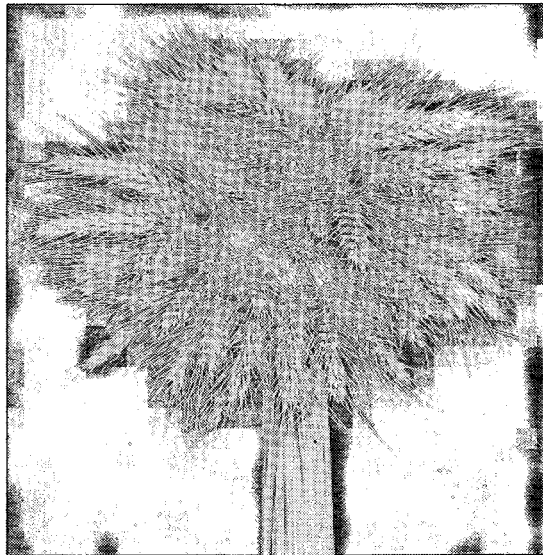# WHEAT INFORMATION SERVICE

Wheat Information Service

Kihara Institute for Biological Research

Yokohama, Japan

Contents

I. Research Notes

Cytological investigations in hexaploid *Triticale*

A.J. SHAH, N.M. SHAHANI and N.N. ANSARI

Department of Plant Breeding & Genetics,
Sind Agriculture University, Tandojam,
Pakistan

Comprehensive work on the cytological behaviour of hexaploid *Triticale* has been carried out during last two decades, which have been verified and supplemented by many workers (KROLOW 1969a, b, MERKER 1973, TSUCHIYA 1974, WEIMARCK 1974, 1975, HAFIZ *et al.* 1982, HAFIZ & LARIK 1984). Present studies were also carried out to investigate the cytological behaviour of five hexaploid *Triticale* lines developed at the Department of Plant Breeding and Genetics, Agricultural University of Norway.

Materials and Methods

Five hexaploid *Triticale* lines namely Beaver-arm, Bacum, Beagle, ITYN$_{78,21}$ (Beagle) and Mapache were obtained through the kind courtesy of Dr. K. AASTVIET, Professor of Plant Breeding and Genetics, Agriculture University of Norway.

The crosses were made between Beaver-arm x Beagle, Beaver-arm x Bacum, Bacum x Beaver-arm, Beagle x Bacum, ITYN$_{78,21}$ (Beagle) x Beaver-arm. The seeds of F$_1$ hybrids, thus obtained, were sown in the field alongwith their parental lines. Ten plants from each of the cross and parental line were selected at random for the study of quantitative characters.

For cytological studies, the young bud spikes were collected and fixed in a fresh Carnoy's solution (a mixture of alcohal and glacial acetic acid in a ratio of 3:1) at room temperature. After 24 hours, the Carnoy's solution was replaced by 70% alcohal and was stored at 4°C. The meiotic observations were made on squash preparations of pollen mother cells using orecien acetic acid stain according to DARLINGTON and LACOUR 1969.

Cytological studies of parental lines and F$_1$ populations were done for all the stages of Meiosis-I and II. A sample of 100 cells per plant for each stage was studied. The chromosomal irregularities for univalents, multivalents, laggards, micronuclei and bridges were recorded in terms of frequencies of irregularities on single cell basis.

Results and Discussions

The results of cytological studies in hexaploid *Triticale* parental lines and their F$_1$ families are presented in Tables 1 and 2.

It is clearly noted from the tables that Meiosis-II was more irregular than Meiosis-I. Number of univalents, micronuclei, laggards and bridges per cell were frequently occuring in all the stages

Table 1. Frequency of cells with irregularities in parental lines and F_1 populations

Families/lines	MI			AI, TI		MII		AII, TII			Tetrads.	
	No. of cells with irregularities	No. of univalents per cell	No. of multivalents per cell	No. of cells with irregularities	No. of univalents per cell	No. of cells with irregularities	No. of laggards or micronuclei per cell	No. of cells with irregularities	No. of bridges per cell	No. of laggards or micronuclei per cell	No. of cells with irregularities	No. of micronuclei per cell
Bacum	0	0	0	0	0	26	1.5	35	0.0	1.7	22	1.2
Beagle	0	0	0	0	0	30	2.7	51	0.19	1.5	19	1.3
ITYN$_{78, 21}$ (Beagle)	40	1.6	0.1	31	2.1	29	1.5	42	0.03	1.9	25	1.3
Beaver-arm	38	1.1	0.07	48	2.1	36	1.2	25	0.04	1.3	26	1.8
Mapache	0	0	0	0	0	4	1.0	5	0.0	1.2	6	2.5
Beaver-arm x Beagle	0	0	0	64	1.5	69	1.3	57	0.1	2.5	71	1.6
Beaver-arm x Bacum	0	0	0	0	0	48	1.7	74	0.0	1.9	40	1.9
Bacum x Beaver-arm	60	1.2	0.1	58	3.1	47	1.2	41	0.0	1.7	49	1.7
Beagle x Bacum	86	2.1	0.2	80	2.9	93	2.0	86	0.0	2.3	44	1.7
ITYN$_{78,21}$ x Beaver-arm	0	0	0	0	0	30	1.2	33	0.0	1.4	24	1.0
Mapache x Beaver-arm	34	2.3	0.1	50	2.4	27	1.7	55	0.07	1.0	46	1.1

Table 2.   Average frequency of cells with irregularities in parental lines and F_1 hybrids

	MI			AI, TI		MII		AII, TII			Tetrads	
	No. of cells with irregularities	No. of univalents per cell	No. of multivalents per cell	No. of cells with irregularities	No. of univalents per cell	No. of cells with irregularities	No. of laggards or micronuclei per cell	No. of cells with irregularities	No. of bridges per cell	No. of laggards or micronuclei per cell	No. of cells with irregularities	No. of micronuclei per cell
Parental lines	15.6	0.54	0.034	15.8	0.84	25	1.58	31.6	0.052	1.52	19.6	1.62
F_1 hybrids	30	0.933	0.067	42	1.65	52.333	1.517	57.667	0.028	1.8	45.667	1.5

of Meiosis-II of all the parental lines and hybrids. Whereas, Bacum, Beagle and Mapache the parental lines and the F_1 families of Beaver-arm × Bacum and ITYN$_{78,21}$ × Beaver-arm did not show any cell with irregular cell division in any stage of Meiosis-I. The normal meiotic-I cell division of Bacum, Beagle and Mapache parental lines indicates that these lines are stable to some extent. Whereas, Mapache the parental line, which shows the minimum number of 4, 5 and 6 irregular cells in AII, TII and Tetrads stages of Meiotic-II division, is comparatively more stable than the other parental lines and hybrids.

In F_1 families, the hybrid of the cross of ITYN$_{78,21}$ × Beaver-arm showed normal cell division in meiosis-I and the minimum percentage of cells with irregularities in Meiosis-II. This indicates that this combination was better in reductional cell division in comparison to all other hybrids. Whereas, the highest percentage of irregular cells was recorded in the cross of Beagle × Bacum.

Table 2 shows that the average number of cells with irregularities in F_1 families were approximately double than that of their parental lines in all the stages of cell divisions. Similarly the average number of univalents per cell in Meiosis-I were also approximately double in F_1 families with comparison to their parental lines. However, the average number of univalents, micronuclei and bridges per cell in Meiosis-II cell division were more or less same in the parental lines and F_1 hybrids. The fact is clear but difficult to explain that why the hybrids between primary strains of hexaploid *Triticale* have a more irregular meiosis than the parents. However, this increased meiotic irregularity in F_1 combinations of hexaploid *Triticale* may be caused by substitutional differences between the parents and also by homozygosity for different kinds of translocations.

The results obtained in this investigations are in agreement with KROLOW (1969 a,b), MERKER (1973), TSUCHIYA (1974), and WEIMARCK (1974-1975) who recorded meiotic disturbances in *Triticale* and reported a high frequency of irregular meiosis cell division in F_1 hybrids than their parents. The results are also in confirmation with HAFIZ *et al.* (1982) and HAFIZ and LARIK (1984) who reported a number of meiotic irregularities in *Triticale*.

References

DARLINGTON, C.D. and L.F. LACOUR. 1969. The handling of chromosomes. 5th edition: 36-39.
HAFIZ, H.M.I., A.S. LARIK and M.A. KHAN. 1982. Genetica Agraria. 36: 201-210.
HAFIZ, H.M.I and A.S. LARIK. 1984. Genetica Agraria. 38: 11-24.
KROLOW, K.D. 1969a, Z. Pflanzenzuchtung (Jr.P.Br.) 62: 241-271.
KROLOW, K.D. 1969b. Z. Pflanzenzuchtung (Jr.P.Br.) 62: 311-342.
MERKER, A. 1973. Hereditas 73: 285-290.
TSUCHIYA, T. 1974. Proc. Inten. Symp. 1973. St. Louis, Miss., U.S.A. Publ. by Amer. ASS. Cereal Chem.: 15-20.
WEIMARCK, A. 1974. Hereditas 77: 281-286.
WEIMARCK, A. 1975. Hereditas 80: 121-130.

Introduction of alien variation into bread wheat through chromosome engineering

B.C. JOSHI and S.M.S. TOMAR

Biotechnology Centre and Division of Genetics,
Indian Agricultural Research Institute, New Delhi, India

Monosomic 5B($2n = 41$) of cv. Chinese Spring was crossed with a rust resistant strain of rye R466 Acca (*Secale cereale*, $2n = 14$) obtained from CIMMYT, Mexico. In the F_1 two types of hybrids were obtained $2n = 27$ and $2n = 28$, the former lacking chromosome 5B of *Triticum aestivum* and the latter having it. In the absence of chromosome 5B of *T. aestivum*, the hybrid with 27 chromosomes exhibited extensive chromosome pairing. The hybrid with 28 chromosomes had mostly univalents, because chromosome 5B of *T. aestivum* does not allow the homoeologous chromosomes to pair (SEARS & OKAMOTO 1958, RILEY & CHAPMAN 1958).

The wheat-rye hybrid with 27-chromosomes, was directly backcrossed to three hexaploid wheat cultivars; Sonalika, Chinese Spring and Lokrin. The BC_1-F_2 families of mono 5B × rye × wheats produced a spectrum of aneuploids (chromosome number ranging from $2n = 34$ to 44). At the appropriate time the field population was infected with a total of about 40 races of stem, leaf and stripe rusts. In the segregating populations only rust resistant hybrid derivatives were selected for further analyses. In the off-season, the progenies of rust resistant plants were grown at the Regional Station of Indian Agricultural Research Institute, Wellington (Nilgiris), a 'hot spot' for rust and powdery mildew. Again rust resistant plants were selected and many possessed high tiller number, high spikelet number and more number of grains per spike. The enormous variability generated by the intergeneric cross of mono 5B × rye × wheats in the BC_1-F_3 generation is evidenced by Table 1.

The procedure of rigorously testing rust resistant progenies, having other desirable traits was continued, and in the BC_1-F_7 generation 93 single plants progenies were tested at Wellington, under natural and artificial epiphytotic conditions of infection. The rust reactions were recorded according to the modified Cobb's scale. To ensure good infection of powdery mildew the outstanding selections were tested in green house under optimal conditions of growth. The seedlings were scored for resistance on 0 - 4 scale (Table 2).

In the BC_1-F_7 generation about 100 rust resistant disome plants ($2n = 42$) have been identified cytologically. The variability maintained in the genetic stocks as exhibited by the disomes is given in Table 3.

Although the source of rust resistance used in the present programme is different than Petkus rye, the adult plant reaction to stem, leaf and stripe rusts and seedling reaction to *Erysiphe graminis tritici* exhibited by the derivatives is more or less similar to that of 1B/1R substitution and 1B/1R translocation lines such as Kaokaz and Burgas-2 which derive their resistance from Petkus rye. These cultivars possess linked genes *Lr* 26 (against leaf rust), *Sr* 31 (against stem rust), *Yr* 9 (against stripe rust) and *Pm* 8 (against powdery mildew). The genetics of adult plant and seedling resistance in the present wheat-rye derivatives to rusts and powdery mildew is under study.

Table 1. Range of variability generated in wheat-rye crosses in the BC_1–F3 generation

Character	M5 × Rye × Lokrin	M5 × Rye × Ch. Spring	M5 × Rye × Sonalika
Tiller no.	4 - 70	5 - 32	2 - 104
Plant height (cm)	59 - 121	63 - 106	65 - 117
Spikelet no. (main spike)	14 - 31	16 - 25	9 - 25
Grain no. (main spike)	1 - 46	4 - 29	1 - 57
Stem rust reaction	F - 80S	F - 100S	F - 100S
Leaf rust reaction	F - 70S	F - 30S	F - 90S

M5 = monosomic 5B of Chinese Spring,   Ch. Spring = Chinese Spring.

Table 2. Rust and powdery mildew reactions of nine selections in the BC_1–F_7 generation of mono 5B × rye × wheats *

Selection	Rusts			
	Stem	Leaf	Stripe	P.Mildew
1	5MS	F	F	1
5-K84	F	F	F	1
9-6-K84	F	F	F	2
9-7-K84	F	F	F	1
6-K84-10	10MR	5MR	F	1
6-K84-13	TS	TMR	F	1
7-K84-24	10MR	5MS	F	1
7-K84-27	5MR	10MS	F	1
7-K84-26	20MR	10MX	F	2
Sonalika	40S	80S	40S	3
Chinese Spring	80S	40S	–	3
Lokrin	30S	50S	F	3
Secale cereale	F	F	F	0
Kaokaz	40MR	TR	F	1
Burgas-2	30MR	TR	F	1

* 93 single plant progenies were tested.

Table 3. Wheat-rye recombinants; range of variability in the disomes as compared with check variety Sonalika

	Ht (cm)	Spike length (cm)	No. spikelet per spike	No. grains per spike	1000 grains wt (gm)
Recombinants	85-124	8.1-16.8	15-31	40-104	26.4-51.7
Sonalika (control)	93.4	11.4	15.8	47.0	39.1

References

RILEY, R. and V. CHAPMAN. 1958. Genetic control of the cytologically diploid behaviour of hexaploid wheat. Nature, Lond. **182**: 713-715.

SEARS, E.R. and M. OKAMOTO. 1958. Intergenomic chromosome relationships in hexaploid wheat. Proc. Xth Int. Cong. Genet. Montreal **2**: 258-259.

Cytoplasmic effects on the competitive ability of wheat

Nobuyoshi WATANABE

Faculty of Agriculture, Gifu University,
Gifu 501-11, Japan

The use of alien cytoplasm in wheat is very important for the broadening of the genetic variability of some quantitative characters. Thus the effects of alien cytoplasm on the competitive ability were evaluated in the present paper. Nine alloplasmic Chinese Spring strains along with euplasmic CS were used in the study (Table 1).

