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I. Research Notes

The meiotic behaviour of a triploid *Triticum monococcum*

D. METTIN, R. SCHLEGEL and W.-D. BLÜTHNER

Martin-Luther-Universität Halle-Wittenberg, Lehrkollektiv für Pflanzerzüchtung, 4104 Hohenthurm b. Halle/S., DDR

From a large number of reciprocal crosses between a diploid *T. monococcum* var. *macedonicum* and the corresponding colchicineinduced autotetraploid strain we obtained a single triploid individual. This plant with 2n=3x=21 chromosomes as expected, was fully normal in appearance, had a somewhat delayed growth and was mainly characterized by an increased tillering capacity.

The triploid was completely male sterile (measured by stainability of the pollen), and all attempts to get seed set after backcrossing to the diploid parent failed. It was thus not possible to obtain any offspring, especially primary trisomics.

Meiotic preparations were made in order to analyze the pairing behaviour in metaphase I. The data obtained are given in Table 1.

In spite of the fact that this particular triploid had three sets of homologous chromosomes the number of trivalents per cell never exceeded three, while most of the cells (about 80%) had either one or two trivalents only (Table 2, see also Fig. 1). There is, in the present material, not only a comparatively low number of trivalents in general, but the kind of association found was always a chain (see Fig. 1).

Comparing the numbers of bivalents and univalents per cell or in general the latter have an excess which is mostly three. This behaviour can be attributed either to premature disjunction of the members of a trivalent or to fully asynapsis. Since most of the unpaired

Table 1. Mean metaphase I configurations in a triploid *T. monococcum*

No. cells analyzed	I	II			III			IV	Xta/cell
		rings	rods	total	pans	chains	total		
50	8.12	2.74	1.98	4.72	0	1.12	1.12	0.02	10.88

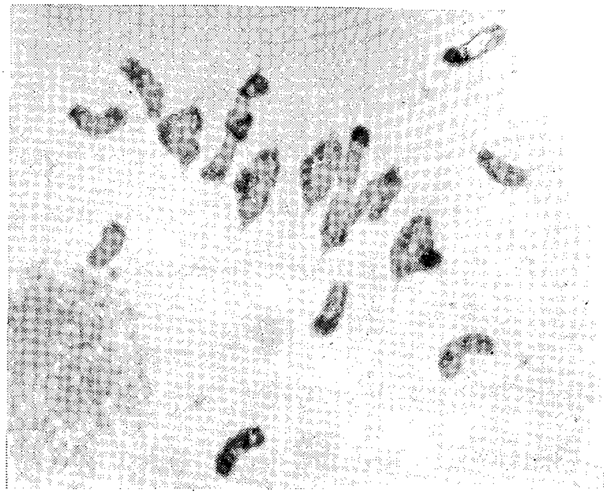

Fig. 1 Metaphase I configuration of 3x-T. monococcum with $1_{III}+5_{II}+8_{I}$

Table 2. Frequencis of different metaphase I configurations

Configuration	%	Configuration	%
$1_{IV}+5_{II}+7_{I}$	2	$1_{III}+4_{II}+10_{I}$	8
$3_{III}+3_{II}+6_{I}$	2	$7_{II}+7_{I}$	2
$2_{III}+4_{II}+7_{I}$	26	$6_{II}+9_{I}$	14
$2_{III}+3_{II}+9_{I}$	4	$5_{II}+11_{I}$	2
$1_{III}+6_{II}+6_{I}$	4	$3_{II}+15_{I}$	2
$1_{III}+5_{II}+8_{I}$	34		100

Table 3. Mean pairing in the 2x- and 4x-parent of the triploid

Ploidy level	No. cells analyzed	I	II			III		IV				Xta/cell
			ring	rod	total	chain	total	ring	chain	others	total	
2x	30	0	6.73	0.27	7.00	0	0	0	0	0	0	15.40
4x	25	0.20	7.56	0.88	8.44	0.12	0.12	2.16	0.40	0.08	2.64	27.80

chromosomes in cells with a high proportion of univalents were not arranged in end-to-end or side-by-side associations but were scattered at random it is assumed that asynapsis is partially restricted.

There is some evidence that the pairing pattern in the triploid is not primarily caused by a reduced chiasma formation. Considering the chiasmata in ring and rod bivalents in the triploid, calculations have shown that the number of chiasmata per ring bivalent is about 2.4 which is within the range of the diploid parent and the tetraploid derivative (Table 3).

New botainical sphaerococcum varieties in *T. aestivum* obtained as a result of EMS treatment

S. Georgiev

Department of Genetics, Faculty of
Biology-Sofia University, Bulgaria

Affter treatment of seeds of *T. aestivum* variety Sadovska ranozreika 2, several sphaerococcum mutants have been induced (Georgiev 1976). Among these mutants four hexaploid varieties with typical sphaerococcum phenotype have also been identified. Two other sphaerococcum varieties separated in F_2 after crossing sphaerococcum mutants No 613 and No 6512 with the original variety Sadovska ranozreika 2 have been reported. These mutants were analysed as regard the phenotype and genotype differentiation through the next 6 generations (F_7).

On the basis of the existing morphological classification of *T. sphaerococcum* Perc., (Dorofeev & Korovina 1979) and taxonomic criterion suggested by Gandilian (1980), we established the varietal diversity among sphaerococcum form in *T. aestivum* obtained. In order to avoid systematical and botanical duplication among the representatives of the hexaploid and tetraploid groups of sphaerococcum mutant forms, we decided all the hexaploid sphaerococcum mutant forms possessing the described typical characters for the respective variety of the *T. sphaerococcum* Perc., to have the same name of this variety plus the suffix "haxa"-e.g. *hexa-rubroaristatum.* A new name was given to all new varieties as follows:

1. *T. sphaerococcum* var. *hexa-ethasulfonicum popovii** 1982 (var. nov.). Plantae spicis ruberis pubibus aristis nigris, granis rubris. Bearded and pubescent ear, red glumes with black awns and red grains. It is obtained after EMS treatment of T. aestivum as a sphaerococcum mutant forms and is characterized by a high sterility (up to 10%). Probably this is due to a structural change in the chromosome set.

2. *T. sphaerococcum* var. *hexa-ethasulfonicum nicolovii** (var. nov.). Plantae spicis ruberis pubibus, aristis nigeris, granis albis. Bearded and pubescent ear, red glumes with red awns and white semispherical grains (Fig. 1, 2). It is induced after EMS treatment of *T. aestivum* variety Sadovska ranozreika 2.

