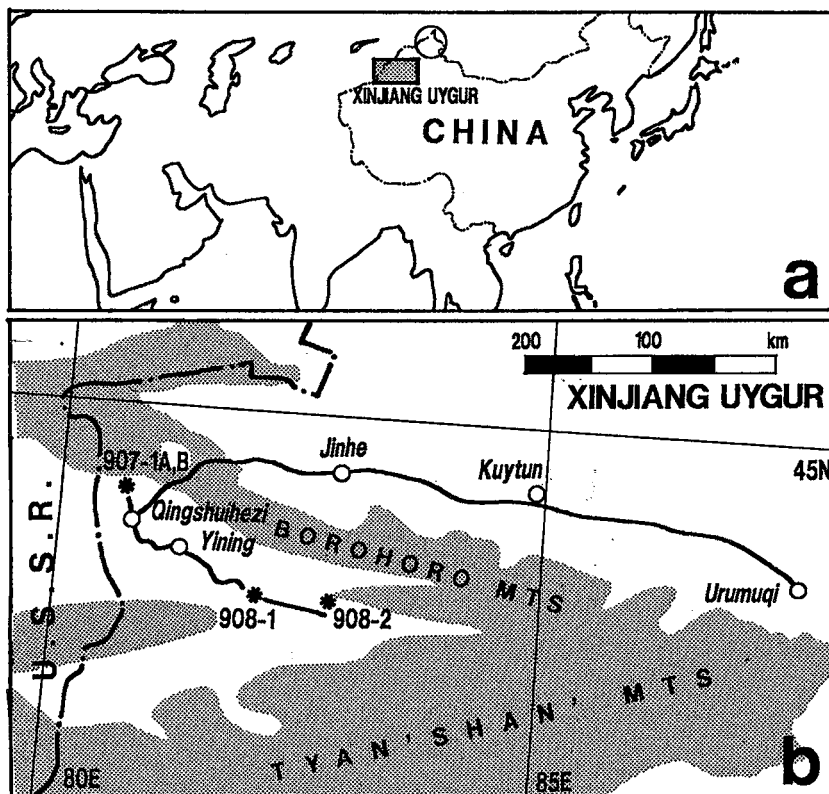


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Tel 45–721–0751

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Characterization of a disomic wheat-*Ae. variabilis* addition line resistant to powdery mildew fungus

P. Spetsov and I. Iliev

Institute for Wheat and Sunflower, General Toshevo, Bulgaria

A disomic addition line ($2n=44$) has been obtained by crossing *T. aestivum* cv. Roussalka with *Aegilops variabilis* (UUSS, $2n=28$)*. It manifested high resistance to powdery mildew in seedling and adult plant stage, both in greenhouse and field conditions. The alien pair of chromosomes slightly suppressed the growth of plants in tillering phase, and necrotic symptom was visually detected, mainly, in glasshouse.

The added chromosome, not carrying a satellite, did not cause negative effects on the sporogenesis in plants. As a result, balanced 22-chromosome gametes were formed.

The present paper deals with the characteristics of the newly obtained disomic addition line.

Materials and Methods

The parents used were *Aegilops variabilis* ($2n=28$), collection number 13.133 (awned type), and *T. aestivum* var. *erythrospermum*, cultivar Roussalka, IWS-Gen. Toshevo's winter type variety. The cross-combination between the parents was made in 1984, and F_1 seeds were irradiated using ^{60}Co , dose of 10 kR.

BC_1 plants with wheat were grown on an infection field and the resistant progenies were obtained each year by self-pollinating the derivatives. A single plant, having the cytoplasm of common wheat and isolated in 1988 with high resistance to powdery mildew, was the ancestor of the disomic addition line (DAL in abbreviation).

First two leaves seedlings grown in a greenhouse were inoculated with five physiological races of *Blumeria graminis* (DC) Speer f. sp. *tritici* (*Erysiphe graminis* f. sp. *tritici* Em. Marchal) i.e., 59, 59^a, 84, 111 and 112 (Iliev 1989). Infection was rated using five progressive grades from 0 to 4: 0, no symptom; 1-2, small areas of mycelium with little or no conidial formation to scant sporulation; 3, reduced sporulation; 4, heavy sporulation.

Field assessments were made on plants, grown in the infection plot that was artificially inoculated by pathogen populations, including the races of powdery mildew fungus from the glasshouse experiment. The estimates for adult plant resistance to powdery mildew comprised leaves and spikes separately, and grouped as follows: VR, high resistant, no symptom to scant sporulation on the lowest leaves; R, resistant, mycelium with little conidial formation; and S, susceptible to the pathogen.

* Genome symbol according to Kimber and Tsunewaki (1988).

Somatic chromosomes were counted in root-tip cells and meiotic phases were analysed from PMCs, using the acetocarmine smear method. Some field observations on plant growth and spike open fertility of the lines were recorded.

Results and Discussion

The wild species, *Ae. variabilis*, showed high resistance to all five races of the pathogen in seedling stage, while the wheat variety was susceptible (Table 1). DAL that possessed a pair of alien chromosomes, expressed a moderate resistance to powdery mildew fungus, except for 59 race. To two other races, 59^a and 111, DAL exhibited no pustules, but to 84 and 112 races it performed scant sporulation. In contrast, the wheat parent was strongly affected by the pathogen.

As regards adult plant resistance, the difference between DAL and the parents, was more distinguishable (Table 2). Variety Roussalka manifested susceptibility, both on leaves and spikes, while the wild species showed high level of resistance, but spikes were affected by the fungus. DAL exhibited high resistance both on leaves and spikes. In some cases, single pustules could be found on the lowest 1-2 leaves, but to a greater extent on spikes (ear assessment R, Table 2).

Table 1. Infection types with five races of *Blumeria graminis* (DC) Speer f. sp. *tritici* in seedling stage.

Lines	Chromosome number 2n	Races of wheat powdery mildew				
		59	59 ^a	84	111	112
DAL	44	4	0	2	0	2
Roussalka	42	4	4	4	4	4
<i>Ae. variabilis</i>	28	0	0	0	0	0

Table 2. Adult plant resistance to powdery mildew fungus, estimated in infection field (averaged for two years).

Lines	Powdery mildew resistance	
	Leaves	Spikes
DAL	VR	R
Roussalka	S	S
<i>Ae. variabilis</i>	VR	S

The resistance of DAL to powdery mildew fungus was due to the presence of a pair of chromosomes, derived from *Ae. variabilis*. Up to now, no information has been available as regards powdery mildew resistance, carried by *Ae. variabilis* chromosomes. Shepherd and Islam (1988) indicated the chromosome O of the same wild species as a carrier of resistance to cereal cyst nematode, while chromosome 6U (formerly A) of *Ae. umbellulata* (donor of U genome to *Ae. variabilis*) as bearing resistance to leaf rust.

Simultaneously, Ceoloni (1985), and Zeller and Heun (1985) used chromosome G of *Ae. longissima*, assumed to be the second genome donor of *Ae. variabilis*, to transfer powdery mildew resistance into the genome of common wheat. Giura and Marinescu (1988) obtained some wheat addition lines with chromosomes of tetraploid *Aegilops* species, including *Ae. variabilis*. Three of those lines exhibited resistance to powdery mildew fungus.

About 30 plants of DAL and 25 F₁ hybrids of the cross DAL x Roussalka were observed to find the mitotic chromosome number, and all had the expected-44 and 43 chromosomes, respectively. Observation in meiotic phases-diakinesis, metaphase I, anaphase I and tetrads led to the conclusion that only 22-chromosome gametes had been functioning in DAL. Consequently, the plants of DAL observed, were meiotically stable, with normal chromosome pairing. The alien chromosome did not carry a satellite.

Two-years field data showed that DAL had the same germination ability as the wheat parent with white coleoptile (Table 3). Necrotic symptom appeared in plants at shooting stage, mainly when grown in the greenhouse. Chlorosis affected first the 2-4 leaves in all their parts from the central to other tillers, then one or two leaves withered and broke. This resulted in slight depression of growth that might have been the reason for the late heading of DAL. Chlorosis on the lowest leaves and some necrotic spots could be detected in field conditions when compared to Roussalka wheat.

Data in Table 3 clearly demonstrated the significant differences between the lines, when grown on the field. DAL fully resembled wheat, but its spikes were shorter and more compact, producing seeds with lighter grain weight per plant than the wheat. The open fertility of DAL was insignificantly higher in comparison to Roussalka wheat.

Data presented in this paper provide all evidence that the newly obtained line is a stable,

Table 3. Some characteristics of DAL compared to Roussalka wheat.

Lines	Germination %	Coleoptile colour	Ear length (cm)	Seed set %	Grain weight per plant (gm)
DAL	90.4	white	6.1***	70.6	6.2*
Roussalka	92.0	white	9.0	62.5	7.3

*, ***, significant at 5 and 0.1 % levels, respectively.

phenotypically distinct and crossable aneuploid genotype of high level of resistance to wheat powdery mildew fungus.

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Identification of sources of resistance against flag smut (*Urocystis agropyri* (Preuss) Schroet) of wheat

G. C. Bhatnagar, S. N. Mali and V. K. Bhatnagar

Wheat Improvement Project, Agriculture Research Station, Durgapura, Jaipur - 302 018, India

Hitherto the flag smut of wheat caused by *Urocystis agropyri* (Preuss) Schroet was considered to be of minor importance in the country. However, in recent past it has been reported in damaging proportions from many parts of the country. The disease was first reported in 1906 by Butler from Layalpur (Punjab) and its sporadic reports are on record from to time. The disease has now become one of the yield reducing factors-in Uttar Pradesh, Punjab, Haryana, Delhi, Himachal Pradesh, Rajasthan and Madhya Pradesh. Even some of the present day cultivars have developed susceptibility and the incidence of the disease has been on increase in these states (Butler 1918; Mundkur 1944; Rao 1952; Bedi 1957; Kothari and Dange 1968; Sethi and Singh 1971 and Bhatnagar and Vijaylaxmi 1975). The situation with respect to Flag smut incidence in Rajasthan during the past five years is more alarming as the losses to the extent of 40-60% have been reported from different parts of the state (Bhatnagar et al 1978). Besides, studies on loss estimation, control through cultural practices and chemicals, studies on varietal susceptibility and screening of promising breeding material at different stages of its development were conducted to identify resistant donars so as to make wheat breeding programme more meaningful.

Materials and Methods

A sick plot (2500 m²) was developed at Agricultural Research Station, Durgapura. The inoculum load in the sick plot was so much that the susceptible varieties exhibited 100% infection. The topography of the infected area was uniform. However, additional inoculum was supplemented through seed and soil at the time of sowing to put maximum selection pressure of the pathogen. Each cultivar was planted in 2 m rows at 5 cm depth with three controls (Lal Bahadur, HD 2009 and D-134) of highly susceptible varieties after every tenth row. The planted material was grown under normal optimum conditions of fertility, irrigation and other cultural practices recommended for wheat crop in this agro-climatic zone. The incidence of flag smut was recorded on individual plants at flag leaf stage, and per cent infection was calculated by formula:

$$\frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

Besides the available commercial varieties, the entries in plant pathological screening nurs-

ery including IET and U. R. T material were subjected to testing. The cultivars or varieties exhibiting less than one per cent infection have been categorised as resistant.

Results and Discussion

Very few attempts have been made in the past to exploit the wheat material for the search of resistance against flag smut in the country, as the disease was always considered of very minor importance. However, Pal and Mundkur (1941) reported IP-4 and IP-111 to be highly resistant out of 97 varieties tested. Tyagi and Anand (1966) identified wheat strains NP 871, NP 876, K-65, Sonora-63 and Sonora-385 to be free from flag smut infection. In similar studies, Singh and Sethi (1975) reported that wheat varieties VL-426, HD 2217, HW 161, HB 121, BH 113, Noreno and 112-P4 exhibited than two per cent infection. Recently, Goel and Jhooty (1984) have screened diversified germplasm and grouped them in various categories including those considered to be immune against flag smut pathogen. In the studies carried out by the present authors, 126 strains of *Triticum aestivum* and strains of *T. durum* were put to vigorous testing in the sick plot and out of them 19 strains of *T. aestivum* and two strains of *T. durum* were found to be free from infection against 80-100% infection in susceptible controls. The screening process was continued during 1980-81, 81-82 and 82-83. Similar observations regarding the immunity of "durums" to *Urocystis agropyri* have been made by Joshi (1978) and Goel and Jhooty (1984). Though Sonalika consistently exhibited immunity in the present studies, contradictory reports are available regarding its performance against flag smut. It was reported to be susceptible by Bedi (1957). However, Goel and Jhooty (1984) observed less than 5% incidence in this variety.

The cultivars or varieties identified to be resistant and showing less than 1% infection in the present investigations against flag smut pathogen are listed below:

Triticum aestivum: HD 2189 (HD 1963/HD 1931), HD 2211 (HD 2136 × HD 1949/HD 1949), HD 2278 (HD 2119 × 249), Raj 821 (NP 875/HD (M) 1508), Raj 1865 ((SD-6485-8156/Chr × Son-Kl. Rend) Bb-Cal zbz (chiroca), Raj 1804 (HD 2009 × Raj 821), Raj 1974 (HD 2185 × HD 2160), Raj 2185 (UP 291 × HD 2206), WH 185 (Norteno × Sh. Sonora), WH 188 (Ciano-India) 23584), WH269 (Cno 'S' × 564-Kl. Rend/C 281-WL 202), WH 291 (HD 1925 × HD 832-23584), WL 927 (Bw 42-HD 1553), WG 1012 (HD 1977 × (WG 143 × USA 255) × PV 18), UP 276 (Pi 62-II-53-5267 Son. 64/Son. 64-Kl. Rend), K 7432 (Cno-India-Bb), IWP 40 (S 64-NP 852 × Kal²), DWL 5023 ((Cr 'S'-Lds) Gr 'S'), Sonalika ((II 53-388 × An) Yt 54 × N 108) LR).

Triticum durum: Raj 911 (Vo-229), Raj 1555 (Cocorit- "S" × Raj 911).

Acknowledgement

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Transfer of leaf rust resistance from durum wheats CPAN 6051 and CPAN 6073 to *Triticum aestivum*

Sanjiv Gupta, A. K. Gupta and R. G. Saini

Department of Genetics, Punjab Agricultural University, Ludhiana-141004, India

Durum wheats are reported to carry leaf rust resistance genes which are different from the *Lr* genes identified in *Triticum aestivum* and very effective against highly virulent races prevalent in the Indian sub-continent (Pasquini et al 1979; Sharma et al 1986; Roelfs, personal communication). These genes can be used to broaden the genetic base of leaf rust resistance in bread wheats. Although successful transfer of genes from durum wheats have been achieved earlier for the improvement of *Triticum aestivum* (McIntosh et al 1967; McIntosh and Dyck 1975), an altered expression of some genes due to change in ploidy level has also been reported (Kerber 1983; Dyck 1987). We report here the transfer of resistance from two highly resistant durums CPAN 6051 and CPAN 6073 to a susceptible hexaploid wheat Agra Local and comparison of the hexaploid derivatives with two commonly grown hexaploid wheats.

