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Research article

Study on utilization of the dominant male sterile triticale in breeding

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Summary

This paper describes the fertile segregating progenies derived from crosses and backcrosses between male sterile triticale lines and hexaploid and octoploid triticale and the populations established for rotational selection. Gene recombinations took place extensively for breaking down adverse gene linkages and improvement of the frequency of favorable genes, seed plumpness, and the synthesis of good characters.

Key words: triticale, male-sterile line, rotational selection

Introduction

Triticale, first grown in China in the 1970's, has shown significant potential in disease resistance, stress tolerance, nutritional quality and yield. However, it has not been used extensively because of poor traits such as plant height, late maturity, low seed test weight and low flour yield due to shrivelled seed. Triticale was grown on approximately 0.4 million mu (one hectare is equal to 15 mu) in the early 1980's in China. However, the sown area later decreased because of the problems mentioned above. Shrivelled seed and the adverse characters of triticale are controlled by multiple factors and are linked with adverse genes; thus the problems cannot be resolved with conventional breeding methods (Wang and Sun 1986). We have done several thousands cross combinations and long term selections without success. The dominant male sterile materials are good tools for rotational selection of triticale. They can be used in the short term for gene recombination and breaking down of adverse gene linkage, but they can also improve the frequency of good genes and the good traits of the dispersed multiple genes can be combined (Liu and Deng 1986; Ji and Deng 1986; Darvey 1986). Therefore, it is an effective method for improving the plumpness of seed and adverse characters of triticale.

Materials and methods

The establishment of triticale male sterile lines

In 1982, crosses were made between male sterile Chinese Spring Ms2, and the rye AR132. The *Ms2* dominant male sterile gene was transferred into octoploid triticale through hybrid's chromosome doubling in the second year. Triticale sterile lines with different characters had been bred through crossing with hexaploid triticale OH1, WOH45, WOH63 and octoploid triticales H1162, H2645, H8301 in 1983-1987.

Group combination

The triticale sterile lines were divided into groups according to breeding objectives such as maturity period, plant height, grain quality, and as food or feed. Ten to 15 lines were selected from each group for intercrossing; a) semi-diallel crosses: fifteen lines for each group and 105 single crosses were made according to the formula n(n-1)/2; b) random crosses: from 1988, sterile plants were interplanted for natural random crosses. Thus the genes in the CO population can be fully combined.

Rotational selection

According to the breeding objectives for each group, 200-500 sterile and fertile plants were

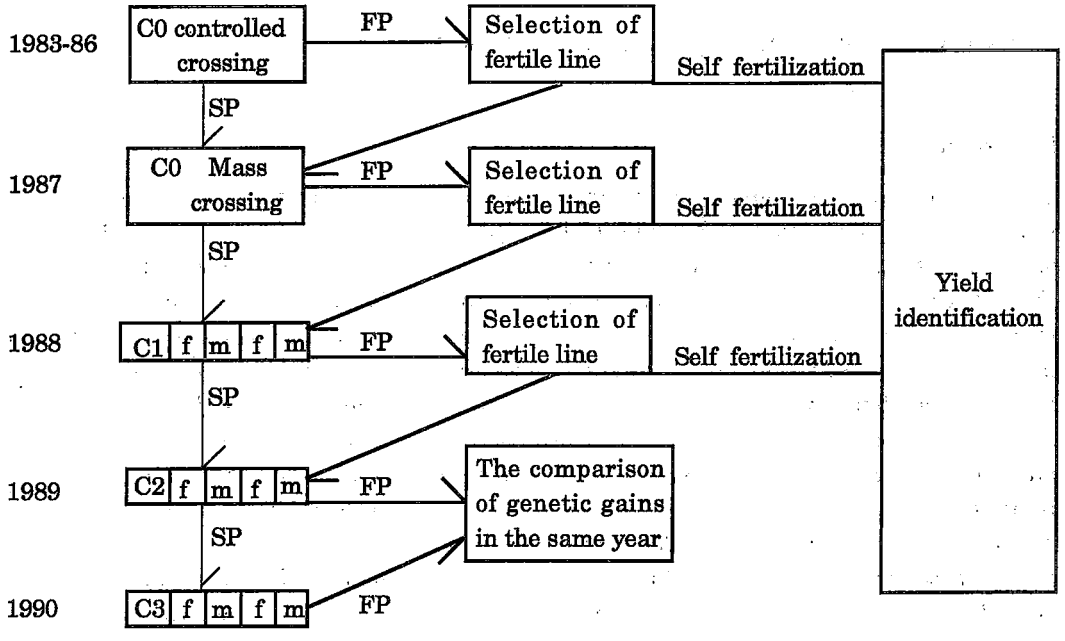

Fig. 1. Rotational selection procedures for triticale.
SP: sterile plants; FP: fertile plants; f: female parent row; m:male plant row.

selected among CO population and sterile plants were mixed and entered into the C1 (Fig.1). The fertile plants whose main traits exceeded the average of the population in female parent row were selected and mixed as male plants of C1 after testing. Selection for C2 was carried out according to the selective method for C1. Thus hybridization and selection can be carried out once at each cycle. Selection concentrated on the female gamete of fertile plants. Selection aimed to improve characters such as plant height, bushiness, winter hardiness, disease resistance, date of heading, etc. It should be carried out before anthesis in order to reduce the diffusing of adverse genes among the population. The results of selection were: a) comparison between each cycle, and b) comparison with conventional selection. The distribution of seed plumpness and the important traits of fertile plants were assessed after each cycle of selection.

Seed plumpness is divided into five grades according to the degree of endosperm development and pericarp smoothness; 1 grade: the endosperm is full of seed coat and pericarp is the most smooth, 2 grade: the pericarp is quite smooth, 3 grade: the endosperm is about 3/4 full of seed coat, 4 grade: the endosperm is about 1/2 full of seed coat, and 5 grade includes others. Each plant may evaluate 2.5, 3.5, or 4.5 seed plumpness depending on percentage of different grade seeds.

Results and discussion

Fertility segregation and utilization of the male sterile gene of Ms2 in triticale

The dominant male sterile *Ms2* gene has been located on the short arm of 4D chromosome by Liu and Deng (1982). We have made several crosses and backcrosses between the male sterile triticale Ms2 and hexaploid and octoploid triticale in order to study and utilize its expression in triticale. The values of χ^2 in Table 1 indicate that the ratio between the sterile plants and the fertile

Table 1. The fertile segregation after crossing and backcrossing of dominant male sterile triticale with different ploidy triticale

Generation	Cross	No. of plants	No. of sterile pl.(S)	No. of fertile pl.(F)	S : F	χ^2	P
(8MS x 8) F_1	244	2794	1367	1472	0.96:1	1.79	0.5-0.2
(8MS x 6) F_1	140	1510	718	792	0.91:1	3.62	0.2-0.05
[(8 x 6)MS x 6] BC_1	50	726	224	502	0.45:1	106.45	<0.01
[(8 x 6)MS x 8] BC_1	69	867	276	591	0.47:1	114.45	<0.01
{[(8 x 6)MS x 6]MS x 6}BC_2	30	332	72	250	0.29:1	106.46	<0.01
{[(8 x 6)MS x 6]MS x 6}MS x 6 BC_3	4	81	11	70	0.16:1	42.98	<0.01

MS: male sterile plants and genotype is *Ms ms*; 8: octoploid triticale; 6: hexaploid triticale and genotype is *ms ms*

plants of octoploid (AABBDDRR) F_1 is 0.96: 1; the ratio between the sterile plants and the fertile plants of (AABBRRD) F_1 of octoploid and hexaploid triticale is 0.91 : 1 which all conform to the predicted ratio 1 : 1. However, the number of sterile plants significantly decreased according to the increase of backcross number. The ratios were 0.47 : 1; 0.45 : 1; 0.29 : 1 and 0.16 : 1 respectively. These ratios are identical with the elimination ratio of 20-50% of D genome chromosome as studied by H. Kihara (Nishiyama 1954). The above results indicate that the dominant male sterile *Ms2* gene expressed steadily. The stamens of the sterile plants is abortive, which induces self sterility. The glume opened normally and was able to produce seed after open or artificial pollination, so it is useful to gene recombination. The stamens and pistil of fertile plants develop normally and they are useful to self-fertilize. Therefore, the dominant male sterile triticale is a very useful cross tool for gene recombination and rotational selection.

Transfer of Ms2 male sterile lines

The sterile plants not only play a role in recombination of genes in rotational selection, but also provide half of the genetic factors of hybrids. Nearly all the lines belong to 4-5 grades, because of their narrow genetic base and poor traits, especially poor plumpness. Therefore, we used AH602 AH685, AH999, AH1005 and 20 triticale lines with different traits in transfer breeding before mass crossing to improve the plumpness and other traits of the primary sterile lines. The plumpness had decreased 0.85 class, from 4.52±0.36 in 1983 to 3.67±0.54 in 1986 (Table 2), through improvement, and the plumpness of all triticale sterile lines had increased nearly one grade. Some combinations even reached 3.2 grade. Thus they have created good base for rotational selection.

Table 2. Seed plumpness improvement of triticale sterile lines

Years	No. of combination	Mean plumpness	Standard deviation
1983	59	4.52	± 0.36
1984	156	4.01	± 0.63
1985	292	3.73	± 0.56
1986	327	3.67	± 0.54

Preliminary results of rotational selection

First, the distribution level of plumpness has increased. It can be seen from the comparison of the mean plumpness of fertile plants in Table 3. C0-C1=0.24, C0-C2=0.72, C0-C3=0.80, C1-C2=0.48, C1-C3=0.56, C2-C3=0.08. The number of fertile plants in C1 population averaged 3.43 and it has not exceeded the mean value 3.26 of parents. However, the number of fertile plants in C2

Table 3. Comparison of preliminary results of rotational selection for plumpness

Population		Plumpness grade									
		2	2.5	3	3.5	4	4.5	5	n	Mean	Standard deviation
CO	S No.	1	4	85	76	134	24	9	333	3.67	0.54
	%	0.3	1.2	25.5	22.8	40.2	7.2	2.7	99.9		
	P No.	212	651	3869	3040	2205	313	2.0	10292	3.36	0.52
	%	2.1	6.3	37.6	29.5	21.4	3.1	0	100		
C1	S No.	2	2	52	123	44	10	3	236	3.52	0.45
	%	0.9	0.9	22.0	52.1	18.6	4.2	1.3	100		
	F No.	2	2	75	160	43	0	0	282	3.43	0.33
	%	0.7	0.7	26.6	56.7	15.3	0	0	100		
	P No.	10	9	118	144	18	2	0	301	3.26	0.40
	%	3.3	3.0	39.2	47.8	12.6	0.7	0	100		
C2	S No.	3	13	189	162	77	19	5	468	3.40	0.49
	%	0.7	2.8	40.4	34.6	16.5	4.0	1	100		
	F No.	34	43	95	47	20	0	0	239	2.95	0.56
	%	14.2	18.0	39.7	19.6	8.4	0	0	100		
	P No.	6	27	373	80	9	10	0	505	3.09	0.35
	%	1.2	5.3	73.9	15.8	1.8	2.0	0	100		
C3	S No.	8	77	234	287	62	3	3	674	3.25	0.46
	%	1.2	11.2	34.9	42.7	9.2	0.4	0.4	100		
	F No.	23	94	266	30	1	0	0	414	2.87	0.34
	%	5.5	22.7	64.3	7.3	0.2	0	0	100		
	P No.	14	46	207	135	113	46	1	562	3.29	0.59
	%	2.5	8.2	36.8	24.0	20.1	8.2	0.2	100		

S: sterile plant; P: bead progeny low; F: fertile plant

population averaged 2.95 which exceeds the mean value 3.09 of their parents. The plumpness of sterile plants in each rotation (year) has increased by 0.23 which is twice the average conventional lines. In addition, the plumpness proportion of each grade in a population has changed. e.g. the percentage of seeds belonging to 4-5 grades in populations of sterile lines or fertile lines has decreased from 40% to 1%, but the percentage of seeds belonging to grade 3 or above has increased significantly, especially in the population of C2 fertile lines, the percentage of seeds of grade 2 and grade 2.5 has increased from 1% to 15 %. In C3 population the percentage has increased to 20% or more. These results indicate that through rotational selection genes favorable to seed plumpness have increased, thus laying a sound foundation for synthesizing other good traits.

Conclusion

Seed plumpness is a difficult problem in triticale breeding. We have done several thousand of cross combinations and long term pedigree selections, but without good results. Transfer of the dominant male sterile *Ms2* gene into octoploid triticale for rotational selection has been made in an attempt to break down the adverse gene linkage with plumpness and to accumulate the favorable quantitative character genes through extensive gene recombination. We attempted to combine good traits such as early maturity, dwarfness, disease resistance and high yield potential on the basis of higher seed plumpness. Rotational selection for seed plumpness improvement is better than pedigree selection and this is related to the basic materials of sterile plants and group combination of recurrent parents. After this work, the mean value of the population was equal to or exceeded that of their parents and showed that it is an effective way for improving seed plumpness of triticale. Further studies are needed in the future because rotational selection has just entered the third rotation.

In the cross and backcross between male sterile octoploid triticale and hexaploid triticale, the proportion of sterile plants was decreased gradually with the increasing number of backcrosses, and this is related to the loss of the D genome chromosome. However, in some combinations there is still a ratio of 1 : 1 between sterile plants and fertile plants. It means that 4D chromosome has not been lost or that substitutions and translocations of chromosomes may have occurred. Therefore, the sterile line of hexaploid triticale should be used in rotational selection. It is possible to select new sterile lines of hexaploid triticale from our work, thus a new field will be opened for the cross breeding of hexaploid and octoploid triticales and studies on chromosome engineering of triticale.

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Research article

The diversity of resources resistant to scab in Triticeae (Poaceae)

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Summary

Resistance to scab was evaluated using 1463 accessions from 85 species belonging to 17 genera in Triticeae. The results indicated that 31 accessions from 5 species were highly resistant to initial infection and spread. The accessions resistant both to initial infection and spread were mainly found in perennial genera *Roegneria*, *Hystrix*, *Kengyilia*, *Agropyron* and *Elymus*. *Roegneria* was the best resistant genera. The differences of resistance to scab in Triticeae are closely related to their ecological conditions where they grow.

Introduction

Wheat blight or scab, caused by *Gibberella zeae* Petch (=*Fusarium graminearum* Schwabe), has been one of the most destructive disease in warm and humid wheat growing area of the world. Up to now, no cultivars with immunity or resistance to both initial infection and spread within spike tissue have been found in *Triticum* and its relatives including *Aegilops*, *Haynaldia* and *Secale* (Hanson et al. 1950; Liu 1985; Mesterhazy 1987; Tomasovic 1989). In this situation, the diversity of resources resistant to scab has to be evaluated in many other species in Triticeae. In the present paper, results of the survey on the scab resistance in Triticeae are reported.

Materials and methods

The conidia of *Gibberella zeae* Petch used for inoculation of the test materials (Table 1) were obtained according to Schroeder and Christensen (1963). The inoculum was a mixed spore suspension of three isolates from scaby wheat kernels, collected at Chengdu, Yaan and Dujiangyan cities, Sichuan province, China. The concentration of spore suspension was, on the average of 10 slides, about 50 spores per 10 x 10 microscope field. Multifloret and single-floret injection were used for determining resistance to initial infection and to the pathogen spread within spike tissue, respectively.

Table 1. The materials used in the analysis

Genera/species	Number of accessions	Genera/species	Number of accessions	Genera/species	Number of accessions
Aegilops		*Elytrigia*		*Kengyilia*	
Ae. bicornis	3	*Et. bessarabica*	1	*K. kokonorica*	1
Ae. biuncialis	1	*Et. elongata*	2	*K. hirsuta*	1
Ae. caudata	1	*Et. elongatiforme*	3	*K. mutica*	1
Ae. comosa	1	*Et. intermedia*	5	*K. melanthera*	1
Ae. columnaris	2	*Et. pycnantha*	1	*Psathyrostachys*	
Ae. crassa	6	*Et. pontica*	3	*Psa. juncea*	1
Ae. cylindrica	3	*Et. repens*	2	*Psa. fragilis*	1
Ae. juvenalis	20	*Eremopyrum*		*Psa. huashanica*	1
Ae. kotschyi	4	*Er. distans*	1	*Pseudoroegneria*	
Ae. ovata	1	*Er. triticeum*	1	*Pse. spicata*	1
Ae. recta	2	*Er. orientale*	1	*Pse. strigosa*	1
Ae. speltoides	3	*Er. bonaepartis*	1	*Pse. stipifolia*	1
Ae. tauschii	15	*Haynaldia*		*Roegneria*	
Ae. triaristata	3	*Ha. villosa*	2	*R. ciliaris*	26
Ae. umbellulata	1	*Henrardia*		*R. dentata*	1
Ae. triuncialis	1	*Her. persica*	1	*R. dolichathera*	1
Ae. vavilovii	2	*Heteranthelium*		*R. gmelinii*	5
Ae. ventricosa	2	*Het. piliferum*	2	*R. hondai*	1
Agropyron		*Hordeum*		*R. longearistata*	1
Ag. cristatum	13	*H. marinum*	14	*R. nakii*	1
Ag. desertorum	5	*H. gussoneanum*	3	*R. pendulina*	1
Crithopsis		*H. leporinum*	3	*R. sinica*	1
C. delileana	2	*H. murinum*	1	*R. stenostachys*	4
Elymus		*H. bogdanii*	2	*R. stricta*	2
E. caninus	1	*H. chilense*	3	*R. varia*	1
E. cylindricus	3	*H. violaceum*	1	*R. tsukushiensis*	24
E. fibrosa	1	*H. parodii*	1	*Taeniatherum*	
E. dahurious	1	*H. bulbosum*	32	*T. crinitum*	1
E. nutans	1	*H. procerum*	1	*Triticum*	
E. tangutorum	3	*H. depression*	1	*T. monococcum*	5
E. trachycaulus	3	*H. vulgare*	112	*T. timopheevi*	2
E. transhycanus	1	*Hystrix*		*T. turgidum*	159
E. scabrus	1	*Hy. duthiei*	1	*T. aestivum*	912

Resistance to initial infection

The first florets of 12 spikelets per spike were injected with a drop of 5 μl conidial suspension with a microsyringe, and each spike was covered with a cellulose bag. These injected spikelets were daily investigated after inoculation to study the latent period of infection. The assessment of resistance to initial infection was made at maturity stage based on the percentage of infected spikelets as follows: 0 = immune (I), 0.1-50% = highly resistant (HR), 50.1-70% = resistant (R), 70.1-90% = moderately resistant (MR), 90.1-100% and latent period of infection longer than 5 days = susceptible (S), 90.1-100% and latent period of infection shorter than 5 days = highly susceptible (HS).

Resistance to spread

The first floret of one intermediate spikelet per spike was injected with a drop of 5 μl conidial suspension. The disease ratings were recorded at wax maturity stage. The method of disease rating was according to Xu and Fang (1982). The assessment of resistance to spread was based on mean disease rating as follows: 0 = immune (I), 0.1-1.99 = highly resistant (HR), 2.00-2.99= resistant (R), 3.00-3.60 = moderately resistant (MR), 3.61-4.20 = susceptible (S), 4.21-5.00 = highly susceptible (HS).

Results

Resistance to scab was evaluated using 1463 accessions of 85 species belonging to 17 genera of Triticeae. The results indicated that there is no immune accession to scab in Triticeae (Table 2). However, 31 accessions from 5 species were highly resistant to initial infection and to spread. Twenty-eight accessions from 13 species showed resistance to initial infection and high resistance to spread. Thirty-five accessions from 15 species showed moderate resistance to initial infection and high resistance to spread. One accession was resistant both to initial infection and spread. Though 45 accessions were susceptible to initial infection, they were highly resistant to spread. Out of the 45 accessions, 30 were hexaploid common wheat.

The accessions that showed resistance to both initial infection and spread were mainly found in the perennial genera *Roegneria*, *Hystrix*, *Kengyilia*, *Agropyron* and *Elymus*. In particular, 67 out of 69 accessions of *Roegneria* were resistant to both initial infection and spread, the response of which was the best among Triticeae (Table 2).

The accessions which are listed in Table 1, but not included in the Table 2 were sensitive to wheat scab.

Discussion

The differences among genera and species in the level of resistance to scab were closely related to the ecological conditions where they grow. The most resistant genera, *Roegneria*, is distributed in temperate and subtropical zone, and usually thrives in meadows, open shrublands and forests,

Table 2. Resistance types to scab in Triticeae

Resistance types/species	Accessions or cultivars
RII:HR and RPS:HR	
Roegneria ciliaris	Pr166, Pr178, Y83008
R. ciliaris var. *japonesis*	Pr179, Y83009, Pr188, Pr189, II19, II38
R. stenostachys	Pr229, Pr230
R. tsukushiensis var. *transiens*	Pr208, Pr212, Pr213, Pr214, Pr211, Pr218, Pr219, Pr220, Pr221, Pr222, Pr237, Pr205, Pr207, Pr238, Pr239, Pr215, Pr243, Pr244
R. stricta	Y0938
Elymus fibrosa	PI439999
RII:R and RPS: HR	
Roegneria ciliaris	Pr170, Pr171, Y83006, Pr175, Pr252, Pr167, Pr247, Pr249
R. ciliaris var. *japonensis*	Pr203, Pr199, Pr187
R. dentata	MA-100-21-25
R. dolichathera	Y1411
R. gmelinii	H25, H36
R. hondai	Y362
R. pendulina	Y340
R. sinica	Y2094
R. strica	Pr233
R. tsukushiensis var. transiens	Pr245, Pr217, Pr218, Pr210, Pr209
Agropyron cristatum	PI297870
Elymus tangutorum	NWC15-818-2
E. trachycaulus	Pr234
Psathyrostachys junoea	Y1603
RII:MR and RPS:HR	
Roegneria ciliaris	Y83007
R. ciliaris var. *japonensis*	H20, Pr195, Pr198, Y83015, Pr202
R. gmelinii	Y2677, Y2683, Y461
R. longearistata	Y425
R. nakai	Y45
R. varia	Y2466
R. tsukushiensis var. *transiens*	Pr206
Agropyron cristatum	PI229909, PI297869, PI297670, PI314596, PI330685, PI314603, PI314802, PI439929, I-2
Ag. desertorum	IM-25, PI439979, PI340061, A20
Kengyilia hirsuta	Y2366
Elymus caninus	Y341
E. dahuricus	NWC28-8-81-4
E. nutans	Y22
E. tangutorum	Pr80, Y503

(Table 2. continued)

Resistance types/species	Accessions or cultivars
E. trachycaulus	Pr235, Pr236
E. transhycanus	Y137
RII:R and RPS:R	
Hystrix duthiei	
RII:S and RPS:HR	
Triticum acstivum	cvs. Wangshuibai, Zaohongmang, Baiyuhua, Shuilizhan, Gunmai, Sanyuhuang, Huoshaotian, Yazitou, Tongzhutou, Zimai, Hongkemai, Heshangtou, Bagutao, Baimangmai, Jiangmai, Yanzisanyuehuang, Huangkeguangtoumai, Guangtoumai, Changmangmai(Guizhou), Huanglamai, Datouhuang, Niqiumai, Jiulan, Chikeguangtoumai, Wuyangmai, Baipuxiaomai, PI36224, Changmangmai (Zhejiang), Huoshaotou, NK+VI
Agropyron cristatum	PI325180
Psathyrostachys spicata	MA-69-42
Psa. strigosa	Y18
Psa. stipifolia	PI440095
Psa. fragilis	Svalov
Elytrigia bessarabica	Y40
Et. elongatiforme	PI383543, PI380625, PI406756
Et. intermedia var. *trichophora*	Pr34, NWC16-8-81-6, PI440043
Et. pycanatha	Pr40
Et. repens	Pr51, Pr53
RII: --and RPS:HR	
Roegeneria stenostachys	Pr231, Pr232
Agropyron cristatum	PI325179, PI439957
Elymus cylindricus	Y45, Y65, P57
Control (Triticum aestivum)	
RII:S and RPS:HR	cv. Wangshuibai
RII:S and RPS:MR	cv. Sumai No.3
RII:S and RPS:S	J-11
RII:S and RPS:HS	cv. Huimai

RII: Resistance to initial infection
I: 0%, HR: 0.1-50.0%, R: 50.1-70.0%
MR: 70.1-90.0%, S: 90.1-100(LPI>5days)
HS: 90.1-100%(LPI<5days)

RPS:Resistance to spread
MDR: Mean disease rating
I: 0, HR: 0.01-1.99, R: 2.00-2.99, MR: 3.00-3.60
S: 3.61-4.20, HS: 4.21-5.00

beside streams and on moist mountain slopes. Other genera that showed good resistance grow in humid area during the flowering stage. *Hystrix* is distributed in sparse forests. The four analyzed species of *Kengyilia* are distributed in high mountain plateau area, from 1100 m to 4750 m altitude, where rain showers are relatively common during their flowering stage. *Elymus* is distributed in temperate zone of the Northern Hemisphere, and grows in the open shrublands and forests, or on moist mountain slopes. *Agropyron* occurs mainly in prairie, slope or hilly land of Asia. On the other hand, the annual wild species of *Hordeum*, *Aegilops*, *Eremopyrum*, *Heteranthelium*, *Henrardia*, *Crithopsis*, *Taeniatherum* and *Haynaldia*, which are susceptible to scab, are distributed in Mediterranean-Central Asiatic regions (Sakamoto, 1973) where it is hot and dry during the flowering period of these genera and species. These results suggest that during the process of mutual adaptation and coevolution of the host and pathogens, genes for scab resistance might have accumulated in particular genera.

Ae. tauschii and *T. monococcum*, which are diploid donor species of D and A genome of the common wheat, respectively, showed high susceptibility to scab. No materials with high resistance to spread were found in tetraploid wheat. However, we found 3.43% of hexaploid common wheat as highly resistant to spread. Most of common wheat resistant to scab are Chinese landraces from Zhejiang, Jiangsu, Hunan, Hubei proveniences and Shanghai City located in the middle and lower reaches of the Yangtse River. Out of 82 landraces, among which 17 were highly resistant to spread, including Wangshuibei from Jiangsu, Gunmai from Hunan, Bagutao from Hubei, Yazitou from Shanghai, Changmangmai from Zhejiang, etc. In Guizhou, Sichuan and Yunnan provinces which locate in southwest of China, eleven out of 98 landraces were highly resistant to spread, including Wuyangmai from Sichuan, Changmangmai from Guizhou, Zimai from Yunnan, etc. No landraces showed high resistance to spread in Hebei, Shanxi, Shaanxi provinces and Beijing City that locate in northern China. Along the middle and lower reaches of the Yangtse River, there is a rainy season called Plum Rains, that affects the climate of southeast of China and results in continuous humid and warm weather during the blooming stage of wheat, while in northern China the weather is dry. The results indicated that variation in resistance to scab is closely related to the ecological conditions where they grow.

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Research article

Production, fertility and cytology of tetrageneric hybrids involving *Triticum*, *Agropyron*, *Haynaldia* and *Secale*

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Summary

Tetrageneric hybrids involving *Triticum*, *Agropyron*, *Haynaldia* and *Secale* were synthesized by means of immature embryo rescue. They can be used: (1) to transfer multi-disease resistance to wheat; (2) to demonstrate the behaviour of each parental chromosome in hybrid cells and rearrangement of the hybrid genomes. Twelve plants of the tetrageneric hybrids were obtained from 53 rescued embryos in 2831 pollinated florets and grew normally with characters inherited from the 4 genera. Seed setting percentage of the hybrid plants was 1.2%, varying from infertile to low-fertile. Most of the hybrids in the cross combination of (TS6xO (AABBRR) x TH6xL (AABBVV)) x TA6xA2 (AABBEE) had 39 chromosomes. Many selfed derivatives have been obtained from the tetrageneric hybrids.