3. *T. sphaerococcum* hexa-rubroaristatum. Plantae spicis ruberis pubibus, aristis rubris, granis rubris. Bearded and pubescent ear, red glumes with red awns and red semispherical grains. (Fig. 1, 2). It is induced after EMS treatment.

4. *T. sphaerococcum* var. *hexa-pakistanicum.* Plantae spicis ruberis pubibus, aristis

* Dedicated to acad. P. Popov on the occasion of his 80th Birthday.

** Dedicated to my teacher of genetics proff. Dr. H. Nicoloff.

Fig. 1-Ears from *T. aestivum* a) Ear from *T. aestivum* variety Sadovska ranozreika 2 b) Ear from *T. sphaerococcum* var. *hexa-ethasulfonicum popovii* 1982, c) Ear from *T. sphaerococcum* var *hexa-etheasufonicum nicolovii,* d) Ear from *T. sphaerococcum* var. *hexa-pakistanicum,* f) Ear from *T. sphaerococcum* var. *hexa-rubiginosum,* g) Ear from *T. sphaerococcum* var. *hexa -jakubzinerii*

Fig. 2-Seeds from *T. aestivum* a) Seeds from *T. aestivum* variety Sadovska ranozreika 2, b) Seeds from *T. sphaerococcum* var. *hexa-ethasulfonicum popovii* 1982 and *T. sphaerococcum* var. *hexa-ethasulfonicum nicolovii,* c) Seeds from *T. sphaerococcum* var. *hexa-rubroaristatum* and *T. sphaerococcum* var. *hexa-rubiginosum,* e) Seeds from *T. sphaerococcum* var. *hexa -jakubzinerii*

rubris, granis albis. Bearded and pubescent ear red glumes with red awns and white grains. It is induced after EMS treatment.

5. *T. sphaerococcum* var. *hexa-rubiginosum.* Plantae spicis ruberis impubibus, aristis curtis rubris, granis rubris. Bearded and glabrous ear, red glumes with red awns and red grains. It is obtained by crossing sphaerococcum mutants No 613 with initial variety Sadovska ranozreika 2.

6. *T. sphaerococcum* var. *hexa-jakubzinerii*. lantae spicis ruberis pubibus, spicis non aristis, granis rubris. Beardles and pubescent ear, red glumes, red grains (Fig. 1, 2). It is obtained by crossing sphaerococcum mutant No 6512 with initial variety Sadovska ranozreika 2. This mutant is characterized by some starility (up to 10%), probably due to structural changes in the karyotype.

In addition to the typical characters for *T. sphaerococcum* Perc., (shortened stem with erect habit, upright disposition and shortened leaves, hemispherical ear glumes and kernels in them) the new varieties described possessed also high protein content and some important amino acide as lysin and tryptophan.

The identification and localization of sphaerococcum gen/s/in the new variethes is in progress.

The new sphaerococcum varieties described in *T. aestivum* are of certain interest for they enrich the botanical and genetical diversity of *T. sphaerococcum* Perc.

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The use of ph mutant increasing homoeologous pairing in wheat × rye hybrids

T.M. SHNAIDER and O.J. PRIILINN

Department of Plant Genetics, Institute of Experimental Biology
Academy of Sciences, Estonian S.S.R., Tallinn, U.S.S.R.

The pairing of homoeologous chromosomes in common wheat, *Triticum aestivum* L. em. Thell. (AABBDD, $2n=6x=42$), is prevented by the activity of suppressor gene located on the long arm of chromosome 5B (OKAMOTO 1957; SEARS & OKAMOTO 1958; RILEY and CHAPMAN 1958; RILEY 1960). In the absence of this gene, named by symbol *Ph*-pairing homoeologous (WALL *et al.* 1971), the homoeologues of the A, B and D genomes pair with each other and also with their homoeologues from related species and genera. The induction of homoeologous pairing by the removal of chromosome 5B or the suppression of its effect afford a possibility of transferring genetic material from alien species to wheat chromosome. Induced pairing and crossing-over of an alien chromosome with one of its wheat homoeologues would seem to offer an excellent chance of accomplishing of an alien segment for a closely related wheat chromosome segment (SEARS 1973). To induce alien chromosomes to pair with their wheat homoeologues, it is only necessary to delete chromosome 5B using mono-5B, nullisomic-5B-tetrasomic-5D or, better, a mutant line *ph 1* (SEARS 1977, 1980) evidently deficient for the pairing suppressor *ph 1*.

In this paper we present analysis of meiosis in F_1 hybrids between common wheat and cultivated rye using mutant *ph 1*.

Materials and Methods

The *ph 1* mutant *Triticum aestivum* L. em. Thell. cv. Chinese Spring (kindly provided to us by Dr. O. MAYSTRENKO from Institute of Cytology and Genetics, Academy of Sciences, U. S.S.R., Novosibirsk) was crossed as a female with a diploid self-fertile line of rye, *Secale cereale*, Kc-517/8 and with diploid rye cv. Pamirskaya. Hybrids between euploid Chinese Spring (CS) and diploid rye cv. Pamirskaya served as control.

The spikes of F_1 hybrids were fixed in Newcomer's fluid. Meiotic observations were made on PMCs from anthers stained in 2 per cent acetocarmine using squash technique.

Results and Discussions

Cytological analysis of meiosis in F_1 plants revealed a great difference in meiotic behaviour between the hybrid combinations. The control cross (CS×Pamirskaya) showed practically no pairing among the 28 chromosomes. In this hybrid the asyndetic type of meiosis was observed with an occurence of more than 90 per cent of PMCs with 28 univalents at MI and rare rod bivalents. The mean numbers of bivalents and univalents per cell in this

Table 1. Associations of chromosomes at MI of meiosis in hybrids from crosses between wheat and rye using mutant *ph*

Hybrids	Number of PMCs analysed	Average number per cell		
		bivalents	univalents	multivalents
mutant *ph* +Kc-517/8	217	5.7 ±0.2**	13.2±0.2***	0.94±0.05***
mutant *ph*×Pamirskaya	269	4.99±0.1**	16.3±0.4***	0.54±0.04***
CS (euploid) ×Pamirskaya	115	0.5 ±0.05	27.1±0.2	0

** $P<0.01$ *** $P<0.001$

Table 2. Mean rate of bivalents, univalents and multivalents in hybrids from crosses between wheat and rye using mutant *ph*

Hybrids	Number of PMCs analysed	Limit numbers of observed		Percent of PMCs with multivalents (from 1 to 4 multivalents per cell)				
		bivalents	univalents	1	2	3	4	Total
mutant *ph*×Kc-517/8	217	2−10	4−24	32.3	19.8	5.5	0.92	58.5
mutant *ph*×Pamirskaya	269	1−10	7−27	27.5	8.6	1.9	0	37.9
CS (euploid) ×Pamirskaya	115	1− 3	22−28	0	0	0	0	0

hybrid were 0.5 and 27.1, respectively. This kind of asyndetic meiosis was described at MI of meiosis in wheat×rye hybrids by many authors.