Cultivars CPAN 6051 and CPAN 6073 were crossed with Agra Local. The F_1 s were selfed and the F_2 seeds thus obtained were sown in an open experimental area under artificial epiphytotic of race 77A which is virulent on all the known genes from *T. aestivum*. Resistant F_2 plants were identified and cytologically examined for chromosome number. A hexaploid derivative D 525-2 was isolated from cross of cultivar CPAN 6051 with Agra Local and D 3542-6 was from cross of CPAN 6073. The infection types on seedlings were recorded according to the scale given by Stakman et al (1962). The seedlings showing infection types 0; , , 1, 2, and X were classified as resistant and those showing infection types 3 and 4 were considered as susceptible. The terminal disease severity was recorded as percentage of leaf area covered with rust according to a modification of Cobb's scale as given by Peterson et al (1948).

The seedling reactions (infection types) of hexaploid derivatives, the donor cultivars, susceptible parent Agra Local and two most commonly grown cultivars HD 2329 and Sonalika against leaf rust (*Puccinia recondita* Rob. ex Desm. f. sp. tritici) races 1, 108 and 77A and their field scores are given in Table 1. The infection types of hexaploid derivative D 525-2 and D 3542-6 against race 1 were ; and ;1, respectively whereas those on CPAN 6051 and CPAN 6073 were ;12⁺ and ;1⁻, respectively. The infection types against race 108 were very close to those on durums and the derivatives. Against race 77A, the infection type on D 3542-6 was 1⁻1 which was very close to its donor parent CPAN 6073 (IT = 11⁺) but that of D 525-2 varied from 2⁻ to 3 which was different from that seen on its donor parent CPAN 6051 (1⁺). This difference might have appeared due to outcrossing of this derivative. Saini (1987) tested cultivar CPAN 6051 and its derivative D 525-2 against 14 Australian leaf

Table 1. Seedling reactions and disease severity on adult plants of two durum wheats, their hexaploid derivatives and some common wheats against three races of leaf rust (*Puccinia recondita*)

Cultivars and hexaploid derivative	Race and Infection type			Disease severity
	1	108	77A	
CPAN 6051 (4X)	;12 ⁺	1+2 ⁻	1 ⁺	Free
D 525-2 (6X)	;	;12	2 ⁻ 3	10 MR
CPAN 6073 (4X)	;1 ⁻	1+2 ⁻	11 ⁺	Free
D 3542-6 (6X)	;1	;1+2	1-1	5 MR
Agra Local (6X)	3 ⁺	3 ⁺	3 ⁺	90S
HD 2329 (6X)	;1	;1	3 ⁺	40 MR
Sonalika (6X)	;1 ⁺	3 ⁺	3 ⁺	50S

rust races and identified *Lr23* from D 525-2 as well as the donor parent CPAN 6051. However, D 525-2 was segregating for *Lr13*. These observations confirm outcrossing of D 525-2. Cultivar Agra Local was susceptible to all these races and disease severity on Agra Local was 90S. The infection type on cultivars HD 2329 and Sonalika against race 1 was ;1 and ;1⁺, respectively. Against race 108 the infection type on seedlings of HD 2329 was ;1 but cultivar Sonalika was susceptible. Both these cultivars were susceptible to race 77A at seedling stage.

The disease severity on HD 2329 and Sonalika was 40MR and 50S, respectively. The disease severity on hexaploid derivative D 525-2 was 10 MR and on D 3542-6 it was 5 MR. Tetraploid donors CPAN 6051 and CPAN 6073 were completely free from leaf rust. The adult plant resistance gene *Lr13* detected from D 525-2 is not effective against race 77A used here for field tests (Gupta et al 1984). Gene *Lr23* present in the donor parent CPAN 6051 gives adult plant resistance against race 77A (Saini et al 1986). The resistance of this derivative under field conditions, therefore, appears to be due to *Lr23* or some other unknown leaf rust resistance gene. Some disease (5 MR) which appeared on D 3542-6 may be due to incomplete expression of the durum resistance from CPAN 6073. The D genome is reported to affect expression of leaf rust resistance genes present on A or B genome (The and Baker 1975; Kerber 1983; Dyck 1987). Since there is only partial change in the resistance of CPAN 6051 and CPAN 6073 in hexaploid background, it appears that the hexaploid derivatives D 525-2 and D 3542-6 can be used for the improvement of commonly grown hexaploid wheats like HD 2329 and Sonalika.

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Effect of *Fusarium graminearum* Schw. on reductions in yield of wheat

S. Tomasović and B. Korić

Institute for Breeding and Production of Field Crops, Faculty of Agricultural Sciences,
University of Zagreb, Marulićev trg 5/1, 41.000 Zagreb, Yugoslavia

Fusarium head blight was described as wheat disease first in England in 1884. That year Smith found out that *Fusarium culmorum* was the cause of this disease. Soon after that, the disease was reportedly spread in Europe, North and South America, Australia and some other parts of the world (Tomasović, 1981; MacInnes and Fogelman 1923). Until mid-sixties, the disease was mainly referred in literature as the one of minor importance (Peterson 1965; Leley 1976) although was in 1915 the cause of yield reductions up to 80% in variety Marquis (MacInnes and Fogelman, 1923). In China, Japan and Brazil, this disease has always been a problem in wheat growing. Today, we might say that fusarium head blight is a problem in countries where narrow crop rotation is used (maize-wheat cropping system); central and eastern parts of the USA, Mexico, Central America, Europe, northern and eastern Africa, southern Asia and Far East (Anderson, 1978).

Today's intensive wheat growing is characterized by high yield potential of the grown varieties. For exploitation of this yield potential, certain preconditions related to increased number of spikes per m² (higher densities) and higher fertilizer rates, especially nitrogen components, have to be met. This leads to a formation of microclimate favourable for development of many diseases, among which one of the most dangerous is fusarium head blight, caused by *Fusarium graminearum* Schw.

In addition to *Fusarium graminearum* species, some other *Fusarium* species also appear, but the mentioned species is most frequent. Apart from causing head blight, this fungus also causes seedling blight, crown rot of basal stem area (Čizmić, 1984; Tomasović, 1987). *Fusarium* head blight is most frequently manifested as spike bleaching (white spikes) or of some of its parts in humid or moderately humid wheat growing regions. In arid and less humid regions, attack on spikes does not occur or is negligible and the disease manifests as infection of root and basal stem area (Tomasović 1987). During past few years, excessive moisture in the period from anthesis to the end of vegetation contributed to the development of moderate or even severe disease intensity, and in certain varieties more than 30% of infected spikes was found (Cvjetković, Balaž, Matijević, 1987).

According to past research, both in the country and abroad, under present conditions of production reduction in yield because of the disease attack can go up to 50% (Tomasović, 1987; Čizmić, 1986; Korić, 1989).

Apart from having epiphytotic attack of *Fusarium graminearum* under artificial infection, with this work we also wanted to study the effect of the disease on yield in some lines developed by this Institute.

Materials and Methods

Failures in yield in some years are often correlated with severe fusarium head blight (Marić et al 1986). How high these damages really are and what their maximum is in our wheat growing areas is hard to determine for sure without exact field testing. Therefore, adequate field trials were conducted at location Botinec, with five wheat lines all developed by this Institute. The aim was to determine the effect of fusarium head blight on reduction in yield. Severe attack (epiphytotic) of the fungus was ensured by artificial infection with a population of selected *Fusarium graminearum* isolates.

Experiments were set following split-plot design in randomized blocks with five replications. Plot size was 1 m². Artificial infection was made with a suspension of spores from selected *Fusarium graminearum* isolates at the flowering stage (stage 10.5 after the Feekes-Large), late in the afternoon, thus avoiding high daily temperature, while requirements in high relative air humidity needed for germination of spore were met, which ensured a successful infection. Apart from the fact that evening dew provides optimal conditions for the infection, artificial infection late in the afternoon allowed us to avoid plastic foil often recommended and used by many authors in their research. For the area where our research was conducted, northwestern Croatia, use of plastic foil is limited because of the high daily temperatures occurring during anthesis. This was proved in our trials when plants, covered with plastic foil immediately after the inoculation died because of extremely high temperatures occurring under the foil.

Identification of *Fusarium* species, collected from infected samples of spike, isolation of pure culture of *Fusarium graminearum* fungus used for artificial infection, and selection of the most suitable isolates for preparation of inoculum was made by Viktorija Vlahović, M. Sc. in a laboratory of this Institute, following the well-known methods (Milatović, Vlahović and Tomasović, 1982; Bekele 1984; Liu 1984; Luzzardi 1984).

Severity of fusarium head blight attack was rated by an international scale (Tomasović 1987) at the milk-dough stage (stage 11.1 and 11.2, Feekes-Large). Other details referring to the mentioned rating scale are discussed in paper by Tomasović (1987) and Milatović, Vlahović and Tomasović (1982). Other management practices usual for trials of such type and purpose were applied. In both years of research trials were treated for weed control.

Results and Discussion

After adequate statistical data processing, analysis of variance showed that both tested factors, artificial infection and variety, as well as their interaction did not always have statistically significant effect on yield in both years (Table 1). From those two factors, only artificial infection had a statistically significant effect on yield in both years. The significance of this effect was demonstrated in "F" and "t" tests. Thus, reduction in yield in 1985 ranged from 53 to 70% and in 1986 from 51 to 53%. Such severe reductions in yield because of the disease should not only be attributed to artificial infection, but also to actual

Table 1. Effect of *Fusarium graminearum* Schw. fungus on wheat yield

Line	Artificial infection		Natural infection		Reduction in yield (%)
	Mean yield (kg/m ²)	Disease severity (0-5)*	Mean yield (kg/m ²)	Disease severity (0-5)*	
Year 1985					
ZG L-1	0.24	4.4	0.80	1.8	70
ZG L-2	0.35	3.6	0.78	0.6	55
ZG L-3	0.34	3.6	0.72	1.6	53
ZG L-4	0.36	3.6	0.79	1.0	54
ZG L-5	0.32	3.8	0.80	2.4	60
Year 1986					
ZG L-1	0.31	3.8	0.65	2.2	52
ZG L-2	0.35	4.6	0.72	2.0	51
ZG L-3	0.32	4.0	0.65	2.4	51
ZG L-4	0.32	4.0	0.66	2.2	51
ZG L-5	0.34	3.8	0.72	2.2	53

* Rating scale 0-5

1985
LSD 5% = 0.03
LSD 1% = 0.05

1986
LSD 5% = 0.14
LSD 1% = 0.23

climatic conditions that favoured the occurrence and development of the disease. This especially refers to the second year of investigation (1986) when moderately severe attack of natural fusarium head blight was observed, which, of course, reflected on percentage of total yield loss in that year. In this way, yield reduction was seemingly lower, though one would not tell that judging by the climatic conditions. Therefore, in presenting data, estimates of fusarium head blight attack both from natural conditions and artificial infection have to be given. Naturally, disease attack must be rated by an accepted international scale and within optimal term, so that the obtained results can be compared with the results already obtained both in this country and from worldwide.

The obtained results suggest that the tested lines were susceptible to the attack, and that in years climatically favourable for the occurrence and development of *Fusarium graminearum*, severe outbreaks of this disease on spikes can be expected. It inevitably leads to high yield reductions, and in seed production of these lines created danger of severe infection which can result in failure to obtain certificate for seeds as commodity, according to our current regulations.

Other diseases that occurred, first of all powdery mildew on leaves were of the same intensity in all variants of trials and did not have any effect on ultimate results of trials.

Instead of a conclusion, one needs to emphasize that in some years the problem of fusarium head blight is pronouncedly manifested. In our struggle for reduced influence of

this fungus on yield, all available means should be used – from cultural practices to development of resistant and tolerant varieties. Unfortunately, chemical protection does not give reliable and safe effects at presents, but they seem to be sporadic and depend more on timing rather than on the effectiveness of the fungicide itself.

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Germination, pollen fertility and crossability between triticale and wheat and reversion patterns in early segregating generations

V. K. Khanna

Department of Plant Breeding, College of Agriculture, Pantnagar-263145, India

Larger or heavier seeds give rise to more vigorous plants and better yields, particularly when equal number of seeds per unit area are planted (Bremner et al 1963; Clark and Peck 1968). However, with the increasing age of plants the superiority of plants from larger seeds decreases and is gradually lost in the long duration crops and perennial plants (Randhawa 1970). Dhillon et al (1976) reported that small seeds showed the highest and the large seeds the lowest emergence capacity in triticale, maize, barley and soybean. A study of germination, pollen sterility and crossability between wheat and triticale and reversion of early segregating generations to the parental types is reported here.

Materials and Methods

The experimental material used in the present study comprised of five strains of hexaploid triticale namely UPT 75233, UPT 7681, UPT 78268, UPT 79339 and UPT 79347 and five varieties of hexaploid wheat namely Sonalika, UP 262, UP 2003, WL 1804 and WL 2087. B_{1t} ($F_1 \times$ triticale), B_{1w} ($F_1 \times$ wheat) and F_2 generations were raised to study the reversion to the parental types. On the basis of the morphological features, plants were classified as having resemblance to either of the parent in each cross.

Results and Discussion

In the present study it was observed that the small seeds showed the highest and the large seeds the lowest emergence capacity (Table 1), except in the case of Sonalika. Similar results were obtained by Dhillon et al (1976) in triticale, maize, barley and soybean.

Pollen sterility in triticales (Table 1) ranged from 5.9 to 15.8 per cent whereas it was 3.7 to 6.2 per cent in wheats. Pollen sterility may be due to poor growth of the plant, chlorophyll deficiency, chromosomal aberrations etc. According to Chauhan (1976) tapetum plays a definite role in the development of microspores.

When triticale was used as the female parent in triticale \times wheat crosses, seed set was low, whereas the germination was good (Table 2). On the contrary, when wheat was used as the female parent, seed set was good but germination was nil. Similar results were reported by Jouve et al (1984). This may be attributed to the high frequency of embryo-less kernels (Behl et al 1981). Singh and Khanna (1983) reported that poor crossability in triticale \times wheat crosses was due to pollen germination and retardation and inhibition of the growth of the pollen tubes in the pistils at the base of the style. Pollen fertility of the

Table 1. Mean 1000 grain weight, germination percentage and pollen fertility percentage in triticales and wheats.

Strain	Grain weight (g)	Germination %	Pollen fertility %
<i>Triticale</i>			
UPT 75233	42.4 ± 1.6	88 ± 1.9	87.3 ± 3.2
UPT 7681	40.1 ± 1.2	92 ± 2.1	89.1 ± 2.7
UPT 78268	44.0 ± 1.9	82 ± 1.1	84.2 ± 2.9
UPT 79339	43.1 ± 0.8	87 ± 1.6	94.1 ± 1.8
UPT 79347	43.8 ± 1.1	87 ± 2.3	93.9 ± 2.1
<i>Wheat</i>			
Sonalika	51.1 ± 1.3	96 ± 2.4	96.3 ± 2.3
UP 262	48.2 ± 2.1	86 ± 1.8	94.7 ± 2.4
UP 2003	42.9 ± 1.7	95 ± 2.2	96.2 ± 2.2
WL 1804	43.5 ± 1.1	94 ± 1.3	93.8 ± 3.4
WL 2087	43.8 ± 1.5	93 ± 1.7	94.4 ± 2.1

F₁ ranged from 42.3 to 64.7 per cent (Table 2).

The percentage of reversion to the parental types is given in Table 3. Plants in the segregating generations were classified into triticales, wheat and intermediate types. Those with compact spike and prominent awns were classified as triticales type, plants with lax spike and comparatively short awns were classified as wheat type. Other plants with mixed morphological features of wheat and triticales were classified as intermediate type. Useful transgressive segregants were observed in all the generations. An unusual observation was that more triticales type plants were recorded in three B_{1w} generations of UPT 75233 × Sonalika, UPT 7681 × UP 262 and UPT 78268 × UP 2003.