Key words: wheat, intergeneric hybrids, embryo culture

Introduction

Distant hybridization has been practised widely in wheat breeding to transfer chromosome segments with useful genes. *Agropyron*, *Secale*, *Haynaldia* and other wild relatives of wheat are important genetic resources to improve wheat varieties. Among them, *Agropyron intermedium* is known to possess genes conferring resistance to barley yellow dwarf virus (BYDV) (Xin et al. 1988) and rusts (Knott 1989), and *Haynaldia villosa* and *Secale cereale* are different resistant resources against powdery mildew. Up to now, more than 10 trigeneric hybrids and few tetrageneric hybrids have been produced in the Triticeae (Kimber and Sallee 1979; Sharma and Gill 1983; Fernandez-Escobar and Martin 1988, 1989; Li and Dong 1993). Most of the papers reported many useful data about chromosome pairing at metaphase I (MI) of meiosis involving multi-genera of wheat wild relatives (Fernandez-Escobar and Martin 1985; Stoinva 1994; Sun et

al. 1995). In recent years, molecular analyses have been used to identify alien chromosomes in the studies of trigeneric hybrids (Islam-Faridi and Mujeeb-Kazi 1995; Svitashev et al. 1995). In order to introduce alien genes for multidisease resistance and to study the relationship of different alien chromosomes, tetrageneric hybrids involving *Triticum* spp., *A. intermedium*, *H. villosa* and *S. cereale* were developed by means of immature embryo culture, and F3 generation plants were successfully obtained in the present report.

This paper presents data on the production, morphology, cytology and fertility of two tetrageneric hybrids and their derivatives involving *Triticum*, *Secale*, *Haynaldia* and *Agropyron*. The results of molecular analyses will be reported in another paper.

Materials and methods

The plant materials used consisted of following amphidiploids: TS6x1330 and TS6xO (Both are hexaploid Triticale, 2n=6x=42, AABBRR); TH6xL and TH6xH (hexaploid Haynatriticum, 2n=6x=42, AABBVV); TA6xA2 (hexaploid Agrotriticum, 2n=6x=42, AABBEE) and TA8x16-3 (octoploid Agrotriticum, 2n=8x=56, AABBDDEE). They were selected or synthesized from intergeneric hybridization (Sun 1981; Liu et al. 1988; Chen and Huang 1991). Trigeneric hybrids TS6xO/TH6xL and TS6x1330/TH6xH obtained as reported (Yuan et al. 1993) were used as a female parent, TA6xA2 and TA8x16-3 as male parents, respectively.

The hybrid embryo was rescued 15-20 days after pollination. The basic culture medium was MS with whole ingredients. The culture media for the induced callus and callus relay were: (1) MS + 200mg/l glutamine + 100mg/l asparagine + 600mg/l hydrolytic lacto-albumin + 2mg/l 2,4-D + 0.1mg/l KT; (2) MS + 1mg/l 2,4-D + 1mg/l NAA + 0.1mg/l KT. Culture medium for differentiation was MS + 3mg/l BA. Sugar was 3%, agar 0.6%, pH5.6, photoperiod 14hr/day and culture temperature 25 ± 1°C. Regenerated plantlets were transplanted to pots.

Root-tip cells were pre-treated for 24hr at 0°C, fixed in ethanol/glacial acetic acid (3:1) and kept in 70% alcohol, then stained with acetic carmine for somatic chromosome counting.

Results

Production

The tetrageneric hybrid F1's were produced from crosses between trigeneric hybrids and doubled diploids or amphidiploids by means of in vitro culture of immature embryo. No high incompatibility was observed. The results of tetrageneric hybrids crossed between trigeneric hybrids (Triticale x Haynatriticum) and Agrotriticum, and their embryo cultures are shown in Table 1. Tetrageneric hybrid seeds were obtained easily, but most of the endosperms were poorly developed or absent. After the embryos had been rescued, ten and two tetrageneric hybrid plantlets were obtained from two cross combinations. Meanwhile, there was a significant difference in percentage of regenerated plantlets when Agrotriticums in different ploidy were used as the male parent.

Table 1. Production of tetrageneric hybrids

Cross combinations	No. of pollinated florets	Embryos No.	(%)	Seedlings No.	(%)
(TS6xO x TH6xL) x TA6xA2	250	25	(10.0)	10	(40.0)
(TS6x1310 x TH6xH) x TA8x 16-3	2581	28	(1.1)	2	(7.1)
Total	2831	53	(1.9)	12	(22.6)

Morphology

Seedlings of the tetrageneric hybrid F_1's were transplanted to pots. Some hybrid plants were vigorous in vegetative appearance. The average number of spikes per plant was 11, varying from 4 to 23. All of the hybrid plants were immune to BYDV, powdery mildew and rusts. The leaves of the hybrid seedlings were wide and long, resembling those of common wheat. Their spikes varied widely in morphology, showing some phenotypes that could not be found in their parents. Some characters were peculiar to *Haynaldia villosa*, such as the midrib bristles on outer glume (Fig. 1), fragile internode of rachis. For characters such as resistance to BYDV, the hybrid plants were similar to their parents of Agrotriticum. The hairy neck appeared in the hybrid plants is a marked character to *Secale cereale*. The hybrid plants maintained these special characters inherited from the four genera, which were helpful to distinguish the true hybrids from the false.

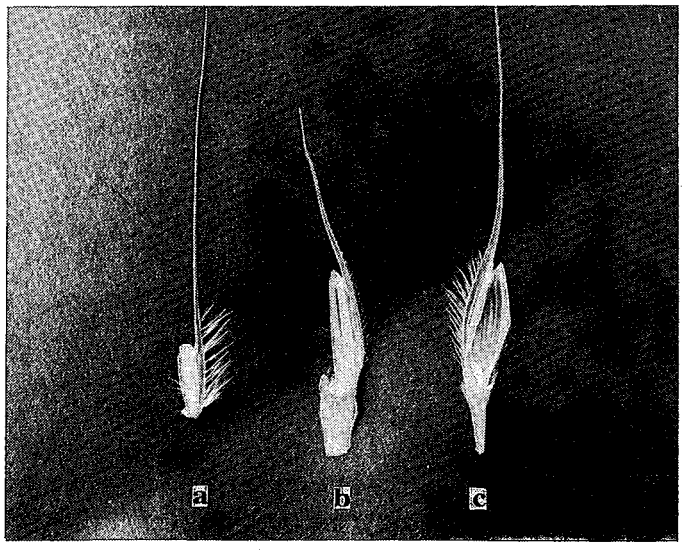

Fig. 1. Comparison of the midrib bristles on outer glumes among *Haynaldia villosa* (a), Haynatriticum (c), and derivative of the tetrageneric hybrid (b).

Table 2. Root tip chromosomes and percentage of fertile pollens in tetrageneric hybrids

Crosses	(TS6xO x TH6xL) x TA6xA2					(TS6x1330 x TH6xH) x TA8x16-3		
(Chromosome No.)	37	38	39	40	Total	47	50	Total
Plants No.	1	2	5	2	10	1	1	2
No. of fertile pollens					33			234
No. of sterile pollens					6531			3878
% of fertile pollens					0.5			5.7

Fertility

The hybrids were infertile or low-fertile types. The tetrageneric hybrids could produce seeds when selfed or backcrossed with wheat. Seed setting percentage averaged 1.2% when self-crossed. Some plants of hybrid F_1 had no pollen or a few fertile pollens in the anther. Only 0.5% of the pollens could be stained by the solution of I_2-KI in the cross combination of ((TS6xO x TH6xL) x TA6xA_2) (Table 2). However, its seed setting rate was significantly improved when backcrossed with a parent of *Triticum* species such as durum wheat, which could reach at 36.6%.

Cytological examination on somatic cells

Observation on the somatic cells of tetrageneric hybrid F_1's showed that most plants had 39 chromosomes in the cross combination of ((TS6xO x TH6xL) x TA6xA_2) varied from 37 to 40. The chromosome numbers were 47 and 50 in two plants of ((TS6x1330 x TH6xH) x TA8x16-3) (Table 2). These materials and their derivatives are being analysed by using DNA markers of their chromosomes and GISH methods (Tomita et al. 1993, 1994; Ma et al. 1994).

Derivatives of the tetrageneric hybrids

All selfed and backcrossed seeds were placed on moist filter paper at room temperature. Most of the seeds did not germinate. The F_2 plants segregated obviously in morphology. The seeds were similar to wheat in morphology. In F_3 generation of ((TS6xO x TH6xL) x TA6xA_2), 3 out of 15 seedlings were chlorinas. This character was inherited from the parent of Agrotriticum. These seedlings died 40 days later after germination. Twenty-one derivatives of F_3 generation have been obtained from the tetrageneric hybrids (Fig. 2). Some plants were morphologically similar to wheat and had good fertility. The seed set percentage was 32.7% on average, varying from 8.7% to 64.9%.

Discussion

Tetrageneric hybrids and their derivatives have been successfully obtained by means of immature embryo rescue when Agrotriticum, Haynatriticum and Triticale were used as bridge parents to overcome the incompatibility and the infertility of direct crossing between wild relative species of wheat. These materials are of particular interest to demonstrate the genomic rearrangement

during wide crossing using molecular cytogenetic methods such as C-banding and in situ hybridization. They can also be used as initial materials to transfer multi-disease resistance into wheat through backcrossing and chromosome engineering.

This study demonstrated that the male parents with different ploidy can significantly affect the production of immature embryos and regenerating ability of seedlings through embryo culture. When all the parents used in ((TS6xO x TH6xL) x TA6xA2) were hexaploids, the production of

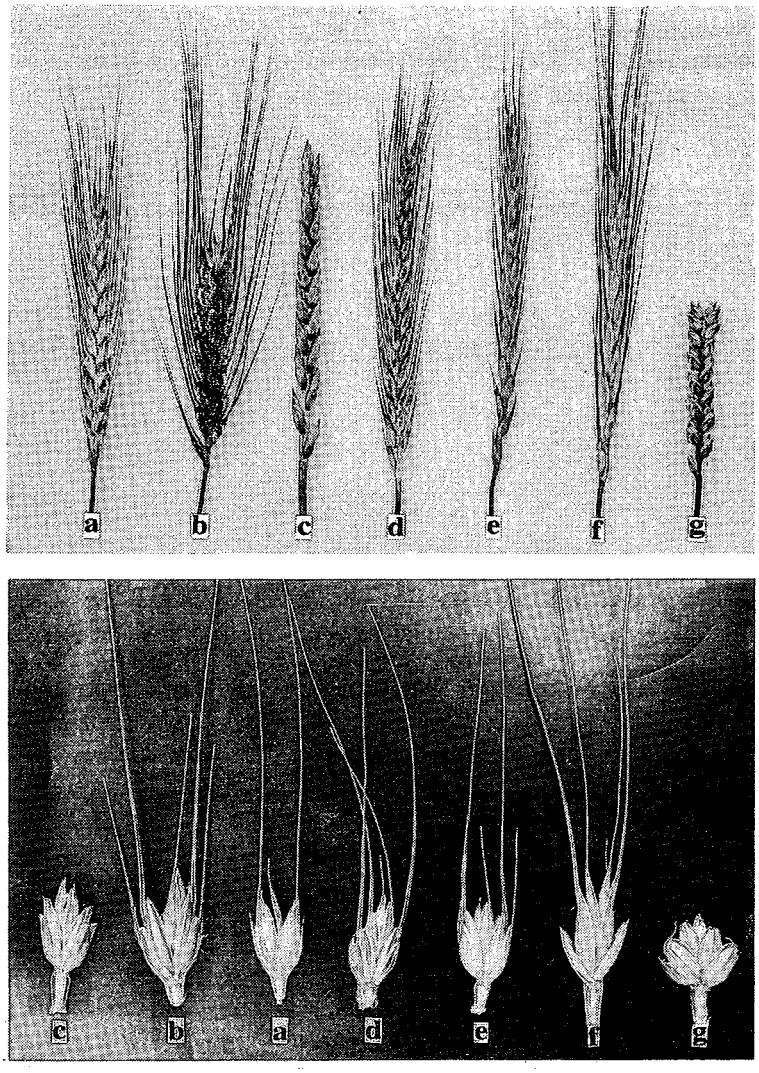

Fig. 2. Different types of the spikes (A) and spikelets (B) in the tetrageneric hybrid derivatives (d, e, f), their parents (a: Triticale, b: Haynatriticum, and c: Agrotriticum) and Chinese Spring (g).

immature embryos reached at 10%, obviously higher than that of 1.1% in ((TS6x1330 x TH6xH) x TA8x16-3). The regenerating ability of seedlings through embryo culture had similar result. Besides, reciprocal crosses, the parental combination and culture media also had some effects on regenerating ability of callus. For example, we found that hexaploid Triticale often causes incompatibility of crosses or sterility of hybrid seeds when used as a male parent.

The chromosomes of tetrageneric hybrids and their derivatives originated from R, V, E and wheat genomes. These materials with the same central genomes AA and BB can develop new types of multi-disease resistance when self-crossed and backcrossed, such as multi-genera's addition lines and multi-genera's translocation lines (Fernandez-Escobar and Martin, 1988). So far, many selfed derivatives have been obtained from the tetrageneric hybrids.

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Research article

Performance of alloplasmic wheat lines in a moisture stress environment

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Summary

Wheat cultivars Chinese Spring, Jones Fife and Zargoon along with their 37 alloplasmic lines were evaluated for a number of agronomic traits under cold and moisture stress in a Mediterranean environment. Both nuclear and cytoplasmic factors seem to be involved in the control of grain yield, frost tolerance, yellow rust resistance and to less extent kernel weight and protein content. Different cytoplasm may be more or less advantageous depending on the donor of the nuclear genes. Cytoplasm from *T. dicoccoides*, *Ae. speltoides*, and *Ae. crassa* seems to confer better performance of related alloplasmic wheat lines grown under drought and cold conditions. The traits such as spike length, grains/spike and plant height are primarily controlled by nuclear genes.

Introduction

Wheat-related species have been used in genetics and breeding research to transfer useful nuclear genes from alien species into the cultivated wheat such as genes controlling resistance to certain diseases (Ceoloni et al. 1988; Knott and Zhang 1990). Cytoplasm of wheat relatives has been found to interact with nuclear genes of *Triticum aestivum* to induce male sterility in wheat (Wilson and Ross 1962), a process that was used to produce hybrid wheat. Nucleus substitution lines with alien cytoplasm have been used to investigate the phylogeny of wheat and to explore the possibility of producing nucleo-cytoplasmic hybrids (Kihara 1963, 1973, 1979, 1980; Maan and Lucken 1971; Tsunewaki et al. 1976; Mukai et al. 1983; Tsunewaki 1988). The effect of alien cytoplasm on gene expression in wheat was highly variable depending on the wheat nucleus and the environment.

Despite the increased interest in alien species by breeders in recent years, little research has been conducted to assess the influence of alien cytoplasm on agronomic traits of wheat grown under moisture and temperature stress. This study reports on the performance of a number of alloplasmic lines evaluated in a dry and cold environment typical of the Mediterranean region.

Materials and methods

Three wheat (*Triticum aestivum* L.) cultivars, Chinese Spring (CS), Jones Fife (JF) and Zargoon (ZR) along with related 37 alloplasmic wheat lines were grown at ICARDA's main research station at Tel Hadya, Syria (36°01'N, 36°56'E) during the 1993-94 season. Planting on 7 December 1993 was made according to a RCB design with 3 replications. Plots consisted of six 3.75 m rows spaced 30 cm apart. The growing season was dry with a total precipitation of 277 mm and relatively cold during the winter months. There were 50 days of frost distributed over the months of November 1993 through March 1994 with the lowest absolute temperatures recorded in January (-8.7°C) and February (-7.5°C). The month of April coinciding with flowering was particularly dry (less than one mm of rain). Data were recorded on a plot basis for the following traits: plant height (cm), spike length (cm), number of grains/spikes, thousand kernel weight (g), protein content of the grain (percent dry matter), and grain yield (kg/ha). Data were also recorded on all entries for their field reaction to frost and yellow rust using the following scale: R (resistant), MR (moderately resistant), MS (moderately susceptible), and S (susceptible) based on the degree of observed damage due to frost or the type of plant reaction and extent of infestation by the disease.

Results and discussion

The investigated traits were generally affected by both nucleus source and cytoplasm type. The performance of alloplasmic lines of cv. Chinese Spring and the euplasmic parent (Table 1) reflects the effect of drought and cold stress on the agronomic characteristics investigated in the study. Alloplasmic lines with cytoplasm from *Aegilops speltoides* and *Ae. crassa* (6x) had significantly greater yield than the corresponding euplasmic parent. These higher yields were associated with a greater cold tolerance and a slightly better resistance to yellow rust under field conditions. The alloplasmic lines with cytoplasm of *Ae. squarrosa*, *Ae. uniaristata* and *Ae. umbellulata* exhibited the best tolerance to frost but were susceptible to yellow rust. Higher grain protein was recorded in *ovata* and *triuncialis*-derived alloplasmic lines but this was associated with significantly lower kernel weight caused by moisture stress. On the other hand, the (*squarrosa*)-CS line presented a high protein content without a reduction in kernel weight. These results point to the possibility of improving spring wheat for certain traits such as frost tolerance, disease resistance and drought tolerance using cytoplasm from alien species.

Jones Fife (JF) is a winter wheat cultivar that proved better adapted than Chinese Spring to the relatively cold winter of the testing environment. All alloplasmic lines of this cultivar were unaffected by frost (Table 2). Disease infestation was heavy with a susceptible reaction type on most entries with the exception of lines with cytoplasm from *T. dicoccoides* and *Ae. uniaristata*. These were also the highest yielding entries with the first line being significantly better than the euplasmic line (2611 kg/ha vs 1889 kg/ha). This alloplasmic line also was the tallest entry in the group, suggesting that taller types may have an advantage in drought stress-prone areas. Despite the differences in protein content observed among this group of entries, no alloplasmic line was better than the euplasmic parent. This contrasts with other results showing a large increase in

Table 1. Performance of alloplasmic lines of cultivar Chinese Spring at ICARDA, Tel Hadya, 1993 - 1994

Alloplasmic Line	Plasma	Plant height	Spike length	Grains/ spike	1000-Kernel weight	Protein content	Yield (kg/h)	Frost	Yellow rust
(*squarrosa*) - CS	D	63	6.7	37	26	16.9	1167	R	S
(*uniaristata*) - CS	M^u	65	6.7	35	26	16.7	1167	R	S
(*speltoides*) - CS	S	68	7.0	42	26	16.0	1889	MS	S
(*sharonensis*) - CS	S^l	68	6.7	32	23	16.6	1389	MS	S
(*bicornis*) - CS	S^b	67	6.3	31	21	16.6	1111	MS	S
(*mutica*) - CS	Mt	65	6.3	31	21	16.7	611	S	S
(*monococcum*) - CS	A	70	6.7	35	27	16.3	1222	MS	MS
(*dicoccoides*) - CS	B	70	6.3	38	27	16.7	1656	MS	MR
(*cylindrica*) - CS	D	60	6.3	34	25	16.7	1333	MR	S
(*columnaris*) - CS	C^u	73	6.7	34	26	16.8	1000	MR	S
(*aestivum*) - CS	B	82	6.7	36	26	15.5	1556	S	S
(*ovata*) - CS	M^o	72	7.0	37	18	17.7	944	S	S
(*kotschyi*)- CS	S^v	63	6.0	34	25	16.7	1222	S	S
(*crassa* 4x) - CS	D^2	72	6.7	35	26	16.8	1550	MR	S
(*triuncialis*) - CS	C	65	8.7	44	17	17.4	1167	MS	S
(*juvenalis*) - CS	D^2	78	6.7	37	25	16.3	1057	MR	S
(*crassa* 6x) - CS	D^2	63	7.0	36	26	16.7	1859	MR	MR
(*umbellulata*) - CS	C^u	82	9.7	45	25	16.7	667	R	S
LSD (0.05)		15.6	1.2	6.5	2.2	0.7	201		
CV (%)		13.4	9.0	10.2	5.1	2.7	18.4		

protein content due to incorporation into wheat of nuclear genes from certain genotypes of *T. dicoccoides* (Tahir 1983). Although protein content may be affected by the cytoplasm to some extent, the trait is primarily controlled by nuclear genes.

Significant differences were observed among the alloplasmic lines of cv. Zargoon for grain yield and kernel weight. Zargoon (ZR) is an improved cultivar which explains its relatively high yield under the testing conditions (Table 3). Only the alloplasmic (*crassa* 4x)-ZR line showed a comparable yield (2667 kg/ha) to that of Zargoon. However, five of the 6 alloplasmic lines were more tolerant to frost than Zargoon itself, suggesting a cytoplasmic effect on cold tolerance in wheat. The *sharonensis* cytoplasm was associated with less cold tolerance and an extremely low kernel weight in the alloplasmic lines of cv. Chinese Spring and cv. Jones Fife. Kinoshita and Kihara (1983) reported the pleiotropic effects of *ovata* cytoplasm for many kinds of economically

Table 2. Preformance of alloplasmic lines of cultivar Jones Fife (JF) at ICARDA, Tel Hadya, 1993 - 1994

Alloplasmic Line	Plasma	Plant height	Spike length	Grains/ spike	1000-Kernel weight	Protein content	Yield (kg/h)	Frost	Yellow rust
(*umbellultata*) - JF	C^u	78	9.7	45	22	17.2	1883	R	S
(*squarrosa*) - JF	D	83	9.7	45	23	16.8	1833	R	S
(*aestivum*) - JF	B	72	9.7	43	25	16.8	1889	R	S
(*uniaristata*) - JF	M^u	82	9.7	45	24	16.6	2389	R	MS
(*speltoides*)- JF	B	78	9.0	42	26	16.3	1944	R	S
(*sharonesis*) - JF	S^1	75	9.0	44	21	17.1	1778	R	S
(*dicoccoides*) - JF	B	90	8.3	41	26	16.2	2611	R	MR
(*timopheevi*) - JF	G	75	10.7	48	27	16.8	722	R	S
(*cylindrica*) - JF	D	83	9.0	46	24	17.1	2000	R	S
(*columnaris*) - JF	C^u	68	8.7	43	24	16.8	1167	R	S
(*kotschyi*) - JF	S^v	75	9.0	42	21	16.6	1556	R	S
(*crassa* 4x) - JF	D^2	78	10.3	46	24	16.9	1722	R	S
(*triuncialis*) - JF	C	80	10.3	46	24	17.1	333	R	S
(*juvenalis*) - JF	D^2	78	9.0	41	24	17.2	1889	R	S
(*crassa* 6x) - JF	D^2	85	9.3	43	23	17.2	2200	R	S
LSD (0.05)		15.6	1.2	6.5	2.2	0.7	669.9		
CV (%)		13.4	9.0	10.2	5.1	2.7	18.4		

important characters. Similarly, in an analysis of yield components in four wheat lines with the cytoplasm of *Aegilops ovata*, Khok and Semerov (1990) found that (*ovata*) - Mironovskaya 808 gave the highest yield of 9.36 t/ha, whereas (*ovata*) - Pavlovka gave the lowest yield (3.97 t/ha) as compared to 5.43 t/ha of euplasmic cv. Mironovskaya 808. The performance of nucleo-cytoplasmic hybrids (alloplasmic lines) depends on nucleo-cytoplasmic interaction, environments and degree of seed set fertility.

The results of this study showed that agronomic traits of wheat grown under moisture and cold stress are primarily controlled by nuclear genes and in some cases by the cytoplasm type as well. This is the case of grain yield, frost tolerance, disease resistance and to some extent kernel weight and protein content. Furthermore, different cytoplasms may be advantageous depending on the donor of the nuclear genes. The *dicoccoides* cytoplasm was best in combination with cv. Jones Fife whereas *speltoides* cytoplasm conferred better performance under stress when combined with nuclear genes from cv. Chinese Spring. The *crassa* cytoplasm seems to have favourable effect on agronomic traits on all the three nucleus donor varieties under stress conditions. These studies indicate a great possibility of advantageous exploitation in breeding program of nucleo-

Table 3. Performace of alloplasmic lines of culitvar Zargoon (ZR) at ICARDA, Tel Hadya, 1993-94

Alloplasmic Line	Plasma	Plant height	Spike length	Grains/ spike	1000-Kernel weight	Protein content	Yield (kg/h)	Frost	Yellow rust
(*aestivum*)-Zr	B	63	7.7	34	41	15.7	2667	MS	R
(*squarrosa*)-Zr	D	72	8.0	31	39	16.4	2167	MS	R
(*uniaristata*)-Zr	M^u	57	7.7	34	40	16.3	1556	R	R
(*speltoides*)-Zr	B	53	8.3	37	40	17.0	1056	MR	R
(*sharonensis*)-Zr	S^1	63	6.0	34	22	16.8	889	MS	R
(*dicoccoides*)-Zr	B	60	8.3	33	40	15.6	2333	MR	R
(*crassa 4x*)-Zr	D^2	65	8.3	37	43	16.7	2667	MR	R
LSD (0.05)		15.6	1.2	6.5	2.2	0.7	669		
CV (%)		13.4	9.0	10.2	5.1	2.7	18.4		

cytplasmic hybrids by broadening the genetic base of alloplasmic lines by a large number of genotypes.

Acknowledgment

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Research article

The rice *Act1* promoter gave high activity of transient *gusA* expression in callus, immature embryos and pollen embryoids of common wheat and its relatives following particle bombardment

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Summary

A wheat transformation system was developed by using particle bombardment and scutellar tissues of immature embryos as its target. The promoter region preceding a marker gene is one of the most important factors affecting transformation frequency. In this study, the 5' upstream sequence of the rice actin 1 gene (*Act1*) showed high activity of transient expression in various wheat cell types including embryogenic calli, immature embryos and pollen embryoids of several wheat accessions. All three callus lines, including two aneuploid lines, showed high activity of transient expression of *gusA* gene. In pollen embryoids, the activity of transient *gusA* expression was similar among four wheat cultivars, but the activity after two days of incubation was slightly higher than that after five days of incubation in three of cultivars. The scutellar tissues of both tetraploid and hexaploid wheats provided an efficient level of the *gusA* expression. The present findings suggest that the rice *Act1* promoter is a useful promoter in the transformation system of common wheat and its relatives.

Key words: *gusA*, cultured cells, microprojectile bombardment, promoter activity, wheat

Introduction

In common wheat (*Triticum aestivum* L.), particle bombardment developed by Sanford et al. (1987) is a useful method for gene delivery to intact cells (Wang et al. 1988). This system has been widely used as the method for obtaining transgenic wheat plants. Transgenic wheat plants have been produced from embryogenic suspension cells (Vasil et al. 1992) and scutellar tissues of immature embryos (Weeks et al. 1993; Vasil et al. 1993; Nehra et al. 1994; Becker et al. 1994), but not from other tissues including pollen embryoids. The pollen embryoid is an attractive

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target for particle bombardment because doubled haploid plants can be regenerated from microspore derived embryos by anther culture (Henry and De Buyser 1990). The scutellar tissues of immature embryos are commonly used targets for production of transgenic plants because multiple plants can be easily regenerated from the calli induced from scutellar tissues through immature embryo culture (Scott et al. 1990).

One of the most important factors affecting the transformation efficiency is the activity of the promoter which should drive the introduced gene. Three promoters, i.e., the promoters of maize alcohol dehydrogenase gene (*Adh1*), maize ubiquitin gene (*Ubi1*) and rice actin gene (*Act1*), are widely used in wheat transformation. The cauliflower mosaic virus (CaMV) 35S promoter which is often used in dicot transformation systems shows low activity in transient *gusA* expression in pollen embryoids of wheat (Shimada et al. 1991), immature embryos (Chibbar et al. 1991) and cultured cells (Wang et al. 1988; Takumi et al. 1994). However, the promoter and the first intron of the maize *Adh1* that were placed after the CaMV 35S promoter greatly stimulate expression of a foreign gene in callus (Wang et al. 1988), leaf base and apical tissue (Oard et al. 1989) and immature embryos (Chibbar et al. 1991) of wheat. Taylor et al. (1993) have demonstrated that the maize *Ubi1* showed higher activity of transient expression in cells of cereals including wheat than the maize *Adh1* promoter plus its first intron. The efficiency of the *Ubi1* promoter has also been confirmed in immature embryos (Vasil et al. 1993) and pollen embryoids (Loeb and Reynolds 1994). On the other hand, Nehra et al. (1994) have demonstrated that the rice *Act1* promoter showed higher transient activity than the maize *Adh1* promoter plus its first intron in wheat immature embryos. In our previous work, the rice *Act1* promoter was also confirmed to show higher activity than any other examined promoters including the *Adh1* promoter plus its first intron in cultured cells of three *Triticum* species (Takumi et al. 1994). These results have indicated that the rice *Act1* promoter was efficient and useful in wheat cells.