The wheat×rye hybrids using mutant *ph* exhibited relatively high homoeologous pairing with mean chromosome associations of 5.7 bivalents, 13.2 univalents and 0.94 multivalents (0.58 trivalents, 0.37 quadrivalents and 0.004 pentavalents) per PMC in *ph*×Kc-517/8, and 4.99 bivalents, 16.3 univalents and 0.54 multivalents (0.41 trivalents, 0.11 quadrivalents and 0.01 hexavalents) in *ph*×Pamirskaya (Table 1). The amount of homoeologous pairing in hybrid derived from crossing between mutant *ph* and self-fertile line Kc-517/8 was significantly higher than in hybrid *ph*×Pamirskaya. Percent of PMCs with multivalents in *ph*×Kc-517/8 was equal 58.5 (from 1 to 4 multivalents per cell). In hybrid *ph*×Pamirskaya 37.9 per cent of PMCs with multivalents was observed (Table 2).

It seems quite probable that the high amount of bivalent and multivalent associations at MI of meiosis in hybrid *ph*×Kc-517/8, compared to the combination *ph*×Pamirskaya, are conditioned by cytogenetical peculiarities of self-fertile line of rye Kc-517/8. Cytological analysis of meiosis in this line of rye has revealed considerable disturbances of meiotic processes, which apparently were the results of mutations which occurred in the course of premeiotic division of mitosis and were determined genotypically (Shinaider & Fadejeva 1983; Shnaider et al. 1983). This line of rye is characterized by unstability of meiosis and may produce gametes with unbalanced chromosome numbers.

In the present experiment the combining of genotypes of mutant ph and self-fertile line of rye resulted in increasing of induced homoeologous pairing with the high average numbers of multivalent configurations at MI of meiosis. Undoubtedly the rye genotype plays an important role in the forming of intergeneric hybrids and has an effect on the behaviour of meiosis. The mutant *ph* was found effective in inducing homoeologous pairing of chromosomes in wheat×rye hybrids.

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Comparative efficiency of grouping methods in triticale.

R.K. BEHL

Haryana agricultural University, Hissar India

Though the utility of genetic divergence among parents entering crosses has long been appreciated (ARUNACHALAM 1981), the choice of grouping method and estimating genetic diversity without making crosses continue to be a debatable issue. In that context, Metroglyph analysis, D^2-statistic and Canonical roots have been used quite often. However, sporadic reports are available on this aspect in triticale. Present study deals with comparative efficiency of these three methods to classify base population and F_1 hybrids involving parents eslected from base polulation.

Materials and Methods

Base population comprising ecogeographically diverse 70 hexaploid triticale lines (exper-

Table 1. Grouping pattern of 70 genotypes (experiment 1).

Group number	No. of Genotypes	Tocher method Genotypes	No. of Genotypes	Canonical roots Genotypes	No. of Genotypes	Metroglyph Genotypes
I	32	5, 7, 12, 13, 14, 15, 16, 17, 19, 20, 21, 23, 27, 29, 30, 31, 33, 34, 36, 42, 43, 44, 45, 53, 54, 55, 62, 65, 66, 67, 68, 69	30	11, 12, 13, 14, 16, 17, 19, 21, 22, 23, 27, 29, 30, 31, 33, 34, 36, 38, 42, 43, 45, 48, 49, 51, 53, 54, 66, 67, 68, 69	34	1, 2, 3, 4, 5, 6, 7, 10, 11, 12, 15, 20, 23, 24, 25, 27, 29, 32, 34, 37, 38, 39, 40, 41, 44, 46, 51, 53, 55, 56, 58, 62, 64, 66
II	19	1, 2, 3, 4, 6, 10, 11, 24, 25, 37, 39, 40, 41, 46, 51, 56, 57, 58, 61	19	1, 2, 4, 5, 7, 10, 15, 20, 25, 32, 39, 40, 44, 46, 47, 55, 56, 58, 60, 61, 62, 65	15	14, 16, 17, 21, 22, 30, 31, 45, 47, 50, 54, 60, 65, 67, 68
III	6	9, 32, 47, 59, 60, 64	5	3, 9, 57, 59, 65	3	9, 57, 59
IV	4	28, 49, 50, 63	7	6, 24, 28, 37, 41, 50, 63	3	8, 26, 63
V	4	18, 22, 26, 52	3	18, 26, 52	8	13, 18, 28, 33, 36, 43, 49, 69
VI	2	38, 48	—	—	4	19, 42, 48, 61
VII	1	8	1	8	—	—
VIII	1	35	1	35	2	35, 52
IX	1	70	1	70	1	70
Resemblence (%)				65.71 % of Tocher method		28.57 % of Tocher method, 27.14 % of Canonical roots

Present address: Institute of Agronomy and Plant Breeding, University of Goettingen, F.R.G.

Table 2. Grouping pattern of 22 parents (1-18, Lines, 19-22, Testers) and 72 hybrids (23-94)

Group number	No. of Genotypes	Tocher method Genotypes	No. of Genotypes	Canonical roots Genotypes	No. of Genotypes	Metroglyph Genotypes
I	49	3, 7, 8, 18, 21, 22, 26, 27, 29, 31, 32, 34, 35, 36, 37, 38, 39, 40, 45, 49, 53, 54, 57, 58, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 74, 75, 76, 79, 80, 83, 85, 86, 89, 90, 91, 93, 94	52	3, 11, 13, 18, 21, 22, 26, 29, 31, 32, 34, 35, 36, 37, 38, 39, 40, 45, 47, 49, 50, 53, 54, 57, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 74, 75, 76, 79, 80, 83, 85, 86, 87, 88, 89, 90, 91, 93, 94	55	2, 3, 5, 8, 14, 16, 17, 21, 23, 25, 26, 29, 30, 32, 35, 36, 37, 38, 39, 41, 42, 44, 45, 46, 48, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 69, 70, 73, 74, 76, 79, 80, 82, 84, 85, 86, 87, 89, 90, 93, 94
II	11	23, 41, 42, 44, 46, 48, 55, 56, 73, 81, 84	12	2, 5, 23, 41, 44, 46, 48, 55, 56, 73, 81, 84	—	—
III	8	19, 24, 25, 28, 30, 43, 59, 92	7	19, 25, 28, 33, 43, 59, 92	12	24, 27, 40, 43, 49, 67, 68, 75, 81, 83, 91, 92
IV	8	11, 14, 20, 33, 50, 72, 87, 88	7	14, 20, 24, 27, 58, 78, 82	4	11, 20, 22, 78
V	7	1, 2, 5, 6, 15, 51, 77	6	1, 6, 8, 15, 51, 77	9	1, 4, 6, 15, 19, 28, 33, 51, 88
VI	4	9, 13, 16, 17	3	7, 16, 17	6	7, 13, 31, 47, 71, 72
VII	2	4, 10	3	4, 10, 30	5	9, 10, 18, 34, 50
VIII	2	12, 52	3	9, 12, 52	1	12
IX	1	47	1	42	1	52
X	1	78	—	—	1	77
XI	1	82	—	—	—	—
Resemblence (%)				77.66 % of Tocher method		51,06 % of Tocher method, 47.87 % of Canonical root