The competitive ability of each alloplasmic CS strains was tested by comparing the relative response of strains to competitive conditions with euplasmic CS. Under the competitive conditions, a row of tested strains was associated with rows of euplasmic CS. Pure stands consisted of three rows of tested strains. The plants of alloplasmic strains were planted in the pure stands and in the mixed stands, 10 cm apart in rows spaced 30 cm apart with three replications. Records were taken on five plants from the middle rows of the pure stand and the mixed stand for grain yield(g)/plant.

Table 1 describes the average of yielding ability of each strain in the pure stand and in the mixed stand. Yielding ability of (speltoides)-CS strain in the mixed stand was higher than that in the pure stand. (juvenalis)-CS strains in the mixed stand showed similar yields to the pure stand. The yielding ability of the other strains in the pure stand were less than that in the mixed stands. (squarrosa)-CS strain and (longissima)-CS strain were very weak competitors with euplasmic CS. The yielding ability in the pure stand was negatively correlated with the competitive gain (Fig. 1).

By introduction of alien cytoplasm, it should be noted that the alien cytoplasm shows a strong influence on the competitive ability.

Table 1. Effects of cytoplasm on the competitive ability

| Strain	No. of BC	Yield (g/plant)		Competitive gain (%)[1]
		Pure	Mixture	
(squarrosa) - CS	12	16.9	9.5	–43.8
(unialistata) - CS	7	14.1	12.4	–12.1
(speltoides) - CS	14	11.7	16.9	+35.9
(longissima) - CS	9	17.8	11.2	–37.1
(cylindrica) - CS	13	10.0	9.6	– 4.0
(ovata) - CS	19	10.3	8.5	–17.5
(kotschyi) - CS	15	11.7	9.8	–16.2
(variabilis) - CS	15	15.5	12.7	–18.1
(juvenalis) - CS	13	11.0	13.2	+20.0
Normal CS	–	11.3	11.3	0.0
L.s.d. (d.f. = 38, p = 0.05)		3.27		–

1) Competitive gain = (Mixture-Pure)/Pure × 100.
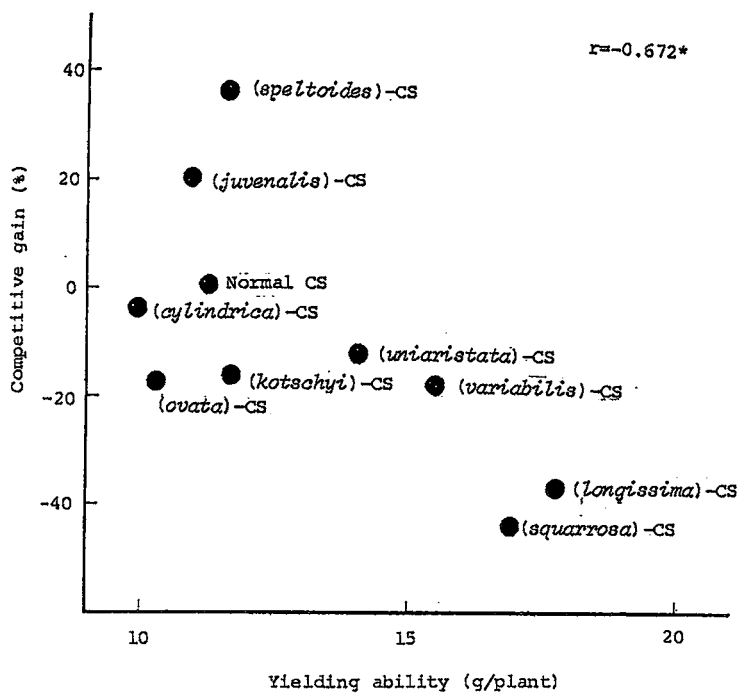
Fig. 1　Relationship between yielding ability in pure stand and competitive gain
　　　*; significant at 5% level (d.f. = 8).

Segregation distortion of Mendelian genes induced by cytoplasm effect

O.G. DAVYDENKO

Institute of Genetics and Cytology of the Byelorussian Academy of Sciences,
Minsk, USSR

Extensive investigations carried out with wheat alloplasmic lines are evidence of various and significant expression changes of morphological and agronomic traits (TSUNEWAKI 1980). At the same time there are some facts demonstrating cytoplasm influence on chromosome transmission processes (ENDO 1979 , TSUJI & MAAN 1981), mutation rate change (PONAJOTOV 1983) and sister chromatid exchange rate (LUGININ et al. 1987). These data show that cytoplasms affect not only characters expression controlled with nuclear genes, but changes of nuclear genes frequency in plant populations.

Introduction of the recessive mutant nuclear gene responsible for genic male sterility in 11 alloplasmic lines with genome of Chinese Spring has demonstrated significant and various changes of segregation distortion, which can be explained by plasmagene effect on selective gametes advantages and changes of nuclear genes recombination (DAVYDENKO 1984, 1985). In this paper it is reported of cytoplasm influence on numeraical segregation ratios for morphological marker traits.

Material and Methods

Alloplasmic wheat lines with genome of var. Chinese Spring and cytoplasms of *Aegilops* and *Triticum* species were used as maternal components of crosses: C04 - cytoplasm of *Ae. squarrosa;* C05 - *Ae. comosa;* C08 - *Ae. speltoides;* C10 - *Ae. sharonensis;* C21 - *T. dicoccoides;* C22 - *T. dicoccum;* C28 - *Ae. cylindrica;* C33 - *Ae. variabilis;* C34 - *Ae. kotschyi;* C36 - *Ae. ventricosa;* C53 - *Ae. juvenalis;* C55 - *Ae. crassa* 6X; C56 - *Ae. vavilovii* and C52 line - euplasmic analogue with cytoplasm of *Triticum aestivum.* Alloplasmic line seeds were kindly given by Prof. K. TSUNEWAKI.

MS63 mutant line (VOLODIN et al. 1982) and K31362 line received from VIR collection were used as pollen parents. Both lines have awned and hairy ear glumes.

F_1 hybrid plants were tested for presence of hairy glumes and among F_2 plants segregation analysis for these two characters was carried out.

Results and Discussion

Segregation analysis of F_2 generation, when crossing alloplasmic lines with both marker lines, has shown, as a whole, digenic control of awnedness trait and monogenic control of glume hairiness trait. At the same time there is observed a strong cytoplasm effect on segregation in some combinations of crosses. Cytoplasms *Ae. kotschyi, Ae. ventricosa* and *Ae. crassa* 6X show segregation distortion for awnedness - awnlessness trait when using MS63 line as a pollen parent

Table 1. F_2 segregation for two marker characters depending on cytoplasm in crosses of alloplasmic lines of Chinese spring with MS63 marker

Cytoplasm of maternal parent	Number of plants	Awnless: awned	χ^2 (9:7)	Hairy: nonhairy	χ^2 (3:1)	Percent of germination
T. aestivum	834	443:391	2.84	604:230	2.96	73.7
Ae. squarrosa	183	94:89	1.75	116:67	13.16	65.6
Ae. comosa	90	81:57	0.34	58:31	4.28	86.5
Ae. sharonensis	72	46:26	1.72	52:20	0.23	83.7
T. dicoccoides	931	509:422	0.94	676:255	2.84	84.4
T. dicoccum	305	155:150	3.65	237:68	1.19	80.1
Ae. cylindrica	761	444:317	1.36	553:208	2.21	74.7
Ae. variabilis	300	169:131	0.01	213:87	2.56	81.3
Ae. kotschyi	812	491:321	5.87	602:210	0.32	74.3
Ae. ventricosa	1319	814:505	15.98	992:327	0.03	80.4
Ae. crassa 6X	795	511:284	20.81	599:196	0.05	80.5

(Table 1). In these crosses a part of awned plants was greatly reduced in F_2. Cytoplasms of Ae. squarrosa and Ae. comosa induced sharp increase of a part of hairy glume plants.

When using another marker - K31362, the effect of the cytoplasms on segregation was different (Table 2). Cytoplasms of T. aestivum and Ae. squarrosa increased considerably awned plant rate, cytoplasms of Ae. cylindrica and Ae. kotschyi decreased it. Cytoplasms of Ae. juvenalis and Ae. vavilovii changed segregation for glume hairiness character in the direction of decreasing the part of hairy plants.

Though germination of F_2 plants in various crossing combinations was different (Table 1 and 2) one couldn't suppose that the reason of segregation change was due to selective mortality of definite combinations of genotypes and cytoplasms as no high negative correlations was revealed between germination and segregation change (r = 0.319 and 0.211 for crossing with MS-63 marker and r = -0.234 and 0.076 for crossing with K31326 marker). At least germination change is not a single and major reason for observed segregation shifts.

Both pollen parents have identical and allelic marker genes, nevertheless different numerical segregation ratio is observed with the same cytoplasms. It can be assumed that cytoplasm effect on segregation is due to different gamete survival or different probability of gamete participation in fertilization depending on cytoplasm and genes linked with markers.

Summarizing data obtained in the present and the previous papers (DAVYDENKO 1984, 1985) one can come to the conclusion that segregation shifts may be observed for diverse traits having different chromosomal localization. Different cytoplasms are "chromosome specific" as they can prefer gametes carrying one of two chromosomes depending on genes located on them. It is interesting that cytoplasmic effect on sister chromatid exchange frequency was also "chromosome specific" and "locus specific" (LUGININ et al. 1987). Probably specificity of nuclear

Table 2. F_2 segregation for two marker characters depending on cytoplasm in crosses of alloplasmic lines of Chinese spring with K31362 marker

Cytoplasm of maternal parent	Number of plants	Awnless: awned	χ^2 (9:7)	Hairy: nonhairy	χ^2 (3:1)	Percent of germination
T. aestivum	565	242:323	46.43	432:133	0.64	70.8
Ae. squarrosa	470	242:228	4.32	346:124	0.48	77.9
Ae. comosa	705	375:330	2.68	518:187	0.88	70.5
Ae. speltoides	829	459:370	0.26	598:231	3.63	82.9
Ae. sharonensis	153	84:69	0.12	120:33	0.96	69.2
T. dococcoides	759	446:313	1.96	585:174	0.13	75.9
T. dicoccum	420	235:285	0.01	321:99	0.45	56.2
Ae. cylindrica	713	433:280	5.83	543:170	0.51	71.3
Ae. variabilis	556	344:212	7.13	413:143	0.15	65.6
Ae. kotschyi	629	392:237	9.42	459:170	1.37	62.8
Ae. ventricosa	610	366:244	3.38	442:168	1.60	65.4
Ae. juvenalis	701	370:331	3.43	554:147	6.07	70.1
Ae. vavilovii	653	385:268	1.94	550:103	33.70	65.3

cytoplasmic effects is a general property becoming apparent both at a plant phenotype level and at individual chromosome and locus level. In any case the obtained data are evidence of the great cytoplasm influence on changes of definite allele rates in plant populations. These facts give ground for speculations about change orientation of nuclear genes frequency by cytoplasmic background change, what was, probably, of great importance in evolution of Triticinae tribe and other higher plants and may be important in selection and breeding processes of crop plants.

References

VOLODIN, V.G., B.I. AVRAMENKO and L.A. SEN. 1982. Genetics of radiation mutants of wheat. Minsk, Nauka i Tekhnika (in Russian).

DAVYDENKO, O.G. 1984. Deviations in segregation for male sterility character influenced by cytoplasms. Cytologia i genetika 18(3): 218-222 (in Russian).

DAVYDENKO O.G. 1985. Expression and transmission of male sterility character in cytoplasms of *Aegilops* and *Triticum*. Biologicheskie osnovy povyshenija produktivnosti zernovykh kultur. Mironovka p. 45-48 (in Russian).

ENDO, T.R. 1979. Selective gametocydal action of chromosome of Aegilops cylindrica in cultivar of common wheat. Wheat Inf. Serv., 50: 24-28.

LUGININ, N.V., O.G. DAVYDENKO and S.R. VEKSHIN. 1987. Effect of cytoplasms on sister chromatid exchange frequency in wheat. Cytologia i genetika, 21(6): 430-433 (in Russian).

PONAJOTOV, I. 1983. Influence of gamma rays on alloplasmic lines of wheat in M_1. Voprosy selekcii i genetiki zernovykh kultur. Moscow p. 79-86 (in Russian).

TSUJI, S. and S.S. MAAN. 1981. Defferential fertility and transmission of male and female gametes in alloplasmic wheat hybrids. Can. J. Genet. and Cytol. **23**: 337-348.

TSUNEWAKI, K. 1980. Genetic diversity of the cytoplasms in *Triticum* and *Aegilops*. Tokyo, Jap. Soc. Prom. Sci.

Thermo-insensitive mutant of WH147 wheat variety

D. SINGH[1], R.S. PARODA[2] and V.P. SINGH[3]

Department of Plant Breeding,
Haryana Agricultural University, Hisar, India

Wheat productivity in India has become more than double *i.e.* from 8.3 g/ha (1965-66) to 18.7 g/ha (1984-85) under irrigated, high fertility and good management conditions. But productivity under rainfed conditions remained static affecting about 40% of the area under this crop. To meet this demand, the work for breeding improved varieties for rainfed areas is going on in wheat section, Department of Plant Breeding and cultivars like C 306 and WH 331 were released/identified. To strengthen this project some mutation breeding programme was also taken up.

Materials and Methods

Wheat variety WH 147 which is found to be the best yielding variety under low input situations was treated with gama rays to isolate desirable mutants for rainfed conditions. From the segregating generation of 10 kR treatment a mutant was isolated. Phenotypically, this mutant was exactly similar to its prototype. However, this mutant was found to be thermo-insensitive while parent variety WH147 is thermo-sensitive.

Results and Discussion

Experimental results indicate that this mutant is most suitable for rainfed conditions and its sowing can be done just after cessation of monsoon to ensure good germination and plant stand.

Table 1 clearly showed that mutant is superior in tillering (17.6%), grains/ear (33.3%); biological yield (32.0%) and in grain yield (10.5%) than parent variety WH147. On the other hand its grain weight (10%) as well as harvest index (24.2%) are low compared to WH147. Translocation of dry matter to the grain was a limiting factor responsible for the low test weight of the seed in mutant (SHEORAN *et al.* 1983). Efforts are being made to improve this character by back crossing this mutant with its prototype WH147.

This mutant was also tested against C306 at Hisar during 1982-83 where it gave 18.5% higher yield than C306. The crop was sown on 27th October under rainfed conditions. The mutant

1. Barley Breeder, HAU, Hisar
2. Director, NBPGR, IARI, New Delhi, India
3. Wheat Breeder, HAU Reg. Res. Station, Kaul (Kurukshetra)

Table 1. Comparative yield performance of WH 147 and its mutant with other ancillary characters under rainfed conditions

Variety	Plant height	Tillers/m.	Ear length (cm)	Grains/ear	1000 grain wt	Biological yield	Yield/ha	Harbest index
WH 147	82	68	6.5	48.0	44	81.5	33.4	0.41
Mutant	102	80	7.8	64.0	40	107.5	35.2	0.33
% Increase/decrease over WH147	24.4	17.6	20.0	33.3	−10.0	32.0	10.5	−24.2

flowered after 133 days of sowing in comparison to 69 days of WH147. Extensive testing of this mutant against C306 was done under rainfed condition during the year 1983-84 at Hisar and Ambala. On the basis of the average yield of 5 trials conducted at each location, mutant gave 26.76 as against 23.25 g/ha of C306 and 35.83 as against 31.70 g/ha of C306 at Ambala and thus recorded 15 and 13% higher yield over C306 at Hisar and Ambala respectively.