In this study, we evaluated the efficiency of the rice *Act1* promoter in various cell types including embryogenic callus, immature embryos and pollen embryoids, as revealed by transient expression of the *gusA* gene encoding ß-glucuronidase (GUS).

Materials and methods

Plant materials

Calli derived from immature embryos of two aneuploid lines of Chinese Spring (CS) and *Aegilops cylindrica*, immature embryos of four common wheat cultivars and two emmer wheats, and pollen embryoids derived from anther culture of four common wheat cultivars were used, as shown in Table 1. Three callus lines were induced from immature embryos, which grew vigorously on Linsmaier-Skoog (LS) medium (Linsmaier and Skoog 1965) containing 2 mg /l 2,4-dichlorophenoxy acetic acid (2,4-D) and 0.25% (w/v) Gelrite (Merck). These calli were subcultured using fresh medium every three weeks. Approximately 1 ml (fresh packed cell volume) of callus was spread onto 90 mm x 15 mm Petri-dishes containing solid LS medium supplemented with 2 mg /l 2,4-D. Immature seeds were sterilized with 70% ethanol and immature embryos isolated were placed

Table 1. Plant materials and cell types in which the *guaA* having the rice *Act1* promoter was introduced by particle bombardment

Accession		Cell type
Triticum aestivum	cv. Chinese Spring ditelo-2DS	embryogenic callus
	cv. Chinese Spring nulli2D-tetra2B	embryogenic callus
	cv. Chinese Spring	immature embryo
	cv. Seri 82	pollen embryoid
	cv. Gernard 81	pollen embryoid
	cv. Glennson 81	pollen embryoid
	cv. Veery "S"	pollen embryoid
	cv. Akadaruma	immature embryo
	cv. Norin 12	immature embryo
	cv. 911-B-8-10	immature embryo
Triticum durum	*sphaerococcum*-like line (white awn)	immature embryo
Triticum aethiopicum		immature embryo
Aegilops cylindrica		embryogenic callus

with scutellar tissues exposed on LS medium containing 2 mg /l 2,4-D. Pollen embryoids (1 to 2 mm) were obtained from anther cultures after the methods of Otani and Shimada (1993) and were also placed on LS medium containing 2 mg /l 2,4-D.

Plasmids, particle bombardment and enzyme assay

The p*Act1*-F (McElroy, Zang et al. 1990) including the *gusA* coding region under the control of the 1.3 kb 5' region of the rice actin 1 gene (*Act1*) was used as the reporter gene. The plasmids were amplified in liquid cultures of *Escherichia coli*, isolated by alkaline lysis, and purified twice by CsCl/ethidium bromide density centrifugation (Maniatis et al. 1982). The Biolistic^R PDS-1000/He Particle Delivery System (Bio-Rad) was used as a particle accelerator. Plasmid DNAs were adsorbed to gold particles (1.6 μm diameter) according to the protocol described for the Biolistic^R PDS-1000/He Particle Delivery System (Klein et al. 1988). The calli, pollen embryoids and immature embryos were bombarded after incubation for several days on the LS medium containing 2 mg /l 2,4-D. GUS activity in cultured cells, immature embryos and pollen embryoids was assessed histochemically by the directed addition of the substrate of glucuronidase enzyme as described previously (Takumi et al. 1994) and the average numbers of blue spots, showing transient expression of the *gusA* gene, per embryo in two separate experiments were counted. In each experiment, more than 20 immature embryos and pollen embryoids were used.

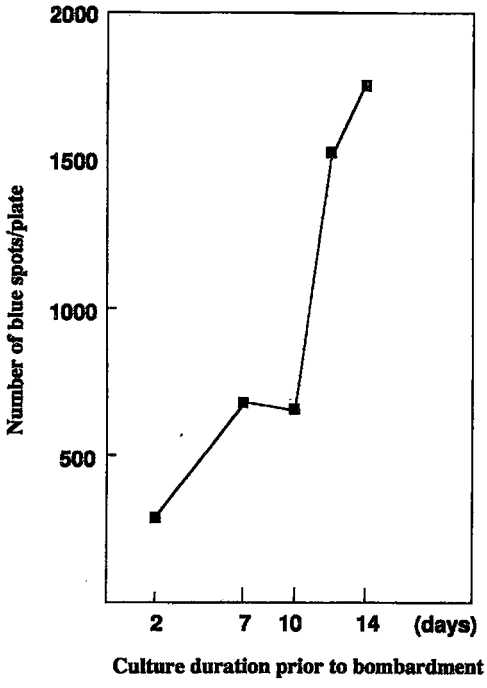

Fig. 1. The *gusA* gene expression in cultured cells of *Ae. cylindrica* bombarded with p*Act1*-F after 2 to 14 days of incubation.
The average number of blue spots/plate was calculated using four to six plates.

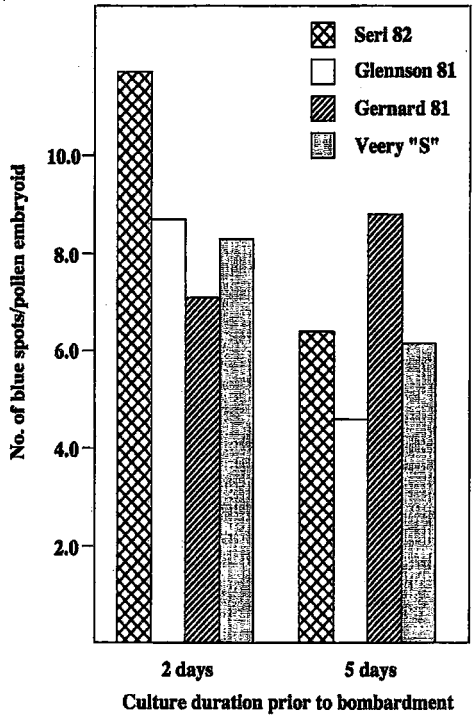

Fig. 2. Influence of the culture duration prior to bombardment on the transient *gusA* expression in pollen embryoids of four common wheat cultivars.
The numbers of blue spots/embryoid in two separate experiments were counted, using more than 20 embryoids in each experiment, and their average is shown.

Results and discussion

Previously, we found that the rice *Act1* promoter showed the highest activity of transient *gusA* expression in three non-embryogenic cultured cell lines of *T. monococcum*, *T. durum* and *T. aestivum* (Takumi et al. 1994). To estimate the efficiency in other cultured cell lines, transient *gusA* expression was confirmed by using three embryogenic cell lines (Table 1). Two of them were cultured cells derived from immature embryos of nullitetrasomic and ditelosomic lines of *T. aestivum* cv. Chinese Spring (Sears 1966; Sears and Sears 1978). The other callus line was *Aegilops cylindrica*, a wild wheat species. These calli were cultured for ten days and then bombarded with the particles coated with a plasmids p*Act1*-F. Transient expression of the *gusA* gene was observed in two days after bombardment by using a histochemical staining. p*Act1*-F yielded a high activity of transient *gusA* expression in all three cell lines (data not shown). This suggests that the rice *Act1* promoter efficiently induces expression of a marker gene in cultured

cells of various wheat species and accessions including aneuploid lines. Of the cultured cells of *Ae. cylindrica* bombarded with p*Act1*-F after 2-14 days of incubation, the highest expression was obtained in the cells bombarded after 14 days incubation (Fig. 1). This supported our previous findings using the cells of *T. monococcum* (Takumi et al. 1994), that the efficiency of transient expression was severely influenced by culture duration of the target tissues before bombardment.

To examine the transient expression of the *gusA* gene connected to the rice *Act1* promoter in wheat pollen embryoids, p*Act1*-F was introduced by particle bombardment into pollen embryos of four wheat cultivars after two or five days incubation. The number of blue spots in pollen embryoids was only few compared to that observed in immature embryos. Fig. 2 shows the number of blue spots per pollen embryoid incubated for two or five days before bombardment. The number in the four wheat cultivars was 7.1 to 11.7 and 4.6 to 8.8 per pollen embryoid incubated for two and five days, respectively. The activity of transient *gusA* expression was similar among the four wheat cultivars, but the activity expressed in two-days old embryoids was slightly higher than that observed in the five-days old embryoids in all cultivars but Gernard 81. Loeb and Reynolds (1994) demonstrated that the CaMV 35S promoter is not effective in wheat pollen embryoids and that the maize *Ubi1* promoter controls a high level of *gusA* expression in the pollen embryoids. It was not known whether the rice *Act1* promoter is as efficient in the pollen embryoids as the maize *Ubi1* promoter, but the activity of the *Act1* promoter in the pollen embryoids was not so high as that in immature embryos. This fact suggests that production of transgenic plants from bombarded pollen embryoids with a selectable marker gene under control of the *Act1* promoter has no promise at present, considering the lower regeneration rate from pollen embryoids than from immature embryos. It is essential for production of transgenic wheats from pollen embryoids to increase drastically their regeneration rate by improving the anther culture.

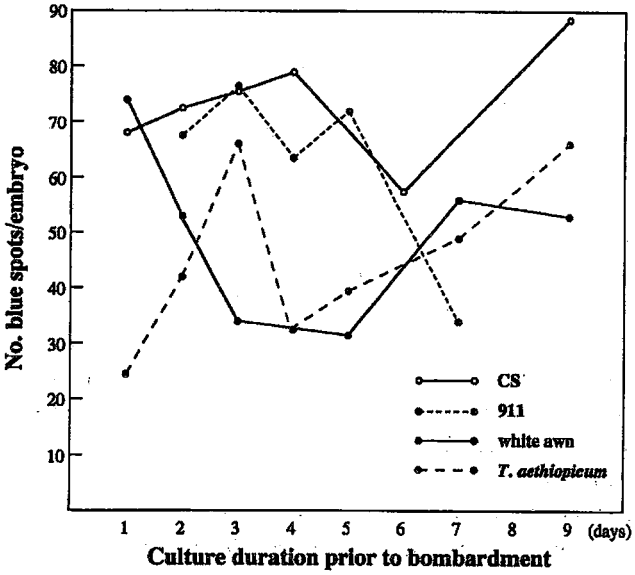

Fig. 3. Effect of the culture duration prior to bombardment on the transient *gusA* expression in immature embryos of two common wheats and two emmer wheats.
The rice *Act1* promoter-*gusA* chimeric gene was introduced to scutellar tissues of immature embryos after one to nine days of incubation. The numbers of blue spots/embryo in two separate experiments were counted using more than 20 embryos in each experiment, and their average is shown.

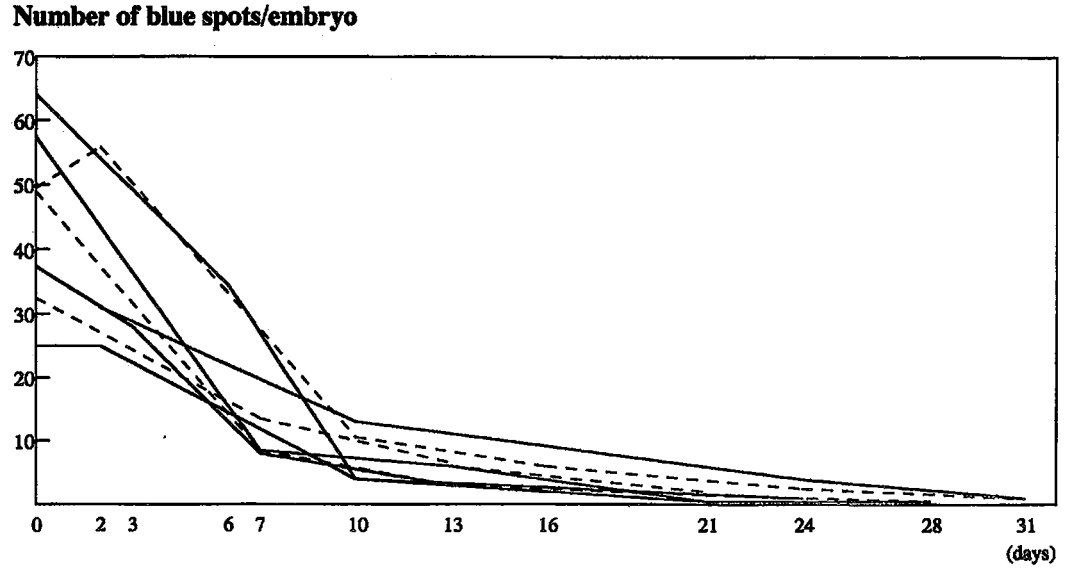

Fig. 4. Decrease in the number of the blue spots per embryo with increased incubation period after bombardment in a common wheat cultivar, Akadaruma.
The immature embryos after four to seven days of incubation were bombarded with p*Act1*-F. Each line indicates the change of blue spot number in eight separate transformation experiments. The number of blue spots shown is the average of five to ten immature embryos.

To examine transient expression of *gusA* gene under control of the rice *Act1* promoter in immature embryos of some tetraploid and hexaploid wheats, the scutellar tissues cultured for one to nine days were bombarded with the particles coated with a plasmid p*Act1*-F. Immature embryos at stage III (14 days after anthesis) were isolated because the developmental stage of immature embryos is important for embryogenesis and immature embryos at stages II and III are most suitable for induction of scutellum callus (Scott et al. 1990). Transient expression of the *gusA* gene was observed in two days after bombardment by using a histochemical staining. Fig. 3 shows the relationship between transient *gusA* expression and culture duration prior to bombardment. No clear correlation between the culture duration and transient *gusA* expression was recognized in all four wheats, as other wheat cultivar Akadaruma (Takumi and Shimada 1996). However, transient expression of *gusA* gene in immature embryos of CS was higher than that in two emmer wheats. The rice *Act1* promoter provided a high level of the *gusA* expression in scutellar tissues of both tetraploid and hexaploid wheats. Transient *gusA* expression was gradually decreased during 1- 31 days after bombardment with p*Act1*-F by using immature embryos of *T. aestivum* cv. Akadaruma (Fig. 4). The number of blue spots in immature embryos decreased with the increasing culture duration after bombardment. A sharp decrease was observed in the first ten days. This indicated that most blue spots are due to transient expression of the

reporter gene and stable transformation is rather difficult.

The rice *Act1* promoter which is known to cause a high level of *gusA* expression in transformed rice and maize cells (McElroy, Zang et al. 1990; McElroy et al 1991) controlled the transient *gusA* expression efficiently in cultured cells, pollen embryoids and scutellar tissues of common wheat and its relatives. The high levels of transient expression in these materials seem to be caused by the constitutive expression of the rice *Act1* (McElroy, Rothernberg et al. 1990; Zang et al. 1991). Moreover, we previously demonstrated that the rice *Act1* promoter showed higher activity of transient expression in cultured cells of common wheat than the maize *Ubi1* promoter, although these two promoters showed similar activity in einkorn wheat cells (Takumi and Shimada 1995). These findings suggest that the rice *Act1* promoter is an efficient and useful promoter in transformation of monocotyledonous crops.

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Research article

C-banding analysis of D-genome chromosome in Chinese landrace of *Triticum tauschii* (Coss.) Schmalh. and *Triticum aestivum* L. cv. Chinese Spring

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Summary

The Giemsa C-banding analysis of 11 accessions of *T. tauschii* from the middle reaches of the Yellow River and Xinjiang province in China and common wheat Chinese Spring was made. The clear C-band polymorphic variation among the *T. tauschii* accessions from the middle reaches of the Yellow River and the accessions from Xinjiang was observed, which is consistent with evidence of RFLPs and esterase analysis in Chinese *T. tauschii*. Modification in the C-banding pattern was noticed on some D-genome chromosomes of Chinese Spring compared with *T. tauschii*. The C-banding polymorphic variation of secondary constriction region in chromosome arm 5DS of *T. tauschii* was found.

Key words: Chinese *Triticum tauschii*, Chinese Spring, C-banding polymorphism

Introduction

The C-banding technique is a good method for cytological differentiation of D-genome chromosomes of *T. tauschii* and *T. aestivum* (Gill et al. 1991; Friebe et al. 1992; Hohmann and Lagudah 1993). A large amount of C-banding polymorphism among different *T. tauschii* accessions from the Middle East has been found, and several chromosomes of them are involed in the modification of the C-banding pattern in comparison with that of D-genome chromosomes of Chinese Spring. In this paper, C-banding analysis of D-genome chromosome in Chinese *T. tauschii* and common wheat Chinese Spring was made.

Materials and methods

The materials analyzed consist of 11 different *T. tauschii* accessions from the middle reaches of

Table 1. Origin of the materials analyzed

Species	Accession no.	Origin
T. tauschii	As*71	Gongnaisi, Xinjiang
T. tauschii	As72	Xinjiang
T. tauschii	As74	Wugong, Shannxi
T. tauschii	As75	Xian, Shannxi
T. tauschii	As76	Xian, Shannxi
T. tauschii	As77	Lushi, Henan
T. tauschii	As78	Lushi, Henan
T. tauschii	As79	Sanmen Gorge, Henan
T. tauschii	As80	Hui Xian, Henan
T. tauschii	As81	Zhongzhuang Commune, Henan
T. tauschii	As82	Xin Xiang, Henan
T. aestivum Chinese Spring	As490	Sichuan

*As: refer to Triticeae Research Institute of Sichuan Agriculture University, China

the Yellow River (including Henan and Shannxi provinces) and Xinjiang province as well as commmon wheat Chinese Spring, and their origins are given in Table 1. The C-banding karyotypes were made using the technique described by Ren and Zhang (1995). Chromosome identification and designation of D-genome chromosomes to homoeologous group follows the generalized C-banding karyotype of *T. aestivum* (Gill et al. 1991) and *T. tauschii* (Friebe et al. 1992). The position of C-bands in each chromosome arm was located relative to C-bands present in hexaploid wheat. The consistent or inconsistent C-bands of each accession were derived from 5 to 8 different C-banded chromosomes of each accession.

Results

The representative C-banded karyotypes of *T. tauschii* and Chinese Spring are given in Fig. 1 and Fig. 2. Within a given accession, the consistent C-bands are shown in black, whereas inconsistent ones are shown in hatching. Whereas only minor variation in C-banding pattern was found within a given accession, a large amount of variation was observed among different accessions except accessions As77 and As78 which show almost no variation (Fig. 1, Fig. 2).

Chromosome 1D

The short arm has a telomeric and an interstitial C-band, which is similar to that of Chinese Spring. An additional sub-terminal C-band was found in *T. tauschii* accessions As72, As74, As75 and As82. Three C-banding patterns were observed for 1DL: the accessions As74, As81 and As82

are identical with that of Chinese Spring in showing one proximal and one distal C-bands. The accessions As71 and As72 usually only show three interstitial C-bands associated to each other. All the other accessions show one proximal and two distal C-bands. Furthermore, 1DL in all of the accessions shows a telomeric C-band.

Chromosome 2D

A large amount of variation exists among different *T. tauschii* accessions. The C-banding patterns of *T. tauschii* differ from that of 2D in Chinese Spring. The result is similar to that reported by Friebe et al. (1992).

Chromosome 3D

One telomeric and one sub-telomeric C-bands were present in all accessions, but these C-bands in accessions As71 and As72 are larger than those of all the other accessions. Moreover, an additional C-band adjacent to the centromere was found in all the accessions. The pattern is similar to that of Chinese Spring. Besides these bands, in accessions As81 and As82, an extra interstitial C-band was found. In 3DL, in addition to telomeric C-band there were several faint interstitial C-bands with a large amount of polymorphism among different accessions. The accessions As71, As72, As77 and As78 show one proximal and one distal C-bands, which are present in the corresponding region of Chinese Spring.

Chromosome 4D

In all accessions, one proximal, one or two interstitial and one terminal C-bands were found in 4DS. With the exception of accession As71, in all the other accessions the short arm shows an additional interstitial C-band. In Chinese Spring, only two proximal C-bands were found. Two distal C-bands were observed in 4DL. They are also present in the corresponining regions of 4DL of Chinese Spring, but they are much smaller than that of *T. tauschii*. An additional interstitial C-band was found in all the other accessions except the accessions As71, As75 and As76. Furthermore, 4DL in all accessions of *T. tauschii* shows a telomeric band.

Chromosome 5D

This is the only SAT chromosome pair in the complement and usually shows a distally located secondary constriction and a small satellite in 5DS, and this region shows up as a terminal C-band which is the largest in the complement (Friebe et al. 1992). In the present study, with the exception of accessions As71 and As72, in which the C-band adjacent to the centromere shows the largest C-band, in all the other accessions the terminal C-band is the largest C-band of the whole genome. The terminal C-band in accession As77, As78 and As79 is much larger than that of all the other accessions, of which the terminal C-band in accession As82 is the smallest. There is an intense C-band adjacent to the centromere. The C-band in As71, As72, As75, As76, As77, As78 and As81 is larger than that of all the other accessions. Furthermore, one more small C-band is present in the middle of 5DS in *T. tauschii*. The pattern is similar to that of Chinese Spring. However, the telomeric C-band and C-band adjacent to centromere present in Chinese Spring is much smaller than that of *T. tauschii*. Moreover, an additonal interstitial C-band was found in the accessions As74, As75 and As80. The telomeric C-band in 5DL of accessions As71 and As72 is larger than that of all the other accessions. Two or three distal C-bands are separately found

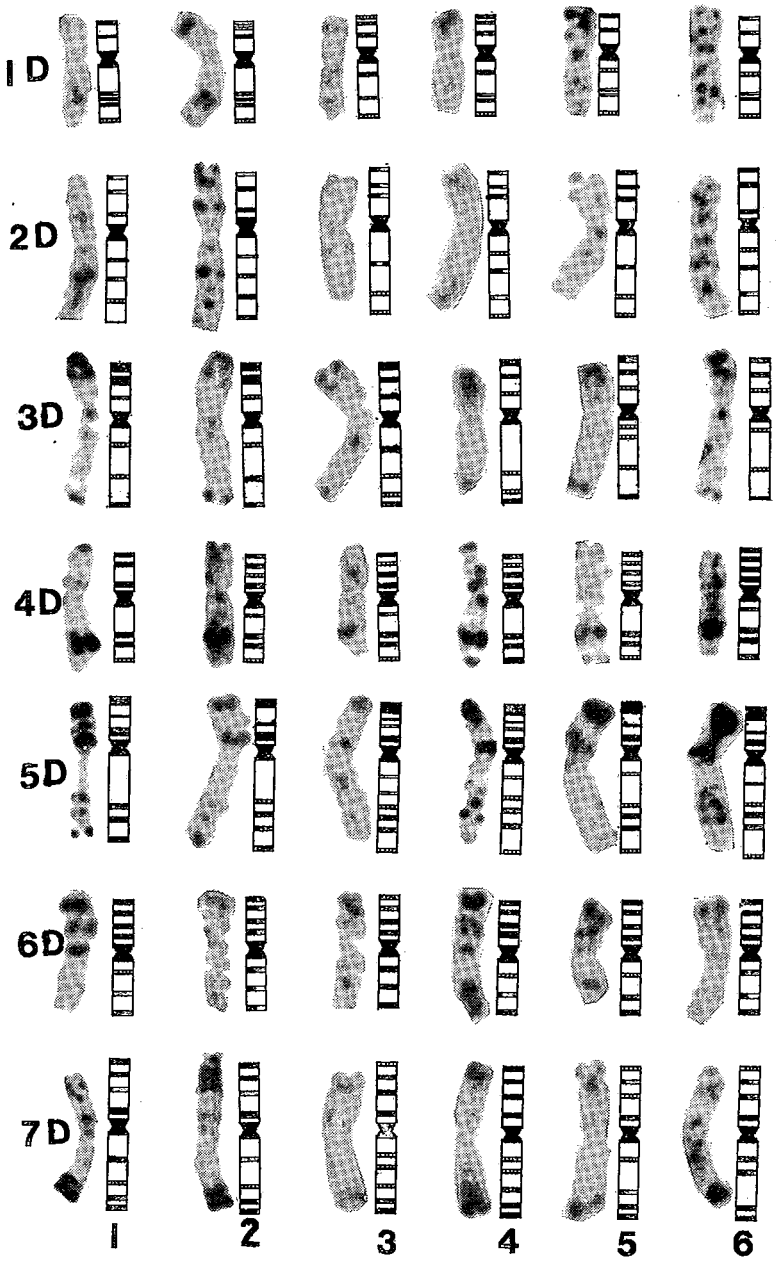

Fig. 1. C-banded kayotypes of Chinese *T. tauschii*
1: As71 Xinjiang, 2: As72 Xinjiang, 3: As74 Shannxi, 4: As75 Shannxi, 5: As76 Shannxi, 6: As77 Henan.

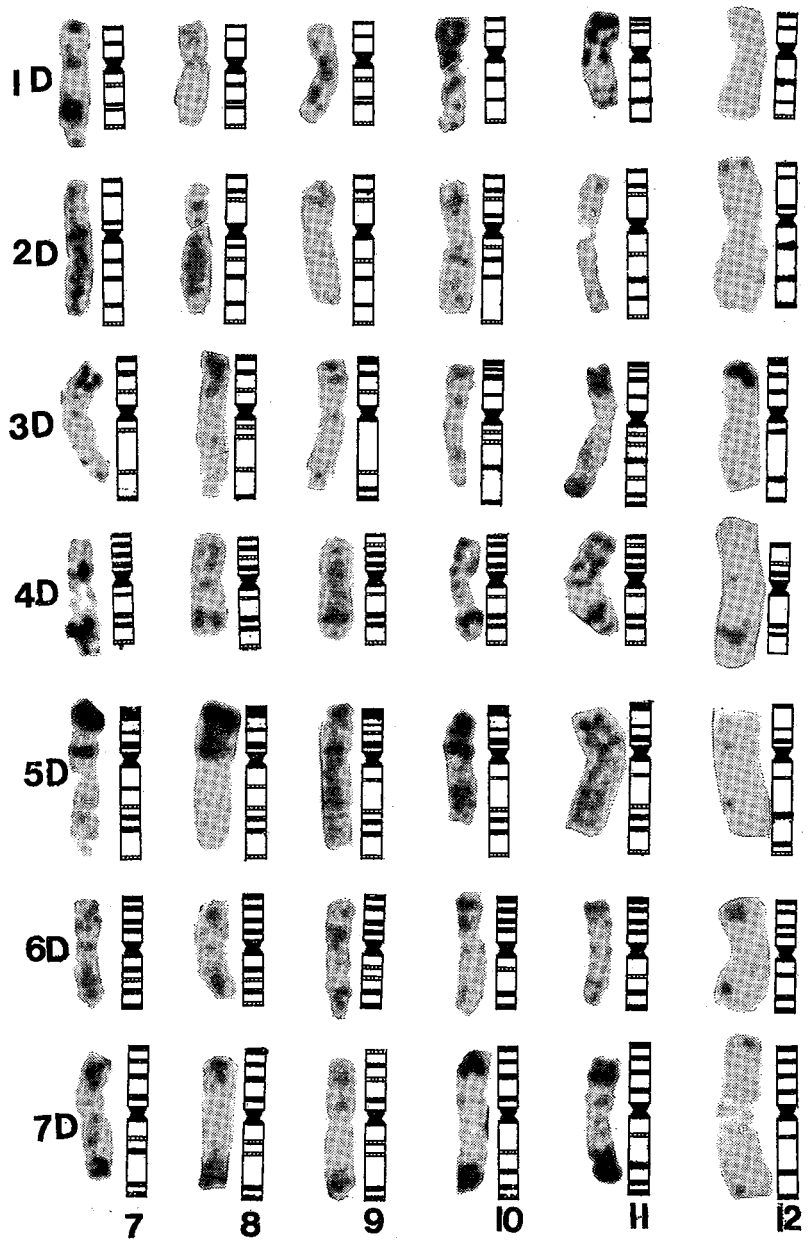

Fig. 1. C-banded kayotypes of Chinese *T. tauschii* (continued)
7: As78 Henan, 8: As79 Henan, 9: As80 Henan, 10: As81 Henan, 11: As82 Henan, 12: As490 *T. aestivum* cv. Chinese Spring.

in the accessions As71and As72. One additional proximal C-band in accessions As75, As76, As77, As78, As79, As80, As81 and As82, and two additional proximal C-bands in accession As74 were found. Three interstitial C-bands, of which the interstitial C-band adjacent to telomere was not detected in any of analyzed accessions of *T. tauschii*, were found in the 5DL of Chinese Spring.