iment I) and 94 progenies including 18 females and 4 males selected from base population and 72 hybrids among them (experiment II) were evaluated in randomised block design with three replication. Observations on randomly selected five plants were recorded for 8 and 14 important characters related to plant growth, grain yield and grain quality attributes in experiment I and II, respectively. Following the analysis of variance, populations in both the experiments were classified using Metroglyph analysis (ANDERSON 1957), Tocher method and Canonical rotts (RAO 1952). Grouping was done in such a way that genotypes clustered in one group resembled with each other, while different groups could be delineated. Resemblence coefficients (%) for similarities in grouping pattern was computed for experiment I (Table 1) and experiment II (Table 2).

Results and Discussion

Substantial genetic variability in base population (exp. I) as well as parents and hybrids (exp. II), as evident from variance analysis warranted the utility of grouping genotypes.

Metroglyph analysis: The method recalls in reducing the quantitative variation into a sort of score and then showing it graphically. Number of tillers per plant and 1000 grain weight (g) being two important characters related to grain yield in triticale were used for plotting the glyphs.

Based on morphological varition 70 and 94 genotypes in two experiments were grouped in 8 and 9 clusters, respectively. Nearly threefourth genotypes could be clustered in first two groups. Thus majority of the genotypes appeared to be more or less similar for these two characters. However, with in a cluster different grades of expression for remaining characters were also noted.

Tocher method: Using generalised distance (square root of D^2) between genotypes for a set of charcters, the 70 genotypes were grouped into nine clusters, whereas, 94 genotypes were grouped into eleven clusters. In both the experiments first two groups were largest and accounted for almost 73 and 64 percent genotypes, respectively. This envisaged that most of the genotypes grouped in these clusters were genetically close to each other and the apparent wide genetic diversity in both the experiments was due to 19 genotypes (exp. I) and 16 parents and 18 F_1 hybrids (exp. II) scattered over remaining groups. There were 3 single genotype clusters in both experiments. These genotypes were extraordinary for one or more characters which made them so divergent.

Canonical root analysis: -Clusters were formed using first two canonical variates (λ_1 and λ_2) which supplied best linear functions and contributed maximum to total variation. Both λ_1 and λ_2 accounted for 61.5 and 55.9 percent of the variability in experiment I and II, respectively. Eight clusters could be recognised in experiment I and nine in experiment II. Majority of the genotypes were grouped in first two groups.

On over all basis, grouping pattern usng canonical roots revealed 65.7 and 77.7 percent resemblence with that of Tocher's method in experiment I and II, respectively, as majority of the genotypes were grouped similarly in both cases. The most divergent groups in Tocher's method were apparent in canonical root analysis also. Discrepencies regarding grouping pattern by two methods are expected as two canonical vectors did not explain total variability. Contrarily, such resemblence between metroglyph analysis and Tocher method and metroglyph analysis and canonical root analysis was of the order of 28.6 and 51.1 percent and 27.1 and 47.9 percent in experiment I and II, respectively. Thus in general, metroglyph analysis showed less resemblence with other two methods, particularly in experiment I, whereas in experiment II such a change was not spectacular. Therefore, it seems that grouping pattern in first two groups is mutually exclusive.

All these techniques suffer from one or more short comings. Metroglyph analysis is based on two characters explaining maximum variability and therefore subjective. So is true with canonical root analysis also. Although, D^2 statistic between any pair of population amounts to a quantitative measure of genetic divergence, yet the grouping pattern is arbitrary, subjective and changeable under the influence of environment (SINGH & GUPTA 1979). Therefere, use of various methods to confirm grouping pattern more objectively has been advocated (VAIRAVAN *et al.*, 1973: Jain *et al.*, 1978). If breeders requriment is fulfilled only by broad classification, metroglyph analysis being simpler offers a suitable alternative

(CHANDRA 1976). In present study also, grouping following metroglyph analysis revealed sizeable similarity over two years as 15 out of 22 parents revealed almost same grouping pattern.

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Some agronomic characters and grain protein content of Chinese Spring monosomics and ditelosomics[1]

H. YOSHIDA and K. KAWAGUCHI

National Agricultural Research Center, Tsukuba 305, Japan

Aneuploid series of *Triticum aestivum* var. Chinese Spring developed by SEARS (1954, 1978) have been available to reduce the complexity of genetic analysis in hexaploid wheat. In the Japanese wheat breeding, it is particularly necessary to grasp the chromosome location of the loci influencing heading time, yield components and grain protein content. Here the chromosomal contribution in the representation of some agronomic characters and grain protein content was estimated by making a comparison between the phenotypic variability of either Chinese Spring monosomics or ditelosomics and that of the normal disomics.

Materials and Methods

The materials for the present study comprised of 21 Chinese Spring monosomic lines, 31 telosomic lines listed in Table 2 and the disomics. Their seeds were kindly obtained from Prof. K. NISHIKAWA of Faculty of Agriculture, Gifu University, Japan.

Three seedlings a line were transplanted with a spacing of 60×10 cm in the alluvial soil field at the beginning of December in 1975 and 1976. On the other hand, three seeds a line were sown in 1/2000a size-pot, and then grown outdoors after the growth of seedlings during 3 weeks in the greenhouse in parallel with the field. Although the chromosomes of their lines were not identified, there seems to be no problem in the most lines because they are stable, excepting monotelodisomic 1AS, 4Aβ and 5AS, ditelosomic 2AS and ditelo 2BS-monotelosomic 2BL (personal communication from Prof. NISHIKAWA).

The observations were recorded on the characters in Table 1. Mean of all 3 plants for each line was calculated except for a few lines. Based on the field and pot trials of the two years, means of either the monosomic or the telosomic lines were compared with the disomic mean of 6 plants. Grain protein content was calculated from % nitrogen of 500 mg grain flour samples measured by autoanalyzer (Technicon Co., Ltd.) using a factor of 5.7. The samples were milled with grains of 1975 cultivation.