The seed of this mutant was also supplied to the Department of Botany of this University for physiological studies. Physiological parameters studied by them also favoured its cultivation in rainfed conditions. Date of sowing experiments conducted by them (SHEORAN et al. 1983) confirmed its thermo-insensitivity as its period of flowering was least affected (125 to 138 days) when the crop is sown from 8th September to 10th December in comparison to WH147 (40 to 98 days).

The results obtained so far clearly showed that this mutant does well in early sowings right from late September. Early sowings are usually required under rainfed situations because we can make use of residual moisture present in the soil just after cessation of monsoon. For early sowing we need varieties insensitive to temperature (ASANA 1974). Since this mutant is thermo-insensitive, hence it is most suitable for early sowings under rainfed conditions, when temperature is too high.

References

ASANA, R.D. 1974. Physiological response of wheat to early sowing under non-irrigated cultivation and to late sowing under irrigation. Indian J. Genet. Plant Breed. 34: 190-196.
SHEORAN, I.S., M.S. KUHAD, R.K. BEHL, A.S. NANDWAL and D. SINGH. 1983. A high yielding heat insensitive mutant of wheat for early sowing. Indian J. Agri. Sci. 53(12): 1076-1078.

Recovery of desirable mutations through chemical treatments in wheat

C.S. KALIA, M.P. SINGH and R.P. PURI

Division of Genetics,
Indian Agricultural Research Inst.,
New Delhi-110012, India

With the discovery of ionizing radiations and mutagenic chemicals, there was considerable optimism for the practical utilization of mutagenesis particularly for improving productivity and for the rectification of specific defects. Subsequently, the results obtained were not comparable with the expectations and thus sceptism was expressed about the relevance of mutagenic techniques (CHOPRA & SHARMA 1985). In the course of present investigation efforts were made to ascertain the mutagenic efficiency of different chemicals and the scope of crop improvement with different mutagenic treatments, particularly with chemosterilants and antileukemic agents. The comparison for their effectiveness and relative efficiency was undertaken with the potent chemical mutagen EMS.

Materials and Methods

Three group of chemical agents viz., Aziridines (Metapa 0.4 and 0.2%, Thiotepa 0.2 and 0.01%), Nitroso compounds (MNG 0.1 and 0.05%, NMU 0.1 and 0.05%), Esters (MMS 0.1 and 0.05% and EMS 0.1 and 0.05%) were used in direct treatment to one variety each of tetraploid (HD 4502) and hexaploid (NP 880) wheat respectively. Two hundred seeds of uniform size were separated and the chemical treatments were given at $20\pm1°C$. In field, the M_1 population was bagged and subsequently in M_2 mutation percentage was calculated on the basis of M_2 population. For estimating seedling rust reaction inoculation was done in a glass house where optimum temperature and humidity conditions were maintained. After two weeks of inoculation, pustule infection types were recorded and classified as described by STAKMAN and LEVINE (1922). Mixture of stem rust races used for seedling infection included 11, 14, 15, 17, 21, 21A-1, 21A-2, 24, 34, 40, 428, 117, 117A, 117A-1, 122, 184, 194, 222, 295 and observations were recorded on the basis of three replications. Adult plant rust testing of selected mutant lines (M_8) was undertaken in 1986 crop season (May-Nov.) at Wellington Nilgiri Hill (South India) which is considered a hot spot for rust infection. Adult plant rust reactions for black, brown and yellow rust were separately recorded by Cobb's scaling method. The protein percentage of checks and selected mutant lines was done on NIR (Near Infrared Analyser, Model 102).

Result and Discussion

Induced mutations for specific characters such as disease resistance and quality aspect in crop plants occur generally at low frequency. Genes for disease and pest resistance available in the existing germplasm are mostly associated with several undesirable linkages, hence their

utilization has certain physical limitations. In order to enlarge gene pool for resistance in high yielding varieties, induced mutagenesis has been advocated as an important methodology (SAWHNEY *et al.* 1979).

At seedling stage, the selected mutants which were tested against mixture of stem rust showed variable range of resistance. In HD 4502 control, the resistance observed on pustule basis was 0-1 type whereas mutant 104-122 was completely free from any infection. It also showed resistance for black, yellow and brown at adult plant stage. Similarly, line 246 which showed resistance to black rust at seedling stage was highest yielder and gave high protein percentage. At adult plant stage it showed only traces of black rust and complete resistance to yellow and brown rust. Another line 268 had manifested resistance to black and brown rust, whereas the parental check was showing moderate susceptibility (Table 1).

Table 1. Comparative yield, protein percentage and rust reaction of some selected mutants (*Triticum durum* − HD 4502)

Treatment	Mutant selection (No.)	100 seed wt. (g)	Yield (q/ha)	Protein content (%)	Seedling reaction (bl)	Rust reaction		
						bl	br	y
Control	−	4.13	26.91	13.3	R 0-1	5_s	80_s	−
NMU 0.1%	104 - 122	5.25	32.29	14.1	R 0-1	T_s	5_s	−
EMS 0.05%	214	4.08	34.88	13.1	R 0-1	5_s	5_s	5_s
	314	4.67	33.29	12.8	−	−	−	−
MMS 0.1%	246	2.78	40.37	15.4	R 2	T_s	5_s	−
EMS 0.05%	268	2.46	30.98	13.7	−	T_s	T_s	10_s
→MMS 0.05%	276	5.65	37.67	12.7	−	T_s	10_s	10_s
MMS 0.05%	286	4.15	29.60	12.0	R 2	20_s	5_s	−
→EMS 0.05%	291	4.48	29.60	13.5	Mixed	5_s	5_s	60_s

In NP 880 the rust reaction recorded for check was of 2 type, but the mutant line 3-25(3), 3-26(1) and 3-11(1) showed '0' type reaction, thereby indicating better resistance over the check. It was an interesting observation that all the seven mutant lines which revealed better resistance at seedling stage had originated from EMS treatments (Table 2). This type of specificity of EMS treatments for the manifestation of mutants with better resistance is of great practical importance. Some sort of specificity with EMS treatments have been reported by FAVRET (1960) in barley and SWAMINATHAN *et al.* (1962) in wheat.

Table 2. Comparative yield, protein percentage and rust reaction of some selected mutants (*T. aestivum* – NP 880)

Treatment	Mutant selection (No.)	100 seed wt. (g)	Yield (q/ha)	Protein content (%)	Seedling reaction (bl)	Rust reaction		
						bl	br	y
Control	—	5.52	28.15	14.3	R 2	5_s	40_s	5_s
Metapa 0.4	13	4.47	26.61	11.7	—	10_s	20_s	5_s
Thiotepa 0.1%	15	5.16	37.11	12.1	—	20_s	5_s	T_s
MNG 0.05	7	4.23	36.20	10.9	—	60_s	5_s	T_s
EMS 0.1%	5 - 1	3.68	26.77	13.9	—	5_s	20_s	—
EMS 0.1%	3 - 11	—	29.43	11.6	R 0	5_s	5_s	T_s
EMS 0.1%	3 - 15	4.04	34.56	10.9	R 2	10_s	5_s	—
EMS 0.1%	3 - 16	4.90	35.90	12.3	R	5_s	20_s	10_s
EMS 0.1%	3 - 17	4.07	27.76	11.0	R	20_s	5_s	—
EMS 0.1%	3 - 25 (3)	4.20	28.20	10.7	R 0	—	—	—
EMS 0.1%	3 - 26 (1)	5.0	30.0	11.4	R 0	—	—	—

Induction of specific type of mutations by EMS has been attributed to its localized chromosomal effects where the respective genes are presumably located. Mutant lines conferring resistance to stem rust both at seedling and adult plant stage have been isolated after NMU treatments in Kharchia Local and Lal Bahadur bread wheat varieties (SAWHNEY *et al.* 1979).

About fifty thousand of M_2 plant population was separately screened for tetraploid and hexaploid wheat varieties to isolate, visible mutations pertaining to alteraction in height, early maturity, and adult plant rust resistance. Subsequently, fifty progenies emerging from different treatments were selected on the basis of M_3 progeny performance. Emphasis for selecting promising progenies was associated with desirable traits of uniform maturity, compact spike length, erect leaf and reduced mottling in kernels in M_4 generation. In this case, observations were confined to single plant yield, 100 kernel weight and protein percentage. Further screening and selection in M_4 and M_5 ultimately culminated in the recovery of sixteen promising mutant lines, which showed variable yield potentials, better resistance and some upgrading in protein percentage. Mutant selection 246 showed yield of 40.3 q/ha against 26.9 q/ha recorded in normal check HD 4502. Mutant lines also exhibited better yield performance in comparison to parental check. It was interesting to note that with the increase in yield there was no corresponding decrease in grain

yield. For 100-seed weight there was substantial increase in mutant line 314, 276 and 104-122. Protein content was not significantly affected in mutant lines of *durum* wheat but moderate increase in mutant selections 104-122, 246 and 268, was recorded. These mutant lines also depicted significant increase in yield over the parental check HD 4502. It was thus evident that some of the negative linkages have been broken and new mutant character association have been formed in some mutant lines. Three mutant selections from *durum* wheat viz., 104-122, 246 and 268 are presently being evaluated at All India initial evaluation trials.

Mutation breeding has also been used for the improvement of grain quality. Higher percentage of protein without affecting grain yield has been achieved in some mutant lines of Lal Bahadur (SAWHNEY *et al.* 1978). Induced variability for protein content in bread wheat was reported by SINGH *et al.* (1979) where the protein range for mutant line was 10.2 to 13.9 per cent as compared to 11.1 per cent in control. Some mutant lines with higher protein content but reduced grain yield was reported by DESAI (1979). Interestingly, the lines which gave higher protein percentage in HD 4502 also gave higher yield than control (Table 1). Yield and seed weight are generally negatively correlated. However, in mutant lines 276, 314 and 104-122 of HD 4502 have not only shown substantial increase in yield but have revealed higher grain weight. It is interesting that 104-122 alongwith increase in yield (control 26.9, mutant 32.3 q/ha) and higher grain weight (control 4.13, mutant 5.25 g/100 seeds) was coupled with higher protein percentage.

In case of NP 880 there was no significant increase for protein percentage in the dwarf mutant lines but there was substantial improvement for yield in mutant selection-15 from thiotepa, selection 7 from MNG and 3-11, 3-15 and 3-16 from EMS treatments (Table 2). From our observations it is obvious that the scope for simultaneous improvement in yield potential and protein percentage through effective selections in mutation breeding is more rewarded in tetraploid, than hexaploid wheats. It could probably be due to the complex nature of genetic architecture and compensating mechanism by triplicate loci. Most of the desirable mutants have been recovered with EMS or with the combination of EMS treatments in tetraploid wheat whereas in hexaploid wheat metapa and thiotepa treatments have also induced some desirable mutants. Thus, the response of chemical treatments in terms of the recovery of desirable mutants pertaining to disease resistance, yield and quality aspect is variable in hexaploid and tetraploid wheats. The inference can thus be drawn that there is ample scope for the induction of disease resistance, alteration/rectification in some negative character association and to improve quality aspects in conjunction with higher yield returns, through appropriate mutagenic treatments in different wheat genotypes.

References

CHOPRA, V.L. and R.P. SHARMA. 1985. Induced mutations in crop improvement. Genetic manipulations for crop improvement. Ed. V.L. Chopra pp. 23-48.

DESAI, R.M. 1979. Improvement of protein quantity and quality in durum wheat using induced mutation approach. Proc. of Symp. on "The role of induced mutations in crop improvement", Hyderabad pp. 99-103.

FAVRET, E.A. 1960. Somatic mutations of four genes for albinism in barley induced by X-rays, EMS. Hereditas, Lund. **46:** 622-634.

SAWHNEY, R.N., V.L. CHOPRA and M.S. SWAMINATHAN. 1978. An analysis of genes for resistance against indian stem rust races in two bread wheat cultivars. Euphytica **28:** 651-660.

SAWHNEY, R.N., CHOPRA, V.L., H.R. MOHINDROO and RAJINDER, KUMAR. 1979. Induced mutagenesis for disease resistance in wheat. Proc. Int. Symp. on improving crop and animal productivity by nuclear and applied techniques, 522.

SINGH, J., SINGH, R.M. and R.B. SINGH. 1979. Induced variability for yield contributing traits and protein content in bread wheat. Proc. Symp. on "The role of induced mutations in crop improvement", Hyderabad pp. 93-98.

STAKMAN, E.C. and M.N. LEVINE. 1922. The determination of biological forms of Puccinia graminis on Triticum spp. Min. Agr. Expt. Sta. Tech. Bull. 8:10.

SWAMINATHAN, M.S., V.L. CHOPRA and S. BHASKARAN. 1962. Chromosome aberrations and the frequency and spectrum of mutations induced by ethyl methane sulfonate in barley and wheat. Indian J. Genet. 22: 192-207.

Field reactions of forty-nine Italian *durum* wheat cultivars to soilborne wheat mosaic

V. VALLEGA and C. RUBIES-AUTONELL

Istituto Sperimentale per la Cerealicoltura, Via Cassia 176, 00191 Rome, Italy
and
Istituto di Patologia Vegetale, Facoltà di Scienze Agrarie, 40100 Bologna, Italy

In Italy, soilborne wheat mosaic is widespread in the traditional common wheat growing areas of the North, as well as in several Central provinces, where both common and *durum* wheats are cultivated (RUBIES-AUTONELL & VALLEGA 1985). The disease often decreases the yield of susceptible cultivars by more than 50%, also affecting test weight, plant height and weediness (TODERI 1969, VALLEGA & RUBIES-AUTONELL 1985).

Losses due to soil infestation by the SBWM-virus can be greatly reduced by growing cultivars exhibiting genetical resistance (WIESE 1977). Worldwide, however, only the reactions of common wheats have been studied extensively, whereas little is known about the behaviour of *durums*. Investigations on SBWM-resistance amongst Italian *durums* were therefore initiated in 1981-82, and a first report on the reactions of 25 cultivars has been recently published (VALLEGA & RUBIES-AUTONELL 1985). Highly significant correlations between symptom-severity evaluations made in March, at growth stage 3 on the Feekes-Large scale (LARGE 1954), and yield losses were found in these preliminary studies.

Further experiments were carried out in 1983/84 and 1985/86 to include newly released materials. The present communication summarizes the data so far collected on the reactions of 49 Italian *durums* to soilborne wheat mosaic.