Chromosome 6D

Similar C-bands are present in 6DS of Chinese Spring and *T. tauschii*. However, the telomeric C-band and C-band adjacent to telomere in Chinese Spring is usually staining lighter in comparison with that found in *T. tauschii*. Besides a telomeric C-band, one proximal and one distal C-bands were found in 6DL of all the accessions, which is similar to that of Chinese Spring.

Chromosome 7D

A telomeric and three interstitial C-bands are present in 7DS of both *T. tauschii* and Chinese Spring. In 7DL, a large amount of variation exists among different *T. tauschii* accessions. A telomeric and two interstitial C-bands were found in 7DL of Chinese Spring, which is a little different from that of *T. tauschii*.

Discussion

Overall, polymorphic variation of C-bands is prevalent on chromosome arms 1DL, 2DS, 2DL, 3DL, 5DS, 5DL and 7DL, which are similar to those reported by Friebe et al. (1992) and Hohmann et al. (1993). However, in the present study a large amount of polymorphism of chromosome arm 5DS and a few polymorphisms on 6DL were found, which is different from their reports. The results of comparison of the C-banding pattern of *T. tauschii* accessions from Middle East (including the varieties *typica*, *meyeri* and *strangulata*) reported by Hohmann et al. (1993) with that of Chinese *T. tauschii*, indicates that the nine Chinese *T. tauschii* from the middle reaches of the Yellow River are more similar to the variety *typica*, although some variation was found. The two accessions from Xinjiang are different from all the three varieties.

Compared with the polymorphic variation between the accessions from the middle reaches of the Yellow River and the accessions from Xinjiang, which shows a large amount of polymorphic variation, there is less variation between the nine *T. tauschii* from the middle reaches of Yellow river or between the two accessions from Xinjiang. The result is consistent with the evidence of esterase and RFLPs analysis in Chinese *T. tauschii* (Yen et al. 1983; Ward et al. 1995). The differences of C-band polymorphism between the accessions from the middle reaches of the Yellow River and the accessions from Xinjiang are significant in chromosome arms 1DL, 3DS, 5DS and 5DL.

Though the C-banding pattern of *T. tauschii* chromosome is similar to that of homologues of Chinese Spring, there are some differences. Modification of C-banding pattern indicates differentiation in the D-genome chromosomes between *T. tauschii* and Chinese Spring (Friebe et al; 1992, Hobmann et al. 1993).

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Inheritance of resistance to stem rust in five bread wheat cultivars

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Summary

Five bread wheat cvs. HD 2135, HD 2160, HD 2189, HD 2285 and Vaishali were crossed with susceptible wheat, Agra local, to study inheritance of resistance to four selected pathotypes 21(9G5), 21A-2(75G5), 40-1(62G29-1) and 117A(36G2) of *P. graminis tritici*. Segregation of seedlings in F_2 and families in F_3 for resistance to above pathotypes suggested the presence of three dominant and one recessive genes for resistance in HD 2135, two dominant and one recessive genes in HD 2160, four dominant genes in HD 2189, 3 dominant and two complementary recessive genes in HD 2285, and five dominant genes in Vaishali. An adult plant resistance gene *Sr2* was also identified in HD 2135, HD 2189, HD 2285 and Vaishali based on mottling effect in the seedlings. Diallele tests further revealed the presence of an additional dominant gene in HD 2189 and two dominant genes in Vaishali for resistance to pathotype 40-1(62G29-1). Genes *Sr11* and *Sr30* were confirmed in HD 2189 and HD 2285 by test of allelism.

Introduction

Wheat (*Triticum aestivum* L.), the most important cereal crop in global agricultural economy, is cultivated in diverse agroclimatic regions of the world. India with 24 million hectares, is the fourth largest wheat producing country contributing about eight per cent of total production in the world. The production in India has risen from 5.6 million tons in 1947-48 to about 63 million tons in 1994-95, showing a dramatic turn during the last 3 decades (Anon. 1996). To enable sustainable wheat production, emphasis is given to develope varieties that have durable resistance to diseases and greater tolerance to environmental stress. Rusts are the most destructive diseases and responsible for the colossal damage to wheat crop. Cultivars HD 2135 and HD 2189 were developed in 1975 and 1979 respectively for cultivation in central and peninsular India, HD 2285 was released in 1983 for North western India and Vaishali was developed in 1993 by incorporating an alien gene *Sr24/Lr24*. HD 2160 is a triple dwarf, widely used as a donor in Indian wheat breeding programme. All the above varieties have high degree of resistance to rusts and other

diseases but their genetic constitution is still not known. Therefore, inheritance of resistance was studied in cultivars, HD 2135, HD 2160, HD 2189, HD 2285 and Vaishali to 4 prevalent test pathotypes 21(9G5), 21A-2(75G5), 40-1(62G29-1), 117A(36G2) of *Puccinia graminis* (Pers.) f. sp. *tritici* (Eriksss. and Henn).

Materials and methods

Seed of five improved wheat cultivars i.e., HD 2135, HD 2160, HD 2189, HD 2285 and Vaishali (test cultivars), was obtained from Division of Genetics, IARI, New Delhi. Cultivar, Agra Local (AL), was used as a susceptible parent in making crosses.

The above test cultivars were crossed with AL to get F_1 seed. Reciprocal crosses were also attempted to study the role of cytoplasm in inheritance of resistance. HD 2189 and HD 2285 were also crossed with isogenic wheat lines *Sr11* and *Sr30* for test of allelism. After emergence of ear heads crossing was attempted following emasculation procedure. A few F_1 seeds were kept in reserve while others were multiplied to raise F_2 seed. A part of F_2 seed was further advanced to get F_3 seed for testing. To identify whether resistance is similar or different in test cultivars, they were crossed among themselves except in reciprocal manner, to make diallele crosses.

For testing, parents, F_1, F_2 and F_3 seedlings were raised in aluminium trays (11" x 4" x 3") filled with soil and farmyard manure. The seedlings in trays were ready for inoculation after 10 days of sowing. A set of differentials (Bahadur et al. 1985) was also sown along with each set for ascertaining the purity of the pathotype. The urediospore inoculum of various pathotypes was obtained from Directorate of Wheat Research, Regional Station, Flowerdale, Shimla. The urediospore-inoculum of each pathotype was multiplied on AL, following standard procedures (Joshi et al. 1988). The urediospore suspension of the pathotype was prepared in a clean petri plate by mixing spore dust with a few drops of water and a pinch of tween 20 to break the surface tension. Adequate water was added to make the spore suspension and filled in an atomizer and sprayed uniformly on the seedlings. Pots/trays were sprayed with tap water and kept in moist chambers for 48h for incubation at a temperature 20-25°C. The above cultivars were also grown along with isogenic lines and inoculated with 12 pathotypes 11(79G31), 21(9G5), 21A-2(75G5), 34-1(10G13), 40-A(62G29), 40-1(62G29-1), 42(19G35), 117-1(166G2), 117-A(36G2), 117A-1(38G18), 122(7G11), 295(7G43) for matching *Sr* genes following Bahadur et al. (1993).

The differential sets were recorded after 15 days of inoculation when disease developed. The infection types were noted according to the classification of Stakman et al. (1962). Further minor variations in infection types were recorded by putting + and - signs after the number, where - sign indicated infection type lower and + sign higher than normal categories. Symbols represent 0 = immune, 0;=nearly immune, 1 = very resistant, 2 = resistant, 3 = moderately susceptible, 4 = susceptible, and N = Necrosis.

F_2 seedlings, showing different infection types were grouped separately and counted to determine F_2 ratios. F_3 seedlings of each family, were also recorded for their segregation into resistant, segregating and susceptible families. The chi square test (χ^2) for goodness of fit, described

by Panse and Sukhatme (1967) was used for testing validity of observations in relation to expected one in segregating population on the basis of Mendelian segregation.

Results and discussion

Host-pathogen interaction

The infection types (ITs) of Test cultivars HD 2135, HD 2160, HD 2189, HD 2285, Vaishali and differential sets A and B, are shown in Table 1. Reaction pattern of above wheat cultivars showed various infection types of resistant category to 12 pathotypes of *P. graminis tritici*, while AL showed susceptibility (IT4). The above reaction pattern did not permit gene postulation in test cultivars.

Inheritance of resistance

An analysis of seedlings of parents, F_1, F_2 and families of F_3 generations with test pathotypes, is shown in Table 2. F_2 ratios were further confirmed by the segregation of families in F_3.

HD 2135

The F_1 of cross HD 2135 x AL showed ;, ;1-, 4 and ; to pathotypes 21(9G5), 21A-2(75G5), 40-1(62G29-1) and 117A(36G2) respectively, which were almost similar to HD 2135 except 40-1(62G29-1), to which HD 2135 showed ; reaction. Out of 205 seedlings, 202 segregated for resistance and 3 susceptibility deriving the ratio 63R : 1S to pathotype 21(9G5). Seedlings of reciprocal cross also segregated in the above ratio. To 21A-2(75G5) F_2 seedlings segregated in 275 resistant and 18 susceptible showing the ratio 15R : 1S, which was also observed in reciprocal cross. F_3 families segregated in 7R : 8Seg : 1S pattern confirming the ratio obtained in F_2. F_2 seedlings were grouped as 100 resistant and 340 susceptible to 40-1(62G29-1). Also F_3 families segregated in the ratio 1R : 2Seg : 1S, thus confirming F_2 ratios both in direct and reciprocal crosses. Out of 266 seedlings, 249 segregated for resistance and 17 susceptible to 117A(36G2) deriving the ratio 15R : 1S, which was also obtained in reciprocal cross. F_3 families segregated in 7R : 8Seg : 1S and further confirmed above segregation pattern. The above analysis confirmed the presence of three dominant independent genes for resistance to 21(9G5); two dominant independent genes for resistance to 21A-2(75G5) and 117A(36G2); and one recessive gene for resistance to 40-1(62G29-1) in HD 2135.

HD 2160

In cross HD 2160 x AL, F_1 showed resistance to all pathotypes except 40-1(62G29-1). In F_2, seedlings segregated in 267 resistant and 18 susceptible to 21(9G5) deriving the ratio 15R : 1S. The above ratio was also obtained in reciprocal cross. To 21A-2(75G5), out of 358 seedlings, 270 were resistant and 88 susceptible segregating in the ratio 3R : 1S. The segregation of F_3 families in 1R : 2 Seg : 1S and seedlings of reciprocal cross in 3R : 1S pattern confirmed the above F_2 ratio. To pathotype 40-1(62G29-1) F_2 seedlings of both direct and reciprocal crosses segregated in the ratio 1R : 3S. Further segregation of F_3 families occurred in 1R : 2Seg :1S. F_2 seedlings segregated in the ratio 3R : 1S of both direct and reciprocal crosses and F_3 families in 1R : 2Seg : 1S to

Table 1. Infection types* of 12 pathotypes of *P. graminis* f. sp. *tritici* on cultivars and differentials of set A and B

Cultivars	Pathotypes											
	11 (79G31)	21 (9G5)	21A-2 (75G5)	34-1 (10G13)	40A (62G29)	40-1 (62G29-1)	42 (19G35)	117-1 (166G2)	117A (36G2)	117A-1 (38G18)	122 (7G11)	295 (7G43)
HD 2135	;	1	;	;	-	;	;	1	;	1	1+	1
HD 2160	1	;	;	1	1	1	0;	1	;	1	1+	1
HD 2189	1	;	;	;	1	;	0	1	;	1	1+	1
HD 2285	1	;	;	;	1	1+	0	1	;N	1-N	1-2	1
Vaishali	;	0	;	;	;	;1	0	;	;	0;	1	1-
Agra Local	4	4	4	4	4	4	4	4	4	4	4	4
Differentials												
Set A												
Sr13 Mq	4	3	4	;	1	1	4	1	2+	1	4	4
Sr9b Mq	3	1	3+	3+	4	3	3	4	;1-	4	4	4
Sr11 Mq	4	;1	;	;	4	4	1	4	4	4	4	3
Sr28 Kota	3+	4	3	4	3	3	;	;	;	0	;	;
Sr8a Mq	;	2,2+	2,2+	1	4	4	3	1-	;	1	;	;
Sr9e Vernstein	1	;1	1	;	4	4	;	3	4	4	1	;
Sr30 Webster	4	1	3	;	1	1	2	1	1	1	;	;
Sr37 Line W	;	;	;-1	;-1	;-1	1	0	4	;	;-1	0	;
Set B												
Marquis (*Sr7b,18,19,20*)	4	4	4	4	4	4	4	2	1	2	4	3
Einkorn (*Sr21*)	3	;1	;1	1	0;	0;	3	3	3	3	4	3
Kota (*Sr7b,19,28*)	4	4	4	4	4	3	0	1	0	0	;	;
Reliance (*Sr5,16,18,20*)	4	;0	0	4	4	4	0	;	0	;	3	4
Charter (*Sr11+*)	3	;	;1-	;	4	4	0	;1-	0	3	0	;
Khapli (*Sr7a,13,14*)	;	;1	1	;	1	1	3	2	0	1	;	4

*0 = No uredia or other symptoms
0; = No uredia but hypersensitive flecks present
1 = Uredia extremely minute and surrounded by necrotic areas
2 = Uredia small to medium
3 = Uredia medium in size usually without necrosis
4 = Pustules large without necrosis
N = Drying of upper part of leaf

Table 2. Mode of segregation of seedlings of different crosses in F2 and F3 to 4 pathotypes of *Puccinia graminis tritici*

Cross Pathotypes	No. of F2† seedling		Expected F2 ratio	χ^2	p value	F3 ratio
	R	S				
HD 2135* x AL						
21(9G5)	202	3	63R : 1S	0.0130	0.95-0.90	-
21A-2(75G5)	275	18	15R : 1S	0.0056	0.95-0.90	7R : 8Seg : 1S
40-1(62G29-1)	100	340	1R : 3S **	1.2121	0.50-0.25	1R : 2Seg : 1S
117A(36G2)	249	17	15R : 1S	0.1240	0.80-0.70	7R : 8Seg : 1S
HD 2160 x AL						
21(9G5)	267	18	15R : 1S	0.0221	0.95-0.90	-
21A-2(75G5)	270	88	3R : 1S	0.0335	0.90-0.75	1R : 2Seg : 1S
40-1(62G29-1)	62	191	1R : 3S	0.0329	0.90-0.80	1R : 2Seg : 1S
117A(36G2)	217	71	3R : 1S	0.0185	0.75-0.50	1R : 2Seg : 1S
HD 2189 x AL						
21(9G5)	435	8	63R : 1S	0.1706	0.75-0.50	37R : 26Seg : 1S
21A-2(75G5)	261	4	63R : 1S	0.0048	0.95-0.90	-
40-1(62G29-1)	464	31	15R : 1S	0.1251	0.75-0.50	7R : 8Seg : 1S
117A(36G2)	344	5	63R : 1S	0.0382	0.90-0.75	37R : 26Seg : 1S
HD 2285 x AL						
21(9G5)	265	4	63R : 1S	0.0099	0.95-0.90	37R : 26Seg : 1S
21A-2(75G5)	264	4	63R : 1S	0.0085	0.95-0.90	-
40-1(62G29-1)	23	367	1R : 15S	0.0827	0.90-0.75	1R : 8Seg : 7S
117A(36G2)	228	16	15R : 1S	0.0393	0.90-0.75	7R : 8Seg : 1S
Vaishali x AL						
21(9G5)	297	2	255R : 1S	0.5950	0.50-0.25	-
21A-2(75G5)	496	2	255R : 1S	0.0015	0.95-0.90	-
40-1(62G29-1)	223	15	15R : 1S	0.0011	0.95-0.90	-
117A(36G2)	284	4	63R : 1S	0.0499	0.50-0.25	37R : 26Seg : 1S

* Reaction of parents given in Table 1

** F1's of HD 2135 x AL, HD 2160 x AL and HD 2285 x AL showed susceptibility to 40-1 (62G29-1) and resistance to other pathotypes; F1's HD 2189 x AL and Vaishali x AL showed resistance to all pathotypes.

† F2 of reciprocal crosses gave expected ratios as in direct crosses.

- Not tested.

pathotype 117A(36G2). The above data showed the presence of two dominant genes to 21(9G5) and one dominant gene to 21A-2(75G5) and 117A(36G2); and one recessive gene to 40-1(62G29-1) in HD 2160.

HD 2189

The interaction of all test pathotypes was ; on F_1 of cross HD 2189 x AL, similar to HD 2189. Out of 443 F_2 seedlings, 435 segregated for resistance and 8 susceptibility deriving the ratio 63R : 1S to 21 (9G5). Seedlings also segregated in the ratio 63R : 1S in reciprocal cross and the F_3 families showed the pattern 37R : 26Seg : 1S. F_2 seedlings of both direct and reciprocal crosses showed 63R : 1S ratio to pathotype 21A-2(75G5) and 117A (36 G 2). The above ratio was further confirmed by F_3 families, which segregated in 37R : 26Seg : 1S. To race 40-1(62G29-1), F_2 seedlings segregated in the ratio 15R : 1S both in direct and reciprocal crosses. The above ratio was further confirmed by the analysis of F_3 families, which segregated in 7R : 8Seg : 1S. The studies revealed the presence of three dominant independent genes for resistance to pathotypes 21(9G5), 21A-2(75G5) and 117A(36G2) and two dominant independent genes for resistance to 40-1(62G29-1).

HD 2285

F_1 of cross HD 2285 x AL showed ;1 reaction to all the test pathotypes except 40-1(62G29-1). Out of 269 seedlings, 265 segregated for resistance and 4 for susceptibility, deriving the ratio 63R : 1S to 21(9G5). The seedlings of direct and reciprocal crosses also segregated in above ratio to 21A-2(75G5). Segregation of F_3 families in 37R : 26Seg : 1S further confirmed the above segregation pattern. To 40-1(62G29-1), seedlings in F_2 segregated in the ratio 1R : 15S and F_3 families in 1R : 8 Seg : 7S indicating the presence of 2 recessive complementary genes in HD 2285. Segregation of seedlings of both direct and reciprocal cross occurred in 15R : 1S ratio to 117A(36G2), which was confirmed by the grouping of F_3 families in 7R : 8Seg : 1S. The above analysis showed the presence of 3 dominant independent genes for resistance to pathotypes 21(9G5) and 21A-2(75G5); two dominant independent genes to 117A(36G2); and two recessive complementary genes to 40-1(62G29-1).

Vaishali

In cross Vaishali x AL, the interaction in F_1 was 0,; and 1 to 21(9G5), 21A2(75G5) and 117A(36G2) respectively. The host pathogen interaction was ;1 to 40-1(62G29-1). Two hundred ninety nine seedlings of F_2 segregated in 297 resistant and 2 susceptible deriving the ratio 255R : 1S to 21(9G5). The above ratio was also obtained with pathotype 21A-2(75G5), which was also confirmed by segregation pattern of the reciprocal crosses to above two pathotypes. To pathotypes 40-1(62G29-1) and 117A(36G2), F_2 seedlings also segregated in the ratio 15R : 1S and 63R : 1S respectively. F_3 families of the above cross also showed the segregation pattern 37R : 26Seg : 1S to pathotype 117A(36G2). F_2 and F_3 analysis confirmed the presence of four dominant independent genes for resistance to pathotype 21(9G5) and 21A-2(75G5); three dominant independent genes for resistance to 117A(36G2) and two dominant independent genes for resistance to 40-1(62G29) in Vaishali.

Inter-relationship among parents

F_2 seedlings of crosses of HD 2135 with four other parents, HD 2160, HD 2189, HD 2285 and Vaishali, when analysed with 21(9G5), 21A-2(75G5) and 117A(36G2) did not segregate for

Table 3. Segregation pattern in diallele crosses and crosses of parents† with selected isogenic lines to different pathotypes of P. *graminis tritici*

Crosses	F2 seedlings 21(9G5)**		Result	F2 seedlings 21A-2(75G5)		Result	F2 seedlings 40-1(62G29-1)		Result	F2 seedlings 117A(36G2)		Result
	R	S		R	S		R	S		R	S	
HD 2135** x HD 2160	371	0	No seg	275	0	No seg*	391	0	No seg	315	0	No seg
HD 2135 x HD 2189	311	0	No seg	322	0	No seg	223	0	No seg	158	0	No seg
HD 2135 x HD 2285	294	0	No seg	105	0	No seg	248	0	No seg	279	0	No seg
HD 2135 x Vaishali	286	0	No seg	290	0	No seg	332	6	61R:3S	307	0	No seg
HD 2160 x HD 2189	264	0	No seg	300	0	No seg	296	0	No seg	417	0	No seg
HD 2160 x HD 2285	228	0	No seg	201	0	No seg*	298	0	No seg	317	0	No seg
HD 2160 x Vaishali	370	0	No seg	190	0	No seg	260	8	61R:3S	329	0	No seg
HD 2189 x HD 2285	307	0	No seg	180	0	No seg	348	0	No seg	395	0	No seg
HD 2189 x Vaishali	272	0	No seg	234	0	No seg	407	0	No seg	353	0	No seg
HD 2285 x Vaishali	262	0	No seg	246	0	No seg	271	0	No seg	258	0	No seg
HD 2189 x *Sr11****	469	0	No seg									
HD 2285 x *Sr11*	411	0	No seg									
HD 2285 x *Sr30*										405	0	No seg
HD 2189 x *Sr30*										405	0	No seg

† Reaction of parents given in Table 1

* Did not segregate due to less population to 21A-2(75G5)

** F1's showed resistance to all pathotypes

*** F1's and *Sr11* and *Sr30* showed resistance to 21(9G5). To race 117A(36G2), F1's and *Sr30* showed resistance.

susceptibility (Table 3). All the seedlings showed ; or 0; reaction and indicated that a common factor(s) provided resistance to above pathotypes. However, segregation in the ratio 61R : 3S in cross HD 2135 x Vaishali to 40-1(62G29-1) showed the involvement of two dominant and one recessive factors for resistance.

With pathotypes 21(9G5), 21A-2(75G5) and 117A(36G2), F_2 seedlings of crosses HD 2160 with HD 2189, HD 2285 and Vaishali showed only resistant seedlings due to common gene(s) for resistance in them. F_2 seedlings of crosses HD 2160 x HD 2189 and HD 2160 x HD 2285 also showed resistance to 40-1(62G29-1), but segregated in 61R : 1S ratio in HD 2160 x Vaishali. The above segregation explains the presence of two dominant and one recessive gene providing resistance to above pathotype.

HD 2189, when crossed with HD 2285 and Vaishali, F_2 population showed resistance to all pathotypes. Also, F_2 seedlings of cross HD 2285 x Vaishali did not segregate for susceptibility and showed a common factor providing resistance to 21(9G5), 21A-2(75G5), 117A(36G2) and 40-1(62G29-1).

Test of allelism with isogenic lines

Sharma (1990) postulated genes *Sr2*, *Sr11* and *Sr30* in HD 2189; and genes *Sr2*, *Sr5*, *Sr11*, *Sr17* and *Sr30* in HD 2285 with Australian pathotypes of stem rust. Therefore, HD 2189 and HD 2285 were crossed with two isogenic wheat lines *Sr11* and *Sr30*. The F_2 seedling analysis of above crosses did not show segregation for susceptibility to pathotypes 21(9G5) and 117A(36G2) and confirmed the presence of *Sr11* and *Sr30* in HD 2189 and HD 2285. Crosses of these parents with *Sr2* and *Sr17* were not made since *Sr2* expresses in adult plants and *Sr17* does not provide resistance to Indian pathotypes of stem rust. Also crosses of parents with *Sr5* could not be made due to non synchronous flowering.

An adult plant resistance gene *Sr2* was identified in HD 2135, HD 2189, HD 2285 and Vaishali based on mottling effect in the seedlings (McIntosh 1992). *Sr2* was initially derived from 'Yaroslav' a tetraploid wheat by McFadden (1930). Inheritance of resistance in CIMMYT semidwarfs is associated with *Sr2* gene complex derived from variety 'Newthatch' (Rajaram et al. 1988). Through CIMMYT wheats, *Sr2* has gone to many developing countries including India. *Sr2* was also identified in many other Indian wheats (Bahadur et al. 1993).

Sharma (1990) identified *Sr30* in 29 wheat varieties with Australian pathotypes of stem rust. Gene *Sr11* was identified in cvs. HD 2189 and HD 2285 in the present study. Gandhi (1967) reported an additional gene along with *Sr11* in E 581. *Sr11* also conferred resistance in two sister selections of Kalyansona- Siete cerros and Indus 66 (McIntosh 1988) and in 15 other wheats of Indian origin (Bahadur et al. 1993). The other genes identified in HD 2135, HD 2160 and Vaishali require further confirmation through test of allelism.

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Wheat Information Service
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Research information

Agronomic performance of semi-dwarf wheat (*Triticum aestivum* L.) genotypes[1]

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During the past four decades the incorporation of semi-dwarf genes into wheat crop in the world has resulted in dramatic yield increases. The majority of semi-dwarf wheat varieties covering more than half the world's wheat acreage now carry either *Rht1* or *Rht2* (Gale and Youssefian 1985). Eight advanced lines and two commercial varieties Sarsabz and Soghat 90 of wheat (*Triticum aestivum* L.) were selected to study the agronomic characters. Presence of semi-dwarf genes were presumed by the parentage of a genotype mentioned in the list of pedigree (Singh et al. 1989).

The varietal comparison results are presented in Table 1. WRS01 (*Rht1*) and SI88155 (*Rht1*) lines had the lowest grain yield per plant than the other genotypes. The remaining eight genotypes were not significantly different from each other for their grain yield per plant. WRS01 had the reduced number of grains and yield of main spike and also lowest number of grains per spikelet. Sarsabz (*Rht1*) and Soghat 90 (*Rht2*) had the highest grain yield of main spike. SI8878 (*Rht1*) had the highest number of grains per spike and spikelet. SI88171 had the lowest number of spikelets per spike. SI88123 (*Rht1*) had the highest grain yield per plant in the non-significant group of genotypes and also had the increased number of spikes per plant. Final yield is a complex character and depends on its various components. Each genotype has its own strategy to produce more yield.

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[1]Contribution No.42 of AEARC Tandojam

Table 1. Comparison in mean values of eight agronomic characters of different wheat genotypes

Genotypes	Plant height (cm)	No. of tillers/ plant	No. of spikes/ plant	No. of spikelets/ spike	No. of grains/ spike	No. of grains/ spikelet	Grain yield/ spike(g)	Grain yield/ plant(g)
WRS01	92.05 CD	4.45 BC	4.10 CDE	20.75 E	45.20 F	2.18 E	1.44 E	4.67 B
SI8878	80.15 E	4.95 B	4.85 BC	21.85 CD	67.70 A	3.10 A	1.96 CD	7.38 A
SI8887	101.30 A	4.45 BC	4.40 CDE	24.60 A	56.35 CD	2.29 E	2.13 BC	7.10 A
SI88123	95.25 B	6.90 A	6.60 A	23.25 B	61.45 BC	2.64 BC	1.80 D	8.10 A
SI88126	95.80 B	6.50 A	5.70 AB	23.45 B	55.55 CD	2.36 DE	1.74 D	6.78 A
SI88155	99.15 A	3.85 BC	3.65 DE	23.45 B	65.10 AB	2.78 B	1.85 D	4.93 B
SI88171	92.10 CD	4.85 B	4.70 BCD	19.70 F	47.80 EF	2.43 CDE	1.89 CD	6.61 A
SI88231	90.10 D	4.30 BC	4.00 CDE	22.25 CD	53.40 DE	2.40 CDE	2.12 BC	6.80 A
Soghat90	94.40 BC	4.55 BC	4.20 CDE	22.70 BC	58.50 CD	2.56 BCD	2.33 AB	7.60 A
Sarsabz	101.85 A	3.55 C	3.40 E	21.60 DE	57.95 CD	2.69 B	2.56 A	6.96 A

Means followed by the same letters do not differ significantly at 5% level.