Air temperature of the growing season was slowly falling after seeding (av. temp ca. 15°C), and became bottom at the middle of January. It rose afterwards. Growth is slow but continuous during winter, and there is no winter-killing.

Results and Discussion

Table 1 shows the monosomic and the telosomic lines making a representation clearly

[1] Contribution from Hokuriku National Agricultural Experiment Station, Joetsu 943-01.

Table 1. Monosomics and telosomics showing marked differences in agronomic characters based on comparison of 21 monosomics, 27 ditelosomics, 3 monotelodisomics and 1 ditelo-monotelosomic of Chinese Spring with the disomics grown at konosu located in the middle part of Japan.

Characters	Monosomics	Telosomics
Vigor	poor : 5A, 5D	poor : 2BL, 3AS, 6BS, 6DL
Heading time	earlier : 3D later : 2B, 3B, 6B, 6D, 7B	earlier : 1AL later : 2AS, 2DS, 5BL, 5DL, 6AS, 6BL
Culm length	shorter : 2A	longer : monotelodisomic 5AS semidwarf : 2AS, 2BL, 2DS, 3BL
No. tillers	more : 1B, 4A, 4B fewer : 5D	more : 1DL, 7BL, monotelodisomic 4Aβ fewer : 1BL, 1BS, 2BL, 7BS
Spike length	longer : 5A(speltoidy)	longer : monotelodisomic 5AS(speltoidy) shorter : 3AS
No. spikelets	more : 5A, fewer : 2A	fewer : 2AS, 2DS, 6AS
Spike density	lax : 2A	lax : 2AL, 2DS
Grain weight per spike	ligher : 5A, 5D	lighter : 2AS, 2BL, 3AS, 6AS, 6DL
100-grains weight	heavier : 1D, 2D, 3A lighter : 3D, 5D	heavier : 3AL, 3BL, 3DL, 4DL, 7AS lighter : 2BL, 6DL, monotelodisomic 4Aβ
Grain yield per plant	slightly higher : 3A, 6A very lower : 5A, 5D (related to poor vigor)	slightly higher : 3AL very lower : 2BL (related to poor vigor)
Others		6AS : shorter 1st internode length than that of 2nd monotelodisomic 1AS : dark green leaf color 4Aα : roll leaf 6BL : chlorosis of 1st leaf

deviated from Chinese Spring disomics on some agronomic characters. There are some differences in characteristics between the monosomics and the ditelosomics. This may be because of the hemizygous effect of the genes. However, the chromosome 2A exhibited a similar effect under both hemizygous and homozygous conditions for culm length, spikelet number and spike density. The monosomic 3A also was similar to the ditelosomic 3AL for expression of 100-grains weight and grain yield per plant.

The ditelosomic lines generally exhibited inferior character(s) as compared with the monosomics and the disomics. From observations on the ditelosomics of Chinese Spring, it was concluded that deficiency of the genes located on the chromosomes of homoeologous group 2 influenced agronomic characters for the deleterious effect, while that of group 4 was hardly affected. This agreed with the previous suggestion reported by ICHII & YAMAGATA (1975).

The chromosomal locations of genes for wheat characters have been reported by numerous workers and summarized by AUSEMUS *et al.* (1967), MCINTOSH (1973, 1978) and LELLEY (1976). The present results could pointed out in respect of the respective characters

Table 2. Yield and protein content of grains produced by selfing of Chinese Spring disomic, 27 ditelosomic, 3 monotelodisomic and 1 ditelo-monotelosomic lines grown in the field at Konosu, Japan.

Chromosome arm	Yield per plant (g)	100-grain weight (g)	Grain protein (%)	Protein per grain (mg)	Protein yield per plant (mg)
Chinese Spring Disomic	8.2	1.87	13.4	2.51	1,099
monotelodisomic 1AS	4.2	1.42	16.6	2.36	697
1AL	4.7	1.49	16.4	2.44	771
1BS	1.3	1.46	18.9	2.76	246
1BL	1.1	1.42	16.6	2.36	183
1DL	7.4	1.47	16.8	2.47	1,243
2AS	1.3	1.32	19.4	2.56	252
ditelo 2BS-monotelo 2BL	2.9	1.39	16.7	2.32	484
2BL	0.1	1.05	22.6	2.37	16
2DS	4.2	1.84	16.2	2.98	680
3AS	2.5	1.53	20.1	3.08	503
3AL	9.3	1.90	17.7	3.36	1,646
3BL	7.8	2.13	13.9	2.96	1,084
3DL	6.9	2.16	13.4	2.89	925
4Aα	2.2	1.33	19.1	2.54	420
monotelodisomic 4Aβ	3.9	1.10	18.0	1.98	702
4BL	2.2	1.37	17.4	2.38	383
4DL	6.3	2.24	16.0	3.58	1,008
monotelodisomic 5AS	3.6	1.33	18.7	2.49	673
5AL	6.5	1.51	17.5	2.64	1,138
5BL	4.8	1.61	16.7	2.69	802
5DL	6.0	1.47	20.4	3.00	1,224
6AS	3.5	1.65	19.7	3.25	690
6BS	2.4	1.33	18.0	2.39	432
6BL	2.6	1.94	17.4	3.38	452
6DS	7.6	1.92	17.1	3.28	1,300
6DL	2.1	0.86	19.2	1.65	403
7AS	2.2	2.06	19.1	3.93	420
7AL	1.9	1.45	15.5	2.25	295
7BS	2.9	1.53	18.5	2.83	537
7BL	6.9	1.31	15.2	1.99	1,049
7DS	6.3	1.74	16.2	2.82	1,021

as follows.

Vigor : The ditelosomic lines, 2BL, 3AS, 6BS, 6DL and monosomic 5A, 5D were growing with poor vigor. Their growth were delayed.

Heading time : Although heading time depends on daylength and temperature, the result is shown in Table 1. It is known that the three members of homoeologous group 5 possess the genes affecting heading time (SEARS 1954 ; DRISCOLL & JENSEN 1964). The lines 5BL and

5DL were delayed, while the line 5AL was similar to disomics.

Culm length: The missing arms of homoeologous group 2, *i.e.* 2AL, 2BS and 2DL were associated with dwarfness.

No. tillers : The long and short arms of chromosome 7B showed opposite effect to each other for tillering. BHAT & GOUD (1979) reported that the monosomic population 7B had a gene for increased tiller number. A tillering controlling gene seems to be located on the chromosome 7B. The chromosome 1B showed opposite effect for tillering between the monosomic and the ditelosomic.