Materials and Methods

During 1981/82, 1983/84 and 1985/86 three different experiments were carried out in a uniformely SBWMV-infested field near Rome, Italy. The trails, each consisting of 25 *durum* wheat cultivars grown in 10m² plots with three replicates, were planted -respectively- on 12.11.81, 26.11.83, and 4.12.85. Disease ratings were in all cases made in March, at growth stage 3 on the Feekes-Large scale (LARGE 1954), using the following scale: Resistant (R) = slight or no symptoms; Moderately Resistant (MR) = mild mottling and stunting; Moderately Susceptible (MS) = mottling and stunting; Susceptible (S) = severe mottling and stunting, with virus-killed plants. Different sets of wheats were tested each year, and SBWM resistance evaluations thus regarded a total of 49 entries. Because the reactions recorded on a few cultivars were somewhat variable, the results obtained in different experiments are presented separately.

Results and Discussion

As can be seen in Table 1, about two thirds of the cultivars tested, including those which are most widely grown in Italy ('Capeiti', 'Appulo', 'Creso' and 'Trinakria') demonstrated to be

Table 1. Field reactions of 49 Italian *Triticum durum* cultivars grown in a field infested with soilborne wheat mosaic virus (SBWMV) near Roma, Italy, during 1981–82, 1983–84 and 1985–86

Cultivar	Field reaction			Cultivar	Field reaction		
	1982	1984	1986		1982	1984	1986
Adamello	–	–	MS	Lira	–	–	S
Aldura	–	R	R	Messapia	–	MR	MR
Amedeo	–	–	MR	Murgia	R	–	–
Appio	–	R	MR	Nora	MS	–	–
Appulo	R	MR	MR	Norba	–	R	R
Arcangelo	–	MS	MR	Orsini	S	MS	–
Athena	MR	–	–	Piceno	–	R	–
Berillo	MS	MS	–	Procace	–	R	–
Bravo	–	–	MS	Produra	MS	MR	–
Brunda	–	MS	–	Quadruro	–	–	R
Capeiti	R	R	MR	Rodeo	–	MS	–
Cappelli	R	–	–	Salapia	–	–	MS
Castello	–	–	MR	Solitario	–	–	MR
Creso	R	MR	MR	Tibula	MR	R	–
Duilio	–	–	R	Trinakria	R	MR	MR
Endura	–	–	R	Valfiora	MR	–	–
Filippo	S	–	–	Valforte	S	MS	–
Gabbiano	R	–	–	Valgerardo	S	MS	–
Giano	MR	–	–	Valitalico	MR	–	–
Grazia	–	–	MS	Valnova	MS	S	MS
Iapigia	–	MR	–	Valriccardo	S	MR	–
Isa I	MR	–	–	Valselva	MS	–	–
Karel	MR	R	MR	Vespro	–	–	MS
Latino	–	R	R	Vezio	MR	MR	–
Lauria	–	–	MR				

resistant or moderately resistant to SBWM. On the contrary, many of the high-yielding semidwarf types launched during the past fifteen years showed to be totally inadeguate for cultivation in heavily SBWMV-infested soils. Extremely susceptible reactions, sometimes entailing severe stand losses, were observed especially for cultivars 'Filoppo', 'Lira', 'Orsini', 'Valforte', 'Valgerardo' and 'Valnova'.

Varietal reactions to SBWM were quite consistent throughout the various trials. 'Valriccardo', whose behaviour was rated as 'resistant' in 1982, and as 'mildly susceptible' in 1984, was the only exception in this respect.

Tall cultivars 'Capeiti', 'Norba' and 'Trinakria', as well as semidwarf 'Aldura', 'Creso' and 'Latino' showed high levels of SBWM-resistance in at least two experiments, and their use as parents in crossing programs is therefore recommended.

References

LARGE, E.C. 1954. Growth stages in cereals. Illustration of the Feekes scale. Plant. Pathol. **3**: 128-129.

RUBIES-AUTONELL, C. and V. VALLEGA. 1985. Soilborne wheat mosaic in the Lazio region. Inf. Fitopat. **35**: 39-42.

TODERI, G. 1969. Agronomical observations on soilborne wheat mosaic. Riv. Agron. **3**: 178-182.

VALLEGA, V. and C. RUBIES-AUTONELL. 1985. Reactions of Italian *Triticum durum* cultivars to soilborne wheat mosaic. Pl. Dis. **69**: 64-66.

WIESE, M.V. 1977. Soilborne wheat mosaic. In 'Compendium of wheat diseases', edited by The Am. Phyto-path. Soc., St. Paul, Minnesota p. 106.

Presence of possible rust resistance genes in genetic stocks used in Indian wheat breeding programme

B.S. MALIK and M.V. RAO

IARI and Indian Council of Agr. Res., New Delhi, India

Host parasite interaction which is highly specific and controlled by corresponding genes in host and the pathogen provides a basis on which information can be derived concerning either the host or the pathogen (BROWDER 1971). The utilization of specific genes for resistance is the major approach for resistance breeding against rust pathogen. The reaction of a genotype of host screened under controlled condition can be correlated with those lines carrying known genes for resistance to wheat rusts. On this basis probable genes in the host genotype are documented which latter can be confirmed by conventional genetic analysis *i.e.* test of allelism. In this article leaf rust effective genes in twelve wheat genetic stocks of groven resistance were identified by matching technique.

Material and Methods

Twelve rust resistant donors viz E 8643, E 8667, HS 1138-64, HB 117-107, V 156, HD 2009, CPAN 1283, CPAN 1436, CPAN 1437, CPAN 1517 and CPAN 1533 belonging to *aestivum* group were taken for these studies. Out of these, V 156 had genes from allied species *i.e. Triticum timopheeve* (Wis-245). These donors were screened against seventeen leaf rust virulences namely 10, 11, 12, 12A, 17, 20, 63, 77, 77A, 77B, 104, 104A, 106, 107, 108, 162 and 162A in the seedling stage under glass house (Table 2). Their seedling reactions were matched with the reactions of lines carrying known genes for leaf rust resistance (NAQVI 1976), (Table 3).

Results and Discussion

Documenting specific genes to rust resistance by conventional method is very laborious on account of crossing of each these donors with all the known *Lr* lines and testing the segregating population in the glass house against different rust virulences. Matching technique in wheat (BARTOS 1969) is based on the reactions of the set of isogenic lines which are genetically pure.

In the present study apart from matching technique, the parentage/pedigree, tonomic evidences and geographical distribution of these donors were also taken into account for ascertaining the possibility of the effective genes (Table 1). On this basis, these donor varieties have been listed under two major groups. The first group comprising two varieties *i.e.* E 8643 and E 8667 resistant to all the leaf rust virulences tested. The second group comprising ten varieties could be further split in to the following distinct groups.

1. HB 117-107, CPAN 1283 and CPAN 1517 showing resistance to virulences 10, 11, 12, 12A, 17, 20 and 63.
2. HS 1138-6-4, HD 2009, CPAN 1437 and CPAN 1438 showing resistance to all virulences

Table 1. Parentage of rust resistant donor parents

Accession	Parentage	Source/Origin
E 8643	Pj 62-Gb^2 x Tzpp x Knott^2 II 18717-3m-24-5m-14-6C	CIMMYT, Mexico
E 8667	Minnesota Cross II-62-3	Minnesota
HS 1138-6-4	Fn x k58/N10B21.P14/kt548 x Sonalika	IARI, Simla India
HB 117-107	Supreme-Mentena x Marquis-Renown^2 x Kiran	IARI, Bhowali, India
V 156	Wisconsin 245 x Supremo 51	U.S.A.
HD 2009	Lr-64A x Nai 60	IARI, New Delhi, India
CPAN 1283	Lr-64 x Son 64 (Son 64-Y50E x Gto^2)	CIMMYT, Mexico
CPAN 1436	Tzpp x Son 64	CIMMYT, Mexico
CPAN 1437 (Ariana 66)	K338 x Edc	Tunisia
CPAN 1438 (Australian line)	Unknown	Australia
CPAN 1517 (Colotana)	Colonista x Frontana	Canada
CPAN 1533	CC-Tob^2	CIMMYT, Mexico

CPAN: Coordinated Project Accession Number.

except virulences 12 and 77 complex.

3. CPAN 1533 resistant to all virulences except virulences 17 and 77 complex.

4. V-156 and CPAN 1436 resistant to all virulences except 10, 77 and 162.

Based on these groups the possible presence of *Lr* genes in these varieties are presented in Table 4. The varieties namely E 8643 and E 8667 showed reactions similar to those to alien gene/s *Lr9* and *Lr19*. On tracing their parantages the possibility of these gene/s are rule out. However, the type of resistance given by these varieties is expected by a combined action of two or more gene *i.e. Lr*10 (Exe) + *Lr*15/or *Lr*10 (Exe) + *Lr*3 (Ka) + *Lr*15/*Lr*16/*Lr*17 or *Lr*10 (*Lee*) + *Lr*15 + *Lr*2 (any of the alleles) or *Lr*3. Gabo being one of the parent in E 8643 indicated the presence of *Lr*10 (ANDERSON 1961, REDDY 1974), wheat variety E 8667 has maintained resistant to leaf rust under Indian conditions for many years (AGARWAL & PANDEY 1976).

HS 1138-6-4 derived from Sonalika cross indicated the presence of $Lr3$ +$Lr11$ if additional genes providing resistance to virulences 162 and 104 are assumed. For the type of resistance showed by HB 117-107 a gene combination of $Lr3$ + $Lr1$ or $Lr3$ (Ka) + $Lr2a$ is expected REDDY & RAO (1979) reported $Lr3$ + $Lr15$ in this variety. The resistance of V156 a derivative of Wiconsin 245 is covered by $Lr2a$. This variety though susceptible to many leaf rust virulences in seedling stage has maintained field resistance. The reactions of HD 2009 are comparable to $Lr10$ (Exe). However, a gene combination of $Lr10$ (Exe) + $Lr23$ + $Lr2b/Lr2c/Lr2d$ may be responsible for imparting resistance to this variety. However, Gabo being one of the parent, the presence of $Lr10$ is evident in this variety.

CPAN 1238 showed susceptible reaction to virulences 77 and 108 and its resistance is covered by a gene combination of $Lr2$ (any of the alleles) + $Lr1$ + $Lr20$. From its pedigree this variety appears to have genes from Lerma rojo 64 and Sonora 64. Presence of $Lr1$ is supported on account of *Sonora* 64. The work of GUPTA and SAINI (1980-1982), SAINI and GUPTA (1979) confirms it. CPAN 1436 (Tobari-66) resistance is covered by a combination of $Lr1$ + $Lr2$ (any of the alleles) + gene for resistance to 104 virulence of $Lr1$ + $Lr12/Lr13/Lr14a/Lr21/Lr22$ + genes for resistance to virulences 17 and 104. In either of these two combinations presence of $Lr1$ is evident which is in agreement with the compiled work of MCINTOSH 1973, GUPTA and SAINI (1980), 1982), SAINI and GUPTA (1979).

Table 2. Seedling reactions of donor parents to Indian leaf rust virulences

Donor varieties	Leaf rust virulences																
	10	11	12	12A	17	20	63	77	77A	77B	104	104A	106	107	108	162	162A
E 8643	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
E 8667	R	R	R	–	R	R	R	R	–	R	R	–	R	R	R	R	R
HS 1138-6-4	R	R	S	R	R	R	R	R	R	S	R	R/S	R	S	R	R	S
HB 117-107	R	R	R	R	R	R	R	S	S	S	S	S	R	R	R	R	R
V 156	S	R	R	–	R	R	R	S	–	–	S	–	R	S	R	S	S
HO 2009	R	R	S	S	R	R	R	R	S	S	R	S	R	R	S	S	S
CPAN 1283	R	R	R	R	R	R	R	S	S	R	R	R	R	R	S	R	R
CPAN 1436	S	S	R	R	R	S	R	S	S	S	R	R	R	R	R	S	R
CPAN 1437	R	R	S	–	R	R	R	R	R	R	R	–	R	R	R	R	R
CPAN 1438	R	R	S	S	R	R	R	R	S	R	R	R.	R	R	R	S	R
CPAN 1517	R	R	R	–	R	R	R	S	R	S	R	–	R	R	R	R	R
CPAN 1533	R	R	R	R	S	R	R	S	S	S	R	R	R	R	R	R	R

R - Resistant, S - Susceptible.

Table 3. Seedling reactions of lines carrying leaf rust resistance genes to Indian leaf rust virulences

Lr-Lines	Background	Reaction to Races/bio types												
		10	11	12	17	20	63	77	104	106	107	108	162	162A
Lr1	TC[6]	S	R	R	S	S	R	S	S	R	R	S	R	R
Lr2	TC[b]	S	R	R	R	S	R	S	S	R	S	S	S	S
LR2b	TC[6]	S	R	S	R	S	R	S	S	S	S	S	S	S
Lr2c	TC[6]	S	S	S	R/S	S	R	S	S	R	S	S	S	S
Lr2d	TC[6]	S	S	S	R	S	R	S	S	S	S	S	S	S
Lr3	TC[6]	R	R	S	R	R	R	S	S	R	R	R	S	S
Lr3(Ka)	Fd[6]	R	R	S	S	S	R	S	S	R	R	R	R	R
Lr9	TC[6]	R	R	R	R	R	R	R	R	R	R	R	R	R
Lr10(Exe)	TC[6]	R	R	S	R	R	R	R	S	R	R	S	S	S
Lr10(Lee)	Pd[6]	S	R	S	S	R	R	R	S	R	R	S	S	S
Lr11	Wichita[6]	R	R	S	S	S	R	S	S	R	S	S	S	S
Lr12	TC[6]	S	R	S	S	S	R	S	S	R	S	S	S	S
Lr13	Manitou	S	R	S	S	S	R	S	S	R	S	S	S	S
Lr14a	TC[6]	S	R	S	S	S	R	S	S	R	S	S	S	S
Lr14b	TC[6]	S	S	S	S	S	R	S	S	S	S	S	S	S
Lr15	Kenya	R	R	R	S	R	R	S	R	R	S	R	R	R
Lr16	TC[6]	R	R	S	S	R	R	S	R	R	R	R	S	S
Lr17	TC[6]	R	S	R	S	R	S	S	R	R	R	R	S	S
Lr18	TC[7]	S	S	S	S	S	R	S	S	R	S	S	S	S
Lr19	Agatha	R	R	R	R	R	R	R	R	R	R	R	R	R
Lr20	Thew	R	S	R	S	S	R	S	R	S	R	S	R	S
Lr21	TC[6]	S	S	S	S	S	R	S	S	R	R	S	R	S
Lr22	TC[3]	S	R	S	S	S	R	S	S	R	S	S	S	S
Lr23	TC[6]	R	R	S	S	S	R	S	S	R	R	S	S	S

R = Resistant,   S = Susceptible.

CPAN 1437 (Ariana-66) showed resistance to all leaf rust virulences excpet 12. A gene combination of Lr3 (Ka) + Lr10 (Exe) + Lr16 or Lr3 + Lr10 (Lee) + Lr21 is postulated in this variety. In CPAN 1438 an Australian line, gene combination of Lr10 (Exe) + Lr16 or Lr3 + Lr10 (Exe)/Lr10 (Lee) + Lr16 or Lr2b/Lr2c/Lr2d with some additional factors to impart resistance against virulence 162A is expected.