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Research information

Morpho-cytogenetics of *Triticum aestivum* L. x *Aegilops speltoides* Tausch. hybrids

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The grain yield of wheat is directly related to the length of the growing season and the grain filling period. High temperature during the second fortnight of April especially in the North Western plains of India leads to grain shrivelling and significant reduction in grain yield. *Aegilops speltoides* Tausch. (2n=2x=14, SS), a wild species, is highly tolerant to high temperature particularly during the grain filling period. Due to relatively much longer photoperiod requirements, *Ae. speltoides* flowers during the second week of May and is found to set seed in the first fortnight of June when the temperature is usually above 40°C. And the harvested seed is normal and plump. Additionally, *Ae. speltoides* is highly resistant to stem rust.

With a view to incorporate desirable traits of *Ae. speltoides* and more specifically high temperature tolerance into the bread wheat, interspecific hybrids between *T. aestivum* (*ph1b* mutant cv. Chinese Spring) and *Ae. speltoides* (Acc. No. 3808) were produced. All the hybrid plants were completely male sterile and resembled *T. aestivum* more closely than *Ae. speltoides* in general morphological traits. The F_1 hybrids, however, exhibited much profuse tillering, had pigmented auricles and their terminal spikelets showed pronounced awning. Auricle pigmentation in conjunction with profuse tillering ability and characteristic awning indicated the expression of *Ae. speltoides* gene(s) in the cytoplasmic background of cultivated wheat. The mean chromosome pairing per pollen mother cell (PMC) was 6.82 bivalents (predominantly ring) + 0.9 trivalents + 0.26 quadrivalents + 10.3 univalents. The maximum chromosome pairing recorded was 12 bivalents (11 ring + 1 rod) + 4 univalents.

Since Chinese Spring is a poor agronomic cultivar, the F_1 hybrids were topcrossed (as females) to *T. turgidum* ssp. *dicoccoides* (Acc. No. 4637) and VL 777, a bread wheat cultivar with good agronomic background. The seed set on topcrossing the allotetraploid F_1 hybrids to the tetraploid and hexaploid wheats was 5% and 3.5%, resdectively which also confirmed the partial fertility (female) of the *Triticum- Aegilops* F_1 hybrids.

Gene transfers from the alien chromosomes into the genomes of the cultivated species are usually achieved through rare recombinational events or through radiation-induced translocations. Alternatively, when the F_1 hybrids are completely sterile, efforts are made to achieve gene transfer across F_1 sterility barriers by producing monosomic alien addition lines (MAALs).

MAALs have primarily been produced and extensively studied in the polypoid species.

Recently, such lines have also been developed in cultivated rice, a diploid species. The alien addition line technique was employed for transferring leaf rust resistance from *Ae. umbellulata* to hexaploid wheat (Sears 1956), stem rust resistance from *Agropyron elongatum* to hexaploid wheat (Knott 1961) and mildew resistance from *Avena barbata* into hexaploid oat (Aung and Thomas 1978). Similarly, Jena and Khush (1989) transferred several genes including those for resistance to BPH and WBPH from *Oryza officinalis* into *O. sativa.*

The successful production of topcross seeds in the present investigation also opens up the possibility of producing alien addition lines of specific *Ae. speltoides* chromosomes for transferring useful traits especially higt temperature resistance from *Ae. speltoides* into the cultivated wheat. Efforts to develop such monosomic alien addition lines are underway.

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Research information

A simple procedure for the production of wheat-barley 5H chromosome recombinant lines utilizing 5B nullisomy and 5H-specific molecular markers

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Barley (*Hordeum vulgare* L.) is a potential new source of genes for wheat (*Triticum aestivum* L.) improvement, e.g., genes conferring resistance to some diseases and cereal cyst nematode (e.g. Islam and Shepherd 1992a). The production of 6 of the 7 possible wheat-barley disomic addition lines by Islam et al. (1981), involving individual pairs of 'Betzes' barley chromosomes added to 'Chinese Spring' wheat, has made it possible to manipulate barley chromosomes in a wheat background.

Wheat-barley disomic addition lines possessing 'New Golden' barley chromosome 5H added to 'Shinchunaga' wheat was two to three days earlier in heading time than the original wheat cultivar under fall-sowing conditions in the field (Koba et al. 1997). Study on earliness of this line revealed that the 'New Golden' 5H accelerates narrow-sense earliness and decreases vernalization requirement (Murai et al. 1997). To introduce the barley genes for early heading on 5H into wheat, we plan to produce wheat-barley 5H chromosome recombinant lines. Here, we propose a simple procedure to develop those lines using 5B nullisomy in combination with molecular markers.

The proposed procedure to isolate recombinants involving 5H and wheat homoeologues 5A or 5D (5A/D) is shown in Fig. 1. In the first cross, 'Chinese Spring' monosomic 5B is pollinated with the wheat-barley 5H addition line. Progeny double monosomic for 5B and 5H (2n=42 and 20"+5B'+5H') are selected and pollinated with 'Chinese Spring' nullisomic-5B tetrasomic-5A/D in the second stage of crossing. Among progeny with 42 chromosomes, plants which are nullisomic-5B trisomic-5A/D monosomic-5H (19"+5A/D'"+5H') will be identified cytologically (utilizing the C-banding technique) and with molecular markers. Barley 5H chromosome-specific RAPD markers developed by Murai (1995) will be used to identify those plants having 5H. Because of the absence of the *Ph1* gene in the 19"+5A/D'"+5H' stocks, 5H is expected to pair with its homoeologues 5A/D. Wheat-barley recombinant chromosomes will be isolated from the selfed progeny of these stocks

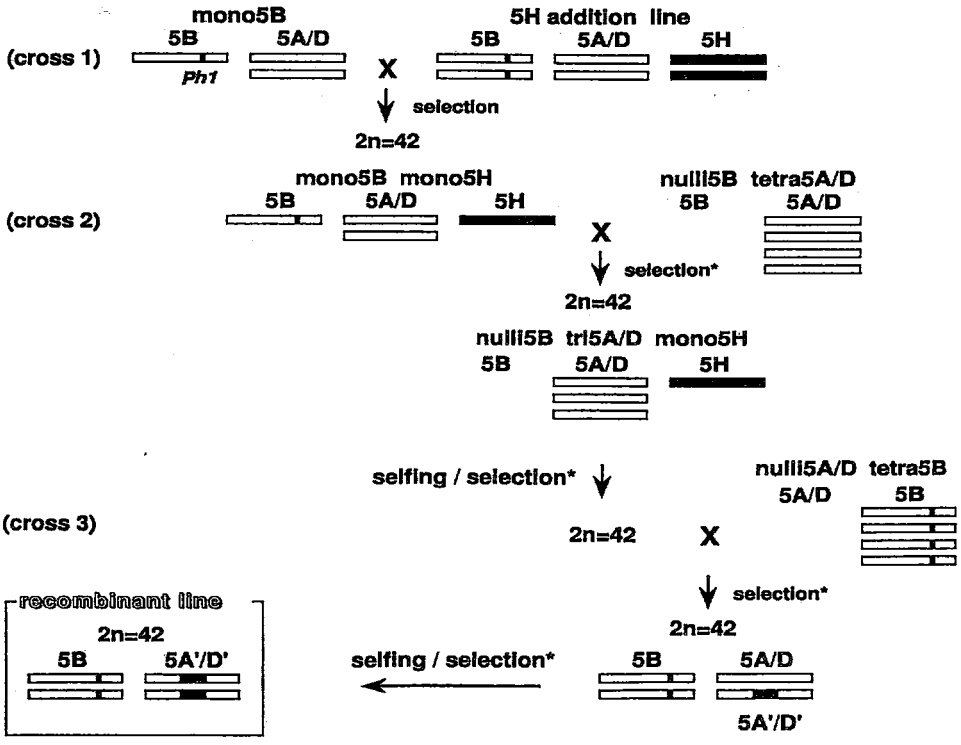

Fig.1 Procedure for production of wheat-barley 5H chromosome recombinant lines utilizing 5B nullisomy and 5H specific molecular markers.
selection*: cytological screening with molecular markers, 5A/D: chromosome 5A or 5D, 5A'/D': recombinant chromosome between 5A or 5D and 5H.

by using molecular markers to screen for dissociation of the barley markers. STS-PCR markers derived from RFLP probes located on 5H (Blake et al. 1996) will be used to allow efficient screening of recombinants. These selected plants (2n=42) possessing recombinant chromosome will be pollinated with nullisomic-5A/D tetrasomic-5B to reintroduce 5B into the progeny. After selfing the putative recombinants, plants homozygous for wheat-barley recombinant chromosomes will be isolated.

Wheat-barley recombinant chromosomes involving barley chromosome arms 3HL or 6HL have been produced by Islam and Shepherd (1992a). In their procedure, wheat plants which were double monosomic for 5B and either 3A or 6A were pollinated with the corresponding ditelosomic wheat-barley substitution lines, i.e., 3HL(3A) or 6HL(6A) (Islam and Shepherd 1992b), and plants with 19"+5B'+t'3HL or t'6HL were selected cytologically. To induce homoeologous recombination, these plants were further crossed with Sears' *phlb* mutant, and triple monosomic

stocks, i.e., 19"+5B'*ph1b*+t'3HL+3A' or 19"+5B'*ph1b*+t'6HL+6A', were selected. Wheat-barley recombinant chromosomes were isolated from the selfed progeny using isozyme markers to screen for dissociation of the barley markers.

The major problem for producing wheat-alien recombinants is the expected low pairing frequency between wheat and alien chromosomes. Islam and Shepherd (1988, 1992a) reported that barley chromosomes paired with frequencies of 0.3% and 2.6% in the triple monosomic stocks, 19"+5B'*ph1b*+t'3HL+3A' and 19"+5B'*ph1b*+t'6HL +6A', respectively. Koebner and Shepherd (1986) have utilized both the *ph1b* mutant and 5B nullisomy to induce homoeologous recombination between wheat and rye chromosomes. They obtained a higher level of homoeologous pairing (three-fold increase of recombination rate) between wheat and rye chromosomes by using 5B nullisomy rather than using the *ph1b* mutant. This finding suggests that 5B nullisomy may induce increased pairing between wheat and barley homoeologous chromosomes.

Because of the expected low pairing frequency between wheat and barley chromosomes, an effective selection system for identifying recombinants is necessary. Isozyme markers,which were used by Islam and Shepherd (1992a), are not widely applicable for identification of recombinants because the number of markers is limited. Numerous molecular markers detecting polymorphism between wheat and alien species have been developed in the past few years. For example, Blake et al. (1996) developed 135 barley chromosome-specific STS-PCR markers, 19 of which are 5H-specific. The selection efficiency is expected to be greatly enhanced by the use of these STS-PCR markers.

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Proposal

The history and the correct nomenclature of the D-genome diploid species in Triticeae (Poaceae)

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Introduction

In the literature, *Aegilops squarrosa* L., *Ae. tauschii* Cosson, and *Triticum tauschii* (Cosson) Schmal. are frequently used as the scientific name for the D-genome diploid species in the tribe Triticeae. According to an incomplete survey, from 1990 to 1995, more than 100 authors used "*Aegilops squarrosa* L." to refer to this taxon in their papers, and, when *Aegilops* and *Triticum* were treated as a single genus, the name *Triticum tauschii* (Cosson) Schmal. is often used. This chaos in nomenclature for this species often leads to misunderstanding of the species referred to by people who are not familiar with Triticeae taxonomy, and may cause problems in researches. Therefore, Dr. Kozo Nishikawa, the editor of Wheat Information Service (WIS), suggested that we write this note to clarify the correct nomenclature for this D-genome diploid Triticeae species.

History of the nomenclature of the diploid D-genome Triticeae species

Two species in the genus now called *Aegilops* were first reported by Scheuchzer (1719) in his Agrostographia. This was before the standard binary system of Linnaeus was established. These two species were later designated as *Aegilops triaristata* by Willdenow in 1805 and as *Ae. ovata* by Linne in 1753, respectively. Linne (1753) established the genus *Aegilops*, based on the type specimen of *Ae. ovata* L., and published the following five *Aegilops* species in his Species Plantarum: *Ae. ovata* L., *Ae. caudata* L., *Ae. squarrosa* L., *Ae. triuncialis* L. and *Ae. incura* L.. In the second edition of this book, *Ae. incura* L. was moved to genus *Lepturus* (Linne 1763). Actually, the species which Linne (1753, 1763) named *Ae. squarrosa* L. is a form of *Ae. triuncialis* L. which differs from the type by only having awns on the top spikelets.

In 1849, Ernest Saint-Charles Cosson published, on the page 69 of "Notes sur quelques

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plantes de France critiques, rares ou nouvelles, fasc. II", a new taxon collected from Iberia (Buxbaum, J.C. loc. cit., near Caucasia, in modern Georgia) and Tauria (Tausch, I.F. loc. cit.). He designated it as *Ae. tauschii* Cosson, in memory of an outstanding botanist, Ignas Friedrich Tausch. This taxon is actually the one which is now known as the D-genome diploid Triticeae species. These specimens were confused with *Ae. squarrosa* L. by J.C.D. von Schreber (1769) and I.F. Tausch (1837). It was confused with *Ae. caudata* L. by James Edward Smith and John Sibthorp in 1806 (see Flora Graeca I, page 76). That specimen from Tauria was confused and designated as *Ae. cylindrica* Host var. *taurica* by Johann Jakob Roemer, and Jos. Augusto Schultes in 1817 (see Caroli a Linne Systema vegetabilium secundum classes, ordines, genera, species, cum characteribus, differtiis et synonymiis, II, page 771).

In 1812, Ambrois Marie Francois Joseph Palisot de Beauvois combined *Ae. squarrosa* L. to the genus *Triticum* and gave it a new species name, *aegilops*. In 1896 he mis-identified the D-genome diploid taxon as *Ae. squarrosa* L.. He reported and named it as *Triticum aegilops* P. Beauv. in Flora of British India, vol. VII, (which was edited by J.D. Hooker. and O. Stapf in 1896). He explained that his description was based on *Ae. squarrosa* L. Because of his big name, de Beauvois' mis-identificatiion had a strong influence on many people, including some experts, such as P.M. Zhukovsky (1928) and A. Eig (1929), who followed de Beauvois and made the same mistake by using the invalid name *Ae. squarrosa* L. for the taxon of the D-genome diploid species.

On page 654 of his book "The Grasses of Burma, Ceylon, India and Pakistan", N.L. Bor (1960) reported :"A recent examination of the type of *Ae. squarrosa* in Linnean Herbarium shows that it is a form of *Ae. triuncialis* Linn., hence the species called *Triticum aegilops* P. Besuv. in the Flora of British India, based on *Ae. squaresa* Linn., must be known by the next available name--*Aegilops tauschii* Cosson". The authors proved this by a high quality photograph of the type specimen which was stored in Copenhagen, Denmark. Therefore, Zeven and Zhukovsky (1975) called the D-genome diploid species *Ae. squarrosa* auct. non L. However, this designation, too, is not valid according to International code of botanical nomenclature (Greuter et al. 1994).

Hackel (1887) combined genera *Aegilops* L. and *Triticum* L. into one genus *Triticum* L. Following the suit, *Aegilops tauschii* Cosson was included in genus *Triticum* ten years later and changed the name to *Triticum tauschii* (Cosson) Schmalh. (see Schmalhausen, Ivan Fedorovich (1827). Fl. Centr. et S. Russia, 2, page 662).

Discussion

Of the two species epithet names, *squarrosa* and *tauschii*, which one is legitimate? This is the question often being asked. A legitimate name has to follow the International Code of Botanic Nomenclature. According to the Code, "the application of names of taxonomic group is determined by means of nomenclature types" (Principle II); "the nomenclature of a taxonomic group is based upon priority of publication" (Principle III); and "each taxonomic group with a particular circumscription, position, and rank can bear only one correct name, the earliest that is in accordance with the Rules, except in specified cases" (Principle IV). Obviously, the legitimate name of the D-genome diploid Triticeae species has to meet these two criteria: priority and correctness. Of the

two popular species names for the D-genome diploid, *squarrosa* was published earlier than *tauschii*, and that is why many researchers regard it the right name. However, Linne (1753, 1763) did not assign the name "*squarrosa*" to the D-genome diploid species but to a form of the tetraploid *triuncialis*. It was a misidentification made by de Beauvois (1896) that led to the popular usage of the "*squarrosa*" to call the D-genome diploid. Cosson (1849) was the first to assign the name "*tauschii*" to the D-genome diploid, based on nomenclature types from Iberia and Tauria. Hence the name *tauschii* has the priority, and, because it follows the Code, it is correct. Obviously, "*tauschii*" is the sole legitimate name of the D-genome diploid species, regardless which genus, *Aegilops* or *Triticum*, it belongs to.

According to the Code, "for any taxon below the rank of genus, the correct name is the combination of the final epithet of the earliest legitimate name of the taxon in the same rank, with the correct name of the genus or species to which it is assigned" (Article 11.4). Therefore, the correct species name should be assigned based not only on the priority, but also on the legitimate name of the genus to which it belongs. Then, there comes the question: which is the legitimate species name: *Aegilops tauschii* or *Triticurn tauschii*? The answer is: Both.

From objective reality, there are only two absolute units of living organisms: individuals and species. A species is a group of individuals which connect to each other as a unit by their indispensable relationships of breeding. There is no absolute boundary among genera, families and the taxa above. Taxonomic treatment above species cannot avoid arbitrariness. It is not surprised that many genus combinations have been proposed. When Cosson (1849) published the species name for the D-genome diploid, he put it in the genus *Aegilops*, and *Aegilops* is a legitimate genus. Hence, *Aegilops tauschii* should be the legitimate name if classification of the genus *Aegilops* is followed. On the other hand, *Triticum* is also a legitimate genus name. The argument is how to define the genus *Triticum*.

Correct taxonomic nomenclature is very important in plant sciences. Mis-identifying a taxon may cause unnecessary waste of the precious time and resources of other scientists. For instance, Jensen et al. (1986) and Jensen (1990) and Yang et al. (1990) worked on an accession, PI 314623. This material was collected in 1967 by USDA-ARS plant explorers Drs. Q. Jones and W. Keller in a mountainous area about 180 km east of Alma Ata, Kazakhstan and mis-named as "*Agropyron batalinii*". When the plants of PI 314623 were compared with the type specimens (it was designated as *Triticum batalinii* Krassn. by the Russian scientist) in herbarium of Komarov Botanical Institute (LE), St. Pertersburg, Russia, they were found to be quite different from the type specimens, but similar to another type specimen named *Roegneria carinata* Ovcz. et Sidor. The mistake made by Jones and Keller caused Jensen et al. (1986) and Jensen (1990) made the wrong conclusion about the genome constitution of "*batalinii*", which they worked on, and led Yang et al. (1990) to wrongly identified taxon "*nana*" as an independent species, though it should only be a variety of *Kengyilia batalinii* (Krassn.) Yang, Yen et Baum (Yen et al. 1996). Recently, J. Dvorak and M.C. Luo conducted RFLP analysis of *Aegilops tauschii* Cosson from China. They were astonished to observe a distinctive band shown in some accessions they analyzed. Based on this observation, they classified these accessions as a new group of this species. After they checked these materials again, they found these materials were actually *Ae. cylindrica* Host. but misclassified to *Ae.*

tauschii Cosson in Crop Germplasm Institute of Chinese Academy of Agricultural Sciences. Therefore, plant scientists are urged to use the correct, legitimate scientific name to call the plant material they work with.

In conclusion, both *Aegilops tauschii* Cosson and *Triticum tauschii* (Cosson) Schmalh. are both valid scientific names for the D-genome diploid Triticeae species in accordance with the Rules of the Code. The name *Ae. squarrosa* L., if it applied to the D-genome diploid species, is not a legitimate name in accordance with the Article 7.4 of the Code, because Linne (1753) described it on the basis of a type specimen that was actually a form of *Ae. triuncialis* L. Trying to make *Aegilops squarrosa* a legitimate name, Zeven and Zhukovsky (1975) offered a compromising proposal: assigning *Ae. squarrosa* auct. non L. to the D-genome diploid. However, this name is also not legitimate according to Article 11.4 of the Code, because the earliest legitimate name of this taxon is *Ae. tauschii* Cosson which was assigned in a valid publication and determined by means of nomenclature type.

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Assembly of North American accessions of *Aegilops cylindrica*

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Aegilops cylindrica Host. is a wide spread species in Mediterranean, West Asia: Asia Minor into Bulgaria, Romania, Yugoslavia and up along the Danube into Hungary; northwards into the Caucasus region and along the Black Sea coast. Probably at the end of the 19th century *Ae. cylindrica* was introduced into the United States and presents in many states from the east to the west coasts, although most abundantly in the western and northwestern states and the plains of Midwest (Donald and Ogg 1991). The weedy growth of *Ae. cylindrica* is dramatically demonstrated by its introduction and subsequent wide spreading in the United States. When the introduction occurred is unclear, but the oldest specimen is from 1918. The species has become troublesome in the fields and pasture. Its growth on the edges and within wheat fields is also troublesome.

Ae. triuncialis L. var. *triuncialis* is also a wide spread species in Mediterranean, West Asia and all over southern Europe and the Near East, extending eastwards into central Asia, Pakistan and Afghanistan and well-represented along the entire Fertile Crescent arc. Also it was found on Cyprus and the southern Crimea as well as in Ciscaucasus, but there predominantly in the eastern parts along the Caspian Sea. Its spread appears to be limited by the 45° N latitude, and only in France, Italy, Slovenia and Croatia it extend beyond the latitude. It was introduced into the United States. The species has become troublesome weed on range in California and Pennsylvania. Fig. 1 shows current infested area surveyed by the weed scientists in the United States in 1988 (Donald and Ogg 1991), and the locations of herbaria summarized by van Slageren (1994).

Potential benefits of collections

Differentiation of the colonizer species must be widely considered in the sight of evolution. It is known that *Bromus tectrum* was introduced into the intermountain region on Western North America ca. 1890, and expanded to its present range within 40 years (Mack 1981). Although not as recently introduced *B. tectrum*, California populations of other alien annuals such as *Bromus mollis* and *Avena barbata* also show distinct regional differentiation in phenology and morphology. Allelic and genotypic composition of ancestral Spanish and colonial Californian gene pools of *A. barbata* has been considered (Garcia et al. 1989; Perez de la Vega et al. 1991).

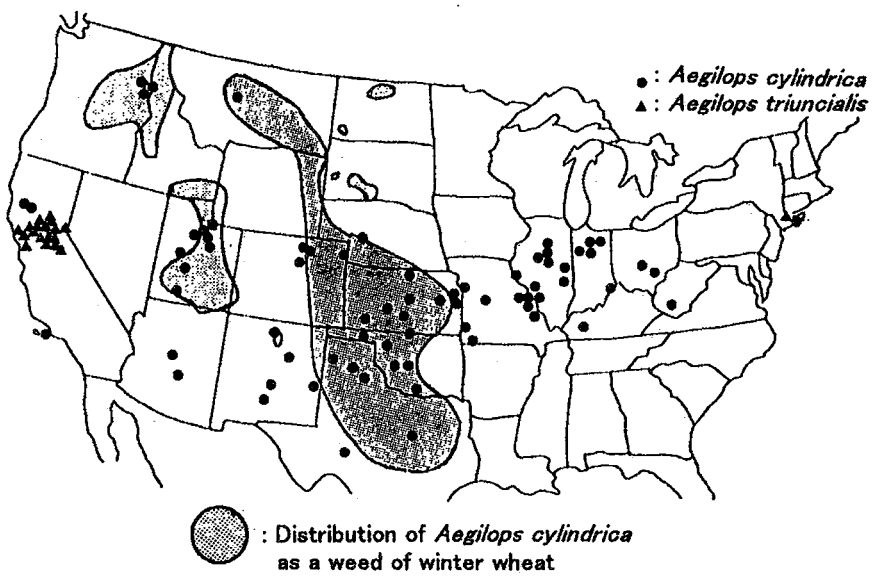

Fig. 1. Distribution of *Aegilops cylindrica* as a weed of winter wheat in the United States and the collection sites of historical herbaria of *Ae. cylindrica* (●) and *Ae. triuncialis* var. *triuncialis* (▲). Data were taken from Donald and Ogg (1991) and van Slageren (1994).

However, North American *Aegilops* has not been investigated by the geneticists, although those species have become troublesome weed in the fields and pasture. I do not know the considerable collections of North American *Aegilops*.

Efforts to assemble North American Accessions

Due to lack of funding, I did not enable to organize the expedition to collect the accessions of *Ae. cylindrica* and *Ae. triuncialis* var. *triuncialis* in the United States, however, fortunately the directory of weed scientists concerning with *Ae. cylindrica* was offered from Dr. D.R. Gealey, Washington State University. I asked them to collect the accessions of *Ae. cylindrica* with the passport data, and if possible, *Ae. triuncialis* at their locality. In 1994, I also proposed Dr. P. Westra, who is the leader of the national collection of *Ae. cylindrica*, to exchange the accessions reciprocally. In the consequence, the collection amounted up to 81 (Table 1). Any accessions of *Ae. triuncialis* var. *triuncialis* was not obtained in this 5 years due to limited distribution at ranges of California and Pennsylvania and lacking of reference.

We did not find any diversity of α-amylase isozymes among my collections (Watanabe et al. 1996), but observed considerable diversity of morphological and physiological characteristics (unpublished results). I expect the North American accession would be utilized broadly and North American *Ae. triuncialis* would be assembled in the future.