Spike length: Spike length of the line 3AS was about 30 per cent less than normal. It is observed that the chromosome 3A shortens spike (BHAT & GOUD 1979).

No. spikelets : The ditelosomic line 2AS and the monosomic line 2A had less number of spikelets. The chromosome 2A is reported for effect on spikelet number (SINGHAL & SINGH 1981).

Spikelet density : The ditelosomic lines, 2AL and 2DS lay lax in spike density. They had spikes about one-half normal density. The monosomic line 2A also reduced around 20 per cent in the density.

100-grains weight: The comparative observations indicated that the absence of the short arm chromosomes of homoeologous group 3 carried the increase in 100-grains weight. The absence of the short arms of chromosomes 2B and 6D were associated with poor vigor, and consequently influenced this character.

Grain yield per plant: Most of the ditelosomic and the monosomic lines fell down the grain yield showing variable range of reduction.

Data are presented in Table 2 for % grain protein and its related characters from Chinese Spring telosomic lines and the disomic control. The ditelosomic line, 2BL showed the highest % of grain protein. However, it was attributable to grain shrinkage. The higher protein values were associated with low yield and/or low grain weight. For this reason, chromosomal contribution of protein production should be estimated by both scales of protein content per grain and protein yield per plant. On this basis, the lines, 1DL, 3AL, 5DL and 6DS were higher than the disomic control for their scales. These results suggest that the arms of chromosomes 1D, 3A, 5D and 6D, i.e. 1DS, 3AS, 5DS and 6DL possess factors which influence the depression of protein production. This finding is in agreement with respect to 1DL, 6DS (MATTERN *et al.* 1978) and 5DL (MORRIS *et al.* 1973). On the other hand, FUJIWARA *et al.* (1977) and NAKATA *et al.* (1980) have reported that there were not found differences among Chinese Spring ditelosomic lines for protein content after removal of influence by seed fertility. This disagreement will be solved hereafter.

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Association of seed protein with grain weight and size in winter and spring wheat crosses.

N.M. SHAHANI and N.N. SAULESCU*

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

Selection of high grain protein content and improved quantitative traits in cereals is faced with a problem to increase protein content without sacrificing high levels of grain yield of the parental lines. The main limitations are the negative correlation between yield v/s grain protein percentage and grain boldness v/s protein percentage (JOHNSON *et al.* 1971; SHAHANI 1980). Complex genetic control of protein content (COWLEY & Wells 1980; KERTESZ *et al.* 1980: SHAHANI *et al.* 1983), influence of the environmental factors on grain protein content (BABYAKIN & PISCUNOVA 1979; SHAHANI *et al.* 1983) and the effect of fertilizers on grain protein percentage (COCHRAN *et al.* 1978; DUBETZ *et al.* 1979) are other major problems to evolve improved varieties with high grain protein percentage.

The present study was, therefore, intended to study the relationship between grain protein percentage and other important quantitative characters in genetically diverse gene pools of winter and spring wheat F_1 and F_2 crosses, in order to improve the theoretical basis by this new wheat breeding approach.

Materials and Methods

Two high yielding winter wheat lines, (F310C3-4 and F21-76) bred at Research Institute for Cereals and Industrial Crops, Fundulea, Romania, were crossed direct and reciprocal with two semidwarf spring wheat varieties (Pak-70 and Tandojam-75) procured from Agricultural Research Institute, Tandoja, Pakistan. Seeds of F_0 hybrids were sown immediately after harvest in the last week of June 1978, in Phytotron. Parents, F_1 and F_2 populations were sown in second fortnight of October, 1978 and March, 1979, using randomized complete block design with three replications in order to study the biological material in two different contrasting environments. Protein content was determined by microkjeldahl method as crude nitrogen times 5.7. Data for coefficient of correlation (r) values, coefficient of determination (r^2) and coefficient of regression (b) values were determined after Snedecor (1956).

Results and Discussions

1000-Grain Weight and Grain Protein Percentage.

Correlation coefficient (r) values of parents and F_1 populations (Table 1) are small and nonsignificant, taking in consideration that practically the parents and F_1 populations are

* Research Institute for Cereals and Industrial Crops, Fundulea, Romania.

Table 1. Correlation coefficients between 1000 grain weight and grain protein percentage of parents and F_1 populations sown in Autumn and Spring seasons.

Parents & combinations.	Autumn sowing				Spring sowing			
	r	r^2	b	Sig.	r	r^2	b	Sig.
F. 310 C3-4	−0.4083	0.1667	−0.1667	N.S.	−0.3859	0.1489	−0.1033	N.S.
F. 21-76	−0.1643	0.0270	−0.0536	N.S.	+0.2473	0.0612	+0.1473	N.S.
Pak-70.	—	—	—	—	+0.3421	0.1170	+0.1396	N.S.
Tandojam-75	—	—	—	—	−0.3358	0.1128	−0.1112	N.S.
F. 310 C3-4×Pak. 70	+0.0091	0.0001	+0.0020	N.S.	−0.1776	0.0315	−0.0317	N.S.
Pak-70×F. 310 C3-4	−0.2075	0.0403	−0.3777	N.S.	−0.0157	0.0002	−0.0053	N.S.
F. 310 C3-4×Tandojam. 75	+0.0403	0.0016	0.0114	N.S.	+0.3454	0.1193	0.0734	N.S.
Tandojam. 75×F. 310 C3-4	+0.0609	0.0037	0.0120	N.S.	−0.1100	0.0121	−0.0187	N.S.
F. 21-76×Pak. 70	−0.3744	0.1402	−0.0979	N.S.	+0.2919	0.0852	0.0513	N.S.
Pak. 70×F. 21-76	−0.4399	0.1935	−0.1354	N.S.	+0.0685	0.0047	0.0124	N.S.
F. 21-76×Tandojam. 75	+0.4972	0.2473	0.1564	N.S.	−0.3117	0.0972	−0.0657	N.S.
Tandojam. 75×F. 21-76	−0.2088	0.0436	−0.0470	N.S.	−0.3064	0.0939	−0.0885	N.S.

N.S.=Nonsignificant.

Table 2. Correlation coefficients between 1000 grain weight and grain protein percentage of F_2 populations sown in Autumn and Spring seasons.