The resistance of CPAN 1517 (Colotana) is possibly covered by two or three gene combination i.e. Lr1 + Lr15 + Lr2 or Lr3 + Lr3 (Ka) + Lr17 or Lr3 + Lr15/Lr1+Lr3 plus additional factor responsible for resistance to virulence 104. These possible combinations suggest the presence of Lr1, Lr3 and Lr15.

The resistance of CPAN 1533 is comparable with gene combination of Lr15 + Lr3(Ka) or Lr15 + Lr16/Lr17/Lr20/Lr21/Lr23. From its pedigree (CC × Tob²), it is evident that Lr3 is present in this variety because both its parents carry this gene. The presence of Lr15 requires further detailed studies by genetic analysis.

Table 4. Possible presence of leaf rust resistant gene(s)

Donors	Leaf rust resistant gene(s)
E 8643	Lr10 (Exe) + Lr15 or Lr10 (Exe) + Lr3 (Ka) or Lr15/Lr17
E 8667	Lr10 + Lr15 or Lr1 + Lr10 + Lr16
HS 1138-6-4	Lr3 or Lr3 + Lr11
HB 117-107	Lr3 + Lr1 or Lr(Ka) + Lr2a
V 156	Lr2b/Lr2c/Lr2d/Lr12 + Lr13/Lr14a/ Lr14b/Lr18/Lr22
HD 2009	Lr10 (Exe) or Lr10 (Lee) + Lr23 + Lr2b/Lr2c/Lr2d
CPAN 1283	Lr2 (alleles) + Lr1 + Lr20
CPAN 1436	Lr1 + Lr2 (alleles) or Lr1 + Lr12/ Lr3/Lr14a/Lr21/Lr22
CPAN 1437	Lr3 (Ka) + Lr10 (Exe) + Lr16 or Lr3 + Lr10 (Lee) + Lr21
CPAN 1438	Lr10 (Exe) + Lr16 or Lr3 + Lr10 (Exe) or Lr10 (Lee) + Lr16
CPAN 1517	Lr1 + Lr15 + Lr2 (allelen) or Lr3 + Lr3 (Ka) + Lr17 or Lr1 + Lr3
CPAN 1533	Lr15 + Lr3 (Ka) or Lr15 + Lr16/ Lr17/Lr20/Lr21/Lr23

References

AGRAWAL, R.K. and PANDAY. 1976. Results of 1975-76. Wheat National Genetic Stock Nursery. Proc. 15th All India Wheat Worker's Workshop, Hissar.

ANDERSON, R.G. 1961. The inheritance of leaf rust resistance in seven varieties of common wheat, Cand. J. Pl. Sc. 41: 342-59.

BARTOS, P.D., J. SAMBORSKI and P.L. DYCK. 1969. Leaf rust resistance of some European Varieties of Wheat, Cand. J. Bot. 7: 543-46.

BROWDER, L.E. 1971. Pathogenic Specialization of cereal rust fungi especially *Puccinia recondita* f.sp. *tritici*: concept, method of study and application. LTSDA, Tech. Bull. 1432, pp. 31.

GUPTA, A.K. and R.G. SAINI. 1980. Genes for resistance to brown rust (*Puccinia recondita*) in wheat III. Genetic analysis of thirteen resistant stocks. Proc. 2nd National Seminar on Genetics and Wheat Improvement, Hissar.

GUPTA, A.K. and R.G. SAINI. 1982. Effectiveness of *Lr genes* against prevalent virulences in leaf rust of wheat in India. Proc. Int. Symposium New Genetic Approaches to Crop Improvement, Karachi, Pakistan

MCINTOSH, R.A. 1973. A catalogue of gene symbols for wheat, Proc. 4th Int. Wheat Genetic, Symp. pp. 893-937.

NAQVI, S.M.A. 1976. Identification of genes for leaf rust in certain varieties of *Triticum aestivum* L. Ph.D Thesis, I.A.R.I. New Delhi, 145 pp.

REDDY, M.S.S. 1974. Genetics of seedling resistance in wheat to leaf rust races of India, Ph.D. Thesis, I.A.R.I., New Delhi.

REDDY, M.S.S. and M.V. RAO. 1977. Genetic classification and control of leaf rust pathogen of wheat in India. Proc. 1st Nat. Sem. Genetics and Wheat Improvement, Ludhiana 78: 85.

SAINI, R.G. and A.K. GUPTA. 1979. Genes for resistance to brown rust (*Puccinia recondita*) in wheat II. *Lr.* genes in Frontana WG. 138 and E 6360, Cereal Res. Commu. 7(4): 289-91.

II. Records

Triticale Persenk (2n = 6x = 42) : A new original variety for grain

Stoyan TSVETKOV

Institute for Wheat and Sunflower, General Toshevo, Bulgaria

In the recent years the periodic and extreme droughts in Bulgaria tested seriously not only wheat but also the new cereal crop- *Triticale* (a wheat - rye hybrid) (TSVETKOV & STEREVA 1986). It is necessary in the breeding of new varieties to take note to their ecological plasticity together with high productive potentialities (TSVETKOV 1982). The insufficient appreciation of the relationship of these two varietal characters could lead to great disappointments in the breeding of some cereal crops and to some unrealized possibilities for the production.

At the 42-plenary session of the State Varietal Committee in February 1987 the *Triticale* Persenk was registered as a original variety and zonated in the whole country.

Origin and Botanical Affiliation

Triticale variety Persenk is developed at the Wheat and Sunflower Institute "Dobroudja", General Toshevo, Bulgaria in the period 1977 - 1986. It will be used for grain production. It came from the complex cross (AD-*durum*-form × AD-No. 8) × AD-No. 8. The first simple crossing AD-*durum*-form × AD-No. 8 was conducted in 1977 while the second complex crossing (AD-*durum*-form × AD-No. 8) × AD-No. 8 in 1978. The mother parent form AD-*durum*-form is a primary 42-chromosome *Triticale* by origin (Charkov, USSR), which was distinguished for a very high cold resistance and a good maturing rate (SHULINDIN & NAUMOVA 1965). The father parent form AD-No. 8 (Mapache) is a Mexican *Triticale* with substituted chromosomes distinguishing for a high fertility of the spike, very good resistance to rusts in the conditions of Bulgaria, a comparatively low stem, whereas its cold resistance is low.

It was established that through the breeding method of hybridization and selection in *Triticale* Persenk were successfully combined the high productive potentialities of the spike taken from the Mexican *Triticale* AD-No. 8 (Mapache) with the good maturing rate of the spike of the Soviet *Triticale* AD-*durum*-form.

Morphological Description

Triticale Persenk (Fig. 1) emerges with a light-ross coleoptile. It forms an half-erect rosete and has an average ability of tillering. The leaves are medium wide being dark green together with the stem till the onset of the milky-wax maturity.
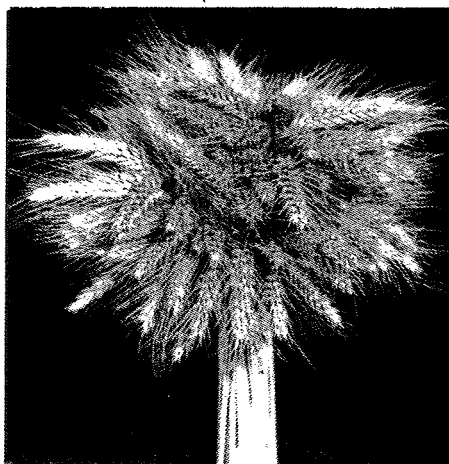
Fig. 1. *Triticale* Persenk (2n = 6x = 42) registered as an original variety
at the 42-plenary session of the State Varietal Committee in 1987

The spikes are white with awns and hairy having a length of 8-10 cm. They are cylindrical with a slightly characteristic sharpening to the apex. In a normal sowing the ear spikelets form 4-5 grains. The shoot edges are covered with well-expressed hairs. Under the ear the stem is hairy. The paleas are also hairy forming a well expressed edge and ending with long awns.

The grain is egg-shaped, medium-large ending by a brush which is well-expressed. It is distinguished for its slight ventral crease. The seed coat is slightly shrunken due to genetic determined reasons.

Breeding Qualities

ECOLOGICAL PLASTICITY.   One of the biggest breeding advantages of *Triticale* Persenk is its high ecological plasticity. This clearly can be seen by the results of the State Varietal Testing (SVT) where on the average in the course of 3 years(1984-1986). *Triticale* Persenk has exceeded annually in grain yield the standard AD-7291 by 7.6% in 1984, in 1985 by 7.0%, and in 1986 by 9.7%. That stability in years can be indicated with difficulty even in the Bulgarian winter soft wheat Sadovo 1 showing high plasticity which in 1984 stepped back in grain yield to the standard AD-7291 by 1.6%, in 1985 exceeded it insignificantly by 1.4% and in 1986 again exceeding it by 5.6%.

PRODUCTIVITY.   *Triticale* Persenk is a variety with high productive potentialities of grain yield per hectar. On the average for 3 years (1984-1986) at the State Varietal Testing it exceeded the standard Mexican *Triticale* AD-7291 by 9.2% (490.0 kg/ha), the winter soft wheat Sadovo 1 by 5.2% (381.0 kg/ha), the winter rye Danae by 3.7%, and the barley Miraj by 29.6%. In the third year Persenk had also no competition in grain yield on the side of wheat, rye and barley (Table 1).

Table 1.   State varietal testing of *Triticale* Persenk compared to wheat, rye and barley on the average for 3 years (1984–1986)

Variety	Crop	Grain yield average for Bulgaria kg/ha	in % to			
			AD-7291	Sadovo 1	Danae	Miraj
AD-7291	*Triticale*	5340	—	96.9	95.0	119.4
Sadovo 1	Wheat	5450	103.2	—	96.3	123.2
Danae	Rye	5620	105.3	103.8	—	127.9
Miraj	Barley	4420	83.7	81.2	78.2	—
Persenk	*Triticale*	5830	109.3	105.2	103.7	129.6

In 1984 at the Varietal Testing Station in Radnevo, Country Stara Zagora, was obtained the highest grain yield per ha of *Triticale* Persenk - 9060 kg/ha, compared to 8170 of the winter soft wheat Sadovo 1, 7830 kg/ha of barley Miraj, 7940 kg/ha of the rye Danae, 8450 kg/ha of AD-7291.

SHORT STEM.   Having a stem shorter by 12.0 cm than that of the standard AD-7291 (110.0 cm) *Triticale* Persenk (98.0 cm) is most suitable for cropping using an intensive technology to produce high grain yield/ha. It is distinguished for a high resistance to lodging.

RESISTANCE TO DISEASES.   The studies conducted in the course of 6 years (1981-1986) showed that under laboratory and field conditions *Triticale* Persenk had not been attacked by powdery mildew. It possesses a high resistance to stem and yellow rust and a very good resistance to brown rust. In comparison with wheat it is distinguished for a higher resistance to root rot which makes Persenk suitable for growing an stubbles.

DROUGHT RESISTANCE.   In contrast to wheat and barley Persenk is distinguished for a significantly higher drought resistance. Its deeper root system (a character obtained by rye) allows it easily to overcome the negative effects of the extreme soil and air droughts.

EARLINESS.   According to data of the State Varietal Testing *Triticale* Persenk matures by 5 days earlier than the standard AD-7291 and by 3 days earlier than the most widely distributed in Bulgaria winter soft wheat Sadovo 1.

PROTEIN.   One of the highest breeding qualities of *Triticale* in comparison with wheat and barlew is its higher protein content in the grain. According to data of the State varietal Testing Persenk contains over 1.5% more protein than the standard AD-7291. Having in mind that AD-7291 on its side forms more protein than the winter soft wheat Sadovo 1 the higher protein content of *Triticale* makes it very valuable for the animal husbandry.

For the time being the plant protein production is basically on the account of cereal crops wheat and barley, which have a low protein content. The increase of the grain protein content as many as 1% (like *Triticale* Persenk) represents a great national task. This will enable us to solve partly the protein problem in the country.

TRITICALE FIRST PRODUCTION TEST IN THE REGION OF ACID SOILS. In our country a significant part of the arrable land is situated in upland and montain regions distinguishing for their poor soil fertility. Another part of about 370,000 ha are with an increased soil acidity. On such soil wheat, barley, maize, sunflower etc. are highly succeptible and yield low, whereas _Triticale_ shows a high tolerance.

At the first production test in a region of acid soils at the farm antonovo, Targoviste Country _Triticale_ Persenk exceeded in grain yield/ha the winter soft wheat variety Pliska by 28.9% and at the farm of Sokolovo village, Gabrovo Country it exceeded the barley variety Miraj in yield by 35.3%.

Literature Cited

TSVETKOV, S. and L. STEREVA. 1986. _Triticale_ (2n = 6x = 42) and Drought. Agricultural science **5**: 24-30.

TSVETKOV, S. 1982. Winter Triticale Breeding (2n = 6x = 42) in Bulgaria. Doct. Sc. dissertation, Gen. Toshevo, Bulgaria p. 1-603.

SHULINDIN, A.F. and L.N. NAUMOVA. 1965. Amphidiploid obtained by the crossing of winter _durum_ wheat with rye. Breeding and Seed Production, No. **1**: 3-8.

Catalogue of gene symbols for wheat: 1987 Supplement

R.A. McIntosh[1] (Co-ordinator), G.E. Hart[2] and M.D. Gale[3]

1. The University of Sydney, Plant Breeding Institute, P.O. Box 180, Castle Hill, N.S.W., Australia, 2154.
2. Department of Soil and Crop Sciences, Texas A & M University, College Station, Texas, U.S.A.
3. Plant Breeding Institute, Trumpington, Cambridge, England, CB2 2LQ.

This Catalogue will be reviewed and updated during 1987. Suggestions for improved sectional presentations, corrections and additions (with reference citations) will be appreciated.

New code to stock lists: **al**: alien species.

Crossability with Rye and *Hordeum bulbosum*

Crossability between wheat and both species is controlled by the same genetic system (907). The evidence for a third gene, *kr3*, in chromosome 5D is discussed (907).

Hairy/Pubescent Auricles

Pa(700).   4AS (700).   **s** : Saratovskaya 29*9/Yanetzk is
Probat 4A(700); Saratovskaya 29*5/Sharbati Sonora 4A(700); Saratovskaya 29*4/Siete Cerros 4A
(700)   **v** : Diamant 1(700); Magali(700);
Sharbati Sonora(700); Siete Cerros(700); Ulyanovka 9(700). *pa* (700).
                                                           v : Gabo(700); Pirotrix 28(700);
                              Saratovskaya 29(700). This phenotype is expressed in Diamant 1
ditelo 4AL (700).

Height

Reduced Height

This section is under review.

Reprints of the 1983 edition: Proc. 6th Int. Wheat Genetics Symposium, Kyoto, Japan, pp. 1197-1254 and certain supplements are available.

Herbicide Response

1. Difenzoquat Insensitivity

Dfql (901).   2B (901).   v : CS (901).
dfql.   s : CS*6/Ciano 67 2B(901);CS*/
                                                                 Sicco 2B (901).
                                                             v : Ciano 67 (901); Sicco (901).