Table 1. List of North American accessions of *Aegilops cylindrica*

Collection				Collection			
State	No.	Collection Site	Donor	State	No.	Collection Site	Donor
Washington	4	Pullman, WA	S. Miller		10	Colorado	D. Gealey
	5	Pullman, WA	D. Gealey		15	Akron, CO	R. Anderson
	57	Pullman, WA	P. Westra		19	Otis, CO	P. Stahlman
	58	Lacrosse, WA	P. Westra		51	Fort Collins, CO	P. Westra
	69	Ritzville, WA	P. Westra		52	Fort Collins, CO	P. Westra
Oregon	6	Pendleton, OR	D. Gealey		53	Kioiwa, CO	P. Westra
	63	Ione, OR	P. Westra		54	Haxton, CO	P. Westra
	77	Pendleton, OR	J.G. Waines		55	Haxton, CO	P. Westra
California	76	Santa Barbara, CA	J.G. Waines		56	Platner, CO	P. Westra
Montana	7	Montana	D. Gealey		61	Rush, CO	P. Westra
	16	Belt, MT	P.K. Fay		62	Cheyenne Wells, CO	P. Westra
	24	Parkcity, MT	P.K. Fay	Nebraska	9	Big Spring, NE	D. Gealey
	25	Columbus, MT	P.K. Fay		17	Angora, NE	D. Lyon
	26	Yellowstone, MT	P.K. Fay		36	Deuel, NE	P. Westra
	27	Cascade, MT	P.K. Fay		37	Garden, NE	P. Westra
Wyoming	8	Lingle, WY	D. Gealey		38	Cheyenne, NE	P. Westra
	70	Archer West, WY	P. Westra		39	Cheyenne, NE	P. Westra
	71	Archer West, WY	P. Westra		40	Kimbal, NE	P. Westra
	72	Pine Bluff, WY	P. Westra		41	Kimbal, NE	P. Westra
	73	Chugwater, WY	P. Westra		42	Scottbluff, NE	P. Westra
	74	Broadview, WY	P. Westra		43	Chardon, NE	P. Westra
Idaho	20	Idaho	D.W. Morishita		44	Chardon, NE	P. Westra
	21	Idaho	D.W. Morishita	Kansas	1	Hays, KS	S. Miller
	28	Ikom, ID	N. Watanabe		11	Lacross, KS	D. Gealey
	29	Ikom, ID	N. Watanabe		12	Lacross, KS	D. Gealey
	49	Bingham, ID	P. Westra		18	Hodgeman, KS	P. Stahlman
	30	Twin Fall, ID	P. Westra		59	Kingman, KS	P. Westra
Utah	30	Utah State Univ.	N. Watanabe		60	Logan, KS	P. Westra
	31	Cache, UT	N. Watanabe	Oklahoma	13	Oklahoma	D. Gealey
	32	Cache, UT	N. Watanabe		14	Woodward, OK	J. Koscelny
	33	Cache, UT	N. Watanabe		45	Oklahoma	P. Westra
	34	Cache, UT	N. Watanabe		47	Oklahoma	P. Westra
	35	Cache, UT	N. Watanabe	Texas	48	Oklahoma	P. Westra
	64	Box Elder, UT	P. Westra		22	Amarillo, TX	A.F. Wiese
	65	Box Elder, UT	P. Westra		23	Bushland, TX	A.F. Wiese
	66	Box Elder, UT	P. Westra		77	Amarillo, TX	A.F. Wiese
	67	Cache, UT	P. Westra		78	Amarillo, TX	A.F. Wiese
	68	Cache, UT	P. Westra		79	Amarillo, TX	A.F. Wiese
Colorado	2	Colorado	S. Miller		80	Amarillo, TX	A.F. Wiese
	3	Otis, CO	S. Miller		81	Amarillo, TX	A.F. Wiese

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Currant list of wheats with rye introgressions of homoeologous group 1
2nd update

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After the first reports on spontaneous wheat-rye chromosome substitutions 5R(5A) by Katterman (1937), O'Mara (1946) and Riley and Chapman (1958), during the past three decades particularly, 1R(1B) substitutions and 1RS.1BL translocations were described in more than 200 cultivars of wheat from all over the world (Zeller and Fischbeck 1971; Zeller 1972, 1973; Bluethner and Mettin 1973; Mettin et al. 1973). Their most important phenotypic deviation from common wheat cultivars is the so-called wheat-rye resistance, i.e. the presence of wide-range resistance to races of powdery mildew and rusts (Bartos and Bares 1971; Zeller 1973), which is linked with decreased breadmaking quality (Zeller et al. 1982), good ecological adaptability and yield performance (Rajaram et al. 1983; Schlegel and Meinel 1994). The origin of the alien chromosome was intensively discussed by genetic and historical reasons. It turned out that basically four sources exist—two in Germany, one in the USA and one in Japan. The variety 'Salmon' (1RS. 1BL) is a representative of the latter (Tsunewaki 1964) and the variety 'Amigo' (1RS. 1DL) is a representative of the penultimate group (Beronsky et al. 1991; The et al. 1992), while almost all remaining cultivars can be traced back to one or to the other German origin (Zeller 1973; Bluethner and Mettin 1977). There was no doubt so far that the Japanese and the American derivatives differ from one another and from the German sources. Although on two places of Germany— Salzmuende near Halle/S (breeder:Riebesel) and Weihenstephan near Munich (breeder : Kattermann)— wheat-rye crosses were already carried out since the twenties and thirties and independent pedigrees could be fragmentally reconstructed by the few reports left (Bluethner 1992), some authors presumed only one German source (Lein 1975; Moonen and Zeven 1984). For breeding programmes additional recombination within the translocated 1RS arm of rye and between the different wheat genetic backgrounds is wished (Mueller et al. 1991a; Lutz et al. 1992). In order to prevent miscrossings and to review the wheat-rye introgressions a second list of the various 1RS sources was compiled including some passport data. Because of space limit the year of release, the proof of the introgression, the characteristics of the varieties and the referencesare not included in the paper. They can be obtained from the author by request:

The first list was published by Schlegel, R., U. Vahl, G. Muller, 1994, A compiled list of wheats carrying homoeologous group 1 wheat-rye translocations and substitutions. Ann. Wheat Newslett.,USA, 40:105-117

(left to right: variety, origin, pedigree, introgression in each column)

Abele	?	?	1RS.1BL
Abritus	BLG*	xAvrora	1RS.1BL
Admiral	GBR	xRiebesel lines	1RS.1BL
Advokat	DEU	xSt14/48 Weihenstephan	1RS.1BL
Agra	CSK	x Avrora	1RS.1BL
Alba	POL	xWeique	1RS.1BL
Albrecht	DEU	xDisponent	1RS.1BL
Almus	DDR	xRiebesel lines	1RS.1BL
Alondra 'S'	MEX	x Weique Redmace	1RS.1BL
Alta 84, *T. durum*	MEX	?	1RS.1BL
Altimir 67	BGR	xSkorospelka 35	1RS.1BL
Amadeus	AUT	xKavkaz	1RS.1BL
Amandus	DEU	xPerseus	1RS.1BL
Ambassador	GBR	xForester	1RS.1BL
Amigo	USA	xInsave rye	1RS.1AL
Amika	CSK	xAvrora	1RS.1BL
Anza deriv.	USA	xtriticale	1R(1D)
Apatinka	YUG	xAvrora	1RS.1BL
Apollo	DEU	xClement	1RS.1BL
Arber	DEU	xKronjuwel	1RS.1BL
Austro BAER	CHL	xKatterman lines	1RS.1BL
Avrora	USS	xNeuzucht	1RS.1BL
Bacanora 88	MEX	?	1RS.1BL
Bagula	MEX	xKavkaz	1RS.1BL
Balkan	YUG	xSkorospelka 35	1RS.1BL
Banatka niska	YUG	xAvrora	1RS.1BL
Baron	?	?	1RS.1BL
Batten	NZL	xKavkaz	1RS.1BL
Beaver	GRB	xMildress	1RS.1BL
Benno	DEU	xZorba	1RS.1BL
Beogradjanka	YUG	xKavkaz	1RS.1BL
Bernina	SCH	xKatterman lines	1RS.1BL
Besostaya 2	USS	xNeuzucht	1RS.1BL
Bobwhite 'S'	MEX	xAvrora	1RS.1BL
Bovictus	DEU	xAvrora	1RS.1BL
Branka	CSK	xSt378/57Weihenstephan	1RS.1BL
Burgas 1	BGR	xNeuzucht	1RS.1BL
Burgas 2	BGR	xNeuzucht	1R(1B)
Butin	CSK	xKavkaz	1RS.1BL
Campus	AUT	xKavkaz	1RS.1BL
Cando deriv.	DEU	xVeery 'S'	1RS.1BL
Capriccio	?	?	1RS.1BL
Carolus	DEU	xPerseus	1RS.1BL
Cazo	MEX	?	1RS.1BL
Cebeco 180	NLD	?	1RS.1BL
Cebeco 97	NLD	?	1RS.1BL
Century	USA	xAmigo	1RS.1AL
Chakwal 86	PAK	xVeery derivatives	1RS.1BL
Charodeijka	BGR	xSkorospelka 35	1RS.1BL
Chat 'S'	MEX	xVeery derivatives	1RS.1BL
Chersonskaja 153	USS	xAvrora1RS.1BL	
Chieftain	?	?	1RS.1BL
Chinese Spring deriv.	AUS	xImperial rye	1R(1D)
Chinese Spring deriv.	AUS	xImperial rye	1RS.1BL
Chinese Spring deriv.	AUS	xImperial rye	1RS.1DL
Chinese Spring deriv.	AUS	xImperial rye	1R(1B)
Chuan Mai	CHN		1RS.1BL
Clement	NLD	xSt.47/51 Riebesel	1RS.1BL
Compact	AUT	xKavkaz	1RS.1BL
Conveyor	GBR	xRiebesel lines	1RS.1BL
Cordillera	PRY	xVeery 3 selection	1RS.1BL
Corinthian	?	?	1RS.1BL
Csongor	HUN	xPredgornaya2	1RS.1BL
Cunco INIA	CHL	xRiebesel lines	1RS.1BL
Custom	GBR	xSt465/62Weihenstephan	1RS.1BL
Dalcachue INIA	CHL	xRiebesel lines	1RS.1BL
Damier	FRA	xClement	1RS.1BL
Danubia	CSK	xAvrora	1RS.1BL
Dauntless	GBR	xMMG435/46/3	1RS.1BL
Delta	POL	?	1RS.1BL
Denislava	BGR	xSkorospelka 35	1RS.1BL
Disponent	DEU	xBenno	1RS.1BL
Dnestrjanka	USS	xKavkaz	1RS.1BL
Donata	NDL	xRiebesel lines	1RS.1BL
Donjon	NDL	xClement	1RS.1BL
Donskaya polukarlik.	USS	xSvereodonskaya	1RS.1BL
Dozent	DEU	xPerseus	1RS.1BL
Druzba 1	USS	xWinnetou	1RS.1BL
Dukat	YUG	xAvrora	1RS.1BL
Dunavka	BGR	xAvrora	1RS.1BL
Esmeralda 86	MEX	?	1RS.1BL
Est-Mottin 72	ITA	?	1RS.1BL
Falestdkaya 2	USS	xKavkaz	1RS.1BL
Falke	MEX	?	1RS.1BL

Famulus	AUT	xKatterman lines	1RS.1BL
Fatima	HUN	?	1RS.1BL
Feldkrone	DEU	xZorba	1RS.1BL
Feldman	DEU	xKatterman lines	1RS.1BL
Florida	DEU	xDisponent	1RS.1BL
Forna	SCH	xKatterman lines	1RS.1BL
Fundulea 4	ROM	?	1RS.1BL
Fundulea 29	ROM	xAvrora	1RS.1BL
Gabo deriv.	AUS	xImperial rye	1RS.1BL
Gabrinus	AUT	xKatterman lines	1RS.1BL
Galvez 87	MEX	?	1RS.1BL
Gamtoos	ZAF	xVeery 3selection	1RS.1BL
Genaro 81	MEX	?	1RS.1BL
Genaro F81	MEX	xVeery 3selection	1RS.1BL
GK Bence	HUN	?	1RS.1BL
GK Odzi	HUN	xAvrora	1RS.1BL
GK Sagvari	HUN	xAvrora	1RS.1BL
GK Szemes	HUN	xAvrora	1RS.1BL
GK Tiborc	HUN	?	1RS.1BL
GK Zombor	HUN	xKavkaz	1RS.1BL
Glennson M81	MEX	xVeery 1 selection	1RS.1BL
Gorbi	DEU	?	1RS.1BL
Götz	DEU	xBenno	1RS.1BL
GR 876	USA	xKavkaz	1RS.1BL
Granada	DEU	xZorba	1RS.1BL
Granka	YUG	xAvrora	1RS.1BL
Grebe	AUS	xSkorospelka 35	1RS.1BL
Hamlet	DEU	xZorba	1RS.1BL
Hammer	NDL	xWeibull2019	1RS.1BL
Haeward	GBR	xKatterman lines	1RS.1BL
Harts	ZAF	?	1RS.1BL
Haven	GBR	xMildress	1RS.1BL
Havik	MEX	?	1RS.1BL
HD2278	IND	?	1RS.1BL
Hedgehog	GBR	xRiebesel lines	1RS.1BL
Heinrich	DEU	xArkos 3	1RS.1BL
Helios	DEU	xPerseus	1RS.1BL
Herzog	DEU	xKronjuwel	1RS.1BL
HI977	IND	?	1RS.1BL
Holdfast deriv.	AUS	xKing II rye	1R(1B)
Hope deriv.	AUS	xImperial rye	1RS.1AL
Hornet	GBR	xRiebesel lines	1RS.1BL
Hyderabad 88	PAK	xVeery derivatives	1RS.1BL
Iapar6 Tapejara	BRA	?	1RS.1BL
Ikarus	DEU	xSt623/65Weihenstephan	1RS.1BL
Ilona	CSK	xKavkaz	1RS.1BL
Impacto BAER	CHL	xKatterman lines	1RS.1BL
Impuls	BGR	xSkorospelka 35	1RS.1BL
Ionija 89	YUG	xAvrora	1RS.1BL
Iris	CSK	xKavkaz	1RS.1BL
Isidor	DEU	xPerseus	1RS.1BL
Iskra	YUG	xSkorospelka 35	1RS.1BL
Istra	CSK	xAvrora	1RS.1BL
Jan. 7770-4	?	?	1RS.1BL
Jantor	BGR	xAvrora	1RS.1BL
Jedina	YUG	xMacvanka 2	1RS.1BL
Jednota	YUG	xAvrora	1RS.1BL
Jejka	USS	xKavkaz	1RS.1BL
Jing-Dan-106	?	?	1RS.1BL
Jubilejnaya 75	USS	xKavkaz	1RS.1BL
Jugoslavija	YUG	xAvrora	1RS.1BL
Jugtina	USS	xKavkaz	1RS.1BL
Kaljevica	YUG	xAvrora	1RS.1BL
Kaloyan	BGR	xAvrora	1RS.1BL
Kardam	BGR	xAvrora	1RS.1BL
Kauz	MEX	xKavkaz	1RS.1BL
Kavkaz	USS	xNeuzucht	1RS.1BL
Kea 'S'	MEX	xVeery derivatives	1RS.1BL
Khyber 87	PAK	xVeery derivatives	1RS.1BL
Knirps	DEU	?	1RS.1BL
Koda	POL	xNadzeija	1RS.1BL
Kohinoor	PAK	xVeery derivatives	1RS.1BL
Kolubara	YUG	xAvrora	1RS.1BL
Kormoran	DEU	xKatterman lines	1RS.1BL
Kosava	YUG	xAvrora	1RS.1BL
Kotovcanka	USS	xAvrora	1RS.1BL
Kozara	YUG	xAvrora	1RS.1BL
Kristall	DEU	xCapriccio	1RS.1BL
Kronjuwel	DEU	xSt465/52Weihenstephan	1RS.1BL
Lanca	POL	xNadzeija	1RS.1BL
Lasta	YUG	xAvrora	1RS.1BL
Laurel INIA	CHL	xRiebesel lines	1RS.1BL
Lesapi	ZWE	xVeery 'S' selection	1RS.1BL
Levchanka	YUG	xKavkaz	1RS.1BL
Licanka	YUG	xAvrora	1RS.1BL
Lichanka	YUG	xAvrora	1RS.1BL
Lihuida	YUG	xKavkaz	1RS.1BL
Lima 1	PRT	xVeery 3 selection	1RS.1BL
Linos	DEU	xZorba	1RS.1BL
Lira 'S'	MEX	xVeery derivatives	1RS.1BL
Livia	CSK	xKavkaz	1RS.1BL
Liz	POR	?	1RS.1BL
Loeri	ZMB	xVeery 5 'S' selection	1RS.1BL
Long Mai 10	CHN	?	1RS.1BL
Lovrin 10	ROM	xNeuzucht	1RS.1BL

Lovrin 12	ROM	xNeuzucht	1RS.1BL
Lovrin 13	ROM	xNeuzucht	1R(1B)
Lovrin 19	ROM	xRiebesel lines	1RS.1BL
Lovrin 24	ROM	xRiebesel lines	1RS.1BL
Lovrin 29	ROM	xRiebesel lines	1RS.1BL
Lovrin 32	ROM	xRiebesel lines	1RS.1BL
Lovrin 34	ROM	xRiebesel lines	1RS.1BL
Lovrin 41	ROM	xRiebesel lines	1RS.1BL
Macvanka 1	YUG	xKavkaz	1RS.1BL
Macvanka 2	YUG	xKavkaz	1RS.1BL
Magister	NDL	?	1RS.1BL
Mamut	POL	?	1RS.1BL
Marabu	DNK	?	1RS.1BL
Marija	CRO	xKavkaz	1RS.1BL
Marina	CRO	?	1RS.1BL
Merkur	DEU	xtriticale	1RS.1BL
Mildress	NDL	xR47/51 Riebesel	1RS.1BL
Millaleau Inia	CHL	xVeery 3 selection	1RS.1BL
Mironovskaya 10	USS	xwheat-rye hybrid 48/49	1R(1B)
Mironovskaya nizkoro.	USS	xMironovskaya 10	1RS.1BL
Momchil	BGR	xAvrora	1RS.1BL
Mona	CSK	xRiebesel lines	1RS.1BL
Mv 14	HUN	xKavkaz	1RS.1BL
Mv 15	HUN	xKavkaz	1RS.1BL
Mv 16	HUN	xKavkaz	1RS.1BL
Mv 20	HUN	xKavkaz	1RS.1BL
Mv 21....86	HUN	?	1RS.1BL
Mv Emma	HUN	xKavkaz	1RS.1BL
Mv Irma	HUN	xKavkaz	1RS.1BL
Mv Koma	HUN	xKavkaz	1RS.1BL
Mv Magma	HUN	xKavkaz	1RS.1BL
Mv Palma	HUN	xKavkaz	1RS.1BL
Mv Szigma	HUN	xKavkaz	1RS.1BL
Nadzeija	USS	xAvrora	1RS.1BL
Nautica	NDL	xMildress	1RS.1BL
Neuzucht	DDR	xSt14/44 Salzmünde	1R(1B)
Niklas	DEU	xGötz	1RS.1BL
Ning 8401	CHN	?	1RS.1BL
Ning8201	CHN	?	1RS.1BL
Ning8319	CHN	?	1RS.1BL
Nova posavka	YUG	xAvrora	1RS.1BL
Nova stopjanka	YUG	xKavkaz	1RS.1BL
Novosadska 100	YUG	?	1RS.1BL
Novosadska Brkulja	YUG	xSkorospelka 35	1RS.1BL
Odesskaya 117	USS	xKavkaz	1RS.1BL
Odesskaya 66	USS	xKavkaz	1RS.1BL
Odilo	DEU	xZorba	1RS.1BL
OH 416	USA	xAmigo	1RS.1AL
Olymp	DEU	xGötz	1RS.1BL
Opata 85	MEX	?	1RS.1BL
Oplenka	YUG	xKavkaz	1RS.1BL
Orlando	DDR	xSt.26/47 Salzmünde	1R(1B)
Pakistan 81	PAK	xVeery 5 'S' selection	1RS.1BL
Palur	DDR	xAlmus	1RS.1BL
Pansevka	YUG	xAvrora	1RS.1BL
Pantus	AUT	xKatterman lines	1RS.1BL
Papago 86	MEX	?	1RS.1BL
Partizanka nisa	YUG	xAvrora	1RS.1BL
Parula	MEX	xVeery 6 selection	1RS.1BL
Pavon	MEX	?	1RS.1BL
Peresvet	USS	xKavkaz	1RS.1BL
Perquenco INIA	CHL	xRiebesel lines	1RS.1BL
Perseus	DEU	xZorba	1RS.1BL
PF8237	BRA	?	1RS.1BL
Pfau	MEX	?	1RS.1BL
Pieta	BGR	xAvrora	1RS.1BL
Pionero Inta	ARG	?	1RS.1BL
Pirsabak	PAK	xKavkaz	1RS.1BL
Pirsabak 85	PAK	xVeery derivatives	1RS.1BL
Pitoma	YUG	xKavkaz	1RS.1BL
PKB Krupna	YUG	xAvrora	1RS.1BL
Pobeda	YUG	xBalkan	1RS.1BL
Podunavka 1	YUG	xAvrora	1RS.1BL
Podunavka 2	YUG	xAvrora	1RS.1BL
Podunavka 3	YUG	xSkorospelka 35	1RS.1BL
Poleskaya 71	USS	xBesostaya 2	1RS.1BL
Polimka	YUG	xKavkaz	1RS.1BL
Pomoravka	YUG	xAvrora	1RS.1BL
Pomoravka	YUG	xAvrora	1RS.1BL
Posavka 1	YUG	xSkorospelka 35	1RS.1BL
Posavka 2	YUG	xSkorospelka 35	1RS.1BL
Predgornaya 2	USS	xErythrospermum315	1RS.1BL
Prjaspa	BGR	xAvrora	1RS.1BL
Prometey	USS	xKavkaz	1RS.1BL
Punjab 85	PAK	xVeery derivatives	1RS.1BL
Punjnad 88	PAK	xVeery derivatives	1RS.1BL
Quiang Feng	CHN	?	1RS.1BL

R 47/51 (Riebesel)	DEU	xPetkus rye	1R(1B)
Rawal 87	PAK	xVeery derivatives	1RS.1BL
Rawhide	USA	xKavkaz	1RS.1BL
Rayon	MEX	see Ures (syn.)	
Requiem	BGR	xSkorospelka 35	1RS.1BL
Ricardo	NDL	xSt.359/48Weihenstephan	1RS.1BL
Roseana	?	?	1RS.1BL
Rosicza	BGR	xAvrora	1RS.1BL
Rotor	DEU	?	1RS.1BL
Roxana	CSK	xKavkaz	1RS.1BL
Rusalka podobrena	BGR	xAvrora	1RS.1BL
Sabina	CSK	xWh 378/57-132b	1RS.1BL
Saladin	DDR	xSt.26/47 Salzmünde	1R(1B)
Salmayo	?	?	1RS.1BL
Salmon	JPN	8x triticale x 6x triticale	1RS.1BL
Salzm. Bartweizen	DEU	xPetkuser rye	1R(1B)
Sansevka	YUG	xAvorora	1RS.1BL
Sarhad 83	PAK	xBobwhrite 'S' selection	1RS.1BL
Sel. 73/36/9-1	CHN	xLovrin 10	1RS.1BL
Sel. 79-4045	CHN	xLovrin 13	1RS.1BL
Sel. 84059-4-2	CHN	?	1RS.1BL
Selekta	CSK	xSt378/57 Weihenstephan	1RS.1BL
Sensor	DEU	xKattermann lines see Granada (syn.)	1RS.1BL
Senta	CSK	xBenno	1RS.1BL
Seri 82	MEX	xVeery 5 'S' selection	1RS.1BL
Seri 82	MEX	?	1RS.1BL
Seric	ZMB	?Veery 4 selection	1RS.1BL
Sfera	USS	xKavkaz	1RS.1BL
Shtorm	USS	xKavkaz	1RS.1BL
Sida	CSK	xKatterman lines	1RS.1BL
Siete Cerros T66	MEX	?	1RS.1BL
Simona	CSK	xKatterman lines	1RS.1BL
Sindi 83	PAK	?	1RS.1BL
Singron	ROM	xAvrora	1RS.1BL
Siouxland	USA	xKavkaz	1RS.1BL
Siouxland 89	USA	xKavkaz	1RS.1BL
Siroka	YUG	xKavkaz	1RS.1BL
Skitija	BGR	xKavkaz	1RS.1BL
Skopjanka	YUG	xKavkaz	1RS.1BL
Skorospelka 35	USS	xErythrospermum 315	1RS.1BL
Sloboda	YUG	xAvrora	1RS.1BL
Sofia	CSK	xSt378/57Weihenstephan	1RS.1BL
Solaris	CSK	xKavkaz	1RS.1BL
Somborka	YUG	xAvrora	1RS.1BL
Soratnitca	USS	xKavkaz	1RS.1BL
Sparta	CSK	xSt378/57Weihenstephan	1RS.1BL
Srbijanka	YUG	xKavkaz	1RS.1BL
Sredez 68	BGR	xSkorospelka	1RS.1BL
Sredez 72	BGR	xSkorospelka	1RS.1BL
Staparka	YUG	xAvrora	1RS.1BL
Stejpner	SWE	?	1RS.1BL
Sterna	YUG	xKavkaz	1RS.1BL
Stetson	GBR	xBenno	1RS.1BL
Stizanka	YUG	xAvrora	1RS.1BL
Stopjanka	YUG	xKavkaz	1RS.1BL
Str. 911-B-8-10	BGR	xSkorospelka 35	1RS.1BL
Stuart	?	?	1RS.1BL
Studenica	YUG	xKavkaz	1RS.1BL
Subotianka	YUG	xAvrora	1RS.1BL
Sunbird 'S'	MEX	xVeery derivatives	1RS.1BL
Sutjeska	YUG	xAvrora	1RS.1BL
Sutlej 86	PAK	xVeery derivatives	1RS.1BL
Svilena	BGR	xKavkaz	1RS.1BL
Takovcanka	YUG	xKavkaz	1RS.1BL
Talafen	CHL	xRiebesel lines	1RS.1BL
TAM 107	USA	?	1RS.1AL
TAM 200	USA	?	1RS.1AL
Tamaro	SCH	xKatterman lines	1RS.1BL
Tara	GBR	xClement	1RS.1BL
Telez	BGR	xKavkaz	1RS.1BL
Temu 39-78	CHL	xRiebesel lines	1RS.1BL
Terter	BGR	xSkorospelka 35	1RS.1BL
Tervel	BGR	xSkorospelka 35	1RS.1BL
Thrush	MEX	?	1RS.1BL
Titus	AUT	xKatterman lines	1RS.1BL
Tjelvar	SWE	?	1RS.1BL
Toronto	DEU	?	1RS.1BL
Trajana	BGR	xAvrora	1RS.1BL
Transilvaniya 1	ROM	xAvrora	1RS.1BL
Trident	NDL	xKattermann lines	1RS.1BL
Tui	MEX	?	1RS.1BL
Turaco	MEX	?	1RS.1BL
Turda 81	ROM	xSkorospelka 35	1RS.1BL
Urban	DEU	xZorba	1RS.1BL
Ures T81	MEX	xVeery 2 selection	1RS.1BL
Ures*2/PRL	MEX	? see Rayon (syn.)	1RS.1BL
Vasco	NDL	xRiebesel lines	1RS.1BL
Veery 'S'	MEX	xKavkaz	1RS.1BL
Veery 10	MEX	xVeery 'S' selection	1RS.1BL
Veselka	USS	xKavkaz	1RS.1BL
Viri	TZA	xVeery 5 selection	1RS.1BL
Vlada	CSK	xKavkaz	1RS.1BL

Voyage	FRA	?	1RS.1BL
Vympel odesskiy	UKR	xAvrora	1RS.1BL
Wand	GBR	xRiebesel lines	1RS.1BL
Warigal deriv.	AUS	xImperial rye	1RS.1DL
Weihenst. St. 1007/53	DEU	4x Petkus rye	1R(1B)
Weique 'Substitution'	DEU	?	1R(1B)
Weique 'Züchter'	DEU	?	1RS.1BL
Wembley	GBR	?	1RS.1BL
Weneda	POL	xKavkaz	1RS.1BL
Wentzel	DEU	xSalzm. str.	1R(1B)
Winnetou	DDR	xSalzm. Bartweizen	1R(1B)
Winnetou	DDR	xSalzm. Bartweizen	1RS.1BL
Xanthos	DEU	?	1RS.1BL
Zelengora	YUG	xAvrora	1RS.1BL
Zemunka 1	YUG	xAvrora	1RS.1BL
Zernogradka 2	YUG	xAvrora	1RS.1BL
Zitarka	YUG	xKavkaz	1RS.1BL
Zorba	DEU	xtriticale	1R(1B)
Zvezda	YUG	xKavkaz	1RS.1BL

*Nationality Code

AFG	Afghanistan
AGL	Angola
ALB	Albania
ALG	Algeria
ARG	Argentina
AUS	Australia
AZR	Azores
BEL	Belgium
BDG	Bangladesh
BGR	Bulgaria
BOL	Bolivia
BRA	Brazil
CAN	Canada
CHL	Chile
CHN	China
CNR	Canary Islands
COL	Columbia
CSK	Czechoslovakia <1990
CYP	Cyprus
DDR	German Dem Rep, 1949-1990
DNK	Denmark
ECU	Ecuador
EGY	Egypt
EIR	Ireland
ESP	Spain
EST	Estonia
ETH	Ethiopia
FIN	Finland
FRA	France
FRG	Fed Rep Germany, 1949-1990
GBR	Great Britain
GER	Germany <1949 and >1990
GRC	Greece
GTM	Guatemala
HUN	Hungary
IDN	India
IRN	Iran
IRQ	Iraq
ISL	Israel
ITA	Italy
JOR	Jordan
JPN	Japan
KEN	Kenya
KOR	Korea
LBN	Lebanon
LBY	Libya
LSO	Lesotho
MAR	Morocco
MDG	Madagascar
MEX	Mexico
NDL	Netherlands
NER	Niger
NGA	Nigeria
NOR	Norway
NPL	Nepal
NZL	New Zealand
OST	Austria
PAK	Pakistan
PER	Peru
PHI	Philippines
POL	Poland
POR	Portugal
PRY	Paraguay
ROM	Rumania
SAF	South Africa
SAU	Saudi Arabia
SCH	Switzerland
SDN	Sudan
SWE	Sweden
SYR	Syria
TAN	Tanzanja
TCD	Chad
TUN	Tunisia
TUR	Turkey
TWN	Taiwan
URU	Uruguay
USA	USA
USS	USSR<1991
VEN	Venezuela
YEM	Yemen
YUG	Yugoslavia<1991
ZAI	Zaire
ZIM	Zimbabwe