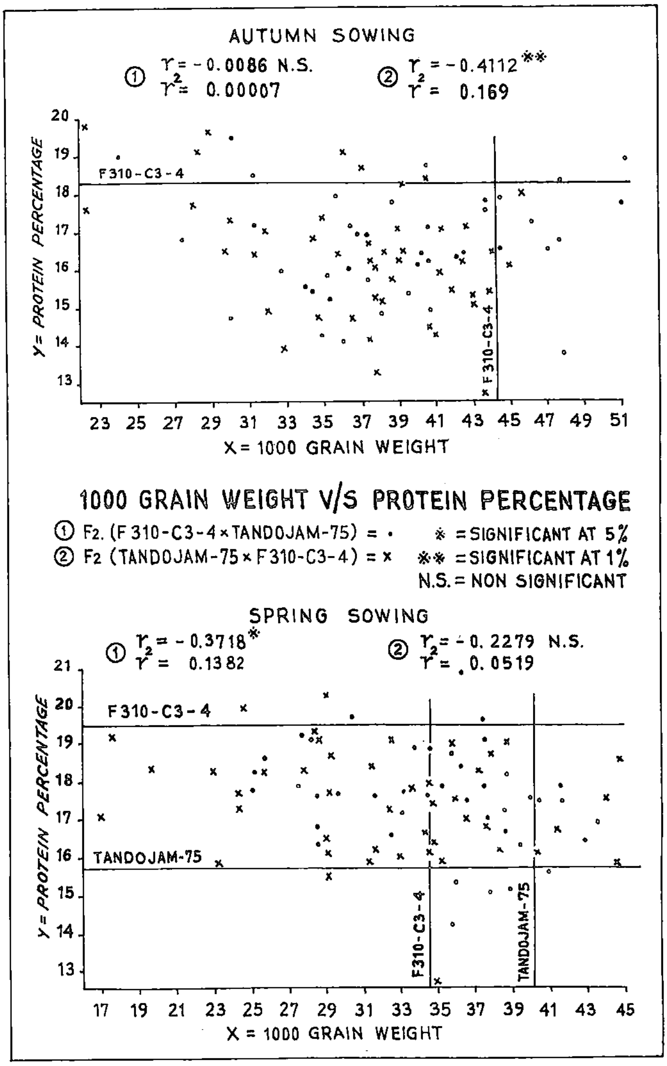
Combinations.	Autumn sowing				Spring sowing			
	r	r^2	b	Sig.	r	r^2	b	Sig.
F. 310 C3-4×Pak. 70	+0.1333	0.0178	+0.0276	N.S.	−0.4723	0.2231	−0.1492	**
Pak. 70×F. 310 C3-4	−0.2303	0.0530	−0.0503	N.S.	−0.2003	0.0401	−0.0444	N.S.
F. 310 C3-4×Tandojam. 75	−0.0086	0.00008	−0.0019	N.S.	−0.3718	0.1382	−0.1096	*
Tandojam. 75×F. 310 C3-4	−0.4112	0.1690	−0.1144	**	−0.2279	0.0519	−0.0502	N.S.
F. 21-76×Pak. 70	−0.0638	0.0041	−0.0104	N.S.	−0.1952	0.0381	−0.0461	N.S.
Pak. 70×F. 21-76.	−0.0842	0.0071	−0.0173	N.S.	−0.1966	0.0386	−0.0447	N.S.
F. 21-76×Tandojam. 75	−0.0127	0.0002	−0.0022	N.S.	−0.1490	0.0222	−0.0348	N.S.
Tandojam. 75×F. 21-76	+0.0946	0.0089	+0.0143	N.S.	−0.5126	0.2628	−0.1281	**

* =Significant at 5% level : ** =Significant at 1% level : N.S.=Nonsignficant.

generally uniform. This means that the variation, which was caused by the environmental factors in grain weight, was not correlated with the corresponding variation of grain protein percentage.

In F_2 generations most of the combinations, except a few, have small and nonsignificant correlation coefficient (r) values (Table 2). These results suggest that grain protein content was highly heterogenous in all the parental forms and parents are genetically different from each other, hence most of the variability for grain protein content was independent to the variation of 1000 grain weight. The results are in confirmation with McNeal *et al.* (1972) and Jain *et al.* (1976).

Frequency distribution (Fig. 2) shows transgressive segregates of more grain weight and



high protein percentage. This sort of transgressive segregations may provide the chances for selection of superior plants.

Single Grain Weight and Protein per Grain.

The results (Table 3 and 4) reveal that the association, between single grain weight and protein per grain of all the parents, F_1 and F_2 combinations, was positive and highly significant ($P > 0.01$). This indicates that absolute protein content closely depends upon the grain size. In F_1 population the coefficient of determination (r^2) values show a maximum variability upto 90.71 percent in protein per grain due to its relationship with grain weight, and regression coefficient (b) values indicate a maximum increase of 0.2268 miligrams of absolute grain protein with the increase of weight of one miligram per grain. Whereas, in

Table 3. Correlation coefficients between single grain weight and protein per grain in miligrams of parents and F_1 populations sown in Autumn and Spring seasons.

Parents and combinations	Autumn sowing				Spring sowing			
	r	r^2	b	Sig.	r	r^2	b	Sig.
F. 310 C3-4.	+0.6288	0.3954	0.1109	**	+0.7884	0.6216	0.1730	**
F. 21-76	+0.7718	0.5958	0.1776	**	+0.8276	0.8604	0.230	**
Pak. 70	—	—	—	—	+0.8519	0.7257	0.1821	**
Tandojam. 75	—	—	—	—	+0.8186	0.7601	0.1170	**
F. 310 C3-4×Pak. 70	+0.8327	0.6934	0.1256	**	+0.9394	0.8740	0.1558	**
Pak. 70×F. 310 C3-4	+0.9014	0.8125	0.1573	**	+0.8088	0.6541	0.1681	**
F. 310 C3-4×Tandojam. 75	+0.6734	0.4534	0.1649	**	+0.8989	0.8080	0.1702	**
Tandojam. 75×F. 310 C3-4	+0.9162	0.8395	0.1605	**	+0.9255	0.8565	0.1630	**
F. 21-76×Pak. 70	+0.5996	0.3596	0.0972	**	+0.9434	0.8900	0.1743	**
Pak. 70×F. 21-76	+0.8075	0.6521	0.0857	**	+0.9524	0.9071	0.1681	**
F. 21-76×Tandojam. 75	+0.8709	0.7584	0.2268	**	+0.8282	0.6859	0.1350	**
Tandojam. 75×F. 21-76	+0.6497	0.4221	0.1058	**	+0.6296	0.3964	0.0922	**

** =Significant at 1% Level.

Table 4. Correlation coefficients between single grain weight and protein per grain in miligrams of F_2 populations sown in Autumn and Spring Seasons.