Hybrid Weakness

1. Hybrid Necrosis
According to Dhaliwal et al. (687) progressive necrosis is suppressed at 28°C.

Male Sterility

Chromosomal

Ms2 (904).   *Tai* (902).   4DS (904).   Dominant allele confers sterility.
                                                             v : Taigu = Line 223 (902, 904).

Meiotic Characters

2. Pairing homoeologous

Ph1c (906).   tv : Cappelli Phi - mutant (906).

Nucleolar Organiser Regions/Ribosomal RNA

1. *18S-5.8S-26S rRna* Genes

Correction: *Nor 1* (543) is synonym for *Nor-B1*, not *Nor-A1*.

Nor-H2.   [*Rrn1* (756)].   6H(728,713,756).   v : Clipper (713).
Nor-H3.   [*Rrn2* (756)].   7H(728,713,756).   v : Clipper (713).

2. *5S rRNA* Genes

Basic symbol: change *5S-rRNA* to *5S-Rrna*

Proteins-Enzymes

1. Acid phosphatase

Acid phosphatase gene loci were reported for 7RL in *S. cereale* (761) and for chromosomes L1 and L4 of *Agropyron intermedium* (735).

2. Alcohol dehydrogenase

Adh-Ag^{i}1.   [*Adh-X1*(735)] .   L4(735).   **v** : CS.

4. α-amylase

α-Amy-R^{m}2 (723).   Delete this entry.
α-Amy-E2 (723).   7EL (723).   **ad** : CS/*E. elongata.*
α-Amy-S^{b}2 (723).   7S^b(723).   **ad** : Holdfast/*Ae. bicornis.*

5. β-amylase

β-Amy-H^{ch}1 (723).   4H^{ch}(723).   **ad** : CS/*H. chilense.*
β-Amy-S^{l}1(723).   4S^1(723).   **ad** : CS/*Ae. sharonesis.*
                                                 su : CS/*Ae. sharonesis.*
                                      D (723).   **ad** : CS/*T. longissima.*
β-Amy-U2 (723).   5U (723).   **ad** : CS/*Ae. umbellulata.*
                                      su : CS/*Ae. umbelluata.*
β-Amy-Ag^{i}1.   Replaces *β-Amy-E^{i}1.*

6. Endopeptidase

Ep-D1
  Ep-D1a.   **v** : CS (133).
  Ep-D1b.   [EP-V1(736)] .   **v** : VPM 1 (736).

7. Esterases

Est-R1.   [*Est$_R$* (522)] .   3R(556,757)   **ad** : CS/Imperial(556);Holdfast/
                                                   King II(557); Kharkov/Dakold (557).

An esterase gene was located in chromosome L7 of *Agropyron intermedium* (735).

8. Glucosephosphate isomerase

Gpi-R1 (59).

1R (59), **ad** : CS/King II (59).
1RS (755). **al** : 2a, 26, and R14 (755).

15. Phosphogluconate dehydrogenase

A rye locus designated *Pgd 2* was located distal to *Glu-R1* in 1RL (755).

16. Phosphoglucomutase

Pgm-Ag^i 1. [*Pgm-X1*(735)] . 1A(735). **v** : CS.

17. Shikimate dehydrogenase

Skdh-U1. Fourth column, add su after ad. i.e. **ad,su** :

20. Aromatic alcohol dehydrogenase

Aadh-A2. Third column, substitute 758 for 729.

<u>Endosperm Storage Proteins</u> [This section has been revised and is presented in full]

1. Glutenins

These are heterogeneous mixtures of proteins comprising subunits linked by disulphide bonds. 'A' are high-molecular-weight (HMW) and 'B', 'C', and 'D' are low-molecular-weight (LMW) sub-units. The *Glu* loci, all of which are compound, encode HMW glutenin subunits.

Each *Glu-1* locus in hexaploid wheat contains two genes, the products of which were described as 'x-type' and 'y-type' based on differences in molecular weight and isoelectric point (738). Other evidence has shown these gene products to differ in electrophoretic finger print pattern (739) and cysteine content (747), and the genes themselves to differ in nucleotide sequence (740, 741, 742). Although early evidence suggested up to 6 genes in total at each locus (744, 742) it appears likely that only a single copy of each gene is present at the 1AL, 1BL, and 1DL loci (743).

No 'y-type' protein from the *Glu-A1* locus has been demonstrated in hexaploid wheat (738) and sequencing experiments have shown the presence of a terminating sequence inside the transcribed portion of the gene (742). The gene coding for 'x-type' proteins within *Glu-A1* is also often silent (738, 641).

The symbols for the genes within the *Glu-1* loci coding for x-type and y-type proteins will be *Glu-1-1* and *Glu-1-2*, respectively, rather than *Glu-1x* and *Glu-1y* (740). The genes are closely linked but recombination has been observed between *Glu-B1-1* and *Glu-B1-2* with a frequency of

3 in 3450 (668). The gene order, relative to the centromere, has not been ascertained.

Although alleles at each gene within the *Glu-1* compound loci could reasonably be named, the system of naming alleles on the combinations of *Glu-1-1* and *Glu-1-2* products has been retained in this edition.

Glu-A1 [643] (320). [Glt-A1, Glt-A2 (641), *Glu 1A* (661)]. 1A (643); 1AL (654, 320).

                                                        v : CS (643, 654), various (641);

                                                        s : CS/Hope (320).

Glu-A1a (321).   v : Hope.

Glu-A1b (321).   v : Bezostaya 1.

Glu-A1c (321).   v : CS.

Six combinations involving 5 HMW subunits [1A (u-z)] are listed in 641, from a study of 109 genotypes including representatives of botanical varieties.

Glu-B1 [551] (320).   [Glt-B1,-B2,-B3 (641), *Glu 1B* (661)].   1BL (551, 643, 320).

                                                       v : CS.

Glu-B1a (321).   v : Flinor.

Glu-B1b (321).   v : CS.

Glu-B1c (321).   v : Bezostaya 1.

Glu-B1d (321).   v : Hope.

Glu-B1e (321).   v : Federation.

Glu-B1f (321).   v : Lancota (rare).

Glu-B1g (321).   v : NS 335 (rare).

Glu-B1h (321).   v : Sappo (rare).

Glu-B1i (321).   v : Gabo.

Glu-B1j (321).   v : Dunav (rare).

Glu-B1k (321).   v : Serbian (rare).

Glu-B1l (748).   v : Spica D.

Fifteen combinations involving 12 HMW subunits [1B(a-o)] are listed in 641.

Glu-D1 [653] (320).   [Glt-D1, -D2 (641), *Glu 1D* (661)].   1DL (653,551,645,643,320).

                                                       v : CS.

Glu-D1a (321).   v : CS.

Glu-D1b (321).   v : Hobbit.

Glu-D1c (321).   v : Champlein.

Glu-D1d (321).   v : Hope.

Glu-D1e (321).   v : Flinor (rare).

Glu-D1f (321).   v : Danchi (rare).

Five combinations involving 6 HMW subunits [1D(p-t)] are listed in 641.

Glu-E1 [654].   1ES (654).   **ad** : CS/*E. elongata.*

Glu-H1 [654]. [*Hor 3* (514)].   1H(654), 1HL (514).

                                                                ad : CS/Betzes (654);

                                                                v : various (514).

Glu-R1 [654] (650). [*Sec 3* (651)]. 1R (654,651), 1RL (650, 648).

                                                                ad : CS/Imperial; Holdfast/King II
                                                                        (648);

                                                                tr : CS 1DS/Imperial 1RL (650).

Glu-R^m 1[659].1R^mL(659,648).   **ad** : CS/*S. montanum* (659, 648).

Glu-U1 [645].   1U (645, 654).   **ad** : CS/*Ae. umbellulata* (645,
                                                                        654).

2.   Gliadins

These are heterogeneous mixtures of alcohol-soluble polypeptides without quaternary structure.

Gli-A1 [402] (320).   [*Gld 1A*(661)].   1AS (402,554,644,645).

                                                                v : CS (402, 554, 645);

                                                                su : CS/Cheyenne (644).

Gli-B1 [554] (320).   [*Gld 1B* (646,661), Gld-B1, -B2, -B3, -B4, -B5, -B6 (641)]
                                             1B(554), 1BS(644,645).

                                                                v : CS (554, 645);

                                                                s : CS/Cheyenne (644).

Gli-D1[670] (320). [Gld-D1, -D2, -D3 (641), *Gld 1D* (661). 1DS (670, 402, 554, 644, 645).

                                                                v : CS (670, 402, 554, 645);

                                                                s : CS/Cheyenne (644).

In hexaploid wheat the *Gli-1* loci are compound and code for gramma-gliadins, omega-gliadins (749, 661) and low molecular weight glutenins (745). Quantitative 'Southern' hybridisations indicate families of 3 to 5 gamma-gliadin genes, and similar numbers of LMW glutenin genes, are present at each *Gli-1* locus (746). The gene order on the chromosomes is not known.

The complexity of the electrophoretic patterns of the products of these loci currently defies the naming of alleles. Nevertheless, variation has been described (644, 657) and applied in mapping experiments (646,320,60,593,649). Sixteen combinations of *Gli-B1* and 4 combinations of *Gli-D1* subunits are listed in 641. Multiple alleles are described in 657, 15 at *Gli-A1*, 18 at *Gli-B1*, and 8 at *Gli-D1*. An indication that the gliadin genes and the LMW glutenin genes, at the loci presently described as *Gli-1*, may be separable was provided by the report of recombination (1.7%) within *Gli-B1* (666).

Gli-E1 [654].   1ES (654).   **ad** : CS/*E. elongata.*

Gli-R1 [402]. [*Sec-R1*(650), *Sec 1*(651)]. 1RS (402, 654, 651, 648).

        ad : CS/Imperial (402, 654, 651, 648), Holdfast/King II (402, 648).

        tr : CS 1DS/Imperial 1RL (650).

Gli-R^{m}1 [648]. 1R^{m}S(648). ad : CS/*S. montanum.*

Gli-U1 [662] 1U(662, 645). ad : CS/*Ae. umbellulata.*

Gli-Ag^{1}1 L3 (580). ad : Vilmor in 27/*Ag. intermedium.*

In barley, the B and C hordeins are controlled by the *Hor 2* and *Hor 1* loci, respectively, which are linked (656) on chromosome 1HS (652, 565). The map distances and homology of the proteins indicate that *Hor 1*, the locus closest to the centromere, is partly equivalent to *Gli-1* (526).

Gli-A2 [402] (320). [*Gld 6A* (661)]. 6A (402), 6AS (660) v : CS.

Gli-B2 [554] (320). [*Gld 6B* (661)]. 6B (554), 6BS (660) v : CS.

Gli-D2 [402] (320). [*Gld 6D* (661)]. 6D (402), 6DS (660) v : CS.

Allelic variation has been demonstrated at all of the *Gli-2* loci, including 13 alleles at *Gli-A2*, 11 at *Gli-B2*, and 10 at *Gli-D2* in a study of 39 varieties (657).

Gli-R2 [654]. [*Sec2* (651)]. 2R (654, 651), 2RS (648).

        ad : CS/Imperial (654, 651, 648), Holdfast/King II (648).

Gli-R^{m}2 [659]. 6R^m (659, 648). ad : CS/*S. montanum.*

The location of *Gli-R2* in *S. cereale* is thought to have envolved from *S. montanum* (659) via a translocation between 2R and 6R (663).

Gli-U2 [662] ; 6U (662). ad : CS/*Ae. umbellulata.*

2. Other

Three other prolamin loci have been identified on the short arms of the group 1 chromosomes of hexaploid wheat but the relationship between them is not clear. A gliadin locus, designated Gld-B6, was described in CS/Thatcher substitution lines and mapped 28 mu proximal to *Gli-B1* (593). Another locus, designated Gld2-1A (760), controlling production of proteins was described in a cross between Bezostaya 1 and Gernot and mapped 31 recombination units from *Gli-A1* (664). A glutenin locus in a similar position on 1BS, 22 mu proximal to *Gli-B1*, was designated as *Glu-B2* and mapped in a Sicco × Chinese Spring cross (599).

A set of two wheat endosperm storage gene loci, *Tri-A* and *Tri-D1* (762), were located 11.0

±1.8% and 10.1±2.2% from the centromeres on 1AS and 1DS, respectively (666). Allelic variation occurred at both loci (762).

Other proteins

1. Lipopurothionins

Pur-R1.	1RL (672).	ad : CS/Imperial; su : several 1R (1B); tr : Aurora, Kavkaz with 1BL/1RS.

2. Lectins

Lec-A1.	1AL (671).	v : CS.
Lec-B1.	1B (671).	su : CS/Hope.
Lec-D1.	1DL (671).	v : CS.
Lec-U1.	1U (671).	ad : CS/*Ae. umbellulata*.

Protease Inhibition

Genes encoding proteins which inhibit the action of mammalian and insect, but not cereal, ∂-amylases were located in 3BS (Inhibitor I=Inh. I), 3DS (Inh. III) and 6DS (Inh. II) of Chinese Spring (751). In barley, genes encoding four inhibitors were located using the CS/Betzes addition lines and other aneuploids:-

Ica1 (Ica 1) and *Ica2 (Ica 2)*.	1HL (753).	– encode inhibitors of chymo-trypsin and bacterial and fungal alkaline proteases.
Isa1 (Isa 1).	2H (753).	– encodes inhibitor of bacterial protease subtilisin and endo-genous ∂-amylase (752).
Itc1 (Itc 1).	3H (753).	– encodes inhibitor of trypsin and chymotrypsin

Genes encoding inhibitors immunochemically related to the above barley inhibitors were located in rye chromosomes 1R, 2R and 3R, respectively, using CS/Imperial and Holdfast/King II addition lines (759).

Response to Photoperiod

ppd1.	v : Diamant 1 *ppd2* (629); Saratovskaya *ppd2* (629).

ppd2.   v : Skorospelka 35 (629). Dia-
                                                                  mant 1 *ppd1* (629); Saratovskaya *ppd1* (629).
Ppd1Ppd2.   v : Sharbati Sonora (629).

Response to Vernalization

According to 628 *Vrn1* is not always fully dominant and not always epistatic. Kuspira et al. (630) attributed single gene variation in *T. monococcum* to variation at the *Vrn1/vrn1* locus. Multiple recessive alleles were suggested (630).

Pathogenic Disease Reaction

Reaction to *Erysiphe graminis*

Pm3a.   v : PI46890 (909).

Reaction to *Puccinia graminis*

Sr5.   v ; Jubilejná (688). Glenlea *Sr6*
                                                                  Sr9b (679).
Sr6.   v : Glenlea (heterogeneous) *Sr5*
                                                                  Sr9b (679).
Sr9b.   v : Glenlea *Sr5 Sr6* (679).
Sr30.   v : Mediterranean W1728 (675).
SrTmp.   v : Triumph 64 (233, 689)
                                                                  Mironovská = Mironovskaja
                                                                  808 (688); Trison (689).

Complex genotype: Kenya Plume *Sr2 Sr5 Sr6 Sr7a Sr9b Sr12 Sr17* (908).