It is suggested that in wheat-triticales hybridization programme, triticales should be used as the female parent and the desirable segregants of triticales and intermediate type in the F₂ generation of triticales × wheat crosses may be further mated *inter se* in order to enlarge the genetic variability.

Table 2. Crossability between wheat and triticale, F₁ seed germination and pollen fertility

Cross	No. of florets pollinated	No. of seeds set	Crossability (%)	No. of F ₁ seed germinated	Seed germination (%)	Pollen fertility of F ₁ (%)
UPT 75233 × Sonalika	1086	117	10.8	84	71.8	54.4
Sonalika × UPT 75233	1054	480	45.5	0	0	—
UPT 7681 × UP 262	1120	141	12.6	90	63.8	51.6
UP 262 × UPT 7681	1062	369	34.7	0	0	—
UPT 78268 × UP 2003	1050	120	11.4	78	65.0	42.3
UP 2003 × UPT 78268	1084	426	39.3	0	0	—
UPT 79339 × WL 1804	1074	174	16.2	124	71.3	61.8
WL 1804 × UPT 79339	1086	462	42.5	0	0	—
UPT 79347 × WL 2087	1144	219	19.1	162	74.0	64.7
WL 2087 × UPT 79347	1132	543	48.0	0	0	—

Table 3. Percentage reversion to parental phenotype in early segregating generations of triticale and wheat crosses.

Cross	Generation	No. of plants observed	Triticale type (%)	Intermediate type (%)	Wheat type (%)
UPT 75233 × Sonalika	F ₂	25	30	24	46
	B _{1t}	25	46	22	32
	B _{1w}	25	64	8	28
UPT 7681 × UP 262	F ₂	25	48	18	34
	B _{1t}	25	51	22	27
	B _{1w}	25	60	12	28
UPT 78268 × UP 2003	F ₂	25	29	38	33
	B _{1t}	25	58	18	24
	B _{1w}	25	46	19	35
UPT 79339 × WL 1804	F ₂	40	51	16	33
	B _{1t}	40	69	19	12
	B _{1w}	40	25	32	43
UPT 79347 × WL 2087	F ₂	40	32	25	43
	B _{1t}	40	64	24	12
	B _{1w}	40	31	27	42

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Relationship of lodging resistance and yield to anatomical characters of stem in wheat, triticale and rye

V. K. Khanna

Department of Plant Breeding, G. B. Pant Agriversity, Pantnagar, India

When wheat (genus *Triticum*) and rye (genus *Secale*) are artificially crossed, the product is an intergeneric hybrid that has characteristics of both parents. The hybrid is called triticale. The early triticales were developed from tall, weakstrawed parents and the sunlight conditions of the lower latitudes encouraged them to grow even taller and weaker. Especially under the stimuli of irrigation and fertilization, intended to exploit their full yield potential, the tall triticales tended to lodge or fall over, severely depressing yield. Lodging has attracted attention due to severity of damage and consequent losses in yield and grain quality. For triticales to be competitive with wheat at the higher level of production, it was essential to improve its lodging resistance. This has been accomplished to quite an extent by improving straw strength, decreasing plant height or both. Triticale may prove to be an important crop for those areas which are marginal for wheat cultivation, e.g., the hills, where it yields about 20% more than wheat. Present study deals with the correlation of vascular bundles and thickness of different stem layers with yield and lodging resistance in triticale, wheat and rye.

Materials and Methods

The study was carried out on seven wheat, seven triticale and four ryes selected on the basis of differences in height and lodging susceptibility. A randomized block design with three replications was used. Stem sections were collected one month after the heading, i.e., at approximately half maturity of the grain. The material was preserved in FAA (5 ml formaldehyde + 5 ml glacial acetic acid + 90 ml of 70% ethyl alcohol). The sample was collected from the main tiller by taking five plants in each replication and the internodes were numbered from the base towards the top. Studies were done on free hand cut sections. For counting the number of vascular bundles whole sections were used. The sections were stained with Safranin-fast green (Johansen 1940). The size of epidermal cells, chlorenchyma and sclerenchyma cells was measured with a calibrated ocular micrometer. The measurements were taken on 10 randomly selected cells in each slide. The readings were converted to microns and the average values were calculated.

Results and Discussion

Epidermis refers to the outermost layer of cells of all parts of the primary plant body-stems, roots, leaves, flowers, fruits, and seeds. The normal functions of epidermis of the aerial

plant parts are considered to be restriction of transpiration, mechanical protection, gaseous exchange through stomata, storage of water and metabolic products, and photosynthesis.

Experimental results revealed that thickness of epidermis ranged from 5.91 microns (Snoopy rye) to 13.1 microns (UPT 72142), and epidermal cells of the tall wheat varieties were thicker than those of the dwarf ones (Table 1). This, however, was not true for triticales and ryes. Amongst triticales three dwarf triticales, TL 419, UPT 78274 and UPT 7440 had a thicker epidermis than one tall strain, i.e., UPT 74303. Two tall wheats, UP 031 and C 306, which showed maximum lodging, had thicker epidermis than all the dwarf varieties with better lodging resistance. Also, UP 301 which showed no lodging and gave a high yield (41.5 q/ha) had the lowest value for this character. UPT 72142 had the thickest epidermis among all the triticales though it showed high lodging. Amongst ryes, Snoopy had the least lodging as well as the thinnest epidermis. Thickness of epidermis does not show any role in lodging resistance in our study.

The term sclerenchyma refers to complexes of thick walled cells, often lignified, whose principal function is mechanical. These cells are supposed to enable plant organs to withstand various strains, such as may result from stretching, bending, weight and pressure, without undue damage to the thin-walled softer cells.

Thickness of sclerenchymatous cells varied from 9.45 microns in UP 301 to 15.46 microns in UPT 72142 (Table 1). Dwarf wheats, with the exception of UP 301, gave a thicker sclerenchyma than the tall wheats. The dwarf wheats, WL 711 and UP 2003, with thick sclerenchyma cells were more resistant to lodging than the tall ones. UP 301, though completely lodging resistant and high yielding, had the lowest value for sclerenchyma thickness. Since this variety is very short in stature, it does not lodge in spite of thin sclerenchyma cells. Sclerenchyma was found to be thicker in all the four dwarf triticales when compared to UPT 74303 and UPT 78015, but the thickness was maximum in UPT 72142 which is tall and high yielding. UPT 72142 had lodging on the higher side in spite of the thickest sclerenchyma which may be due to the thinnest hypodermis. Similar correlation is seen in UPT 7440 which shows maximum lodging in spite of having less plant height. In general, thick sclerenchyma resulted in less lodging. Amongst ryes this relationship is clear cut. Murdy (1960) in maize and Vaidya (1956) in wheat reported that the thickness of sclerenchyma was greater in lodging resistant varieties.

One or more layers of cells beneath the epidermis in leaf, stem, and root may be morphologically and physiologically distinct from the deeper-lying ground tissue. This may be known as hypodermis.

The relationship between hypodermis and lodging resistance followed a pattern more or less similar to sclerenchyma (Table 1). Wheats with thicker hypodermis showed the least lodging except UP 301 which did not lodge in spite of having a thin hypodermis due to its very less height. UPT 72142 had the thinnest hypodermis amongst triticales but it did not show too much lodging, which may be due to its thickest sclerenchyma. The two dwarf triticales, UPT 78274 and UPT 78268 had higher values and the least lodging. Another

Table 1. Thickness of epidermal cells, sclerenchyma cells and hypodermis (microns), and plant height (cm), lodging percentage and yield (q/ha)

Variety	Epidermis	Sclerenchyma	Hypodermis	Plant height	Lodging	Yield
Wheat						
UP 301	8.56	9.45	50.00	68.00	0	41.50
UP 2003	8.99	14.64	77.75	83.60	15	35.11
WL 711	9.25	13.92	75.00	93.20	15	39.31
Sonalika	9.88	13.38	75.11	100.00	20	42.00
UP 1050	11.02	13.10	70.50	113.00	20	32.40
UP 031	11.23	12.95	62.50	117.50	80	30.45
C 306	11.60	12.88	65.50	135.60	85	26.00
Triticale						
TL 419	10.46	13.43	83.64	85.00	10	41.00
UPT 78268	9.84	13.42	86.25	89.70	5	40.65
UPT 78274	11.42	13.24	90.50	90.10	0	36.80
UPT 7440	10.41	13.20	76.50	96.50	20	36.00
UPT 78015	10.96	12.13	82.75	104.90	10	32.77
UPT 72142	13.10	15.46	68.75	108.00	15	38.45
UPT 74303	8.65	10.49	81.75	109.50	10	35.55
Rye						
Snoopy	5.91	8.63	68.26	100.00	35	Not known
Asian	6.62	7.27	55.42	125.00	80	"
Australian	6.95	7.41	55.91	130.00	80	"
Russian	6.48	6.98	53.23	135.00	85	"

Table 2. Thickness of chlorenchyma cells (microns)

Variety	Internode					Average for internode
	I	II	III	IV	V	
Wheat						
UP 301	19.08	24.91	21.40	22.80	—	22.05
UP 2003	17.92	18.72	20.64	19.05	—	19.09
WL 711	20.48	19.28	18.96	18.48	19.52	19.34
Sonalika	Absent	23.32	24.81	21.43	22.81	23.09
UP 1050	Absent	19.17	17.01	20.86	22.35	19.85
UP 031	Absent	19.50	20.43	18.00	19.08	19.25
C 306	Absent	20.32	18.56	18.30	20.40	19.39
Triticale						
TL 419	19.62	19.43	20.44	18.62	—	19.53
UPT 78268	17.60	17.44	21.20	24.20	—	20.11
UPT 78274	17.76	17.04	18.80	23.18	—	19.19
UPT 7440	17.92	17.45	20.50	20.00	—	18.96
UPT 78015	18.64	18.60	19.65	18.12	17.20	18.44
UPT 72142	Absent	Absent	16.82	17.01	32.43	22.09
UPT 74303	18.72	16.84	17.80	17.00	20.72	18.22
Rye						
Snoopy	17.62	18.48	17.51	16.21	—	17.46
Asian	Absent	Absent	17.80	16.92	16.43	17.05
Australian	Absent	Absent	16.98	17.46	17.84	17.43
Russian	Absent	Absent	17.32	17.03	16.78	17.04

Table 3. Number of vascular bundles in different internodes

Variety		Internodes					Average per internode
		I	II	III	IV	V	
Wheat							
UP 301	A	36	34	35	32	—	63.25
	B	28	34	27	27	—	
UP 2003	A	38	32	36	37	—	58.00
	B	18	20	26	25	—	
WL 711	A	42	35	37	37	30	61.40
	B	25	22	24	24	31	
Sonalika	A	X	35	33	33	32	65.00
	B	X	29	34	32	32	
UP 1050	A	36	30	33	32	23	56.60
	B	18	25	30	30	26	
UP 031	A	40	36	38	28	27	55.00
	B	10	14	26	28	28	
C 306	A	36	34	30	30	22	54.80
	B	18	22	24	28	30	
Triticale							
TL 419	A	37	35	32	30	—	55.25
	B	19	22	22	24	—	
UPT 78268	A	39	35	34	26	—	54.75
	B	19	21	25	20	—	
UPT 78274	A	34	36	28	25	—	50.00
	B	15	22	20	20	—	
UPT 7440	A	37	31	33	20	—	48.25
	B	14	13	14	31	—	
UPT 78015	A	34	30	28	27	24	47.60
	B	20	17	20	20	18	
UPT 72142	A	38	33	33	28	30	56.60
	B	21	19	24	25	32	
UPT 74303	A	30	34	27	27	22	47.80
	B	21	19	20	19	20	
Rye							
Snoopy	A	32	31	32	27	—	52.00
	B	19	23	23	21	—	
Asian	A	X	X	28	25	24	43.33
	B	X	X	16	19	18	
Australian	A	X	X	27	24	24	42.66
	B	X	X	19	19	15	
Russian	A	X	X	25	25	23	44.66
	B	X	X	21	20	20	

A = Inner Vascular bundles; B = Outer Vascular bundles;
X = Internode absent; — = Vascular bundles absent.

dwarf triticales UPT 7440 showed a thinner hypodermis and also the maximum (20 per cent) lodging amongst triticales. Amongst ryes thick hypodermis results in less lodging. Gobo et al (1971) gave similar results in wheat.

Because of its high chlorophyll content, the photosynthetic parenchyma is sometimes called chlorenchyma. The thickness of chlorenchyma did not show much variation amongst wheat strains except in Sonalika and UP 301 which had the thickest cells and the highest yields (Table 2). Even the cells in the tall wheats which were low yielding were quite thick. It is likely that in spite of thick cells their yields may be less because of lodging. Chlorenchyma was absent in the first internode of all the tall wheats. The strains showing thicker chlorenchyma in triticales had a higher yield except UPT 72142, which, in spite of lacking these cells in the first and second internode, was high yielding. This may be due to the thickest cells in the fifth internode of this strain.

Vascular bundles occur in two rings in the stems of wheat, triticales and rye. The number of vascular bundles in the inner ring of first internode exceeded those of the last internode in all the cases (Table 3). The inner ring had more vascular bundles than the outer ring with a few exceptions. In wheat, the maximum number of vascular bundles were observed in UP 301 and in all varieties they showed a positive correlation with yield. The three dwarf varieties had higher number of vascular bundles than the tall ones and at the same time they were more productive and lodging resistant. The dwarf triticales had a higher number of vascular bundles but a tall type UPT 72142 had the highest value but its yield was lesser than the highest which may be due to lodging. In general, wheat strains had more vascular bundles than triticales and ryes. Sowa (1961) in barley, Natr (1964) in winter wheat and Gobo et al (1972) found a positive relationship between the number of vascular bundles and lodging resistance.

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Interrelationship among grain yield and its economic characters in wheat, *Triticum aestivum* L.

S. M. Qayyum, A. H. Ansari, A. A. Mirza*

Department of Agronomy, S. A. U., Tandojam, Pakistan

* Department of Statistics, S. U. Jamshoro, Pakistan

The knowledge about the association of factors influencing yield is a pre-requisite for designing an effective plant breeding programme (Worley et al 1976). The information about the simple correlation of agronomic and morphological characters with yield is helpful in the identification of the components of this character. Keeping the above facts in view an experiment was performed to assess the interrelationship among yield and its components in wheat, under agro-ecological conditions of Tandojam.

Materials and methods

To assess the interrelationship among yield and its components in wheat, an experiment was conducted at Agronomy Experimental Fields, A. R. I. Tandojam during winter 1987-88. Six cultivars of bread wheat (M-141, M-154, TJ-83, Pavon, Pak-70 and Blue Silver) were grown in four replicated complete randomized block design at a rate of 125kg seeds per ha in a net plot area of 5 × 3m, maintaining 30cm row distance. A basal fertilizer was applied with dose of 100kg N and 70kg P₂O₅ per ha prior to sowing in the form of urea and single super phosphate. All the required cultural operations were adopted uniformly in all the plots throughout the growing period according to the crop requirements. At maturity 12 plants were randomly selected from each variety. The plant population was recorded per m² from each plot. The following characters were measured; plant population/m², days to flag leaf, days to ear heading, plant height, number of tillers/plant, spikelets/spike, spike length, number of kernels/spike, kernel weight/spike and grain yield/plant.

Simple and multiple correlation and regression coefficients were calculated, following Steel and Torrie (1980).