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Number 84: 70-85 (1997)

Recent publications on wheat genetics

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

1996

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(20)
ACCN:001669609 CTLN:3923654
ABSJ:G (Genetics Abstracts)
AUTH:Bougri, O.V.;Korzun, V.N.;Grimm, B.*
AFFN:Inst. Plant Genet. and Crop Plant Res., Dep. Molecular Cell Biol., Correnssstr. 3, D-06466 Gatersleben, Germany
TITL:Chromosomal assignment of the genes encoding glutamyl-tRNA reductase in barley, wheat, and rye and their organization in the barley genome
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1996
HCOL:vol. 124, no. 1, pp. 1-6

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(21)
ACCN:001673287 CTLN:3927859
ABSJ:G (Genetics Abstracts)
AUTH:Dubcovsky, J.;Luo, M.-C.;Zhong, G.-Y.; Bransteitter, R.;Desai, A.; Kilian, A.;Kleinhofs, A.; Dvorak, J.*
AFFN:Dep. Agronomy and Range Sci., Univ. California, Davis, CA 95616, USA
TITL:Genetic map of diploid wheat, Triticum monococcum L. and its comparison with maps of Hordeum vulgare L.
HTIL:GENETICS
HSSN:0065-2660
HYER:1996
HCOL:vol. 143, no. 2, pp. 983-999

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(22)
ACCN:001673288 CTLN:3927860
ABSJ:G (Genetics Abstracts)
AUTH:Gill, K.S.;Gill, B.S.;Endo, T.R.;Boyko, E.V.
AFFN:Genet. Resour. Cent., Dep. Plant Pathol., 4307 Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506, USA
TITL:Identification and high-density mapping of gene-rich regions in chromosome group 5 of wheat
HTIL:GENETICS
HSSN:0065-2660
HYER:1996
HCOL:vol. 143, no. 2, pp. 1001-1012

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(23)
ACCN:001673735 CTLN:3928307
ABSJ:G (Genetics Abstracts)
AUTH:Kuo, A.;Cappelluti, S.;Cervantes-Cervantes, M.;Rodriguez, M.;Bush, D.S.*
AFFN:Dep. Biol. Sci., Rutgers Univ., 101 Warren St., Newark, NJ 07102, USA
TITL:Okadaic acid, a protein phosphatase inhibitor, blocks calcium changes, gene expression, and cell death induced by gibberellin in wheat aleurone cells
HTIL:PLANT CELL
HSSN:1040-4651
HYER:1996
HCOL:vol. 8, no. 2, pp. 259-269

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(24)
ACCN:001673760 CTLN:3928332
ABSJ:G (Genetics Abstracts)
AUTH:Felix, I.;Martinant, J.P.;Bernard, M.; Bernard, S.;Branlard, G.
AFFN:INRA, Stn. d'Amelioration des Plantes, Domaine de Crouelle, 63039 Clermont-Ferrand Cedex, France
TITL:Genetic characterization of storage proteins in a set of F sub(1)-derived haploid lines in bread wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 3-4, pp. 340-346

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(25)
ACCN:001673799 CTLN:3928371
ABSJ:G (Genetics Abstracts)
AUTH:Dubcovsky, J.;Santa Maria, G.;Epstein, E.; Luo, M.-C.;Dvorak, J.
AFFN:Dep. Agron. and Range Sci., Univ. California, Davis, CA 95616, USA

TITL:Mapping of the K super(+)/Na super(+) discrimination locus Kna1 in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 3-4, pp. 448-454

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(26)
ACCN:001673811 CTLN:3928383
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Jia, J.;Devos, K.M.;Chao, S.;Miller, T.E.;Reader, S.M.;Gale, M.D.*
AFFN:John Innes Cent., Norwich Res. Park, Colney, Norwich NR4 7UH, UK
TITL:RFLP-based maps of the homoeologous group-6 chromosomes of wheat and their application in the tagging of Pm12, a powdery mildew resistance gene transferred from Aegilops speltoides to wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 5, pp. 559-565

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(27)
ACCN:001673835 CTLN:3928407
ABSJ:G (Genetics Abstracts)
AUTH:Fennell, S.;Bohorova, N.*;Van Ginkel, M.;Crossa, J.;Hoisington, D.
AFFN:CIMMYT, Intl. Maize and Wheat Improvement Cent., Lisboa 27, Apdo. Postal 6-641, 06600 Mexico D.F., Mexico
TITL:Plant regeneration from immature embryos of 48 elite CIMMYT bread wheats
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 2, pp. 163-169

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(28)
ACCN:001673846 CTLN:3928418
ABSJ:G (Genetics Abstracts)
AUTH:Wang, Y.B.;Hu, H.;Snape, J.W.*
AFFN:John Innes Cent., Colney Lane, Norwich NR4 7UH, UK
TITL:The genetic and molecular characterization of pollen-derived plant lines from octoploid triticale x wheat hybrids
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 7, pp. 811-816

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(29)
ACCN:001673854 CTLN:3928426
ABSJ:G (Genetics Abstracts)
AUTH:Zhong, S.B.;Zhang, D.Y.;Li, H.B.;Yao, J.X.
AFFN:Inst. Agrobiol. Genet. and Physiol., Jiangsu Acad. Agric. Sci., Nanjing 210014, People's Rep. China
TITL:Identification of Haynaldia villosa chromosomes added to wheat using a sequential C-banding and genomic in situ hybridization technique
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 1, pp. 116-120

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(30)
ACCN:001673990 CTLN:3928572
ABSJ:G (Genetics Abstracts)
AUTH:Sibikeeva, Yu.E.;Sibikeev, S.N.
AFFN:Lab. Genet. and Cytology, Agric. Res. Inst. for South-East Regions, Tulaikov St., 7, Saratov, 410020, Russia
TITL:Genetic analysis of anther culture response in wheat carrying alien translocations
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 6, pp. 782-785

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(31)
ACCN:001673995 CTLN:3928577
ABSJ:G (Genetics Abstracts)
AUTH:Tsegaye, S.;Becker, H.C.;Tesemma, T.
AFFN:Swedish Univ. Agric. Sci., Dep. Plant Breeding Res., S-26831, Svaloev, Sweden
TITL:Variation of leaf esterases in some Ethiopian tetraploid wheat landraces
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:1996
HCOL:vol. 43, no. 2, pp. 119-123

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(32)
ACCN:001673997 CTLN:3928579
ABSJ:G (Genetics Abstracts)
AUTH:Mujeeb-Kazi, A.;Rosas, V.;Roldan, S.
AFFN:CIMMYT, Lisboa 27, Apartado Postal 6-641, Deleg. Cuauhtemoc, 06600 Mexico, DF, Mexico
TITL:Conservation of the genetic variation of Triticum tauschii (Coss.) Schmalh. (Aegilops squarrosa auct. non L.) in synthetic hexaploid wheats (T. turgidum L. s.lat. x T. tauschii; 2n =

6x = 42, AABBDD) and its potential utilization for wheat improvement
HTIL:GENET. RESOUR. CROP EVOL.
HSSN:0925-9864
HYER:1996
HCOL:vol. 43, no. 2, pp. 129-134

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(33)
ACCN:001674081 CTLN:3928663
ABSJ:G (Genetics Abstracts)
AUTH:Tahir, M.;Pavoni, A.;Tucci, G.F.;Turchetta, T.;Lafiandra, D.
AFFN:Dep. Agrobiology and Agrochemistry, Univ. Tuscia, Via S. Camillo de Lellis, 01100 Viterbo, Italy
TITL:Detection and characterization of a glutenin subunit with unusual high Mr at the Glu-A1 locus in hexaploid wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 6, pp. 654-659

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(34)
ACCN:001674082 CTLN:3928664
ABSJ:G (Genetics Abstracts)
AUTH:Akanda, S.I.;Mundt, C.C.*
AFFN:Dep. Botany and Plant Pathol., Oregon State Univ., 2082 Cordley Hall, Corvallis, OR 97331-2902, USA
TITL:Path coefficient analysis of the effects of stripe rust and cultivar mixtures on yield and yield components of winter wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 92, no. 6, pp. 666-672

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(35)
ACCN:001674408 CTLN:3928995
ABSJ:G (Genetics Abstracts)
AUTH:Linacero, R.;Lopez-Bilbao, M.G.;Romero, C.;Laurie, D.A.;Vazquez, A.M.
AFFN:Dpto. Genet., Fac. Biol., Univ. Complutense, Madrid, Spain
TITL:Genotypic differences in polyembryo formation and somatic embryogenesis increment in wheat (Triticum aestivum L.), following 2,4-D treatment
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 3, pp. 345-348

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(36)
ACCN:001674612 CTLN:3929199
ABSJ:G (Genetics Abstracts)
AUTH:McIntosh, R.A.;Silk, J.;The, T.T.
AFFN:Univ. Sydney, Plant Breeding Inst. Cobbitty, Private Bag 11, Camden N. S.W. 2570, Australia
TITL:Cytogenetic studies in wheat XVII. Monosomic analysis and linkage relationships of gene Yr15 for resistance to stripe rust
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 3, pp. 395-399

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(37)
ACCN:001674743 CTLN:3929333
ABSJ:G (Genetics Abstracts)
AUTH:McIntosh, R.A.;Arts, C.
AFFN:Univ. Sydney, Plant Breeding Inst. Cobbitty, Private Bag 11, Camden, N. S.W. 2570, Australia
TITL:Genetic linkage of the Yr1 and Pm4 genes for stripe rust and powdery mildew resistances in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 3, pp. 401-403

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(38)
ACCN:001677111 CTLN:3931764
ABSJ:G (Genetics Abstracts)
AUTH:Peusha, H.;Hsam, S.L.K.;Enno, T.;Zeller, F.J.
AFFN:Inst. Experimental Biol., Dep. Plant Genet., EE-3051 Tallinn, Estonia
TITL:Identification of powdery mildew resistance genes in common wheat (Triticum aestivum L. em. Thell.) VIII. Cultivars and advanced breeding lines grown in Finland
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1996
HCOL:vol. 124, no. 1, pp. 91-93

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(39)
ACCN:001677152 CTLN:3931805
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Goerlach, J.;Volrath, S.;Knauf-Beiter, G.;Hengy, G.;Beckhove, U.;Kogel, K.-H.;Oostendorp, M.;Staub, T.;Ryals, J.*;et al.
AFFN:Ciba-Geigy Agric. Biotechnol. Res. Unit, Research Triangle Park, NC 27709-2257, USA
TITL:Benzothiadiazole, a novel class of inducers of

systemic acquired resistance, activates gene expression and disease resistance in wheat
HTIL:PLANT CELL
HSSN:1040-4651
HYER:1996
HCOL:vol. 8, no. 4, pp. 629-643

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(40)
ACCN:001680617 CTLN:3934368
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:William, M.D.H.M.;Mujeeb-Kazi, A.*
AFFN:Intl. Maize and Wheat Improvement Cent. (CIMMYT), Lisboa 27, Apartado Postal 6-641 06600 Mexico, D.F., Mexico
TITL:Development of genetic stocks and biochemical markers to facilitate utilization of Aegilops variabilis in wheat improvement
HTIL:CYTOLOGIA
HSSN:0011-4545
HYER:1996
HCOL:vol. 61, no. 1, pp. 7-13

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(41)
ACCN:001680634 CTLN:3934385
ABSJ:G (Genetics Abstracts); V (Virology & AIDS Abstracts)
AUTH:Hohmann, U.;Badaeva, K.;Busch, W.;Friebe, B.;Gill, B.S.
AFFN:Botanisches Institut der Ludwig-Maximilians-Universitaet Muenchen, Menzinger Str. 67, D-80638 Muenchen, Germany
TITL:Molecular cytogenetic analysis of Agropyron chromatin specifying resistance to barley yellow dwarf virus in wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 2, pp. 336-347

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(42)
ACCN:001680652 CTLN:3934403
ABSJ:G (Genetics Abstracts)
AUTH:Ceoloni, C.;Biagetti, M.;Ciaffi, M.;Forte, P.;Pasquini, M.
AFFN:Dep. Agrobiology and Agrochemistry, Univ. Tuscia, 01100 Viterbo, Italy
TITL:Wheat chromosome engineering at the 4x level: The potential of different alien gene transfers into durum wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 87-97

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(43)
ACCN:001680653 CTLN:3934404
ABSJ:G (Genetics Abstracts)
AUTH:King, I.P.;Cant, K.A.;Law, C.N.;Worland, A.J.;Orford, S.E.;Reader, S. M.;Miller, T.E.
AFFN:Cytogenetics Group, Inst. Grassland and Environ. Res., Aberystwyth, Dyfed SY23 3EB, UK
TITL:An assessment of the potential of 4DS.4DL-4s super(l)L translocation lines as a means of eliminating tall off types in semi-dwarf wheat varieties
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 103-106

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(44)
ACCN:001680654 CTLN:3934405
ABSJ:G (Genetics Abstracts)
AUTH:Cuadrado, A.;Rubio, P.;Ferrer, E.;Jouve, N.
AFFN:Dep. Cellular Biol. and Genet., Univ. Alcala de Henares, E-28871 Alcala de Henares, Madrid, Spain
TITL:Sequential combinations of C-banding and in situ hybridization and their use in the detection of interspecific introgressions into wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 107-112

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(45)
ACCN:001680655 CTLN:3934406
ABSJ:G (Genetics Abstracts)
AUTH:Miller, T.E.;Reader, S.M.;Purdie, K.A.;King, I.P.
AFFN:John Innes Cent., Colney, Norwich NR4 7UH, UK
TITL:Fluorescent in situ hybridization - A useful aid to the introduction of alien genetic variation into wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 113-119

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(46)
ACCN:001680659 CTLN:3934410
ABSJ:G (Genetics Abstracts)
AUTH:Cyran, M.;Rakowska, M.;Miazga, D.
AFFN:Inst. Plant Breeding and Acclimatization,

Radzikow, 05-870 Blonie, Poland
TITL:Chromosomal location of factors affecting content and composition of non-starch polysaccharides in wheat-rye addition lines
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 153-157

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(47)
ACCN:001680661 CTLN:3934412
ABSJ:G (Genetics Abstracts)
AUTH:Daud, H.M.;Gustafson, J.P.
AFFN:Biotechnol. Cent., MARDI, P.O. Box 12301, 50774 Kuala Lumpur, Malaysia
TITL:Molecular evidence for Triticum speltoides as a B-genome progenitor of wheat (Triticum aestivum)
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 3, pp. 543-548

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(48)
ACCN:001680964 CTLN:3934716
ABSJ:G (Genetics Abstracts)
AUTH:Friebe, B.;Tuleen, N.A.;Badaeva, E.D.;Gill, B.S.
AFFN:Dep. Plant Pathol., Wheat Genet. Resour. Cent., Throckmorton Hall, Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:Cytogenetic identification of Triticum peregrinum chromosomes added to common wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 2, pp. 272-276

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(49)
ACCN:001680966 CTLN:3934718
ABSJ:G (Genetics Abstracts); N (Biochemistry Abstracts 2: Nucleic Acids)
AUTH:Sardana, R.K.;Flavell, R.B.
AFFN:Dep. Biochem., Fac. Sci., Univ. Ottawa, 40 Marie Curie Private, Ottawa, ON K1N 6N5, Canada
TITL:Molecular cloning and characterization of an unusually large intergenic spacer from the Nor-B2 locus of hexaploid wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 2, pp. 288-292

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(50)
ACCN:001680972 CTLN:3934724
ABSJ:G (Genetics Abstracts)
AUTH:Marino, C.L.;Nelson, J.C.;Lu, Y.H.;Sorrells, M.E.;Leroy, P.;Tuleen, N. A.;Lopes, C.R.;Hart, G.E.*
AFFN:Dep. Soil and Crop Sci., Texas A&M Univ., Coll. Stn., TX 77840, USA
TITL:Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (Triticum aestivum L. em. Thell.)
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 2, pp. 359-366

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(51)
ACCN:001682113 CTLN:3936025
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Michael, A.J.;Hofer, J.M.I.;Ellis, T.H.N.
AFFN:Dep. Genet. and Microbiol., Inst. Food Res., Norwich NR4 7UA, UK
TITL:Isolation by PCR of a cDNA clone from pea petals with similarity to petunia and wheat zinc finger proteins
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1996
HCOL:vol. 30, no. 5, pp. 1051-1058

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(52)
ACCN:001682368 CTLN:3936280
ABSJ:G (Genetics Abstracts)
AUTH:Plaschke, J.;Boerner, A.;Wendehake, K.;Ganal, M.W.;Roeder, M.S.
AFFN:Inst. Plant Genet. and Crop Plant Res., Corrensstrass 3, 06466 Gatersleben, Germany
TITL:The use of wheat aneuploids for the chromosomal assignment of microsatellite loci
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 33-40

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(53)
ACCN:001682370 CTLN:3936282
ABSJ:G (Genetics Abstracts)
AUTH:Worland, A.J.
AFFN:Cereals Dep. John Innes Cent., Colney, Norwich, NR4 7UH, UK

TITL:The influence of flowering time genes on environmental adaptability in European wheats
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 49-57

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(54)
ACCN:001682372 CTLN:3936284
ABSJ:G (Genetics Abstracts)
AUTH:Kosner, J.;Zurkova, D.
AFFN:Res. Inst. Crop Prod., Praha - Ruzyne, Czech Rep.
TITL:Photoperiodic response and its relation to earliness in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 59-64

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(55)
ACCN:001682373 CTLN:3936285
ABSJ:G (Genetics Abstracts)
AUTH:Stelmakh, A.F.;Avsenin, V.I.
AFFN:Plant Breeding and Genet. Inst. (SGI), 270036 Odessa, Ukraine
TITL:Alien introgression of spring habit dominant genes into bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 65-68

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(56)
ACCN:001682374 CTLN:3936286
ABSJ:G (Genetics Abstracts)
AUTH:Boerner, A.;Plaschke, J.;Korzun, V.;Worland, A.J.
AFFN:Inst. Plant Genet. and Crop Plant Res., D-06466 Gatersleben, Germany
TITL:The relationships between the dwarfing genes of wheat and rye
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 69-75

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(57)
ACCN:001682375 CTLN:3936287
ABSJ:G (Genetics Abstracts)
AUTH:Giura, A.;Saulescu, N.N.
AFFN:Res. Inst. for Cereals and Industrial Crops (I.C.C.P.T.), Jud. Calarasi, 8264 Fundulea, Romania
TITL:Chromosomal location of genes controlling grain size in a large grained selection of wheat (Triticum aestivum L.)
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 77-80

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(58)
ACCN:001682376 CTLN:3936288
ABSJ:G (Genetics Abstracts)
AUTH:Ben Amer, I.M.;Worland, A.J.;Boerner, A.
AFFN:Inst. fuer Pflanzengenetik und Kulturpflanzenforschung, Corrensstrasse 3, D-06466 Gatersleben, Germany
TITL:The effects of whole chromosome substitutions differing in alleles for hybrid dwarfing and photoperiodic sensitivity on tissue culture response (TCR) in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 81-86

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(59)
ACCN:001682377 CTLN:3936289
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Davoyan, R.O.;Ternovskaya, T.K.
AFFN:Dep. Biotechnol., Krasnodar Res. Inst. Agric., Krasnodar 350012, Russia
TITL:Use of a synthetic hexaploid Triticum miguschovae for transfer of leaf rust resistance to common wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 99-102

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(60)
ACCN:001682510 CTLN:3936484
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Broers, L.H.M.;Subias, X.C.;Atilano, R.M.L.
AFFN:Lochow Petkus France EURL, Route Nationale 154, 28150 Allonnes, France
TITL:Field assessment of quantitative resistance to yellow rust in ten spring bread wheat cultivars
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 90, no. 1, pp. 9-16

(61)
ACCN:001682760 CTLN:3936734
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Loughman, R.;Wilson, R.E.;Thomas, G.J.
AFFN:Dep. Agric. Western Australia, South Perth 6151, Australia
TITL:Components of resistance to Mycosphaerella graminicola and Phaeosphaeria nodorum in spring wheats
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 3, pp. 377-385

(62)
ACCN:001683312 CTLN:3937335
ABSJ:G (Genetics Abstracts)
AUTH:Wang, W.C.;Marshall, D.
AFFN:Texas A&M Univ., Res. and Extension Cent., 17360 Coit Rd., Dallas, TX 75252, USA
TITL:Genomic rearrangement in long-term shoot competent cell cultures of hexaploid wheat
HTIL:IN VITRO CELL. DEV. BIOL. PLANT
HSSN:1054-5476
HYER:1996
HCOL:vol. 32, no. 1, pp. 18-25

(63)
ACCN:001683326 CTLN:3937349
ABSJ:G (Genetics Abstracts); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Sawhney, R.N.;Joshi, B.C.
AFFN:Indian Agric. Res. Inst., New Delhi - 110012, India
TITL:Genetic research as the valid base of strategies for breeding rust resistant wheats
HTIL:GENETICA
HSSN:0016-6707
HYER:1996
HCOL:vol. 97, no. 3, pp. 243-254

(64)
ACCN:001683327 CTLN:3937350
ABSJ:G (Genetics Abstracts)
AUTH:Sawhney, R.N.;Sharma, J.B.
AFFN:Div. Genet., Indian Agric. Res. Inst., New Delhi - 110012, India
TITL:Introgression of diverse genes for resistance to rusts into an improved wheat variety, Kalyansona
HTIL:GENETICA
HSSN:0016-6707
HYER:1996
HCOL:vol. 97, no. 3, pp. 255-261

(65)
ACCN:001683345 CTLN:3937368
ABSJ:G (Genetics Abstracts)
AUTH:Law, C.N.;Worland, A.J.
AFFN:Cereal Res. Dep., John Innes Cent., Norwich, UK
TITL:Inter-varietal chromosome substitution lines in wheat - Revisited
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 1-10

(66)
ACCN:001683346 CTLN:3937369
ABSJ:G (Genetics Abstracts)
AUTH:Arbuzova, V.S.;Efremova, T.T.;Laikova, L.I.;Maystrenko, O.I.;Popova, O. M.;Pshenichnikova, T.A.
AFFN:Inst. Cytology and Genet., Siberian Branch Russian Acad. Sci., Novosibirsk, Russia
TITL:The development of precise genetic stocks in two wheat cultivars and their use in genetic analysis
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 11-15

(67)
ACCN:001683347 CTLN:3937370
ABSJ:G (Genetics Abstracts)
AUTH:Krattiger, A.F.;Payne, P.I.;Law, C.N.
AFFN:Intl. Serv. for Acquisition Agri-biotech Applications (ISAAA), Ithaca, NY, USA
TITL:Effects of homoeologous group 1 and 6 chromosomes of the Cappelle-Desprez (Bezostaya 1) substitution lines on aspects of bread-making quality of wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 17-25

(68)
ACCN:001683348 CTLN:3937371
ABSJ:G (Genetics Abstracts)
AUTH:Snape, J.W.;Quarrie, S.A.;Laurie, D.A.
AFFN:Johns Innes Cent., Norwich Res. Park,

Colney, Norwich, NR4 7UJ, UK
TITL:Comparative mapping and its use for the genetic analysis of agronomic characters in wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 89, no. 1, pp. 27-31

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(69)
ACCN:001684862 CTLN:3938929
ABSJ:G (Genetics Abstracts)
AUTH:Deswal, R.K.;Grakh, S.S.;Berwal, K.K.
AFFN:Dep. Plant Breeding, CCS Haryana Agricultural Univ., Hisar-125 004, India
TITL:Genetic variability and characters association between grain yield and its components in wheat
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 221-224

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(70)
ACCN:001693667 CTLN:3947616
ABSJ:G (Genetics Abstracts)
AUTH:Racz, I.;Kovacs, M.;Lasztity, D.;Veisz, O.;Szalai, G.;Paldi, E.
AFFN:Dep. Plant Physiol., Eoetvoes Lorand Univ., H-1088 Budapest, Muzeum krt 4, Hungary
TITL:Effect of short-term and long-term low temperature stress on polyamine biosynthesis in wheat genotypes with varying degrees of frost tolerance
HTIL:J. PLANT PHYSIOL.
HSSN:0176-1617
HYER:1996
HCOL:vol. 148, no. 3-4, pp. 368-373

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(71)
ACCN:001694877 CTLN:3948910
ABSJ:G (Genetics Abstracts)
AUTH:Bechere, E.;Belay, G.;Mitiku, D.;Merker, A.
AFFN:Dep. Plant Breeding Res., Box 7003, S-750 07 Uppsala, Sweden
TITL:Phenotypic diversity of tetraploid wheat landraces from northern and north-central regions of Ethiopia
HTIL:HEREDITAS
HSSN:0018-0661
HYER:1996
HCOL:vol. 124, no. 2, pp. 165-172

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(72)
ACCN:001694881 CTLN:3948914
ABSJ:G (Genetics Abstracts)
AUTH:Chaudhary, B.D.;Pannu, R.K.;Singh, D.P.;Singh, P.
AFFN:Directorate Res., CCS Haryana Agric. Univ., Hisar-125 004, India
TITL:Genetics of metric traits related with biomass partitioning in wheat under drought stress
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 361-367

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(73)
ACCN:001694895 CTLN:3948928
ABSJ:G (Genetics Abstracts)
AUTH:Hooda, J.S.;Singh, D.P.;Pannu, R.K.
AFFN:Dep. Agronomy, CCS Haryana Agric. Univ., Hisar-125 004, India
TITL:Performance of wheat (Triticum aestivum L.) genotypes under different environmental conditions
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 294-298

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(74)
ACCN:001694896 CTLN:3948929
ABSJ:G (Genetics Abstracts)
AUTH:Dhaubhadel, S.;Khanna, V.K.;Jain, R.K.;Garg, G.K.
AFFN:Dep. Mol. Biol. and Genet. Eng., Cornell Univ., NY, USA
TITL:Development of wheat-barley hybrids (tritordeum) through embryo rescue
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 182-187

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(75)
ACCN:001694897 CTLN:3948930
ABSJ:G (Genetics Abstracts)
AUTH:Sharma, H.P.;Bhargava, S.C.
AFFN:Dep. Genet. and Plant Breeding, S. K. N. Coll. Agric., Jobner-303 329 (Jaipur), India
TITL:Genotypic variability in wheat for total water content and excised leaf water loss under moisture stress conditions
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 225-228

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(76)
ACCN:001694898 CTLN:3948931
ABSJ:G (Genetics Abstracts)
AUTH:Luthra, O.P.;Chawla, V.;Sharma, S.K.; Tripathi, I.D.
AFFN:Dep. Genet., CCS Haryana Agric. Univ. Hisar-125 004, India
TITL:Genetic studies on slow leaf rusting characters in wheat
HTIL:ANN. BIOL.
HSSN:0970-0153
HYER:1996
HCOL:vol. 12, no. 2, pp. 229-231

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(77)
ACCN:001697488 CTLN:3951631
ABSJ:G (Genetics Abstracts)
AUTH:Williams, K.J.;Fisher, J.M.;Langridge, P.*
AFFN:Dep. Plant Sci., Univ. Adelaide, Waite Campus, Urrbrae 5064, South Australia, Australia
TITL:Development of a PCR-based allele-specific assay from an RFLP probe linked to resistance to cereal cyst nematode in wheat
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 4, pp. 798-801

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(78)
ACCN:001697489 CTLN:3951632
ABSJ:G (Genetics Abstracts)
AUTH:Erpelding, J.E.;Blake, N.K.;Blake, T.K.; Talbert, L.E.*
AFFN:Dep. Plant, Soil, and Environ. Sci., Montana State Univ., Bozeman, MT 59717, USA
TITL:Transfer of sequence tagged site PCR markers between wheat and barley
HTIL:GENOME
HSSN:0831-2796
HYER:1996
HCOL:vol. 39, no. 4, pp. 802-810