Reaction to *Puccinia recondita*

Lr2a.   v : Mediterranean W1728 *Lr3*
                                                                  (675).
Lr3.   v : Hana (688); Juilejná (688);
                 Mara(688);Mediterranean W3732 (675); Viginta (688). Mediterranean W1728 *Lr2a* (675).
Lr9.   v : PI468940 (909).
Lr13.   v : Kenya Plume (908).
Lr32 (632).   3D (632).   dv : *T. tauschii* RL5497-1 (632).
                                                                  v : Tetra Canthatch/ *T.tauschii*
                 RL5497-1, RL5713 (632); RL5713/Marquis-K (632).

Lr33 (639). | 1BL (639). | i : RL6057=Tc*6/PI58458(637, 638, 639).

v : PI268316 (637); PI268548 (637). PI58548 *Lr34* (637).

Lr34 (640). *LrT2* (638). 7D (640). i : Line 897 (638); Line 920 (638); RL6058=Tc*6/Terenzio *Lr33* (637). RL6069=Tc*6/Lageadinho *LrT3* (638); RL6070=Tc*5/PI321999 *LrT3* (638); RL6050=Tc*6/Terenzio *LrT3* (638).

v : PI268454 (637).PI58548 *Lr33* (637, 638). Lageadinho *LrT3* (638). Terenzio *Lr3 Lr30 LrT3* (638). Others (638).

In addition to conferring seedling and adult plant resistance, *Lr34* responds in a complementary manner when combined with *Lr33* or *LrT3* (638). In the Thatcher background, *Lr33* is associated with increased resistance to stem rust (638, 640).

Reaction to *Puccinia striiformis*

Yr1. | 2A (903). | v : Feng-Kang 13 (903).
Yr9. | 1R (1B). | v : Roxana (688); Sabina (688).
| 1RS-1BL. | v : Agra (688); Danubia (688); Roxana (688); Sabina (688); Solaris (688); Selekta (688).

Reaction to *Tilletia carries*

Bt4. | | v : Tres (heterogeneous) (677).

Reaction to *Mayetiola destructor* (Say)

H3. | | v : Frankenmuth (673).

Likage of 10.5±2% involving *H3* and *Pm3a* in PI148960 was attributed to a chromosome 5A-1A translocation (910).

H6. | | v : Adder (674).

H7 + H8. | | v : Adena (633).

Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.) – Greenbug

Gb1. | *gb1* (67). | Recesstive. | v : CI9058 (67); Dickinson Selection 28A (67).

Gb2 (685).	1A (681).	v : Amigo CI17609 (685).
Gb3 (682).	7D (681).	v : Largo CI17895 (683).
Gb4 (680).		v : CI17959 (684).
Gb5 (686).		v : CI17882 (686); CI17884
		(686); CI17885 (686).

Genetic Linkages

Chromosome 1A

1AS.	*Hg — Gli-A1.*	2.95 ± 1.18% (905).
	Hg — Lr10.	5.97 ± 1.70% (905).
	Gli-A1 — Lr10.	3.95 ± 1.38% (905).
	Gli-A1 — Tri-A1.	40.1 ± 2.9% (762).
	Tri-A1 — centromere.	11.0 ± 1.8% (666).

Chromosome 1B

1BS.	*Glu-B1 — Glu-B2.*	16.7 ± 5.2cM (599).
	Glu-B2 — Gli-B1.	22.4 ± 6.3cM (599).
tv:	Gene for gliadin band 42 — Gene for gliadin band 45.	0 (635).
tv:	*Rg1* — Gene for gliadin band 45.	10.32 ± 2.44% (635).
tv:	*Rg1* — Gene for gliadin band 42.	7.87 ± 2.39% (635).
tv:	*Rg1* — Band 42/45 (*Gli-B1*).	2.0 ± 0.6% (911).
		8.7 ± 1.2% (911).
	Lr26 — Lr32.	2.6 ± 0.8% (639).
1BL.	*Lr33* — centromere.	3.1 ± 1.2% (639).

'Probable gene order *Glu-B1 — Glu-B2 — Nor 1* (599).

Chromosome 1D

1DS.	*Gli-D1 — Tri-D1.*	36.5 ± 3.6% (762).
	Tri-D1 — centromere.	10.1 ± 2.2% (666).

Chromosome 2B

2BS-2BL.	*Lr13 — Sr9b.*	17.6 ± 3.1% (908).

Chromosome 2D

Ppd1 (2DL) – *Rht8.*	16.6%	(692).
Ppd1 – *Rht8.*	25%	(692).
Yr16 – *Rht8.*	38%	(692).

Chromosome 4D

4DS.	*Ms2* – centromere.	31.16%	(904).

Chromosome 5A

5AL.	*B1* – *q.*	25cM	(676).
	q – *Vrn1.*	34cM	(676).
	q – *Kr2.*	38.1 ± 10.60%	(907).
	Vrn1 – *Kr2.*	4.8 ± 4.66%	(907).

Gene order: *β-Amy-A2* – *B1* – *Hn* – *Q* – *Vrn1* – *Kr* (518, 676, 907).

Chronosome 5B

5BL.	centromere – *Kr1.*	44.8 ± 3.28%	(907).

References

512. AINSWORTH, C.C. 1983. Genet. Res., Camb. **42**: 219-227.
526. SHEWRY, P.R., B. MIFLIN and D.D. KASARDA. 1983. Phil. Trans. Soc. Lond. Ser. B. **304**: 297-308.
551. BIETZ, J.A., K.W. SHEPHERD and J.S. WALL. 1975. Single-kernel analysis of glutenin: Use in wheat genetics and breeding. Cer. Chem. **52**: 513-532.
554. WRINGLEY, C.W. and K.W. SHEPHERD. 1973. Electrofocusing of grain proteins from wheat genotypes. Ann. N.Y. Acad. Sci **209**: 154-162.
588. NEUMAN, P.R. and G.E. HART. 1986. Biochem. Genet. **24**: 435-446.
595. SINGH, R.P., and R.A. MCINTOSH. 1984. Can. J. Genet. Cytol. **26**: 723-735.
596. SINGH, R.P., and R.A. MCINTOSH. 1984. Can. J. Genet. Cytol. **26**: 736-742.
597. SINGH, R.P. and R.A. MCINTOSH. 1985. Can. J. Genet. Cytol. **28**: 189-197.
599. JACKSON, E.A., L.M. HOLT and P.I. PAYNE. 1985. Genet. Res., Camb. **46**: 11-17.
615. THOMAS, J.B., and R.L. CONNER. 1986. Crop Sci. **26**: 527-530.
629. MAYSTRENKO, O.I., and E.B. ALIEV. 1985. Chromosomal location of genes responsible for photoperiodic reaction in a non-sensitive spring variety of common wheat Sharbati Sonora. Cer. Res. Comm. **13**: 363-369.
630. KUSPIRA, J., J. MACLAGAN, K. KERBY and R.N. BHAMBHANI. 1986. Genetic and cytogenetic analysis of the A genome of *Triticum monococcum* II. The mode of inheritance of spring versus winter growth habit. Can. J. Genet. Cytol. **28**: 88-95.
631. JOHNSON, R., A.J. TAYLOR and G.M.B. SMITH. 1986. Personal communication.
632. KERBER, E.R. 1986. Personal communication.

633. LAFEVER, H.N. 1985. Registration of 'Adena' wheat. Crop Sci. **25:** 1131.

634. SCHMIDT, J.W., V.A. JOHNSON, P.J. MATTERN, A.F. DREIER, D.V. MCVEY and J.H. HATCHETT. 1985. Registration of 'Siouxland' wheat. Crop Sci. **25:** 1130-1131.

635. LEISLE, D., M.I. KOVACS and N. HOWES. 1985. Inheritance of linkage relationships of gliadin proteins and glume colour in *durum* wheat. Can. J. Genet. Cytol. **27:** 716-721.

636. NEWTON, A.C., R. JOHNSON and C.E. CATEN. 1985. Virulence analysis of local populations of *Puccinia striiformis* f. sp. *tritici.* Cereal Rusts Bull. **13:** 11-15.

637. DYCK, P.L. 1977. Genetics of leaf rust reaction in three introductions of common wheat. Can. J. Genet. Cytol. **19:** 711-716.

638. DYCK, P.L., and D.J. SAMBORSKI. 1982. The inheritance of resistance to *Puccinia recondita* in a group of common wheat cultivars. Can. J. Genet Cytol. **24:** 273-283.

639. DYCK, P.L. 1986a. Personal communication.

640. DYCK, P.L. 1986b. Personal communication.

641. GALILI, G., and M. FELDMAN. 1983. Genetic control of endosperm proteins in wheat 2. Variation in high-molecular-weight glutenin and gliadin subunits of *Triticum aestivum.* Theor. Appl. Genet. **66:** 77-86.

642. MURAMATSU, M. 1986. The *vulgare* super gene, Q: its universality in *durum* wheat and its phenotypic effects in tetraploid and hexaploid wheats. Can. J. Genet. Cytol. **28:** 30-41.

643. LAWRENCE, G.J., and K.W. SHEPHERD. 1980. Variation in glutenin protein subunits in wheat. Aust. J. Biol. Sci. **33:** 221-233.

644. KASARDA, D.D., J.E. BERNARDIN and C.O. QUALSET. 1976. Relationship of gliadin protein components to chromosomes in hexaploid wheats (*Triticum aestivum*). Proc. Natl. Acad. Sci. USA **73:** 3646-3650.

645. BROWN, J.W.S., R.J. KEMBLE, C.N. LAW and R.B. FLAVELL. 1979. Control of endosperm proteins in *Triticum aestivum* (var. Chinese Spring) and *Aegilops umbellulata* by homoeologous group 1 chromosomes. Genetics **93:** 189-200.

646. RYBALKA, A.I., and A.A. SOZINOV. 1979. Mapping the locus of *Gld 1B* which controls the biosynthesis of reserve proteins in soft wheat. Tsitologiyai Genetika **13:** 276-282.

648. SHEWRY, P.R., S. PARMAR, N. FULRATH, D.D. KASARDA and T.E. MILLER. 1986. Chromosomal locations of the structural gene for secalins in wild perennial rye (*Secale montanum* Guss.) and cultivated rye (*S. cereale* L.) determined by two-dimensional electrophoresis. Can. J. Genet. Cytol. **28:** 76-83.

649. PAYNE, P.I., L.M. HOLT, J. HUTCHINSON and M.D. BENNETT. 1984. Development and characterisation of a line of bread wheat, *Triticum aestivum,* which lacks the short-arm satellite of chromosome 1B and the *Gli-B1* locus. Theor. Appl. Genet. **68:** 327-334.

650. SINGH, N.K., and K.W. SHEPHERD. 1984. Mapping of the genes controlling high-molecular-weight glutenin subunits of rye on the long arm of chromosome 1R. Genet. Res., Camb. **44:** 117-123.

651. SHEWRY, P.R., D. BRADBERRY, J. FRANKLIN and R.P. WHITE. 1985. The chromosomal locations and linkage relationships of the structural genes for the prolamin storage proteins (secalin) of rye. Theor. Appl. Genet. **69:** 63-69.

652. NETSVETAEV, V.P. 1978. Mapping of loci Hrd in chromosome 5 of barley with the help of reciprocal translocations. "Biologicheskie Osmovy Ratseonalnogo Ispolzovaniya Jivotnogo i Rastitelnogo Myra" USSR. Riga "Zinatne", pp. 145-146.

653. ORTH, R.A., and W. BUSHUK. 1974. VI. Chromosomal location of genes coding for subunits of glutenin of common wheat. Cereal Chem. **51:** 118-126.

654. LAWRENCE, G.J., and K.W. SHEPHERD. 1981. Chromosomal locations of genes controlling seed proteins in species related to wheat. Theor. Appl. Genet. **59:** 25-31.

656. SHEWRY, P.R., H.M. PRATT, R.A. FINCH and B.J. MIFLIN. 1978. Genetic analysis of hordein polypeptides from single seeds of barley. Heredity **40:** 463-466.

657. METAKOVSKY, E.V., A. YU NOVOSELSKAYA, M.M. KOPUS, T.A. SOBKO and A.A. SOZINOV. 1984. Blocks of gliadin components in winter wheat detected by one-dimensional polyacrylamide gel electrophoresis. Theor. Appl. Genet. **67:** 559-568.

659. SHEWRY, P.R., S. PARMAR and T.E. MILLER. 1985. Chromosomal location of the structural genes for the M_r 75,000 - secalins in *Secale montanum* Guss: evidence for a translocation involving chromosomes 2R and 6R in cultivated rye (*Secale cereale* L.). Heredity **54:** 381-383.

660. PAYNE, P.I., L.M. HOLT, G.J. LAWRENCE and C.N. LAW 1982. The genetics of gliadin and glutenin, the major storage proteins of the wheat endosperm. Qual. Plant Foods Hum. Nutr. **31**: 229-241.

661. SOZINOV, A. 1984. Blocks of cereal storage proteins as genetic markers. Proc. 2nd Int. Workshop on Gluten Proteins, Wageningen, pp. 121-127.

662. SHEPHERD, K.W. 1973. Homoeology of wheat and alien chromosomes controlling endosperm protein phenotypes. Proc. 4th Int. Wheat Genet. Symp., Columbia, Missouri. pp. 745-760.

663. VAN HEEMERT, C., and J. SYBENGA. 1972. Identification of the three chromosomes involved in the translocations which structurally differentiate the genome of *Secale cereale* L. from those of *Secale montanum* Guss. and *Secale vavilovii* Grossh. Genetica **43**: 387-393.

664. SOBKO, T.O. 1984. Identification of the locus which controls the synthesis of alcohol-soluble endosperm proteins in soft winter wheat. J. Agric. Sci., Kiev. N7 **320**: 78-80.

666. SINGH, N.K., and K.W. SHEPHERD. 1984. A new approach to studying the variation and genetic control of disulphide- linked endosperm proteins in wheat and rye. Proc. 2nd Int. Workshop on Gluten Proteins, Wageningen, pp. 129-136.

667. PAYNE, P.I., E.A. JACKSON, L.M. HOLT and C.N. LAW. 1984. Genetic linkage between endosperm storage protein genes on each of the short arms of chromosomes 1A and 1B of wheat. Theor. Appl. Genet. **67**: 235-243.

668. PAYNE, P.I., L.M. HOLT and E.A. JACKSON. 1984. Genetical analysis of wheat endoperm storage proteins. Proc. 2nd Int. Workshop on Gluten Proteins, Wageningen, pp. 111-120.

670. BOYD, W.J.R., and J.W. LEE. 1967. The control of wheat gluten synthesis at the genome and chromosome level. Experientia **23**: 332-333.

671. STINISSEN, H.M., W.J. PEUMANS, C.N. LAW and P.I. PAYNE. 1983. Control of lectins in *Triticum aestivum* and *Aegilops umbellulata* by homoeologous group 1 chromosomes. Theor. Appl. Genet. **67**: 53-58.