Results and discussion

Simple correlation among yield and its components (Table 1) showed that plant population/m² had strong negative association with number of tillers/plant, indicating that population/m² decreased the tillering capacity/plant. Similarly spike length had negative significant correlation with plant population/m². This relation shows that increasing plant population/m² reduced the length of spike. Yield/plant revealed high negative relationship with plant population/m² indicating that increasing plant stand/m² reduced the single plant yield.

Table 1. Phenotypic correlation among yield and its components in wheat.

Character	Plant population /m ²	Days to flag leaf	Days to ear-heading	Plant height	No. of tillers /plant	No. of spikelets /spike	Spike length	Kernels /spike	Kernels weight /spike	Grain yield /plant
Plant population/m ²	—	0.273	0.287	0.022	-0.673**	-0.020	-0.423**	-0.123	-0.178	-0.670**
Days to flag leaf	—	—	0.881**	0.170	-0.008	0.113	-0.183	0.187	-0.053	-0.006
Days to ear heading	—	—	—	0.141	0.032	0.078	-0.152	0.145	-0.097	0.014
Plant height	—	—	—	—	0.273	0.239	0.372**	0.385**	0.361*	0.362**
No. of tillers/plant	—	—	—	—	—	0.001	0.287	0.114	0.090	0.938**
No. of spikelets/spike	—	—	—	—	—	—	0.424**	0.598**	0.704**	0.242
Spike length	—	—	—	—	—	—	—	0.403**	0.558**	0.465**
Kernels/spike	—	—	—	—	—	—	—	—	0.728**	0.353**
Kernel weight/spike	—	—	—	—	—	—	—	—	—	0.417**
Grain yield/plant	—	—	—	—	—	—	—	—	—	—

* and ** : Significant at the 5% and 1% levels of probability, respectively.

These results suggest that plant population can possibly be used as yield predictor. These results are in agreement with those of Breggs and Aytenfisu (1980).

Days to flag leaf had strong and positive correlation with days to ear heading. However, it did not have any correlation with plant height, kernels/spike, kernel weight/spike and yield, respectively. Days to ear heading did not have any association with plant height, number of tillers/plant, number of spikelets/spike, spike length, number of kernels/spike, kernel weight/spike and yield/plant, respectively. These relationship explain that days to flag leaf and ear heading are not sure signs in improving yield.

Plant height had highly significant and positive association with number of kernels/spike showing that taller plants produced greater number of kernels/spike. The correlations between plant height and weight of kernels/spike, and yield/plant were positive and significant. These high magnitude of correlations show that plant height can be used in selection criteria. It was noted that number of tillers/plant, number of spikelets/spike and spike length had no association with plant height.

Number of tillers/plant revealed high positive correlation with yield indicating that selection based on tiller number/plant could be more rewarding to improve the grain yield. Similar results were reported by Larik (1979). No relationships were found in number of tillers/plant with number of spikelets/spike, spike length, number of kernels/spike and kernel weight/spike.

Number of spikelets/spike had high positive correlations with spike length, number of kernels/spike and kernels weight/spike. These correlations show that longer spike bears more spikelets, resulting increased number and wight of kernels. It was noted that number of spikelets/spike had positive but not significant association with yield/plant. These results are not in agreement with the findings of Kumbhar et al (1983) who reported significant and positive association between number of spikelets/spike and yield/plant. Spike length showed strong and positive association with number of kernels/spike, kernel weight/spike and yield/plant. These relationships suggest that longer spike produce greater number and weight of grains per spike and yield, and can be used for selection criteria. Similar results were reported by Larik (1979), Kumbhar et al (1983), and Soomro and Qureshi (1987).

Number of kernels/spike had significant and positive association with weight of kernels/spike and yield/plant. This relation explains that kernels/spike can be used in breeding purposes. These results are supported by Kumbhar et al (1983), and Soomro and Qureshi (1987).

A highly positive association was found between kernels weight/spike and yield/plant. This shows that kernel weight/spike can be used in selecting a high yielding strain. Similar results were reported by Larik (1979), Kumbhar et al (1983), and Soomro and Qureshi (1987).

Table 2. Estimates of simple correlation, multiple correlation and regression among yield and its components in wheat

Character	Simple correlation (r)	Partial regression coefficients	t-test
X ₁ . Plant population/m ²	-0.670**	0.009 ±0.005	0.181
X ₂ . Plant height	0.362**	-0.007 ±0.104	-0.715
X ₃ . No. of tillers/plant	0.938**	2.582 ±0.066	38.946**
X ₄ . Spike length	0.465**	0.106 ±0.064	1.655
X ₅ . No. of kernels/spike	0.353**	0.001 ±0.009	0.127
X ₆ . Kernel weight/spike	0.417**	3.060 ±0.266	11.475**
Y ₁ . Yield/plant (Dependent character)	—	—	—

$Y = -10.439 + 0.009x_1 - 0.007x_2 + 2.582x_3 + 0.166x_4 + 0.001x_5 + 3.060x_6$
 Multiple R = 0.996
 Multiple R² = 0.992
 Estimated Error = 0.377

** : Significant at the 1% level of probability

Table 3. Test of significance for multiple regression

Source of Variation	df	SS	MS	F
Regression	6	647.789	107.96	817.88**
Residual	41	5.411	0.132	—
Total	47	653.20	—	—

** : Significant at the 1% level of probability

Multiple correlation and regression

Detail information on the effectiveness of different quantitative attributes and their contribution towards final yield was obtained by working out multiple correlation and regression (Table 2). This was accomplished by assessing the cumulative effect of yield components on grain yield per plant, i.e., taking grain yield/plant as dependent character and the other traits which were strongly associated with yield/plant as independent variables. The multiple correlation coefficient between yield/plant and other characters was 0.996 which means that 99.2 per cent of the variation in yield/plant can be attributed to six independent variables. The calculated F value 817.99 (Table 3) shows that the multiple regression was highly significant. The *t*-test indicated that number of tillers/plant, and kernels weight/plant contributed significantly towards yield/plant while the other four variables not. These results are in accordance with the results obtained by Lark (1979) and Kumbhar et al (1983). From the multiple regression coefficient carried out in the present study, it may be inferred that number of tillers/plant and kernel weight/spike are the effective yield components of the bread wheat.

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Identification and location of chlorophyll synthetic genes in a wheat variety Mara

Dalmir Singh

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

Summary

A study was undertaken to identify and locate gene(s) for chlorophyll synthesis on specific chromosomes in an Italian hexaploid dwarf wheat variety Mara. For this purpose a variety Mara was crossed as a male parent with a monosomic line 3A of a variety Pb. C591 which produce albino seedlings (nullisomics) upon selfing (Singh and Joshi, 1979). All the F_1 hybrid plants were analysed cytologically at the first meiotic metaphase. Seeds were taken from all the F_1 hybrids separately. Observations made on the F_2 seedlings suggested that the variety Mara carries two independent genes which are involved in the biosynthesis of chlorophyll. One of the genes is located on chromosome 3A.

Introduction

It has been demonstrated that the flag leaves of wild species of wheat have higher photosynthetic capacity (P_{max}) than those of the bread wheat varieties when expressed per unit leaf area or per unit mass of chlorophyll (Austin, et al., 1986) which indicates that chlorophyll content might be related to P_{max} . It is necessary to identify genes for the higher photosynthetic efficiency in wild diploid wheat species in order to transfer them to bread wheat. In fact this kind of selective transfer in the absence of the knowledge of chlorophyll synthetic genes present in the recipient varieties may be difficult. Logically, along with the identification of the genes for higher photosynthetic capacity it is important to identify and locate chlorophyll synthetic gene(s) in the recipient varieties too. With this objective in mind, an Italian hexaploid dwarf wheat Mara was used to identify and locate the gene(s) for chlorophyll synthesis.

Materials and methods

To determine the chromosome(s) carrying genes involved in the biosynthesis of chlorophyll in the variety Mara, it was crossed as a male parent with a monosomic line 3A of a variety Pb. C591 which was reported to carry a gene for chlorophyll synthesis on chromosome 3A (Singh and Joshi, 1979). Seeds obtained from these crosses were planted in the field. All the F_1 hybrid plants were analysed cytologically at the first meiotic metaphase (Table 1). Seeds were taken from all the hybrid plants separately and the presence or absence of chlorophyll was determined by germinating these F_2 seeds in the petri dishes. The observations were made on the seedlings on individual hybrid plant population basis (Table 1).

Observations were also recorded on the seedlings of all the parents involved in the experiment.

Results and discussion

Seedling data recorded on the parents showed that all the parents produced only green seedlings except a monosomic line 3A of a variety Pb. C591 which produced green and albino seedlings. The frequency of albino seedlings in this line was 12.6% which agreed to 13.7% of albino seedlings (nullisomics) produced upon selfing of a monosomic line 3A of the variety Pb. C591(Singh, 1986).

All the F₁ hybrid seedlings produced chlorophyll. Complete absence of chlorophyll-deficient seedlings in the F₁ seedlings suggested that all the F₁ seedlings possess at least one gene for chlorophyll synthesis because the chlorophyll synthetic gene is hemizygous effective (Singh and Joshi, 1979).

The F₂ seedlings of monosomic F₁ hybrids involving monosomic 3A (var. Pb. C591) and Mara were found to segregate for green and albino seedlings while the F₂ seedlings of disomic F₁ hybrids produced only green seedlings (Table 1). The occurrence of only green seedlings in the F₂ generation of the disomic F₁ hybrids showed that the variety Mara possess at least one gene for chlorophyll synthesis on chromosome 3A. The variety Pb. C591 was shown to carry a gene for chlorophyll synthesis. It was therefore presumed that a gene on chromosome 3A of the variety Mara for chlorophyll synthesis might be allelic to the gene present on chromosome 3A of the variety Pb. C591. The monosomic F₁ hybrid plants produced albino F₂ seedlings with an overall frequency of 4.0% which was much lower than 12.6% of albino seedlings observed in the selfed population of a monosomic 3A of the variety Pb. C 591 (Table 1). This reduced frequency of albino seedlings in the F₂ generation

Table 1. Meiotic chromosome configurations of hybrids and segregation of albino seedlings in F₂.

Parents and crosses	Parental and F ₁ chromosome configurations	Number of F ₂ seeds germinated	Number of F ₂ seedling		
			Green	Albino	(%)
Mono 3A (Pb. C591)	20" + 1'	200	173	25	(12.6)
Mara	21"	200	195	0	(0)
Mono 3A × Mara -1	21"	605	591	0	(0)
" " -2	20" + 1'	326	311	12	(3.71)
" " -3	20" + 1'	515	486	21	(4.14)
" " -4	20" + 1'	395	375	15	(3.84)
" " -5	20" + 1'	458	432	19	(4.21)
Overall frequency of albino in Mono hybrids			1604	67	(4.0)

of the monosomic hybrids suggested that the variety Mara might carry an additional chlorophyll synthesis gene which reduced the occurrence of albino seedling (nullisomics) from 12.6% to 4.0%.

The results suggested that the variety Mara might carry two independent genes involved for some critical function in the biosynthesis of chlorophyll. One of the genes is located on chromosome 3A, which may be allelic to the gene present in the variety Pb. C591.

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Natural habitat of *Aegilops squarrosa* in Xinjiang Uygur, China

M. Tanaka and H. Tsujimoto*

Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences

* Kihara Institute for Biological Research, Yokohama City University,
Mutsukawa 3-112-20, Minami-ku, Yokohama 232, Japan

We took part in the field research trips of North Xinjiang Uygur Autonomous Region, China, in 1989 and 1990. One of the objectives of the trips was to investigate the natural habitat of *Aegilops squarrosa* in northern mountainous region of China that is thought to be north and east margins of the distribution of the *Aegilops* species.

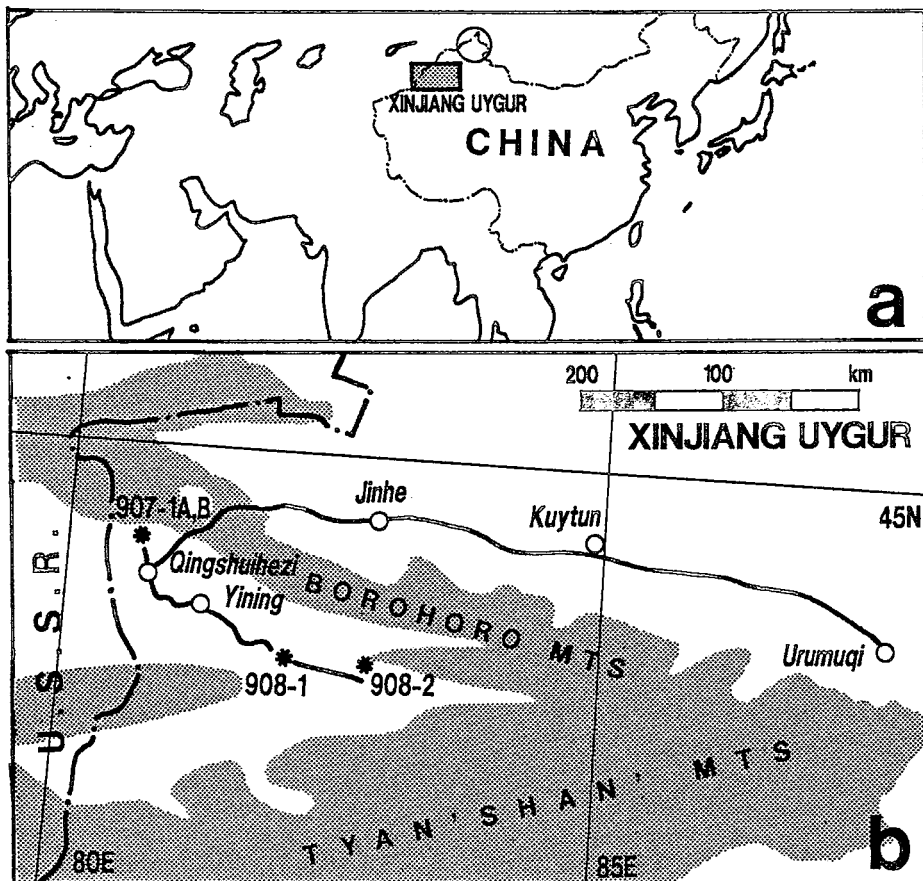


Fig. 1. Route of the present research trip. In a, the open circle indicates Altay region and the shadowed box is Ili region of which enlarged map is shown in b. In b, asterisks indicate the places where we collected *Ae. squarrosa*.

Table 1. Location and altitude of the stations where we collected *Ae. squarrosa*

Station	Location	Altitude (m)
907-1A	20 km north from Qingshuihezi. Side of forest near small river.	930
907-1B	20 km north from Qingshuihezi. On a hillside.	950
908-1	98 km east from Yining. Road sides.	730
908-2	130 km, east from Yining. On a mountainside.	1000

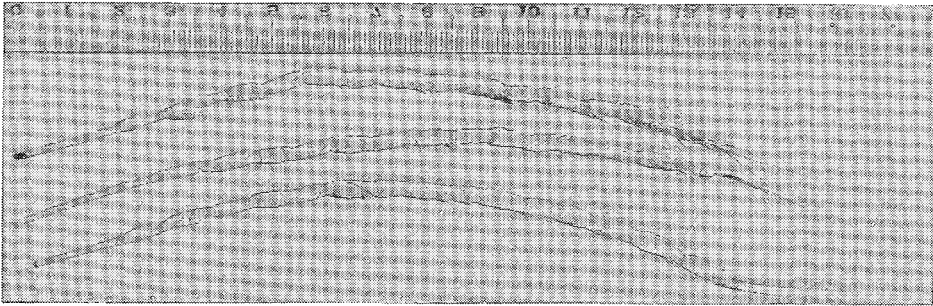


Fig. 3. Spikes of *Ae. squarrosa* collected at station No. 908-1A

In the trip of 1989, we investigated Altay region bordering on U. S. S. R. and Mongolia. We did not find any species of *Aegilops* in this region although we found many species of perennial *Triticeae* such as *Roegneria* and *Elymus*.

