catalogue

Information is given in the following order, where possible:

1. Gene symbol, with principal reference to the particular gene or gene symbol in parenthesis.
2. Synonyms (with reference(s) in parenthesis).
3. Chromosome and chromosome-arm location, if known, with references in parenthesis.
4. Stocks carrying the particular gene in order of presentation.

   i: = Near-isogenic stocks, with number of backcrosses indicated.

   s: = Homologous chromosome-substitution stocks, with number of backcrosses indicated.

   v: = Cultivaral hexaploid stocks in increasing order of genetic complexity.

   v2: = Cultivaral hexaploid stocks with two or more genes affecting the trait

   d: = Alien chromosome addition line.

   su: = Alien chromosome substitution line.

   itv: = Near-isogenic tetraploid stocks.

   tv: = Tetraploid stocks.

   tv2: = Tetraploid stocks with two or more genes affecting the trait

   dv: = Diploid stocks.

   al: = Alien species.

   ma: = Reference to mapping information involving agronomic and morphological traits and molecular markers under gene entries will generally be restricted to values of less than 10 cM. Values higher than this would be of less use in genetics and plant breeding and, in any case, should be available from the genetic linkage section of the Catalogue or from genetic maps. Higher values will be used in the case of flanking markers.

Where more than a single gene affecting a character is listed, e.g., Gabo *D3* {645} under *D1*, the reference refers to the literature source reporting *D1* in Gabo, and not necessarily to *D3*.

Abbreviations: CS= Chinese Spring; Tc=Thatcher.

Note: Due to limitations with the database, Greek symbols were converted to words or Roman letters (alpha or a, beta or b, etc.). For author names with accents or special letters, the most similar Roman letter was used.

11. DNA Markers

See 'Genetic nomenclature proposal' above for a proposal for the naming of AFLP loci. The following list catalogues DNA-marker loci that (1) have been detected either by Southern hybridization of DNA restriction fragments or as sequence-tagged-sites by amplification of DNA fragments with primers and (2) have been localized to specific wheat chromosomes. The formal listings of the 5S-RNA or 18S-5.8S-26S rRNA (Nor) loci are included elsewhere in the catalogue. No attempt has been made to list orthologous loci in related species, although many have been identified {e.g., 1329,1330}. In addition we list genes that appear on consensus maps prepared by Dr R. Appels and various colleagues. The nomenclature used is that originally published in the 1994 Supplement, except for some loci detected with 'known-function' clones for which other nomenclature has been used in the publications cited. The reference(s) that follow the locus symbols designate the publication(s) in which the chromosomal locations or map positions of the loci were first reported. References that are in parentheses { } contain the listed locus symbol. Temporary symbols for a few DNA markers detected with known-function DNA probes are marked with an asterisk, *, ; these are temporary, pending assignment of the laboratory designator.

Synonyms are listed in parentheses [ ] in the second column. Where symbols were assigned by the curators to comply with nomenclature guidelines the same reference numbers follow the gene symbol and the synonym. Other chromosomes bearing markers detected with the same probe or the same primers are indicated in parentheses after the probe or the primers. To permit flexibility in using the database, each homoeologous group is bracketed separately. Three revisions were made in the organization of

the DNA Markers section, as follows:

1. Markers in homoeologous chromosome groups 4, 5 and 7 (with the exception of those in *T. monococcum* chromosome $4A^m$; see #2 below) are listed in groups composed of loci located in homoeologous segments. The groups include the six classical homoeologous arm groups, namely, 4S (4AL:4BS:4DS), 4L (4AS:4BL:4DL), 5S (5AS:5BS:5DS), 5L (5AL:5BL:5DL), 7S (7AS:7BS:7DS) and 7L (7AL:7BL:7DL), and five new groups, 4AL:4BL:4DL, 5AL:4BL:4DL, 4AL:5BL:5DL, 7BS:5BL:7DS, and 7AS:4AL:7DS. Evidence is not available regarding the correct group location for a few of the markers listed in groups 4S, 4L, and 7S; a double asterisk (**) after the locus reference identifies these markers.
2. Markers in *T. monococcum* $4A^m$ are listed separately (under $4A^mS$, $4A^mL$, or $4A^m$), due to the several rearrangements that distinguish 4A and $4A^m$.
3. Superscripts appended to locus references designate the species in which loci were analyzed, as follows:
   '1' *T. aestivum*,
   '2' *T. turgidum*,
   '3' *T. monococcum*,
   '4' *Ae. tauschii*, and
   '5' Species hybrid,
   with the exception that the superscript is omitted for markers studied only in *T. aestivum*.

a' Designates primer pairs that identify loci that cap the genetic maps. The forward primer is a degenerate telomeric sequence and the reverse primer is a specific sequence. Each primer combination identified multiple loci; however, only telomeric *(Tel)* loci are included {888}.

b' Designates loci detected by hybridization with DNA clones whose sequences are largely homologous with known gene in the EMBL database (1392).

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

Order of presentation: Gene, synonym, map location (approximate distance in cM from the terminal end of the short arm), probe, all known locations in homoeologous groups. In the output files genes appear in alphabetical order with locus numbers in ascending order.

(Editorial remarks)

This article is a partial citation from the report by Dr. R. A. McIntosh at the 10th International Wheat Genetics Symposium (Paestum, Italy). The citation was allowed by the author as well as Dr. N. E. Pogna, Chairperson of Local Organization Committee. The full text and the contents are available in Proc. 10th IWGS (edited by N. E. Pogna et al; Istituto Sperimentale per la Cerealicoltura, Via Cassia 176, 00191 Roma, Italy: http://www.cerealicoltura.it), or through data base KOMUGI (http://www.shigen.nig.ac.jp/wheat/genecalog/macgene/

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Record

The 10th International Wheat Genetics Symposium (TIWGS)

The Tenth International Wheat Genetics Symposium (TIWGS) was held at Ariston Conference Centre in Paestum, Italy, in 1 - 6 September 2003.