672. SANCHEZ-MONGE, R., A. DELIBES, C. HERNANDEZ-LUCAS, P. CARBONARO and F. GARCIA-OLMEDO. 1979. Homoeologous chromosmal location of the genes encoding thionins in wheat and rye. Theor. Appl. Genet. **54**: 61-63.

673. EVERSON, E.H., R.D. FREED, P.K. ZWER, L.W. MORRISON, B.L. MARCHETTI, J.L. CLAYTON, R.L. GALLUN and W.T. YAMAZAKI, 1986. Registration of 'Frankenmuth' wheat. Crop Sci. **26**: 202-203.

674. SHANER, G.E., H.W. OHM, J.E. FOSTER, F.L. PATTERSON, R.L. GALLEN, D.M. HUBER, G.C. BUECHLEY, C.G. SAFRANSKI and J.M. HERTEL. 1986. Registration of 'Adder' wheat. Crop. Sci. **26**: 201.

675. SINGH, R.P. and R.A. MCINTOSH. 1985. Genetic basis of leaf rust resistance in wheat cultivar Mediterranean. Cereal Rusts Bull. **13**: 31-36.

676. SNAPE, J.W., C.N. LAW, B.B. PARKER and A.J. WORLAND. 1985. Genetical analysis of chromosome 5A of wheat and its influence on important agronomic traits. Theor. Appl. Genet. **71**: 518-526.

677. ALLAN, R.E., C. J. PETERSON, G.L. RUBENTHAL, R.F. LINE and K.J. MORRISON. 1986. Registration of 'Tres' wheat. Crop Sci. **26**: 203-204.

678. KOEBNER, R.M.D., K.W. SHEPHERD and R. APPELS. 1986. Controlled introgression to wheat of genes from rye chromosome IRS by induction of allosyndesis. II. Characterisation of recombinants. Theor. Appl. Genet. Submitted.

679. DYCK, P.L., D.J. SAMBORSKI and J.W. MARTENS. 1985. Inheritance of resistance to leaf rust and stem rust in the wheat cultivar Glenlea. Can. J. Plant Path. **7**: 351-354.

680. HARVEY, T.L., T.J. MARTIN and R.W. LIVERS. 1980. Resistance to biotype C greenbug in synthetic hexaploid wheats derived from *Triticum tauschii*. J. Econ. Entomol. **73**: 387-389.

681. HOLLENHORST, M.M., and L.R. JOPPA. 1983. Chromosomal location of genes for resistance to greenbug in 'Largo' and 'Amigo' wheats. Crop Sci. **23**: 91-93.

682. JOPPA, L.R., R.G. TIMIAN and N.D. WILLIAMS. 1980. Inheritance of resistance to greenbug toxicity in an amphiploid of *Triticum turgidum/T. tauschii*. Crop Sci. **20**: 343-344.

683. JOPPA, L.R., and N.D. WILLIAMS. 1982. Registration of Largo, a greenbug resistant hexaploid wheat. Sci. **22**: 901-902.

684. MARTIN, T.J., T.L. HARVEY and J.H. HATCHETT. 1982. Registration of greenbug and hessian fly resistant wheat germplasm. Crop Sci. **22**: 1089.

685. SEBESTA, E.E., and E.A. WOOD, Jr. 1978. Transfer of greenbug resistance from rye to wheat with X-rays. Agron. Abstr. pp. 61-62.

686. TYLER, J.M., J.A. WEBSTER and E.L. SMITH. 1985. Biotype E greenbug resistance in WSMV resistant wheat germplasm lines. Crop Sci. **25**: 686-688.

687. DHALIWAL, H.S., S.K. SHARMA and A.S. RANDHAWA. 1986. How to overcome hybrid necrosis in wheat. Wheat Inform. Serv. **61**: 27-28.

688. BARTOS. P., and E. STUCHLIKOVA. 1986. Genes for rust resistance. Ann. Wheat Newsl. **32**: 65-66.

689. ROELFS, A.P., and D.V. MCVEY. 1979. Low infection types produced by *Puccinia graminis* f.sp. *tritici* and wheat lines with designated genes for resistance. Phytopathology **69**: 722-730.

690-699. References reserved for section on Height - under review.

700. MAYSTRENKO, O.I. 1986. Personal communication.

723. Replace with: AINSWORTH, C.C., T.E. MILLER and M.D. GALE. 1987. α-amylase and β-amylase homoeoloci in species related to wheat. Genet. Res., Cam. (In Press).

725. AINSWORTH, C.C., T.E. MILLER and M.D. GALE 1986. Theor. Appl. Genet. **72**: 219-225.

734. FLAVELL, R.B. and M. O'DELL. 1976. Ribosomal RNA genes on homoeologous chromosomes of group 5 and 6 in hexaploid wheat. Heredity **37**: 377-385.

735. FIGUEIRAS, A.M., M.T. GONZALES- JAEN and C. BENITO. 1986. Biochemical evidence of homoeology between *Triticum aestivum* and *Agropyon intermedium* chromosomes. Theor. Appl. Genet. **72**: 826-832.

736. MCMILLAN, D.E., R.E. ALLAN and D.E. ROBERTS. 1986. Association of an isozyme locus and strawbreaker foot rot resistance derived from *Aegilops ventricosa* in wheat. Theor. Appl. Genet. **72**: 743-747.

738. PAYNE, P.I., L.M. HOLT and C.N. LAW. 1981. Structural and genetical studies on the high-molecular-weight subunits of wheat glutenin. Theor. Appl. Genet. **60**: 229-236.

739. PAYNE, P.I., L.M. HOLT, R.D. THOMPSON, D. BARTELS, N.P. HARBERD, P.A. HARRIS and C.N. LAW. 1983. The high-molecular-weight subunits of glutenin: classical genetics, molecular genetics and the relationship of bread-making quality. Proc. 6th Int. Wheat Genet Symp. pp. 827-834.

740. THOMPSON, R.D., D. BARTELS and N.P. HARBERD. 1985. Nucleotide sequence of a gene from chromosome ID of wheat encoding a HMW-glutenin subunit. Nucleic Acids Res. **13**: 6833-6846.

741. SUGIYAMA, T., A. RATALSKI, D. PETERSON and D. SOLL. 1985. A wheat HMW glutenin subunit gene reveals ahighly repeated structure. Nucleic Acids Res. **13**: 8729-8737.

742. FORDE, J. J.M. MALPICA, N.G. HALFORD, P.R. SHEWRY, O.D. ANDERSON, F.C. GREENE and B.J. MIFLIN. 1985. The nucleotide sequence of an HMW glutenin subunit gene located on chromosome 1A of wheat (*Triticum aestivum* L.) Nucleic Acids Res. **13**: 6817-6832.

743. HARBERD, N.P., D. BARTELS and R.D. THOMPSON. 1986. DNA restriction-fragment variation in the gene family encoding high-molecular-weight (HMW) glutenin subunits of wheat. Biochem. Genet. **24**: 579-596.

744. THOMPSON, R.D., D. BARTELS, N.P. HARBERD and R.B. FLAVELL. 1983. Characterisation of the multigene family coding for HMW glutenin subunits in wheat using cDNA clones. Theor. Appl. Genet. **67**: 87-96.

745. JACKSON, E.A., L.M. HOLT and P.I. PAYNE. 1983. Characterisation of high-molecular-weight gliadin and low-molecular-weight glutenin subunits of wheat endosperm by two-dimensional electrophoresis and the chromosomal localisation of their controlling genes. Theor. Appl. Genet. **66**: 29-37.

746. HARBERD, N.P., D. BARTELS and R.D. THOMPSON. 1985. Analysis of the gliadin multigene loci in bread wheat using nullisomic-tetrasomic lines. Mol. Gen. Genet. **198**: 234-242.

747. MOONEN, J.H.E., A. SCHEEPSTRA and A. GRAVELAND. 1985. Biochemical properties of some high-molecular-weight subunits of wheat glutenin. J. Cereal Sci. **3**: 17-27.

748. LAWRENCE, G.J. 1986. The high-molecular-weight glutenin subunit composition of Australian wheat cultivars. Aust. J. Agric. Res. **37**: 125-133.

749. MECHAM, D.K., D.D. KASARDA and C.O. QUALSET. 1978. Genetic aspects of wheat gliadin proteins. Biochem. Genet. **16**: 831-853.

751. SANCHEZ-MONGE, R., D. BARBER, E. MENDEZ, F. GARCIA-OLMEDO and G. SALCEDO. 1986. Genes encoding α-amylase inhibitors are located in the short arms of chromosomes 3B, 3D and 6D of wheat (*Triticum aestivum* L.). Theor. Appl. Genet. **72**: 108-113.

752. MUNDY, J., I. SVENDSEN and J. HEJGAARD. 1983. Barley α-amylase/subtilism inhibitor. 1. Isolation and characterisation. Carlsberg Res. Commun. **48**: 81-90.

753. HEJGAARD, J., S.E. BJORN and G. NIELSEN. 1984. Localisation to chromosomes of structural genes for the major protease inhibitors of barley grains. Theor. Appl. Genet. **68**: 127-130.

755. LAWRENCE, G.J., and R. APPELS. 1985. Mapping the nucleolus organiser region, seed protein loci, and isozyme loci on chromosome 1R in rye. Theor. Appl. Genet. **71**: 742-749.

756. SAGHAI-MAROOF, M.A., K.M. SOLIMAN, R.A. JORGENSON and R.W. ALLARD. 1984. Ribosomal DNA spacer-length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. Proc. Natl. Acad. Sci., USA **81**: 8014-8018.

757. SALINAS, J. and C. BENITO. 1985. Esterase isozymes in rye - characterisation, genetic control, and chromosomal location. Theor. Appl. Genet. **71**: 136-140.

758. JAASKA, V. 1984. NAD-dependent aromatic alcohol dehydrogenase in wheats (*Triticum* L.) and goatgrasses (*Aegilops* L.): evolutionary genetics. Theor. Appl. Genet. **67**: 535-540.

759. HEJGAARD, J., S.E. BJORN and G. NIELSEN. 1984. Ryechromosomes carrying structural genes for the major grain protease inhibitors. Hereditas **101**: 257-259.

760. SOZIONOV, A.A. 1985. Protein polymophisms and study in genetics and breeding Nauka, Moscow.

761. SALINAS, J., and C. BENITO. 1984. Phosphatase isozymes in rye. Characterisation, genetic control and chromosomal location. Z. Pflanzenzuchtg. **93**: 115-136.

762. SINGH, N.K., and K.W. SHEPHERD. 1985. The structure and genetic control of a new class of disulphide-linked proteins in wheat endosperm. Theor. Appl. Genet. **71**: 79-92.

901. SNAPE, J.W., W.J. ANGUS, B. PARKER and D. LECHE. The chromosomal locations of genes conferring differential response to the wild oat herbicide, difenzoquat. J. Agric. Sci. Camb. (In Press).

902. DENG, J.Y. and Z.L. GAO. 1982. Discovery and determination of a dominant male-sterile gene and its importance in genetics and wheat breeding. Scientia Sinica (Series B) **25**: 508-516.

903. XIN, Z.Y., R. JOHNSON, C.N. LAW and A.J. WORLAND. 1984. A genetic analysis of genes for yellow rust resistance in the winter wheat variety Feng-Kang 13. Acta Agron. Sinica **10**: 217-222.

904. LIU, B.H., and J.Y. DENG. 1986. A dominant gene for male sterility in wheat. Plant Breeding **97**: 204-209.

905. HOWES, N.K. 1986. Linkage between the *Lr10* gene conditioning resistance to leaf rust, two endosperm proteins and hairy glumes in hexaploid wheat. Can. J. Genet. Cytol. **28**: 595-600.

906. JAMPOTES, R., and J. DVORAK. 1986. Location of the *Ph1* locus in the metaphase chromosome map and the linkage map of the 5Bq arm of wheat. Can. J. Genet. Cytol. **28**: 511-519.

907. SITCH, L.A., J.W. SNAPE and S.J. FIRMAN. 1985. Intra chromosomal mapping of crossability genes in wheat (*Triticum aestivum*). Theor. Appl. Genet. **70**: 309-314.

908. SINGH, R.P., and R.A. McINTOSH. 1986. Genetics of resistance to *Puccinia graminis tritici* and *Puccina recondita tritici* in Kenya Plume wheat. Euphtica **35**: 245-256.

909. SUNDERMAN, D.W., B. O'CONNELL and J.H. HATCHETT. 1986. Registration of PI468960 hessian fly resistant soft spring wheat germplasm. Crop. Sci. **26**: 1093.

910. SUNDERMAN, D.W., and J.H. HATCHETT. 1986. Relationship between resistance to hessian fly and powdery mildew in soft white spring wheat PI468960. Crop. Sci **26**: 1071-1072.

911. HARE, R.A., D.L. DU CROS and W.C. BARNES. 1986. Genetic linkage between glume colour and certain giladin proteins in durum wheat Crop. Sci. **26**: 831-833.

III. Announcement

Second International Symposium on Genetic Manipulation in Crops

29 to 31 August 1988

International Maize and Wheat Improvement Center, Mexico

Scheduled sessions on anther culture and haploid breeding, protoplast culture and plant regeneration, protoplast fusion and somatic hybrids, distant hybridization, somaclonal variation, endosperm culture, international collaboration in genetic manipulation of crop plants.

Organizing committee: Prof. Li Zhensheng, Prof. Hu Han, Prof. Shao Qiquan, Institute of Genetics, Academia Sinica, China; Dr. A. Mujeeb-Kazi, CIMMYT, Mexico; Dr. G. S. Khush, Dr. L. A. Sitch, IRRI, Philippines.

For information and forms write:

Dr. L. A. Sitch
IRRI, P. O. 933
Manila, Philippines

IV. Editorial Remarks

Announcement for Future Issues

WIS No. 67 will be planned for publication in September, 1988, Manuscripts for this issue are most welcome and accepted any time, not later than July 31, 1988.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics, breeding and cytology of *Triticum, Aegilops, Secale, Haynaldia* and related genera. Manuscripts should be typewritten (double-space) in English, and submitted with duplicates. One article should not exceed five printed pages, including two textfigures (smaller than 7×7 cm^2). Lists of stocks are exempted from this page limit. Off-prints could be printed by order at cost price. Communications regarding editorial matters should be addressed to:

Wheat Information Service,
c/o Kihara Institute for Biological Research,
Mutsukawa 3-122, Minami-ku,
Yokohama 232, Japan

Membership Fee

WIS is distributed only to the member, and yearly Membership Fee is ¥2,000. The Fee should be paid with Foreign Postal Money Order, or through The Mitsubishi Trust and Banking Co. (account number; 410-1305325WIS), otherwise considerable loss is caused due to the bank charges. Neither personal nor bank checks are accepted. For Japanese members, Postal Transfer (account number; Yokohama 1-52192 WIS) is available.

Back numbers are available by order at cost price.

Acknowledgement

The Managing Editor

Explanation of the Figure on the Cover

Triticale Persenk ($2n=6x=42$) registered as an original variety at the 42-plenary session of the State Varietal Committee of Bulgaria. See the article by TSVETKOV in the present issue for details.