In the trip of 1990, we visited Ili region locating between Tyan'shan' and Borohoro Mountains. We found the population of *Ae. squarrosa* var. *typica* in several places of this region (Fig. 1 and 2). They grew in *Artemisia-Sophora* step with *Cirsium* spp. We have collected the samples at three locations (Table 1). At station No. 908-1 *Ae. squarrosa* was found only along the road sides. All the other population were apparently wild, which should not regard the recent introduction by men or animals. In the population of 908-2, plants with yellow and black spikes coexisted. The spikes of one of the collections are shown in Fig. 3.

Ae. squarrosa in this region is supposed to have immigrated from the West along the Ili River because the other directions are surrounded with two high mountains. The geographical block by the mountains seems to hinder the transfer of this species to more eastern regions. Although *Ae. squarrosa* is known to grow in the wheat field or the margins placed along the Yellow River, it might have transferred together with wheat as a weed.

Therefore, the Ili region thus far is the most east and north margin of the distribution of *Ae. squarrosa*.

Acknowledgment

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Location of genes for awnedness and waxiness using monosomic analysis in wheat (*Triticum aestivum*)*

O. Sridevi, J. V. Goud and K. V. Bhat**

Division of Genetics and Plant Breeding University of Agricultural Sciences. Dharwad-5, Karnataka, India

Several varieties of common wheat (*Triticum aestivum* L.) and of other species are waxy on various parts of the plants, e.g., leaves, leaf sheaths, glume surface etc. The genotypes are classified based on this into waxy and non-waxy.

The awn is the extension of flowering glume. Wheats have been classified as awned and awnless. Monosomic analysis has revealed that awning in bread wheat is controlled by a series of awn promoter genes and three major epistatic genes 'Hd', on chromosome VIII (4B), B1 on IX (5A) and B2 on X (6B). A series of 'A' genes have been proposed by Heyne and Livers (1953) to explain awn development in different varieties. An 'A' gene is hypothetically non-epistatic but incompletely dominant over an awn producing 'a' allele. A single locus in the homozygous recessive condition 'aa' could produce full awns, if not inhibited by partially epistatic Hd or B1 or B2. The present study was aimed at identifying the chromosomes associated with the genes influencing these traits by using all the twentyone monosomic lines of variety Kalyansona.

Materials and Methods

Twentyone monosomic lines of Kalyansona were crossed with DWR-39 and in F₁, confirmed monosomic plants were carried to F₂ generation. Segregation for waxiness, i.e., waxy and nonwaxy types and for awn character viz., fully awned, sparsely awned, hooded and awnless was observed.

In the same manner, normal disomic cross was made using both the parents and forwarded to F₂ generation and observations made in disomic F₂ were compared with those of monosomic F₂ populations.

Results and Discussion

The values in Table 1 reveal that plants in 17 monosomic F₂ populations segregated into different types whereas in disomic F₂ cross there was no segregation. This difference in awning seemed to be controlled by factors located on at least seventeen chromosomes.

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** Present Address—NBPGR, IARI, New Delhi-110 012.

Similar situation was observed in the report on tetraploid wheat Khapli by Mokhtarzadeh (1975) where he explained that awning is controlled by factors located on nine chromosomes. Similar type of explanation was given to describe the inheritance of glume colour in Red Bobs (Sadananda, 1977), in Cadet (Bhowal and Jha, 1969) and in Khapli (Mokhtarzadeh, 1975).

This indicates that there is a complex interaction among genes present on these seventeen chromosomes with the genotype of the male gamete when the genes are present in hemizygous condition (single dose). This is the reason why segregation was not observed in four populations where these seventeen chromosomes are present in homozygous condition. Depending on the type of interaction the gene is engaged in, the ultimate ratios in the

Table 1. Segregation pattern for awn character in monosomic F₂ population

Mono	Awnless	Fully awned	Sparsely awned	Hooded	Total
1A	69	26	32	13	140
2A	75	21	31	5	132
3A	81	35	35	22	191
4A	0	188	0	0	188
5A	87	57	17	16	174
6A	0	140	0	0	140
7A	125	40	26	18	209
1B	101	47	24	18	193
2B	84	38	52	28	205
3B	102	35	54	14	205
4B	10	28	49	5	82
5B	19	32	26	52	131
6B	98	38	14	29	181
7B	66	36	12	19	133
1D	67	43	24	55	189
2D	91	41	12	19	165
3D	88	46	22	24	185
4D	42	34	32	13	175
5D	0	143	0	0	143
6D	72	36	34	33	175
7D	0	212	0	0	212
Disomic	0	490	0	0	490

Kalyansona

Fully awned

DWR-39

Fully awned

critical families are bound to vary. That is why the segregation ratio differed among the critical families or it may be due to the modifying factors, which affect the expression of main factors, *A*, *B* and *Hd* (Clark, 1926).

For waxiness also, segregation into waxy and nonwaxy was not observed in disomic, F_2 population (Table 2). But seventeen monosomic populations showed segregation, the remaining four viz., 4A, 6A, 5D and 7D did not, thus, indicating the presence of genes for waxiness on these seventeen chromosomes and simultaneous absence of segregation for the two characters, i.e., waxiness and awnedness in four populations. From this we can infer that these two genes affecting awnedness and waxiness are closely associated or may be that there is pleiotropic effect of the concerned genes on these two characters.

Table 2. Segregation pattern for waxiness character in monosomic F_2 population

Mono	Waxy	Non-waxy	Total
1A	93	47	140
2A	51	81	132
3A	123	68	191
4A	188	0	188
5A	124	50	174
6A	140	0	140
7A	94	115	209
1B	147	46	193
2B	106	99	205
3B	140	65	205
4B	38	46	82
5B	77	52	131
6B	136	45	181
7B	76	57	133
1D	100	89	189
2D	108	57	165
3D	114	66	185
4D	59	116	175
5D	143	0	143
6D	64	111	175
7D	212	0	212
Disomic	490	0	490
Kalyansona	Waxy		
DWR-39	Waxy		

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Catalogue of gene symbols for wheat: 1991 Supplement

R. A. McIntosh¹ (Co-ordinator), G. E. Hart² and M. D. Gale³

1. The University of Sydney, Plant Breeding Institute, Cobbitty Rd., Cobbitty, N. S. W., 2570, Australia.
2. Department of Soil and Crop Sciences, Texas A & M University, College Station, Texas, U. S. A., 77843-2474.
3. Institute of Plant Science Research, Cambridge Laboratory, Colney Lane, Norwich, Norfolk, England, UR4 7UJ.

The most recent edition of the Catalogue appears in the Proceedings of the 7th International Wheat Genetics Symposium held at Cambridge, England (pp. 1225-1323). This supplement has been offered to the editors of Annual Wheat Newsletter, Cereal Research Communications and Wheat Information Service for inclusion in their respective journals.

Additions to Symbols List.

<i>Bo</i>	Boron toxicity.
<i>Em</i>	Early-methionine-labelled polypeptide.
<i>Gc</i>	Gametocidal genes.
<i>Igc</i>	Suppression of gametocidal activity.
<i>Si</i>	Subtilisin inhibitor.
<i>Stb</i>	Reaction to <i>Septoria tritici</i> blotch.

Levy and Feldman (1968) studied the inheritance of more than 20 morphological and biochemical traits in crosses of four *T. dicoccoides* lines and *T. durum*. Similarly, Kuspira *et al.* (1973) studied 12 qualitative characters in *T. monococcum*. The symbols applied to the characters examined in these studies are not being reserved and listed in the Catalogue. However, both studies should serve as bases for future work.

Anthocyanin Pigmentation

Purple/Red auricles, Purple leaf base.

<i>Ra2</i> (1085).	4B (1085).	v: Rye line with added wheat chromosomes.
<i>Ra3</i> (1085).	6B (1085).	v: Rye line with added wheat chromosomes.

Purple leaf base was expressed only when both chromosomes 4B and 6B containing *Ra2* and *Ra3*, respectively, were added to a rye with purple coleoptiles. It was not expressed when the same genes were added to a rye line with green coleoptiles (1085).

Boron Tolerance

Genes controlling tolerance to high concentrations of soil boron act additively.

<i>Bo1</i> (1082).	v: Halberd <i>Bo2 Bo3</i> .
<i>Bo2</i> (1082).	v: (W1*MMC). Warigal <i>Bo3</i> . Halberd <i>Bo1 Bo3</i> .
<i>Bo3</i> (1082).	v: Warigal <i>Bo2</i> . Halberd <i>Bo1 Bo2</i> .

Very sensitive genotype : Kenya Farmer *bo1 bo2 bo3*.

DNA Markers

Group 1L

XEm-1A,B,D (1122). p10-15.

Group 1

<i>XksuD3-1D</i> (1133).	pTtksuD3.	v: CS.
<i>XksuD16-1,5D</i> (1133).	pTtksuD16.	v: CS (1D). dv: <i>Ae. squarrosa</i> (5D).
<i>XksuD49-1D</i> (1133).	pTtksuD49.	v: CS.
<i>XksuG40-1D</i> (1133).	pTtksuG40.	v: CS.
<i>XksuI23-1D</i> (1133).	pTtksuI23.	v: CS.
<i>XksuM88-1D</i> (1133).	pTtksuM88.	v: CS.
<i>Xadh3'-1D</i> (1133).	padh3'.	v: CS.

Group 2L

<i>XksuD22-2D</i> (1133).	pTtksuD22.	v: CS.
<i>XksuD23-2D</i> (1133).	pTtksuD23.	v: CS.

Group 2

<i>XksuA2-2D</i> (1133).	pTtksuA2.	v: CS.
<i>XksuB3-2D</i> (1133).	pTtksuB3.	v: CS.
<i>XksuC3-2D</i> (1133).	pTtksuC3.	v: CS.
<i>XksuD8-2D</i> (1133).	pTtksuD8.	v: CS.
<i>XksuD18(A)-2,4D</i> (1133).	pTtksuD18.	v: CS (2D). dv: <i>Ae. squarrosa</i> (4D).
<i>XksuD18(B)-2D</i> (1133).	pTtksuD18.	v: CS.
<i>XksuF19-2,6D</i> (1133).	pTtksuF19.	v: CS (2D). dv: <i>Ae. squarrosa</i> (6D).
<i>XksuF41-2D</i> (1133).	pTtksuF41.	v: CS.
<i>XksuG5-2D</i> (1133).	pTtksuG5.	v: CS.

Group 3S

<i>XksuB8-3D</i> (1133).	pTtksuB8.	v: CS.
<i>XksuD19-3D</i> (1133).	pTtksuD19.	v: CS.

Group 3

<i>XksuD4-3D</i> (1133).	pTtksuD4.	v: CS.
<i>XksuD7-3,7D</i> (1133).	pTtksuD7.	v: CS (3D). dv: <i>Ae. squarrosa</i> (7D).
<i>XksuD24-3D</i> (1133).	pTtksuD24.	v: CS.
<i>XksuD45-3D</i> (1133).	pTtksuD45.	v: CS.
<i>XksuF28-3D</i> (1133).	pTtksuF28.	v: CS.
<i>XksuG45-3D</i> (1133).	pTtksuG45.	v: CS.

<i>XksuH2-3D</i> (1133).	pTtksuH2.	v: CS.
<i>XksuM9L-3D</i> (1133).	pTtksuM9L.	v: CS.
<i>Xp300-3D</i> (1133).	pP300.	v: CS.
Group 4S		
<i>Xpsr110-4A*</i> (1125) <i>4B*,D</i> (999).	PSR110.	v: CS.
Group 4L		
<i>Xpsr104-4A*</i> (1125) <i>4B*,D</i> (999).	PSR104.	v: CS.
Group 4		
<i>XksuB5-4D</i> (1133).	pTtksuB5.	v: CS.
<i>XksuC2-4D</i> (1133).	pTtksuC2.	v: CS.
<i>XksuD21-4D</i> (1133).	pTtksuD21.	v: CS.
<i>XksuF43-4,5,6D</i> (1133).	pTtksuF43	v: CS (4D,5D).
[<i>XKsuF43(A)-6D</i> ,		dv: <i>Ae. squarrosa</i> (6D).
<i>XKsuF43(B)-4,5D</i> (1133)].		
<i>XksuF43(B)-4,5D</i> (1133).	pTtksuF43.	v: CS.
Group 5		
<i>XksuD42-5D</i> (1133).	pTtksuD42.	v: CS.
<i>XksuF43-4,5,6D</i> (1133).	pTtksuF43.	v: CS (4D,5D).
[<i>XKsuF43(A)-6D</i> ,	pTtksuF43.	dv: <i>Ae. squarrosa</i> (6D).
<i>XKsuF43(B)-4,5D</i> (1133)].		
<i>XksuM2-5D</i> (1133).	pTtksuM2.	v: CS.
<i>XksuM4-5D</i> (1133).	pTtksuM4.	v: CS.
<i>XksuM70-5D</i> (1133).	pTtksuM70.	v: CS.
<i>Nor-D3</i> .	pTa71.	v: CS.
Group 6S		
<i>XksuG44-5,6D</i> (1133).	pTtksuG44.	v: CS (6DS).
		dv: <i>Ae. squarrosa</i> (5D).
<i>XksuH3-6D</i> (1133).	pTtksuH3.	v: CS.
Group 6L		
<i>XksuD17-6D</i> (1133).	pTtksuD17.	v: CS.
Group 6		
<i>XksuB6-6D</i> (1133).	pTtksuB6.	v: CS.
<i>XksuD1-6D</i> (1133).	pTtksuD1.	v: CS.
<i>XksuD11-6D</i> (1133).	pTtksuD11.	v: CS.
<i>XksuF24-6,7D</i> (1133).	pTtksuF24.	v: CS.
<i>XksuM9S-5,6D</i> (1133).	pTtksuM9S.	v: CS (6D).
		dv: <i>Ae. squarrosa</i> (5D).
Group 7S		
<i>XksuA1-1D</i> (1133).	pTtksuA1.	v: CS.
Group 7L		
<i>XksuA5-7D</i> (1133).	pTtksuA5.	v: CS.
Group 7		
<i>XksuB7-7D</i> (1133).	pTtksuB7.	v: CS.
<i>XksuD6-7D</i> (1133).	pTtksuD6.	v: CS.
<i>XksuD10-7D</i> (1133).	pTtksuD10.	v: CS.

<i>XksuD25-7D</i> (1133).	pTtksuD25.	v: CS.
<i>XksuD46-7D</i> (1133).	pTtksuD46.	v: CS.
<i>XksuE7-7D</i> (1133).	pTtksuE7.	v: CS.
<i>XksuF2(A)-2,7D</i> (1133).	pTtksuF2.	v: CS (7D). dv: <i>Ae. squarrosa</i> (2D).
<i>XksuF2(B)-2,7D</i> (1133).	pTtksuF2.	v: CS (7D). dv: <i>Ae. squarrosa</i> (2D).
<i>XksuF2(C)-7D</i> (1133).	pTtksuF2.	v: CS.
<i>XksuF2(D)-2,7D</i> (1133).	pTtksuF2.	v: CS (7D). dv: <i>Ae. squarrosa</i> (2D).
<i>XksuF2(E)-2,7D</i> (1133).	pTtksuF2.	v: CS (7D). dv: <i>Ae. squarrosa</i> (2D).
<i>XksuF24-6,7D</i> (1133).	pTtksuF24.	v: CS.