The symposium was organized by the local organization committee under chairpersonships of Dr. Norberto Pogna, Dr. Gian Tommaso Scarascia Mugnozza, and Dr. Angelo Bianchi with the direction from the International Organization Committee (chaired by Dr. Peirre Hucl). Members of the Local Organizing Committee are; Drs A. Bianchi, A. Blanco, G. Boggini, A. Bozzini, C. Ceoloni ,R. D'Ovidio, N. Di Fonzo, D. Lafiandra, M. Motto, E. Porceddu, N. Pogna, L. Rossi, F. Salamini, M. Sari Gola, G. T. Scarascia Mugnozza, P. Spagnoletti Zeuli and P. Tusa. It was patronized by Italian Ministry of Agriculture and Forestry.

365 wheat scientists were formally registered from 56 countries. They discussed in the following seven sessions with 101 oral and 322 poster presentations;

1) Evolution and Genetic Diversity
2) Cytogenetics and Germplasm Evaluation
3) Classical and Molecular Breeding
4) Transgenesis
5) Structural and Functional Genomics
6) Biotic and Abiotic Stresses
7) Grain Quality

The poster and oral papers presented at the Symposium were printed in three volumes of proceedings. The proceeding is available by mail order to the local organization committee c/o Istituto Sperimentale per la Cerealicoltura, Via Cassia 176–00191, Roma, Italy (phone;+39 06 32 95 705,and fax;+39 06 36 30 60 22) or by web order through http://www.cerealicoltura.it/.

In addition to the research topics, workshops were organized as follows;

1) Conservation of Genetic Resouces and its International Cooparation.
2) 100 Years of Wheat Breeding and Breeding Goals in the Third Millennium
3) International Project on Wheat Genomics
4) Gene Symbol and Gene Catalogue

International Triticeae Mapping Initiative (ITMI) workshop had provided an opportunity for presentations and discussions on mapping of Triticeae species.

In the business session held in the last program on Sept. 6, the following four issues were discussed:

1) Reports from Wheat Information Service: 1) Historical review of WIS, 2) Difficulties and limitation of publishing in the present style, 3) Publishing an special issue of 100th anniversary in 2006, 4) Possibility to shift to publication on web.
2. The 11th Symposium: After voting among two candidate countries, it was decided that the next symposium will be in Australia in 2008.
3. Honoring distinguished contributors to wheat genetics research: Dr. Mike Gale (England), Dr. Robert McIntosh (Australia), Dr. Koichiro Tsunewaki (Japan).
4. New board of International Committee: Drs. N. Pogna (Chair, Italy), O. D. Anderson (USA), P. Sharp (Australia), D. J. Liu (China), H. Tsujimoto (Japan), and P. Hucl (Canada).

The symposium gathered various and informative information, and eager discussion were held during and after the sessions. Especially they must understand the studies on functional genomics had provided various and new aspects of wheat research including bioinformatics and systematic molecular breeding. The researchers should have realized significance of genetic studies on biotic and abiotic stresses for basic science and practical breeding and large potential with wheat study on it to solve worldwide food problems. Among all, importance and effectiveness of international cooperation on conservation and exchange of genetic stocks and resources, construction of genetic maps, and databases for stocks and gene clones were commonly realized. Especially

the database system of wheat gene catalogue constructed by Dr. McIntosh , Dr. Y. Yamazaki and others would be appreciated very, as a big fruit of the 10th IWGS. The database catalogue was provided to the attendances with a CD. It is also visible through the database KOMUGI (http://www.shigen.nig.ac.jp/wheat/genecalog/macgene/).

The symposium was held in Paestum where is a Mediterranean resort area inherited pre- and mid-Roman histories. Without doubt, the attendance must have enjoyed the programmed evening events as well as post-symposium tours.

(A tentative report for 10th IWGS by Tetsuo SASAKUMA, Kihara Institute for Biological Research, Yokohama, Japan)

Editorial remarks

Many subscribers must have enjoyed in attending the 10th International Wheat Genetics Symposium held in Paestum, Italy in the last September. To researchers who could not attend it, please know the atmospheres of fruitful and enjoyable meeting in the present issue.

We are very proud that Dr. Bob McIntosh (Univ. of Sydney) and Dr. Yukiko Yamazaki (National Institute of Genetics, Japan) had contributed for construction of new system of gene catalogue of wheat. Since 1983, the annual supplement of wheat gene catalogue has been printed in WIS, and it was one of the raison d'ètre of WIS. Now, since the new system has established (it is called as MacGene after initializing the contributors), updating is easy, and construction of 'my catalogue' is possible after downloading from the database of KOMUGI (http://www.shigen.nig.ac.jp/wheat/genecalog/macgene/).

We are glad to have continuous contributions of sending manuscript of research article. The proportion of acceptance after reviewing is about 40% in the last year. However, there are several problems faced: 1) financial difficulty, 2) contribution from limited countries, 3) poor quality for scientific description and manner (some had sent the revised article after rejection). Please support to develop WIS as the worldwide informative journals.

December, 2003
Editors of WIS
K. Nishikawa (Chief), T. Sasakuma, H. Tsujimoto and K. Furukawa (Publication secretary)

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.

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