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(79)
ACCN:001709443 CTLN:3964743
ABSJ:G (Genetics Abstracts)
AUTH:Endo, T.R.;Gill, B.S.*
AFFN:Dep. Plant Pathol., Kansas State Univ., Manhattan, KS 66506-5502, USA
TITL:The deletion stocks of common wheat
HTIL:J. HERED.
HSSN:0022-1503
HYER:1996
HCOL:vol. 87, pp. 295-307

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(80)
ACCN:001709473 CTLN:3964773
ABSJ:G (Genetics Abstracts)
AUTH:Molnar-Lang, M.;Linc, G.;Sutka, J.
AFFN:Agric. Res. Inst. Hungarian Acad. Sci., H-2462 Martonvasar, P.O. Box 19, Hungary
TITL:Transfer of the recessive crossability allele kr1 from Chinese Spring into the winter wheat variety Martonvasari 9
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 90, no. 3, pp. 301-305

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(81)
ACCN:001714444 CTLN:3970250
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Kanazin, V.;Blake, T.;Shoemaker, R.C.*
AFFN:Dep. Agronomy and USDA-ARS-FCR, Iowa State Univ., Ames, IA 50011, USA
TITL:Organization of the histone H3 genes in soybean, barley and wheat
HTIL:MOL. GEN. GENET.
HSSN:0026-8925
HYER:1996
HCOL:vol. 250, no. 2, pp. 137-147

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(82)
ACCN:001716201 CTLN:3972085
ABSJ:J (Microbiology Abstracts B: Bacteriology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:El Attari, H.;Sarrafi, A.*;Alizadeh, A.; Dechamp-Guillaume, G.;Barrault, G.
AFFN:Dep. Biotechnol. and Plant Breeding ENSAT-INP, 145 Ave. de Muret, F- 31076 Toulouse-Cedex, France
TITL:Genetic analysis of partial resistance to bacterial leaf streak (Xanthomonas campestris pv. cerealis) in wheat
HTIL:PLANT PATHOL.
HSSN:0032-0862
HYER:1996
HCOL:vol. 45, no. 4, pp. 736-741

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(83)
ACCN:001717594 CTLN:3972533
ABSJ:Z (Entomology Abstracts); G (Genetics Abstracts)
AUTH:Formusoh, E.S.;Hatchett, J.H.*;Black, W.C.,

IV;Stuart, J.J.
AFFN:Plant Science and Entomology, USDA-ARS, Department of Entomology, Kansas State University, Manhattan, KS 66506, USA
TITL:Sex-linked inheritance of virulence against wheat resistance gene H9 in the Hessian fly (Diptera: Cecidomyiidae)
HTIL:ANN. ENTOMOL. SOC. AM.
HSSN:0013-8746
HYER:1996
HCOL:vol. 89, no. 3, pp. 428-434

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(84)
ACCN:001718050 CTLN:3972992
ABSJ:G (Genetics Abstracts)
AUTH:Benavente, E.;Fernandez-Calvin, B.; Orellana, J.
AFFN:Unidad Genet., E.T.S.I. Agron., Univ. Politecnica Madrid, Ciudad Univ., E-28040 Madrid, Spain
TITL:Relationship between the levels of wheat-rye metaphase I chromosomal pairing and recombination revealed by GISH
HTIL:CHROMOSOMA
HSSN:0009-5915
HYER:1996
HCOL:vol. 105, no. 2, pp. 92-96

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(85)
ACCN:001718158 CTLN:3973100
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Subramaniam, K.;Abbo, S.;Ueng, P.P.*
AFFN:Plant Mol. Biol. Lab., USDA-ARS, BARC-West, Beltsville, MD 20705, USA
TITL:Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1996
HCOL:vol. 31, no. 5, pp. 1009-1020

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(86)
ACCN:001721522 CTLN:3977138
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); W2(Agricultural and Environmental Biotechnology Abstracts)
AUTH:Anderson, Olin D.;Kuhl, Joseph C.;Tam, Angie
AFFN:Western Regional Research Center, Agricultural Research Service, U.S. Department of Agriculture, 800 Buchanan Street, Albany, CA 94710, USA
TITL:Construction and expression of a synthetic wheat storage protein gene
PBSR:ELSEVIER SCIENCE B.V.
HTIL:GENE
HSSN:0378-1119
HYER:1996
HCOL:vol. 174, no. 1, pp. 51-58

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(87)
ACCN:001723112 CTLN:3978844
ABSJ:G (Genetics Abstracts); V (Virology & AIDS Abstracts); Z (Entomology Abstracts)
AUTH:Nkongolo, K.K.
AFFN:Department of Biological Sciences, Laurentian University, Sudbury, Ontario, P3E - 2C6, Canada
TITL:Expression of barley yellow dwarf virus and Russian wheat aphid resistance genes in and fertility of spring wheat X triticale hybrids and backcross lines
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 90, no. 3, pp. 337-344

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(88)
ACCN:001723601 CTLN:3979333
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); N (Biochemistry Abstracts 2: Nucleic Acids)
AUTH:Faris, J.D.;Anderson, J.A.;Francl, L.J.; Jordahl, J.G.
AFFN:Department of Plant Sciences, North Dakota State University, Fargo, ND 58105, USA
TITL:Chromosomal location of a gene conditioning insensitivity in wheat to a necrosis-inducing culture filtrate from Pyrenophora tritici-repentis
HTIL:PHYTOPATHOLOGY
HSSN:0031-949X
HYER:1996
HCOL:vol. 86, no. 5, pp. 459-463

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(89)
ACCN:001724174 CTLN:3979943
ABSJ:G (Genetics Abstracts)
AUTH:Myllyharju, J.;Nokkala, S.
AFFN:Laboratory of Genetics, Department of Biology, University of Turku, Turku, Finland,
TITL:Glycoproteins with N-acetylglucosamine and mannose residues in Chinese hamster metaphase chromosomes

HTIL:HEREDITAS
HSSN:0018-0661
HYER:1996
HCOL:vol. 124, no. 3, pp. 251-259

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(90)
ACCN:001724292 CTLN:3980061
ABSJ:A (Microbiology Abstracts A: Industrial & Applied Microbiology); K (Microbiology Abstracts C: Algology, Mycology & Protozoology); G (Genetics Abstracts)
AUTH:Lehman, J.S.;Shaner, G.
AFFN:Department of Botany and Plant Pathology, Purdue University, 1155 Lilly Hall, West Lafayette, IN 47907-1155, USA
TITL:Genetic variation in latent period among isolates of Puccinia recondita f. sp. tritici on partially resistant wheat cultivars
HTIL:PHYTO PATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 6, pp. 633-641

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(91)
ACCN:001724293 CTLN:3980062
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Liu, J.Q.;Harder, D.E.*;Kolmer, J.A.
AFFN:Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg, Manitoba R3T 2M9, Canada
TITL:Competitive ability of races of Puccinia graminis f. sp. tritici on three barley cultivars and a susceptible wheat cultivar
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 6, pp. 627-632

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(92)
ACCN:001728606 CTLN:3984608
ABSJ:G (Genetics Abstracts)
AUTH:Pecetti, L.;Damania, A.B.
AFFN:Istituto Sperimentale per le Colture Foraggere, viale Piacenza 29, 20075 Lodi, Italy
TITL:Geographic variation in tetraploid wheat (Triticum turgidum ssp. turgidum convar. durum) landraces from two provinces in Ethiopia
HTIL:GENET. RES. CROP EVOL.
HSSN:0925-9864
HYER:1996
HCOL:vol. 43, no. 5, pp. 395-407

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(93)
ACCN:001728607 CTLN:3984609
ABSJ:G (Genetics Abstracts)
AUTH:Damania, A.B.;Pecetti, L.;Qualset, C.O.*; Humeid, B.O.
AFFN:Genet. Resour. Conserv. Prog., Univ. California, Davis, CA 95616-8602, USA
TITL:Diversity and geographic distribution of adaptive traits in Triticum turgidum L. (durum group) wheat landraces from Turkey
HTIL:GENET. RES. CROP EVOL.
HSSN:0925-9864
HYER:1996
HCOL:vol. 43, no. 5, pp. 409-422

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(94)
ACCN:001728608 CTLN:3984610
ABSJ:G (Genetics Abstracts)
AUTH:O'Hara, R.B.;Brown, J.K.M.
AFFN:Environ. Sci. and Technol. Dep., Riso Natl. Lab., Post Box 49, DK-4000 Roskilde, Denmark
TITL:Frequency- and density-dependent selection in wheat powdery mildew
HTIL:HEREDITY
HSSN:0018-067X
HYER:1996
HCOL:vol. 77, no. 4, pp. 439-447

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(95)
ACCN:001728619 CTLN:3984621
ABSJ:G (Genetics Abstracts)
AUTH:Friebe, B.;Jiang, J.;Raupp, W.J.;McIntosh, R.A.;Gill, B.S.
AFFN:Wheat Genet. Resour. Cent. and Dep. Plant Pathol., State Univ., Manhattan, KS 66506-5502, USA
TITL:Characterization of wheat-alien translocations conferring resistance to diseases and pests: Current status
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 1, pp. 59-87

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(96)
ACCN:001728621 CTLN:3984623
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Hu, X.;Bostwick, D.;Sharma, H.;Ohm, H.; Shaner, G.
AFFN:CIMMYT, Int., Lasbo, Mexico DF, Mexico
TITL:Chromosome and chromosomal arm locations

of genes for resistance to Septoria glume blotch in wheat cultivar Cotipora
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 2, pp. 251-257

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(97)
ACCN:001728622 CTLN:3984624
ABSJ:G (Genetics Abstracts)
AUTH:Watanabe, N.;Yotani, Y.;Furuta, Y.
AFFN:Lab. Genet. and Plant Breeding, Fac. Agric., Gifu Univ., Gifu 501-11, Japan
TITL:The inheritance and chromosomal location of a gene for long glume in durum wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 2, pp. 235-239

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(98)
ACCN:001728629 CTLN:3984631
ABSJ:G (Genetics Abstracts)
AUTH:Motsny, I.I.;Simonenko, V.K.
AFFN:Dep. Genet. and Cytology Plants, Plant Breeding and Genet. Inst., 270036 Odessa, Ukraine
TITL:The influence of Elymus sibiricus L. genome on the diploidization system of wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 2, pp. 189-193

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(99)
ACCN:001733613 CTLN:3988995
ABSJ:G (Genetics Abstracts); V (Virology & AIDS Abstracts)
AUTH:Talbert, L.E.;Bruckner, P.L.;Smith, L.Y.; Sears, R.;Martin, T.J.
AFFN:Department of Plant, Soil, and Environmental Sciences, Montana State University, Bozeman, MT 59717, USA
TITL:Development of PCR markers linked to resistance to wheat streak mosaic virus in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 3, pp. 463-467

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(100)
ACCN:001735692 CTLN:3991577
ABSJ:G (Genetics Abstracts)
AUTH:Hanusova, R.;Hsam, S.L.K.;Bartos, P.;Zeller, F.J.*
AFFN:Technische Univ. Muenchen, Inst. fuer Pflanzenbau und Pflanzenzuechtung, D-85350 Freising-Weihenstephan, Germany
TITL:Suppression of powdery mildew resistance gene Pm8 in Triticum aestivum L. (common wheat) cultivars carrying wheat-rye translocation T1BL -1RS
HTIL:HEREDITY
HSSN:0018-067X
HYER:1996
HCOL:vol. 77, no. 4, pp. 383-387

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(101)
ACCN:001735762 CTLN:3991647
ABSJ:G (Genetics Abstracts)
AUTH:Cakmak, I.;Sari, N.;Marschner, H.;Kalayci, M.;Yilmaz, A.;Eker, S.; Gueluet, K.Y.
AFFN:Cukurova Univ., Fac. Agric., Dep. Soil Sci. Adana, Turkey
TITL:Dry matter production and distribution of zinc in bread and durum wheat genotypes differing in zinc efficiency
HTIL:PLANT SOIL
HSSN:0032-079X
HYER:1996
HCOL:vol. 180, no. 2, pp. 173-181

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(102)
ACCN:001735763 CTLN:3991648
ABSJ:G (Genetics Abstracts)
AUTH:Cakmak, I.;Sari, N.;Marschner, H.;Ekiz, H.; Kalayci, M.;Yilmaz, A.; Braun, H.J.
AFFN:Cukurova Univ., Fac. Agric., Dep. Soil Sci. Adana, Turkey
TITL:Phytosiderophore release in bread and durum wheat genotypes differing in zinc efficiency
HTIL:PLANT SOIL
HSSN:0032-079X
HYER:1996
HCOL:vol. 180, no. 2, pp. 183-189

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(103)
ACCN:001735769 CTLN:3991654
ABSJ:G (Genetics Abstracts)
AUTH:May, C.E.;Zhiyong, X.
AFFN:Agric. Res. Inst., NSW Agric., Wagga Wagga, NSW 2650, Australia
TITL:Nucleolus organizer regions (Nor loci) of Chinese wheats
HTIL:SCI. CHINA SER. C
HSSN:1006-9305

HYER:1996
HCOL:vol. 39, no. 2, pp. 189-198

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(104)
ACCN:001736158 CTLN:3992050
ABSJ:N (Biochemistry Abstracts 2: Nucleic Acids); G (Genetics Abstracts)
AUTH:Guiltinan, M.J.;Niu, Xiping
AFFN:Dep. Horticulture, Biotechnol. Inst., Intercollege Prog. in Plant Physiol., Cent. for Gene Regulation, Pennsylvania State Univ., 51 Wartik Lab., Univ. Park, PA 16802, USA
TITL:cDNA encoding a wheat (Triticum aestivum cv. Chinese Spring) glycine-rich RNA-binding protein
HTIL:PLANT MOL. BIOL.
HSSN:0167-4412
HYER:1996
HCOL:vol. 30, no. 6, pp. 1301-1306

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(105)
ACCN:001736418 CTLN:3992389
ABSJ:G (Genetics Abstracts)
AUTH:Luo, M.-.C.;Dvorak, J.
AFFN:Dep. Agron. and Range Sci., Univ. California, Davis, CA 95616, USA
TITL:Molecular mapping of an aluminum tolerance locus on chromosome 4D of Chinese Spring wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 1, pp. 31-35

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(106)
ACCN:001736421 CTLN:3992392
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Peusha, H.;Hsam, S.L.K.;Zeller, F.J.*
AFFN:Technische Univ. Muenchen, Inst. fuer Pflanzenbau und Pflanzenzuechtung, D-85350 Freising-Weihenstephan, Germany
TITL:Chromosomal location of powdery mildew resistance genes in common wheat (Triticum aestivum L. em. Thell.) 3. Gene Pm22 in cultivar Virest
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 2, pp. 149-152

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(107)
ACCN:001736422 CTLN:3992393
ABSJ:G (Genetics Abstracts)
AUTH:Rodriguez-Ouijano, M.;Carrillo, J.M.
AFFN:Unidad de Genetica, E.T.S.I. Agronomos, Univ. Politecnica de Madrid, Spain
TITL:Relationship between allelic variation of Glu-1 and Gli-1/Glu-3 prolamin loci and gluten strength in hexaploid wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 2, pp. 141-148

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(108)
ACCN:001738565 CTLN:3994662
ABSJ:G (Genetics Abstracts)
AUTH:Fowler, D.B.;Chauvin, L.P.;Limin, A.E.;Sarhan, F.
AFFN:Crop Dev. Cent., Univ. Saskatchewan, 51 Campus Dr., Saskatoon, SK S7N 5A8, Canada
TITL:The regulatory role of vernalization in the expression of low-temperature-induced genes in wheat and rye
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 4, pp. 554-559

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(109)
ACCN:001738569 CTLN:3994666
ABSJ:G (Genetics Abstracts)
AUTH:Sourdille, P.;Perretant, M.R.;Charmet, G.;Leroy, P.;Gautier, M.F.;Joudrier, P.;Nelson, J.C.;Sorrells, M.E.;Bernard, M.*
AFFN:INRA Stn. d'Amelioration des Plantes, Domaine de Crouelle, 63039 Clermont-Ferrand Cedex, France
TITL:Linkage between RFLP markers and genes affecting kernel hardness in wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 4, pp. 580-586

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(110)
ACCN:001738571 CTLN:3994668
ABSJ:G (Genetics Abstracts)
AUTH:Mercado, L.A.;Souza, E.*;Kephart, K.D.
AFFN:Plant, Soil, and Entomol. Sci., Univ. Idaho, Aberdeen R and E Cent., PO Box AA, Aberdeen, ID 83210, USA
TITL:Origin and diversity of North American hard spring wheats
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752

HYER:1996
HCOL:vol. 93, no. 4, pp. 593-599

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(111)
ACCN:001738572 CTLN:3994669
ABSJ:G (Genetics Abstracts)
AUTH:Tsegaye, S.;Tesemma, T.;Belay, G.
AFFN:Swedish Univ. Agric. Sci., Dep. Plant Breeding Res., S-268 31 Svaloev, Sweden
TITL:Relationships among tetraploid wheat (Triticum turgidum L.) landrace populations revealed by isozyme markers and agronomic traits
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 4, pp. 600-605

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(112)
ACCN:001738578 CTLN:3994675
ABSJ:G (Genetics Abstracts)
AUTH:Yen, Y.;Baenziger, P.S.
AFFN:Dep. Agron., Univ. Nebraska, Lincoln, NE 68583-0915, USA
TITL:Chromosomal locations of genes that control major RNA-degrading activities in common wheat (Triticum aestivum L.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 4, pp. 645-648

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(113)
ACCN:001738595 CTLN:3994692
ABSJ:G (Genetics Abstracts)
AUTH:Zeller, F.J.;Hsam, S.L.K.
AFFN:Technische Univ. Muenchen, Inst. fuer Pflanzenbau und Pflanzenzuechtung, D-85350 Freising-Weihenstephan, Germany
TITL:Chromosomal location of a gene suppressing powdery mildew resistance genes Pm8 and Pm17 in common wheat (Triticum aestivum L. em. Thell.)
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 1-2, pp. 38-40

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(114)
ACCN:001738613 CTLN:3994710
ABSJ:G (Genetics Abstracts)
AUTH:Robert, N.;Denis, J.-B.
AFFN:INRA, Stn. d'Amelioration des Plantes, Domaine de Crouelle, Clermont- Ferrand, F-63039 Cedex, France
TITL:Stability of baking quality in bread wheat using several statistical parameters
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 1-2, pp. 172-178

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(115)
ACCN:001738636 CTLN:3994733
ABSJ:G (Genetics Abstracts)
AUTH:Naranjo, T.;Fernandez-Rueda, P.
AFFN:Depto. de Genetica, Fac. de Biol., Univ. Complutense de Madrid, 28040 Madrid, Spain
TITL:Pairing and recombination between individual chromosomes of wheat and rye in hybrids carrying the ph1b mutation
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 1-2, pp. 242-248

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(116)
ACCN:001738642 CTLN:3994739
ABSJ:G (Genetics Abstracts)
AUTH:Yamamori, M.;Endo, T.R.
AFFN:Natl. Inst. Agrobiological Resour., Tsukuba, Ibaraki 305, Japan
TITL:Variation of starch granule proteins and chromosome mapping of their coding genes in common wheat
HTIL:THEOR. APPL. GENET.
HSSN:0040-5752
HYER:1996
HCOL:vol. 93, no. 1-2, pp. 275-281

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(117)
ACCN:001739688 CTLN:3995851
ABSJ:V (Virology & AIDS Abstracts); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:McNeil, J.E.;French, R.*;Hein, G.L.;Baenziger, P.S.;Eskridge, K.M.
AFFN:USDA, ARS, Dep. Plant Pathol., Univ. Nebraska, Lincoln, NE 68583, USA
TITL:Characterization of genetic variability among natural populations of wheat streak mosaic virus
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 11, pp. 1222-1227

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(118)

ACCN:001744848 CTLN:4000521
ABSJ:K (Microbiology Abstracts C: Algology, Mycology & Protozoology); A (Microbiology Abstracts A: Industrial & Applied Microbiology); G (Genetics Abstracts)
AUTH:Chen, X.;Jones, S.S.;Line, R.F.*
AFFN:Agricultural Research Service, U.S. Department of Agriculture, Pullman, WA 99164-6430, USA
TITL:Chromosomal location of genes for resistance to Puccinia striiformis in seven wheat cultivars with resistance genes at the Yr3 and Yr4 loci
HTIL:PHYTOPATHOLOGY
HSSN:0331-949X
HYER:1996
HCOL:vol. 86, no. 11, pp. 1228-1233

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(119)
ACCN:001746461 CTLN:4002225
ABSJ:G (Genetics Abstracts)
AUTH:Colombo, N.;Favret, E.A.
AFFN:Inst. de Genetica, INTA, C.C. 25, 1712 Castelar, Argentina
TITL:The effect of gibberellic acid on male fertility in bread wheat
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 3, pp. 297-303

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(120)
ACCN:001746490 CTLN:4002254
ABSJ:G (Genetics Abstracts)
AUTH:Le Gouis, J.;Pluchard, P.
AFFN:Inst. Natl. de la Recherche Agronomique (INRA), Domaine de Brunehaut, 80200 Estrees-Mons, France
TITL:Genetic variation for nitrogen use efficiency in winter wheat (Triticum aestivum L.)
CONF:Selected Papers from the XIV EUCARPIA Congress on Adaptation in Plant Breeding
LOCN:Jyvaskyla (Finland) DATE:31 Jul - 4 Aug, 1996
ISSN:0014-2336
HAUT:P.M.A Tigerstedt
HTIL:EUPHYTICA
HYER:1996
HCOL:vol. 92, no. 1-2, pp. 1-286

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(121)
ACCN:001746494 CTLN:4002258
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:McDonald, B.A.;Mundt, C.C.;Chen, R.-S.
AFFN:Dep. Plant Pathol. and Microbiol., Texas A&M Univ., College Station, TX 77843-2132, USA
TITL:The role of selection on the genetic structure of pathogen populations: Evidence from field experiments with Mycosphaerella graminicola on wheat
CONF:Selected Papers from the XIV EUCARPIA Congress on Adaptation in Plant Breeding
LOCN:Jyvaskyla (Finland) DATE:31 Jul - 4 Aug, 1996
ISSN:0014-2336
HAUT:P.M.A Tigerstedt
HTIL:EUPHYTICA
HYER:1996
HCOL:vol. 92, no. 1-2, pp. 1-286

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(122)
ACCN:001746503 CTLN:4002267
ABSJ:G (Genetics Abstracts)
AUTH:Berzonsky, W.A.
AFFN:Agron. Dep., Purdue Univ., West Lafayette, IN 47907, USA
TITL:Brazilian origin and inheritance of a heterozygous reciprocal chromosome translocation in wheat (Triticum aestivum L.)
HTIL:CYTOLOGIA
HSSN:0011-4545
HYER:1996
HCOL:vol. 61, no. 3, pp. 253-258

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(123)
ACCN:001747550 CTLN:4003321
ABSJ:G (Genetics Abstracts); K (Microbiology Abstracts C: Algology, Mycology & Protozoology)
AUTH:Bartos, P.;Stuchlikova, E.;Hanusova, R.
AFFN:Res. Inst. Crop Prod., 161 06 Praha-Ruzyne, Czech Rep.
TITL:Adaptation of wheat rusts to the wheat cultivars in former Czechoslovakia
CONF:Selected Papers from the XIV EUCARPIA Congress on Adaptation in Plant Breeding
LOCN:Jyvaskyla (Finland) DATE:31 Jul - 4 Aug, 1996
ISSN:0014-2336
HAUT:P.M.A Tigerstedt
HTIL:EUPHYTICA
HYER:1996
HCOL:vol. 92, no. 1-2, pp. 1-286

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(124)
ACCN:001747568 CTLN:4003339
ABSJ:G (Genetics Abstracts); W2(Agricultural and

Environmental Biotechnology Abstracts)
AUTH:Ahmed, K.Z.;Mesterhazy, A.;Bartok, T.;Sagi, F.
AFFN:Dep. Genet., Fac. Agric., Minia Univ., Minia, Egypt 61517
TITL:In vitro techniques for selecting wheat (Triticum aestivum L.) for Fusarium-resistance. II. Culture filtrate-technique and inheritance of Fusarium-resistance in the somaclones
HTIL:EUPHYTICA
HSSN:0014-2336
HYER:1996
HCOL:vol. 91, no. 3, pp. 341-349

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(125)
ACCN:001747589 CTLN:4003360
ABSJ:G (Genetics Abstracts)
AUTH:Mujeeb-Kazi, A.;Islam-Faridi, M.N.;Cortes, A.
AFFN:Intl. Maize and Wheat Improvement Cent. (CIMMYT), Lisboa 27, Apartado Postal 6-641, 06600 Mexico, D. F., Mexico
TITL:Genome identification in some wheat and alien Triticeae species intergeneric hybrids by fluorescent in situ hybridization
HTIL:CYTOLOGIA
HSSN:0011-4545
HYER:1996
HCOL:vol. 61, no. 3, pp. 307-315

1997

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(1)
ACCN:001752504 CTLN:4008821
ABSJ:J (Microbiology Abstracts B: Bacteriology); G (Genetics Abstracts); A (Microbiology Abstracts A: Industrial & Applied Microbiology)
AUTH:Troxler, J.;Azelvandre, P.;Zala, M.;Defago, G.;Haas, D.*
AFFN:Lab. de Biologie Microbienne, Univ. de Lausanne, CH-1015 Lausanne, Switzerland
TITL:Conjugative transfer of chromosomal genes between fluorescent pseudomonads in the rhizosphere of wheat
HTIL:APPL. ENVIRON. MICROBIOL.
HSSN:0099-2240
HYER:1997
HCOL:vol. 63, no. 1, pp. 213-219

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Number 84: 86 (1997)

Information

9th International Wheat Genetics Symposium

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

Forty years after the first Symposium took place in Canada at the University of Manitoba, the 9th IWGS will return to Canada and be held at the University of Saskatchewan. The highlight of the first symposium were the reports by Sears and Okamoto, and Riley and Bell on the discovery of the *Ph1* gene that prevents homoeologous pairing in *Triticum aestivum*. Many exciting new discoveries are being made in wheat genetics. The 9th IWGS will cover all aspects of wheat genetics and breeding.

University of Saskatchewan
The University of Saskatchewan has extensive crop research facilities and a large phytotron. Saskatoon is a major centre for plant biotechnology. Located on the campus are the National Research Council of Canada's Plant Biotechnology Institute, Agriculture and Agri-Food Canada's Research Centre, the POS (Protein, Oilseed and Starch) Pilot Plant Corporation and numerous biotechnology companies in a research park, Innovation Place. Tours will be arranged to visit some of these facilities.

Program
The program will include invited and contributed papers and posters. A refereed proceedings including both papers and posters will be published and available at the Symposium. A separate program for accompanying persons is planned.

Accommodations
With the low value of the Canadian dollar, costs in Canada are very reasonable. Accommodation for the Symposium will range from university residence units at $20 Cdn. per person per night to first class hotels at $60-90 Cdn. per room per night.

For furthewr information, contact the symposium secretary, Carolyn Ouellet
E-mail: Carolyn.Ouellet@USask.ca

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Editorial remarks

During fiscal year 1996-1997, 146 supporters have contributed to the donation to Wheat Information Service, which allowed us to improve financial condition and editorial affairs. Thank you very much, again, for these contributors, to whom we have sent a beautiful card of the receipt. Based on this, we have made effort on grading-up of the journal, probably resulting in increased number of contribution papers. Also, the reviewing system seems to function well: the proportion of acceptance for the original articles is about 70% at present time, and the journal could include several articles for Research information.

Wheat Information Service are now circulated over 700 subscribers including institutions and personals across 64 countries. Computer-based internet system has been rapidly developed in recent, but, still in the world, there must be many wheat researchers who do not participate in the benefits of these magic services and working hard for wheat researches for science and food problems. Wheat Information Service would like to connect these researchers with the modern, and the regional information to the world. The present issue contains a list of recent publications on wheat genetics cited from a computer database. Also, we would like to accumulate information on conserved genetic stocks in database.

In the present issue, No.84, Dr. C. Yen in Triticeae Research Institute, Sichuan Agricultural University, China proposes a nomenclature of the D-genome species, based on historical and taxonomic review. Editors would like to open the space for discussion on this subject in the future issues from subscribers.

Hope for your continuous contribution to WIS.

Editor, T. S.

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