Gametocidal Activity

Gametocidal genes, that may cause abortion of both male and female gametes, are expressed in the heterozygous or hemizygous condition. Gametes lacking the gametocidal allele abort. Some gametocidal genes have dysgenic effects including chromosome breakage, mutation and seed abnormality.

1. Gametocidal Genes

Gc1a (1306). *Gc* (1031). 2B (1306). i: CS*8/*Aegilops speltoides* ssp. *aucheri* (1081).
Gc1b (1306). 2B (1306). i: CS*8/*A. speltoides* ssp. *ligustica* (1306).

2. Suppressors of Gametocidal Genes

Igc1 (1304). 3B (1303). Causes suppression of the 3C chromosome gametocidal gene of *Ae. triuncialis*. This chromosome breakage (1303).
 alien gametocidal factor also promotes v: Norin 26 (1302, 1305). Nineteen wheats listed in 1302 and/or 1305.

Wheats lacking *Igc1*. Chinese Spring (1302, 1305). Forty wheats listed in 1302 and/or 1305.

Grass-Clump Dwarfness / Grass Dwarfness

Knott (1074) described a lethal dwarf condition controlled by a dominant gene closely linked with *Sr30* (chromosome 5D) in Webster and a complementary recessive gene in LMPG.

Phenotypes resembling grass clump dwarfs in hybrids carrying a 2BL.2RS translocation were reported by May and Appels (1308). The complementary gene(s) in wheat was not *D1*, *D2* or *D3*. The effect was suppressed at high temperature.

Hairy Glumes

Hg. Ref. 1073 presents evidence for multiple alleles in *T. monococcum*.

Hairy Node

Multiple alleles in *T. monococcum* (1073).

Hairy Leaf

Kuspira *et al.* (1073) provided evidence for at least three alleles at a *H1* locus in *T. monococcum*.

With the reversal of chromosome designations for 4A and 4B, this locus in *T. monococcum* cannot be allelic with the gene *T. aestivum*.

Height

Reduced Height

Rht1

v: list in 1301, 1098.

Rht2

v: list in 1301, 1098.

Hybrid Weakness

1. Progressive Necrosis

Lists appear in 1080, 1091, 1092, 1096.

2. Hybrid Chlorosis

List appears in 1091.

Ner1.

5RL (1100).

Ner2.

7RL (1100).

Proteins

Enzymes

I. Acid phosphatase

Add to note,

....*intermedium* (168) "and chromosome E of *Ae. umbellulata* (1131). Two loci on 7R separated by 25 ± 5.2 cM were reported (1127)".

III. Aminopeptidase

Amp-R2.

Change location from '4RL (991)' to '4R (991), 4RS (1112).'

VI. Endopeptidase

Ep-D1b.

v: Hyak (1086); Madsen (1087).

Add after *Ep-VI*:

"*Ep-H¹I* (1128).

7H¹p (1128).

ad: CS/*E.trachycaulus*".

VII. Esterase

1. Delete reference 453 from *Est-5* listings.

2. Add below *Est-D6b*:

"*Est-M6* (986).

2MS (986).

su: CS/*Ae.comosa*.

EST-7 are monomeric isozymes extractable from green tissues (1123).

Est-A7 (1123).

2AL (1123).

v: CS.

Est-B7 (1123).

2BL (1123).

v: CS.

Est-D7 (1123).

2DL (1123).

v: CS.

Est-D7a (1123).

v: CS.

Est-D7b (1123).

v: Synthetic (IPSR 1190903).

Est-H7 (1123).

2HL (1123).

ad: CS/Betzes.

Est-R7 (1123).

2RL (1123).

ad: CS/Imperial,

su: Holdfast/King II.

Est-R^m7 (1123).

2R^ma (1123).

ad: CS/*S.montanum*.

Est-U7 (1123).

2U (1123).

ad: CS/*Ae.umbellulata*.

<i>Est-E7</i> (1123).	2E (1123).	ad: CS/ <i>Ag.elongatum</i> .
<i>Est-V7</i> (1123).	2V (1123).	ad: CS/ <i>D.villosa</i> .

A group of leaf esterase isozymes were found to be controlled by the long arms of the homoeologous group 3 chromosomes (453). The relationship of these esterases to EST-2 and to the leaf esterases designed EST-6 reported in 1124 has not been determined."

VIII. Glucosephosphate isomerase

Add after *Gpi-D1b*:

"Varietal differences in GPI zymograms are noted in 1129".

IX. Glutamic oxaloacetic transaminase

Add after *Got-V2*:

" <i>Got-H¹2</i> (1128).	6H ¹ (1128).	ad: CS/ <i>E.trachycaulus</i> ."
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XVII. Shikimate dehydrogenase

<i>Skdh-H¹1</i> (1128).	5H ¹ (1128).	ad: CS/ <i>E.trachycaulus</i> ."
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XXI. Aconitase

Add note after *Aco-D1*:

"Further alleles at *Aco-A1* and *Aco-B1* are listed in 1129; these have not been tested against those found in 807".

Add after *Aco-B2*:

<i>Aco-B2a</i> (942).	v: CS.
<i>Aco-B2b</i> (942).	v: PI 278437.
<i>Aco-B2c</i> (942).	v: PI 182575.
<i>Aco-B2d</i> (942).	v: PI 157589.

XXII. NADH dehydrogenase

Change *Ndh-A1* entry to:

Ndh-A1 [243](1128). [*Ndh-B1* (243)]. 4AL*(243).v: CS.

Add after *Ndh-A1c*:

<i>Ndh-A1d</i> [1128].	[<i>Ndh-A1b</i> (1128)].	v: Hope, Timgalen.
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Add to <i>Ndh-H1</i>	4HS (1125).	
<i>Ndh-H^{ch}1</i> (1125).	4H ^{ch} (1125).	ad: CS/ <i>H.chilense</i> .
<i>Ndh-R1</i> (1125).	4RS (1125)	ad: CS/Imperial, King II.
<i>Ndh-S4</i> (1125).	4S ¹ (1125).	ad: CS/ <i>Ae.longissima</i> .

<i>Ndh-A2</i> (1125).	7A (1125).	v: Hope.
<i>Ndh-D2</i> (1125).	7DS (1125).	v: CS.
<i>Ndh-R2</i> (1125).	7RS (1125).	ad: CS/Imperial, CS/King II, Holdfast/King II(7R).

<i>Ndh-A3</i> (1125).	3AL(1125).	v: CS.
<i>Ndh-B3</i> (1125).	3BL (1125).	v: CS.
<i>Ndh-B3a</i> (1125).		v: CS.
<i>Ndh-B3b</i> (1125).		v: Carmen.

<i>Ndh-D3</i> (1125).	3DL (1125).	v: CS.
<i>Ndh-H3</i> (1125).	3HL (1125).	ad: CS/Betzes.
<i>Ndh-R3</i> (1125).	6RL (1125).	ad: Holdfast/King II, CS/Imperial(6R), CS/King II(6R).
<i>Ndh-S¹3</i> (1125).	3S ¹ L (1125).	ad: CS/ <i>Ae.longissima</i> . ad: CS/ <i>Ag.sharonesis</i> (3S ¹).
<i>Ndh-A4</i> (1125).	3AS (1125).	v: CS.
<i>Ndh-B4</i> (1125).	3BS (1125).	v: CS.
<i>Ndh-H4</i> (1125).	3HS (1125).	ad: CS/Betzes, CS/King II.
<i>Ndh-E4</i> (1125).	3ES (1125).	ad: CS/ <i>Ag.elongatum</i> .
<i>Ndh-R4</i> (1125).	3RS (1125).	ad: CS/King II, CS/Imperial (3R).

XXV. Adenylate kinase

<i>Adk-A1</i> (1121).[<i>Adk-a</i> (1121)].	7AL (1121).	v: CS.
<i>Adk-B1</i> (1121).[<i>Adk-b</i> (1121)].	7BL (1121).	v: CS.
<i>Adk-D1</i> (1121).[<i>Adk-d</i> (1121)].	7DL (1121).	v: CS.
<i>Adk-H1</i> (1121).	7H (1121).	ad: CS/Betzes.
<i>Adk-R1</i> (1121).	7RL (1121).	ad: CS/Imperial, Holdfast/King II.
<i>Adk-E1</i> (1121).	7E (1121).	ad: CS/ <i>E.elongatum</i> .
<i>Adk-U1</i> (1121).	E (1121).	ad: CS/ <i>Ae.umbellulata</i> .
<i>Adk-Agⁱ</i> (1121).	7Ag ⁱ (1121).	ad: CS/ <i>Ag.intermedium</i> .

Endosperm storage proteins

I. Glutenins

After preamble, add:

A first attempt at assigning alleles at the *Glu-1-1* and *Glu-1-2* loci is provided. This list is derived directly, and uncritically, from the *Glu-1* lists, and, as such, does not have references appended this year. Comments on the list are welcome.

Add to *Glu-A1* list:

Glu-A1r [1101]. 39+40 [1101]. i: *T. thaouidar* accession IPSR 1020006/6*Sicco.

Glu-A1s (1110). 41+42 (1110). i: *T. thaouidar* accession G3152/6*Sicco.

Correction to *Glu-B1* list:

Subunits encoded by *Glu-B1g* should be numbered 13+19, not 3+19.

In *Glu-B1* list, replace variety Norstar with variety Owens as prototype for *Glu-B1u*.

In *Glu-D1* list, note Flinor is the prototype variety for *Glu-D1q* encoding subunits 2+11. Flinor was formerly given as the prototype variety for *Glu-D1e* encoding subunits 2+10. A new prototype for *Glu-D1e* will be provided next year.

Add to *Glu-B1* list:

<i>Glu-B1ak</i> (1109).	7*+8* (1109).	v: Norstar.
<i>Glu-B1al</i> (1109).	7+8* (1109).	v: Glenlea.
<i>Glu-B1am</i> [1102].	18 (1102).	v: Royo.
<i>Glu-B1an</i> [1102].	6 (1102).	v: BG-2013.
<i>Glu-B1ao</i> [1102].	7+16 (1102).	v: BG-3545.
<i>Glu-B1ap</i> [1102].	30+31 (1102).	v: Marinar.
<i>Glu-B1aq</i> [1102].	32+33 (1102).	v: BG-1943.
<i>Glu-B1ar</i> [1102].	34+35 (1102).	v: Jeja Almendros.

<i>Glu-B1as</i> [1102].	13 (1102).	v: PI 348435.
<i>Glu-B1-1o.</i>		v: Supreza, Canada.
<i>Glu-B1-1p.</i>		v: Mondor.
<i>Glu-B1-1q.</i>		tv: Canoco de Grao Escuro, Portugal, <i>T. turgidum</i> .
<i>Glu-B1-1r.</i>		tv: Tremez Mollez, Portugal, <i>T. durum</i> .
<i>Glu-B1-1s.</i>		tv: Quaduro, Italy, <i>T. durum</i> .
<i>Glu-B1-1t.</i>		tv: Athena, Italy, <i>T. durum</i> .
<i>Glu-B1-1u.</i>	26.	v: Cologne 1.
<i>Glu-B1-1v.</i>	28.	v: Forlani.
<i>Glu-B1-1w.</i>	null.	v: Olympic mutant.
<i>Glu-B1-1x.</i>	30.	v: Mariñar.
<i>Glu-B1-1y.</i>	32.	v: BG-1943.
<i>Glu-B1-1z.</i>	34.	v: Jeja Almedros.
<i>Glu-B1-1aa.</i>	37.	v: Shedraya Polesja.
<i>Glu-B1-2.</i>		
<i>Glu-B1-2a.</i>	8.	v: CS.
<i>Glu-B1-2b.</i>	9.	v: Bezostaya 1.
<i>Glu-B1-2c.</i>	16.	v: Lancota.
<i>Glu-B1-2d.</i>	19.	v: NS 335.
<i>Glu-B1-2e.</i>	15.	v: Sappo.
<i>Glu-B1-2f.</i>	18.	v: Gabo.
<i>Glu-B1-2g.</i>	22.	v: Serbian.
<i>Glu-B1-2h.</i>	24.	v: Spica D.
<i>Glu-B1-2i.</i>		tv: PI 355505, Germany, <i>T. dicoccum</i> .
<i>Glu-B1-2j.</i>		tv: PI 352354, Ethiopia, <i>T. dicoccum</i> .
<i>Glu-B1-2k.</i>		tv: PI 94633, Morocco, <i>T. dicoccum</i> .
<i>Glu-B1-2l.</i>	11.	v: BT-2288.
<i>Glu-B1-2m.</i>		v: Supreza, Canada.
<i>Glu-B1-2n.</i>		v: Mondor.
<i>Glu-B1-2o.</i>	8*.	v: Dawbull.
<i>Glu-B1-2p.</i>		tv: Canoco de Grao Escuro, Portugal, <i>T. turgidum</i> .
<i>Glu-B1-2q.</i>		tv: Tremez Mollez, Portugal, <i>T. durum</i> .
<i>Glu-B1-2r.</i>		tv: Quaduro, Italy, <i>T. durum</i> .
<i>Glu-B1-2s.</i>	18*.	v: David.
<i>Glu-B1-2t.</i>	27.	v: Cologne 1.
<i>Glu-B1-2u.</i>	29.	v: Forlani.
<i>Glu-B1-2v.</i>	null.	v: Olympic mutant.
<i>Glu-B1-2w.</i>	31.	v: Mariñar.
<i>Glu-B1-2x.</i>	33.	v: BG-1943.
<i>Glu-B1-2y.</i>	35.	v: Jeja Almedros.
<i>Glu-D1-1.</i>		
<i>Glu-D1-1a.</i>	2.	v: CS.
<i>Glu-D1-1b.</i>	3.	v: Hobbit.
<i>Glu-D1-1c.</i>	4.	v: Champlein.
<i>Glu-D1-1d.</i>	5.	v: Hope.
<i>Glu-D1-1e.</i>	2.2.	v: Danchi.
<i>Glu-D1-1f.</i>	null.	v: Nap Hal, Nepal.
<i>Glu-D1-1g.</i>	2.1.	v: AUS 14653, Afghanistan.
<i>Glu-D1-1h.</i>	2.3.	v: PI 348465.
<i>Glu-D1-1i.</i>	38.	v: Leningradka.

<i>Glu-D1-2.</i>		
<i>Glu-D1-2a.</i>	12.	v: CS.
<i>Glu-D1-2b.</i>	10.	v: Hope.
<i>Glu-D1-2c.</i>	9.	v: BT-2288.
<i>Glu-D1-2d.</i>	null.	v: Nap Hal, Nepal.
<i>Glu-D1-2e.</i>	12*.	v: Tudest.
<i>Glu-D1-2f.</i>	13.	v: AUS 14519, <i>T. macha</i> .
<i>Glu-D1-2g.</i>	36.	! Iranian landrace accession 3048/5*Sicco.
<i>Glu-D1-2h.</i>	11.	v: Flinor.

Add:

Glu-H¹1 (1128). 1H^tq (1128). ad: CS/*E.trachycaulum*.

After *Glu-A3*, insert:

<i>Glu-A3a</i> (1105).		v: CS.
<i>Glu-A3b</i> (1105).		v: Gabo.
<i>Glu-A3c</i> (1105).		v: Cheyenne.
<i>Glu-A3d</i> (1105).		v: Capelle Desprez, Orca.
<i>Glu-A3e</i> (1105).		v: Hope, Insignia.
<i>Glu-A3f</i> (1105).		v: Rescue.

After *Glu-B3*, insert:

<i>Glu-B3a</i> (1105).		v: CS.
<i>Glu-B3b</i> (1105).		v: Gabo, Timstein, Hope.
<i>Glu-B3c</i> (1105).		v: Insignia, Halberd.
<i>Glu-B3d</i> (1105).		v: Orca.
<i>Glu-B3e</i> (1105).		v: Cheyenne.
<i>Glu-B3f</i> (1105).		v: Radja.
<i>Glu-B3g</i> (1105).		v: Kharkov, Bungulla.
<i>Glu-B3h</i> (1105).		v: Thatcher, Rescue.
<i>Glu-B3i</i> (1105).		v: Norin-61.
<i>Glu-B3j</i> (1106).		tv: Duramba-B, Duramba-D, Langdon.
<i>Glu-B3k</i> (1106).		tv: ALP-153, Dural, Durati, Edmore.
<i>Glu-B3l</i> (1106).		tv: Gionp-1954.

After *Glu-D3*, insert:

<i>Glu-D3a</i> (1105).		v: CS.
<i>Glu-D3b</i> (1105).		v: Gabo.
<i>Glu-D3c</i> (1105).		v: Insignia, Capelle Desprez.
<i>Glu-D3d</i> (1105).		v: Norin-61A.
<i>Glu-D3e</i> (1105).		v: Orca, Thatcher.

<i>Glu-E3</i> [1107].	1ES (1107).	su: CS/ <i>E. elongata</i> .
<i>Glu-S¹3</i> [1107].	1S ¹ (1107).	su: CS/ <i>T. longissimum</i> .
<i>Glu-U3</i> [1107].	1U (1107).	su: CS/ <i>T. umbellulatum</i> .

II. Gliadins

After preamble, add:

Variation at the *Gli-1* loci was described earlier (321, 491, 566) and applied in mapping experiments (617, 565, 108, 200, 558). A rational system of naming the alleles was produced by E.V. Metakovsky, N.I. Vavilov Institute of General Genetics, Moscow (1108). This nomenclature

is reproduced below. Where two varieties are given as prototypes for an allele, the first named is from the USSR and the second from elsewhere.

After *Gli-A1*, insert:

<i>Gli-A1a</i> (1108).	v: CS.
<i>Gli-A1b</i> (1108).	v: Bezostaya 1, Mercia.
<i>Gli-A1c</i> (1108).	v: Ukrainka.
<i>Gli-A1d</i> (1108).	v: Dankowska.
<i>Gli-A1e</i> (1108).	v: Falchetto.
<i>Gli-A1f</i> (1108).	v: Mironovskaya 808, Maris Freeman.
<i>Gli-A1g</i> (1108).	v: Gabo.
<i>Gli-A1h</i> (1108).	v: Sadovo I.
<i>Gli-A1i</i> (1108).	v: Saratovskaya 36.
<i>Gli-A1j</i> (1108).	v: Lutescens 62.
<i>Gli-A1k</i> (1108).	v: Skala.
<i>Gli-A1l</i> (1108).	v: Lesostepka 75.
<i>Gli-A1m</i> (1108).	v: Marquis.
<i>Gli-A1n</i> (1108).	v: Intensivnaya.
<i>Gli-A1o</i> (1108).	v: Odesskaya 16, Riband.
<i>Gli-A1p</i> (1108).	v: Pyrotrix 28.
<i>Gli-A1q</i> (1108).	v: Akmolinka 1.
<i>Gli-A1r</i> (1108).	v: Rannaya 73.

After *Gli-B1*, insert:

<i>Gli-B1a</i> (1108).	v: CS.
<i>Gli-B1b</i> (1108).	v: Bezostaya 1, Gabo.
<i>Gli-B1c</i> (1108).	v: Siete Cerros 66.
<i>Gli-B1d</i> (1108).	v: Dneprovskaya 521, Falchetto.
<i>Gli-B1e</i> (1108).	v: Lutescens 62.
<i>Gli-B1f</i> (1108).	v: Maris Freeman.
<i>Gli-B1g</i> (1108).	v: Galahad.
<i>Gli-B1h</i> (1108).	v: Krasnodonka.
<i>Gli-B1i</i> (1108).	v: Insignia.
<i>Gli-B1j</i> (1108).	v: Cluj 650.
<i>Gli-B1k</i> (1108).	v: Kremena.
<i>Gli-B1l</i> (1108).	v: Dukat.
<i>Gli-B1m</i> (1108).	v: Pyrotrix 28.
<i>Gli-B1n</i> (1108).	v: Intensivnaya.
<i>Gli-B1o</i> (1108).	v: Levent.
<i>Gli-B1p</i> (1108).	v: New Pusa 834.

After *Gli-D1*, insert:

<i>Gli-D1a</i> (1108).	v: CS.
<i>Gli-D1b</i> (1108).	v: Bezostaya 1, Mercia.
<i>Gli-D1c</i> (1108).	v: Skorospelka Uluchshennaya (biotype).
<i>Gli-D1d</i> (1108).	v: Solo.
<i>Gli-D1e</i> (1108).	v: Gerek.
<i>Gli-D1f</i> (1108).	v: Maris Freeman.
<i>Gli-D1g</i> (1108).	v: Mironovskaya 808, Ghurka.
<i>Gli-D1h</i> (1108).	v: Sadovo I.
<i>Gli-D1i</i> (1108).	v: Zelinogradka, Insignia.
<i>Gli-D1j</i> (1108).	v: Promin.
<i>Gli-D1k</i> (1108).	v: Kremena.

Gli-D11 (1108).

v: Longbow.

After *Gli-A2*, insert:

Gli-A2a (1108).

v: CS.

Gli-A2b (1108).

v: Bezostaya 1.

Gli-A2c (1108).

v: Siete Cerros 66.

Gli-A2d (1108).

v: Dneprovskaya 521.

Gli-A2e (1108).

v: Sadovo 1.

Gli-A2f (1108).

v: Maris Freeman.

Gli-A2g (1108).

v: Ducat.

Gli-A2h (1108).

v: Hereward.

Gli-A2i (1108).

v: Lesostepka 75.

Gli-A2j (1108).

v: Cluj 650.

Gli-A2k (1108).

v: Skala.

Gli-A2l (1108).

v: Longbow.

Gli-A2m (1108).

v: Marquis.

Gli-A2n (1108).

v: Mironovskaya 808.

Gli-A2o (1108).

v: Ducat.

Gli-A2p (1108).

v: Pliska.

Gli-A2q (1108).

v: Saratovskaya 39.

Gli-A2r (1108).

v: Riband.

Gli-A2s (1108).

v: Saratovskaya 36.

Gli-A2t (1108).

v: Tarasovskaya 2 (biotype).

Gli-A2u (1108).

v: Kirgizskaya Yubileinaya.

Gli-A2v (1108).

v: Kzyl-Bas.

Gli-A2w (1108).

v: Bezenchukskaya 98.

Gli-A2x (1108).

v: Solo.

After *Gli-B2*, insert:

Gli-B2a (1108).

v: CS.

Gli-B2b (1108).

v: Bezostaya 1, Kremena.

Gli-B2c (1108).

v: Siete Cerros 66.

Gli-B2d (1108).

v: Tselinnaya 20.

Gli-B2e (1108).

v: Lesostepka 75.

Gli-B2f (1108).

v: Maris Freeman.

Gli-B2g (1108).

v: Galahad.

Gli-B2h (1108).

v: Sadovo 1.

Gli-B2i (1108).

v: Insignia.

Gli-B2j (1108).

v: Cluj 650.

Gli-B2k (1108).

v: Skala.

Gli-B2l (1108).

v: Longbow.

Gli-B2m (1108).

v: Mironovskaya 808.

Gli-B2n (1108).

v: Solo.

Gli-B2o (1108).

v: Odesskaya 16.

Gli-B2p (1108).

v: Pliska.

Gli-B2q (1108).

v: Saratovskaya 39.

Gli-B2r (1108).

v: Omskaya 12.

Gli-B2s (1108).

v: Saratovskaya 36.

Gli-B2t (1108).

v: Tselinogradka.

Gli-B2u (1108).

v: Kirgizskaya Yubileinaya.

Gli-B2v (1108).

v: Poljarka.

After *Gli-D2*, insert:

<i>Gli-D2a</i> (1108).	v: CS.
<i>Gli-D2b</i> (1108).	v: Bezostaya 1, Levent (biotype).
<i>Gli-D2c</i> (1108).	v: Siete Cerros 66.
<i>Gli-D2d</i> (1108).	v: Dneprovskaya 521.
<i>Gli-D2e</i> (1108).	v: Mironovskaya 808.
<i>Gli-D2f</i> (1108).	v: Kirgizskaya Yubileinaya, Falchetto.
<i>Gli-D2g</i> (1108).	v: Ghurka.
<i>Gli-D2h</i> (1108).	v: Ducat.
<i>Gli-D2i</i> (1108).	v: Insignia.
<i>Gli-D2j</i> (1108).	v: Promin.
<i>Gli-D2k</i> (1108).	v: Skala.
<i>Gli-D2l</i> (1108).	v: Condor.
<i>Gli-D2m</i> (1108).	v: Marquis.
<i>Gli-D2n</i> (1108).	v: Mercia.
<i>Gli-D2o</i> (1108).	v: Omskaya 12.
<i>Gli-D2p</i> (1108).	v: New Pusa 834.
<i>Gli-D2q</i> (1108).	v: Volshebnitsa (biotype).
<i>Gli-D2r</i> (1108).	v: Kremena.
<i>Gli-D2s</i> (1108).	v: Bezenchukskaya 98.

In notes before *Gli-Ap¹*, delete the sentence beginning 'The complexity....' and change 'Nevertheless', to 'Elsewhere' in the next sentence.

Add:

Gli-H¹ (1128). 1H¹p (1128). ad: CS/*E.trachycaulum*.

After *Gli-B3*, insert:

<i>Gli-B3a</i> [200, 297, 562].	v: CS.
<i>Gli-B3b</i> [297].	v: Sicco.
<i>Gli-B3c</i> [200, 562].	s: CS/Thatcher.

4. Protease inhibition

Immediately below "4. Protease inhibition," add "Trypsin inhibitor" as title for *Ti* section. Below *Ti-U2*, delete the paragraph that begins "In barley, in addition to *Ti-H1*" and ends ". . . addition lines (255)" and add:

Subtilisin inhibitor:

<i>Si-R1</i> [255].	2R(255);2RS(1126).	ad: CS/Imperial, Holdfast/KII.
<i>Si-H1</i> (254). [<i>Isa 1</i> (254)].	2H (254).	ad: CS/Betzes.
<i>Si-B2</i> (1126).	1BS (1126).	su: Bersee (Koga II).
<i>Si-D2</i> (1126).	1DS (1126).	v: Koga II.
<i>Si-R2</i> [255](1126).	1R(255);1RS(1126).	ad: CS/Imperial (255).
		tr: Gabo 1BL.1RS (1126).
<i>Si-H2</i> [254](1126).		
[<i>Ica 1</i> , <i>Ica 2</i> (254)]	1H (254).	ad: CS/Betzes.
<i>Si-U2</i> (1126).	1U (1126).	ad: CS/ <i>Ae.umbellulata</i> .
<i>Si-S²</i> (1126).	1S ¹ (1126).	ad: CS/ <i>Ae.longissima</i> .

Considerable varietal variation for *Si-2* was noted in 1126. A location for *Si-H2* on 1HL was inferred in 254 but questioned in 1126.

Other Proteins

Ribosomal RNA

5S rRNA genes: 5S DNA loci

Within the Triticeae there are basically two loci for 5S DNA. One locus identified by repetitive units 320–468 bp in length is located on group 1 chromosomes. The other locus identified by repetitive units 469–500 bp in length is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

<i>SSDna-A1</i> (1076).	1AS (1076).	dv: <i>T. monococcum</i> .
<i>SSDna-B1</i> (1076).	1BS (29, 1076).	v: Chinese Spring.
[<i>5S-Rrna-B1</i> (938)].		
<i>SSDna-D1</i> (1076).	1D (1076, 1077).	v: Chinese Spring (1076, 1077).
	1DS (1076).	dv: <i>T. tauschii</i> (1077).
<i>SSDna-E1</i> (1097).	1E (1097).	dv: <i>L. elongatum</i> .
<i>SSDna-R1</i> (1078).	1RS (29, 1078)	al: <i>S. cereale</i> .
[<i>5S-Rrna-R1</i> (938)].		
<i>SSDna-S²I</i> .	1S ^c (1097).	al: <i>Elymus ciliaris</i> .
<i>SSDna-S⁴I</i> .	1S ^t (1097).	al: <i>E. trachycaulus</i> .
<i>SSDna-Y1</i> .	1Y (1097).	al: <i>E. ciliaris</i> .
<i>SSDna-A2</i> (1076).	5AS (1076).	v: Chinese Spring. al: <i>T. monococcum</i> .
		v: Chinese Spring.
<i>SSDna-B2</i> (1076).	5BS (1076).	v: Chinese Spring (1076, 1077).
<i>SSDna-D2</i> (1076).	5D (1076, 1077).	dv: <i>T. tauschii</i> (1077).
	5DS (1077).	dv: <i>T. tauschii</i> (1077).
<i>SSDna-R2</i> (1078).	5RS (1078).	al: <i>S. cereale</i> .
<i>SSDna-H²2</i> (1078).	5H ^t (1097).	al: <i>E. trachycaulus</i> .
<i>SSDna-U2</i> (1076).	5U (1076).	al: <i>T. umbellulatum</i> .
<i>SSDna-V2</i> (1097).	5V (1097).	al: <i>D. villosa</i> .

A single 5S rRNA hybridisation site was observed in barley. The chromosome involved was not one of those identified by the presence of secondary constrictions (29), but Kolchinsky *et al.* (1084) located a predominant short repetitive sequence (320bp) to 2H.

Reaction to *Erysiphe graminis*

<i>Pm3a</i> .	v: Coker 797 (1307); Florida 301 (1307); Florida 302 (1307); Saluda (1307).
<i>Pm5</i> .	v: Caldwell (1307); Ga 1123 (1307); Hardired (1307). Arthur <i>Pm6</i> (1307); Coker 983 <i>Pm6</i> (1307); Double Crop <i>Pm6</i> (1307).
<i>Pm6</i> .	v: Abe (1037); Coker 747 (1307); Oasis (1307). Arthur <i>Pm5</i> (1307); Coker 983 <i>Pm5</i> (1307);
Double Crop <i>Pm5</i> (1307).	
Chancellor used as a susceptible genetic background for a near-isogenic series probably carries <i>Pm10</i> and <i>Pm15</i> (1090).	
<i>Mli</i> is probably identical to <i>Pm5</i> (1095).	

Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Disease : Septoria tritici blotch

- Stb1.* *Sib1* (1089). v: Bulgaria 88 (1089); Oasis (1089); Sullivan (1089).
Stb2. *Sib2* (1089). v: Nova Prata (1089); Veranopolis (1089).
Stb3. *Sib3* (1089) v: Israel 493 (1089).
Stb4 (1083). v: Cleo (1083); Tadinia (1083); Tadorna (1083).

Stb4 segregated independently of *Stb1* but its relationship with *Stb2* and *Stb3* is unknown.

Reaction to *Pseudocercospora herpotrichoides*

- Pch.* v: Hyak (1086); Madsen (1087).

Eyespot resistance and *Ep-A1b* in chromosome 7A were genetically associated (1093).

Reaction to *Puccinia graminis*

- Sr11.* v: Prospect *SrWld* (1094).
Sr38 (1088). 2AS (1088). v: See *Lr37*. RL6081 will carry additional genes from Thatcher.
SrWld (612). v: Prospect *Sr11* (1099).

Reaction to *Puccinia recondita*

- Lr33.* v: Others (1094).
Lr34. v: Others (1094).
Lr35 (1071). 2B (1071). v: RL5711 (1071).
Lr36. 6BS (1072). v: Line 2-9-2, Line E84018.
Lr37 (1088). 2AS (1088). al: *Aegilops speltoides* Popn.2.
i: RL6081 = Tc*/VPM1 (454).
v: Hyak (1086); Madsen (1087); Rendezvous (1088). VPM1 (1088); VPM1 derivatives (454).

Lr37 is recognised in seedlings at low temperatures (17C) and is highly effective in adult plants under field conditions.

Complex genotype : Prospect *Lr1 Lr2a Lr10 Lr13* (1099).

Reaction to *Puccinia striiformis*

- Yr17* (1088). 2AS (1088). v: See *Lr37*. RL6081 probably carries *Yr7*.

Resistance to Colonisation by *Eriophyes tulipae*

- Cmcl.* 6DS (1079).

Genetic Linkages

- 1R
Sec 1 - Sec 3 36.0 ± 4.6% (394)
40.8 ± 3.76% (688)
36.03 ± 4.12% (1075)

Sr38, *Lr37* and *Yr17* were closely linked in coupling and showed close repulsion linkage with *Lr17* (1088).

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Proposal

In the International Symposium of Cytoplasmic Engineering in Wheat held in July, 1991 at Sapporo, Japan, the following proposal for nomenclature of genetic symbols for cytoplasmic genomes in *Triticum* and *Aegilops* was presented by Dr. Koichiro Tsunewaki, Kyoto University. The editorial board of WIS would like to call wheat researchers to discuss on this proposal. Articles for or against this proposal will be welcomed by WIS.

Genome, plasmon, plastome, and chondriome designation for *Triticum* and *Aegilops* species
Koichiro Tsunewaki (July, 1991)

Species	Code	Genome		Plasmon		Plastome		Chondriome	
		Pre-vious ¹	Pro-posed ²	Pre-vious ³	Pro-posed	Pre-vious ⁴	Pro-posed	Pre-vious ⁵	Pro-posed
<i>boeoticum</i>	01	A	A	A	A	1a	1	—	—
<i>monococcum</i>	16	A	A	A	A	1a	1	—	—
<i>dicoccoides</i>	21	AB	AB	B	B	7	7	VIIb	VIIb
<i>dicoccum</i>	22	AB	AB	B	B	7	7	VIIa	VIIa
<i>durum</i>		AB	AB	B	B	7	7	VIIa	VIIa
<i>spelta</i>	52K	ABD	ABD	B	B	7	7	VIIb	VIIb
<i>aestivum</i>	52C	ABD	ABD	B	B	7	7	VIIa	VIIa
" (<i>tibetanum</i>)	58	ABD	ABD	B	B	7	7	VIIa	VIIa
<i>caudata</i>	02,27	C	C	C	C	2a	2a	—	II
"	—	C	C	—	—	—	2b	—	—
<i>triuncialis</i>	38	C ^u C	UC	C	C	2a	2a	—	—
"	39	C ^u C	UC	—	—	2b	2b	—	—
<i>umbellutata</i>	03	C ^u	U	C ^u	U	3	3	IIIa	IIIa
<i>triuncialis</i>	26	C ^u C	UC	C ^u	U	3	3	IIIb	IIIb
<i>biuncialis</i>	29, 37	C ^u M ^b	UM	C ^u	U	3	3	IIIb	IIIb
<i>triaristata</i> 4x	32	C ^u M ^f	UM	C ^u	U	3	3	IIIc	IIIc
" 6x	54, 57	C ^u M ^f M ^h	UMN	C ^u	U	3	3	IIIc	IIIc
<i>columnaris</i>	30	C ^u M ^c	UM	C ^{u2}	U ²	3	3	IIIId	IIIId
<i>squarrosa</i>	04, 19	D	D	D	D	9a	9a	IX	IX
<i>ventricosa</i>	36	DM ^v	DN	D	D	9a	9a	—	—
<i>cylindrica</i>	28	CD	CD	D	D	9b	9b	—	—
<i>crassa</i> 4x	35	DM ^{cr}	DM	D ²	D ²	1d	16	—	XVI
" 6x	55	DD ² M ^{cr}	DDM	D ²	D ²	1d	16	—	—
<i>juvenalis</i>	53	C ^u DM ^j	DMJ	D ²	D ²	1d	16	—	—
<i>vavilovii</i>	56	DM ^{cr} SP	DMS	D ²	D ²	1d	16	—	—

<i>aucheri</i>	09	S	S	G	G	5	6	Va	VIa
<i>speltoides</i>	15	S	S	G	G	5	6	—	—
<i>araraticum</i>	23, 24	AG	AG	G	G	5	6	Vb	VIb
<i>timopheevi</i>	25	AG	AG	G	G	5	6	Va	VIa
<i>zhukovskiyi</i>	51	AAG	AAG	G	G	5	6	Va	VIa
<i>comosa</i>	05	M	M	M	M	11a	11	—	XI
<i>heldreichii</i>	06	M	M	M ^h	M ^h	11b	12	—	XII
<i>ovata</i>	31	C ^u M ^o	UM	M ^o	M ^o	6	5	—	V
<i>uniaristata</i>	07	M ^u	N	M ^u	N	10	10	—	X
<i>mutica</i>	13	Mt	T	Mt	T	4	4	IVa	IVa
"	14	Mt	T	Mt ²	T ²	4	4	IVb	IVb
<i>aucheri</i>	17	S	S	(S)	—	8	8	—	—
<i>speltoides</i>	08	S	S	S	S	8	8	VIII	VIII
<i>sharonensis</i>	10	S ¹	S ¹	S ¹	S ¹	1c	13	Ic	XIII
<i>bicornis</i>	12	S ^b	S ^b	S ^b	S ^b	1b	14a	Ib1	XIVa
<i>searsli</i>	18	S ^s	S ^s	S ^v	S ^v	1b	14b	Ib2	XIVb
<i>kotschyi</i>	33	C ^u S ^v	US	S ^v	S ^v	1b	14b	Ib3	XIVc
<i>variabilis</i>	34	C ^u S ^v	US	S ^v	S ^v	1b	14b	Ib3	XIVc
<i>longissima</i>	20	S ¹	S ¹	?	?	—	15(?)	?	?

- 1) Kihara (1951), Kihara and Tanaka (1970)
- 2) Kimber and Sears (1983), Kimber and Tsunewaki (1988)
- 3) Tsunewaki (1980)
- 4) Ogihara and Tsunewaki (1982, 1988)
- 5) Terachi and Tsunewaki (1966), Terachi et al. (1990)

Records

KIHARA MEMORIAL

INTERNATIONAL SYMPOSIUM ON CYTOPLASMIC ENGINEERING IN WHEAT

More than eighty wheat researchers from nine countries had attended to Kihara Memorial International Symposium on Cytoplasmic Engineering in Wheat (ISCEW) held on July 3-6, 1991 at Hokkaido University, Sapporo, Japan, under chairmanships of Drs. T. Kinoshita (Hokkaido Univ.) and T. Sasakuma (Kihara Inst.). The Symposium was an informative opportunity to discuss the comprehensive subjects of cytoplasmic inheritance, evolution, and its utilization for plant breeding.

The followings are the program of the Symposium, which include three special lectures and six sessions, the field trip to wheat research fields, in addition to Dr. H. Kihara memorial banquet in which a document film on his career was presented. The sessions were organized under free atmosphere with hot discussions. The proceedings will be published in the end of 1991 in the special issue of SEIKEN ZIHO.

Keynote Lecture

Progress of NC-heterosis studies in wheat

Chaired by Dr. M. Muramatsu

Dr. T. Kinoshita (Hokkaido Univ.)

Special Lecture

A historical review of cytoplasmic studies in wheat Dr. K. Tsunewaki (Kyoto Univ.)
mRNA editing and tRNA import in plant mitochondria

Dr. J. H. Weil (Univ. of L. Pasteur)

Nuclear and cytoplasmic control of anther culture response in wheat.

—Potential for use in breeding

Dr. C. F. Konzak (Washington St. Univ.)

Session I. ORGANELLAR GENOMES AND GENES

Chaired by Dr. M. Murata

I-1 Y. Ogihara (Kihara Inst.): Molecular structures and evolution of chloroplast genomes in *Triticinae*

I-2 Li Jigeng (Academia Sinica): Localization and sequence analysis of chloroplast DNA related to pollen fertility

I-3 T. Terachi (Kyoto Sangyo Univ.): Molecular evolution of mitochondrial genomes in *Triticum* and *Aegilops*

I-4 T. Mikami (Hokkaido Univ.): Mitochondrial gene mutations and cytoplasmic male sterility

I-5 L. Bonen (Univ. of Ottawa): Wheat mitochondrial protein-coding gene structure and expression

Session II. PLASMON DIVERSITY

Chaired by Dr. S. Tsuji

II-1 S. Maan (N. Dakota St. Univ.): Cytoplasmic variability in wheat revealed by nucleo-cytoplasm interactions

- II-2 I. Panayotov (Bulgaria Agr. Academy): The cytoplasm of *Triticinae* and wheat improvement
- II-3 A. Breiman (USDA): Variability of mitochondrial DNA in populations of putative ancestors of common wheat
- II-4 C. Nakamura (Kobe Univ.): Cytoplasmic variability in wheat and its related genera revealed by photosynthesis and respiration

Session III. ORIGIN OF POLYPLOID WHEATS Chaired by Dr. T. R. Endo

- III-1 K. Tsunewaki (Kyoto Univ.): Origin of polyploid wheats revealed by RFLP analysis
- III-2 J. Dvorak (Univ. of California): Do polyploid *Triticum* species have cytoplasm of their nuclear genome donors?
- III-3 B. S. Gill (Kansas St. Univ.): Experimental evidence for cytoplasmic specific introgression and its role in the evolution of polyploid wheats
- III-4 T. Kawahara (Kyoto Univ.): Cytogenetical aspects in the evolution of polyploid species of *Triticum* and *Aegilops*
- III-5 R. Appels (CSIRO): The structure, function and evolution of the group 1 chromosomes of wheat

Session IV. NUCLEUS-CYTOPLASMIC INTERACTIONS Chaired by Dr. J. Fujigaki

- IV-1 Y. Mukai (Osaka Kyoiku Univ.): Physical mapping of cytoplasm-specific nuclear genes in wheat
- IV-2 O. Davydenko (BSSR Academy): Cytoplasmic effect on expression of some morphological traits, transmission and mitotic recombination in allo and isoplasmic lines
- IV-3 Li Ji-Lin (Harbin Univ.): Cytogenetic study on crossing alloplasmic wheat
- IV-4 Y. Yasumuro (Tottori Univ.): Nucleo-cytoplasmic interactions in wheat-rye hybrids and their significance in triticale breeding and genome differentiation
- IV-5 N. Watanabe (Gifu Univ.): Is it possible to increase photosynthetic capacity of wheat utilizing cytoplasmic diversity?

Dr. Kihara Memorial Banquet at Pole Star Hotel

Welcome by Drs. M. Tanaka, M. Takahashi and Ms. Y. Kihara

Session V. WHEAT BREEDING —PROBLEMS AND NEW APPROACHES

Chaired by Drs. Y. Ogihara and H. Tsujimoto

- V-1 R. Allan (USDA): Potential for practical exploitation of alloplasmon in winter wheat breeding
- V-2 R. McIntosh (Univ. of Sydney): Alien sources of disease resistance in wheat
- V-3 K. Murai (Sumitomo Chemical Co.): Two-line system for hybrid wheat production using photoperiod-sensitive cytoplasmic male sterility
- V-4 K. Toriyama (Zen-no; NFACA): Trial of development of hybrid wheat using S^v cytoplasm and 1RS-1BL chromosome

V-6 T. Koba (Ishikawa Agr. Univ.): Chromosomal irregularities in barley-wheat hybrids and their backcrossed generations with wheat

Poster Session

- K. Mori (Hokkaido Univ.): Transfer of male sterile cytoplasm through asymmetrical fusion in rice
- I. Takamura (Hokkaido Univ.): The effect of *ovata* cytoplasm for expression of growth characters in NC-hybrid wheats
- T. M. Ikeda (Kyoto Univ.): Biochemical and molecular studies on mitochondria in four alloplasmic wheats showing growth abnormality
- S. Nasuda (Kyoto Univ.): Identification of the carrier chromosome arms and the position of centromere in the RFLP linkage maps of common wheat
- H. Tsujimoto (Yokohama City Univ.): DNA structure of rye B chromosome
- I. Ohtsuka (Kanagawa Univ.): Genetic analysis of the compatible relationship between tetraploid wheat genomes and *Ae. squarrosa* cytoplasm
- S. Matsubara (Ryokuei-Bio Co.): Transmission of D genome chromosomes in the progenies from pentaploid hybrids (AABB) under *Ae. squarrosa* cytoplasm
- S. Nakata (Yokohama City Univ.): Genetic flux between chloroplast and mitochondria DNA in *Triticum* and *Aegilops*
- H. Katayama (Yokohama City Univ.): Molecular genetical characterization of chloroplast genomes in gramineous plants
- K. Isono (Yokohama City Univ.): Characteristics of repetitive pAs1 clone isolated from *Ae. squarrosa*
- M. Yamamoto (Kansai Women's Junior College): Detection of the ribosomal RNA genes in *Ae. triuncialis* by *in situ* hybridization

Business Discussion

T. Sasakuma

1. Proposal of genomic symbols for cytoplasmic genomes in Triticeae.
by K. Tsunewaki (Kyoto Univ.)
2. New regulations of Wheat Information Service
by H. Tsujimoto (Kihara Inst.)

Concluding Remarks

T. Kinoshita

Field Trip

Hokkaido Agricultural Experiment Station
Green-Bio Institute
Hokuren Experimental Farm

Editorial Remarks

Announcement

From this volume WIS starts as a publication of Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences. We are going to introduce new systems useful for wheat researches in the future issues.

WIS No. 74 will be published in March 1992. Research articles that are accepted by the editorial board by February 15, 1992, will be published in No. 74. Records, genetic lists or information that will be received by that time will also be included. Facsimile is opened for business correspondence (Country code of Japan 81, FAX No. 45-715-0022).

WIS is distributed to the members on the mailing list that is now being revised. Please notify us whether you want to be listed in or withdrawn from the member list.

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Explanation of the picture on the cover

Route of the research trip to Xinjiang Uygur, China. In a, the open circle indicates Altay region and the shadowed box is Ili region of which enlarged map is shown in b. In b, asterisks indicate the places where we collected *Ae. squarrosa*. (See the article by M. Tanaka and H. Tsujimoto in this volume for the details).

WIS No. 73

編集 国際小麦研究連絡会議

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