F_2 combination	Autumn sowing				Spring sowing			
	r	r^2	b	Sig.	r	r^2	b	Sig.
F. 310 C3-4×Pak. 70	+0.9213	0.8488	0.1565	**	+0.7649	0.5851	0.1192	**
Pak. 70×F. 310 C3-4	+0.7182	0.5158	0.1093	**	+0.9091	0.8265	0.1538	**
F. 310 C3-4×Tandojam. 75	+0.8949	0.8009	0.1634	**	+0.7953	0.6325	0.1343	**
Tandojam. 75×F. 310 C3-4	+0.8181	0.6693	0.1312	**	+0.8967	0.8041	0.1554	*
F. 21-76×Pak. 70	+0.9480	0.8987	0.1778	**	+0.8654	0.7489	0.1581	**
Pak. 70×F. 21-76	+0.890	0.792	0.1671	**	+0.8636	0.7458	0.1517	**
F. 21-76×Tandojam. 75	+0.8814	0.7768	0.1445	**	+0.8814	0.7769	0.1550	**
Tandojam. 75×F. 21-76	+0.9399	0.8834	0.1660	**	+0.8038	0.6461	0.1295	**

** =Significant at 1% level.

F_2 population the maximum variability 89.87 percent was recorded in absolute protein content due to its relationship with grain weight and the maximum increase of 0.1778 miligrams of protein per grain was noted with the increase of weight of one miligram per grain. This confirms the possibility of using the single grain weight as a phenotypic marker in selecting high grain protein yield. The results are in agreement with JAIN *et al.* (1976), who reported the similar results while working on breeding for higher protein yields in bread wheat.

Boldness of Grains and Grain Protein Percentage.

The grains were grouped into three categories viz. bold grains, intermediate grains and

Table 5. Mean Values of Grain Protein percentage from Bold, Intermediate and Shrivelled Seeds of F_2 populations sown in Autumn and Spring seasons.

Combinations		Autumn			Spring		
		Bold grains	Inter-mediate grains.	Sheri-velled grains.	Bold grains	Inter-mediate grains.	Sheri-velled grains.
F310-C3-4×Pak. 70	$\bar{X}$	15.717	16.273	16.394	15.198	16.545	16.873
	S	1.1038	1.6945	1.2030	1.4878	1.1024	1.4681
Pak. 70×F310-C3-4.	$\bar{X}$	16.054	16.231	16.696	16.158	16.368	17.576
	S	1.3149	1.3184	0.6542	0.8254	0.9714	1.3101
F310-C3-4×Tandojam. 75	$\bar{X}$	16.016	16.394	17.187	15.764	16.802	17.932
	S	0.8494	1.2787	1.3423	1.165	1.2360	1.3897
Tandojam. 75×F310-C3-4.	$\bar{X}$	14.989	16.013	17.486	16.457	16.571	17.910
	S	1.2833	1.2078	1.2900	0.8568	1.4648	1.2572
F21-76×Pak. 70	$\bar{X}$	16.938	17.473	17.511	15.570	16.812	17.666
	S	1.6238	1.6048	1.2507	1.2406	1.2954	1.6595
Pak. 70×F21-76	$\bar{X}$	16.093	17.554	18.255	15.535	16.766	17.608
	S	1.5828	1.5142	1.4508	1.6655	1.3804	1.5189
F. 21-76×Tandojam. 75	$\bar{X}$	16.110	16.938	16.609	16.813	17.220	17.602
	S	1.0708	1.3422	0.6600	1.8987	1.4769	1.4442
Tandojam. 75×F. 21-76.	$\bar{X}$	16.289	16.360	16.927	16.113	17.356	18.438
	S	1.0087	1.3082	0.8756	1.642	1.7336	1.4819

$\bar{X}$=Mean. S=Standard deviation.

shrivelled grains. It is quite clear from the results (Table 5) that shrivelled grains, in all the combinations, had a higher grain protein content than the bold grains. This tendency of association, of high protein percentage with shrivelled grains, is probably the cause of negative correlation between grain yield and grain protein percentage. These results confirm the conclusion that incomplete development of seeds, which is caused by unsuitable climatic conditions greatly affect on the grain stract deposition and proportionately protein percentage is increased. The results are in confirmation with IONESCU *et al.* (1967), who reported the similar results while working on some biochemical characters of winter bread wheat in Romania.

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Salt tolerance of wheat in relation to nature of salinity

R.P.S. CHAUHAN and J. PRASAD

Department of Agricultural Chemistry, R.B.S. College,
Bichpuri, Agra, India-283105

Wheat is one of the important cereal crops of the world which is reported to be grown successfully upto an ECe level as high as 6.00 and 6.5-7.5 mmhos/cm by MASS *et al.* (1977) and CHAUHAN *et al.* (1980) respectively. So far salt-tolerance of wheat has been evaluated as its non-specific response to decreased water potential caused by excessive amount of salts in the root medium. Salt-tolerance of crops varies with the nature of the salt constituting salinity to which wheat may not be an exception. A study was, therefore, undertaken to find out the effect of type of salinity on wheat (*Triticum aestivum* Linn. emend. Thell) grown on alkaline sandy loam soils under semi-arid climatic conditions of India.

Materials and Methods

Pot experiments were conducted in 1980-81 in R.B.S. College, Bichpuri, Agra. Seven sets of experiments were conducted with NaCl, $CaCl_2$ $MgCl_2$, $NaHCO_3$, Na_2SO_4, NaCl+Na_2SO_4+$NaHCO_3$ (1 : 1 : 1) and NaCl+MgCl2+CaCl2 (1 : 1 : 1) each at two levels of salinity, viz 7.5 and 15.0, 7 and 11.5, 7.0 and 11.5, 6 and 12.0, 6 and 11.5, 7.0 and 11.2 and 7.5 and 11.5 mmhos/cm ECe respectively excluding a common control. The soil used had ECe 3 mmhos/cm, pH 8.2, organic carbon 0.32% and 9.6, 3.4, 16.0, 16.1 and 12.6 me/l Ca^{2+}, Mg^{2+}, Na^{+}, Cl^{-} and SO_4^{2} respectively were present in saturation extract with 6.3 sodium adsoprtion ratio. The experiments were conducted in china-clay cylindrical pots, having a diameter of 30 cm and capacity of 10 kg, arranged in a randomized block design, with 3 replications. Each pot was filled with 10 kg soil, and recommended amounts of N, P and K were mixed in each pot before sowing. In each pot 10 seeds of wheat (WL 711) were sown on 28 November, 1980. After emergence, seedlings were thinned 6 to a pot. The crop was raised with standard management practices and irrigated six times each with 2litres of good quality canal water.

Grain and plant samples at flowering stage collected from each pot, were mixed treatmentwise and anlysed for Ca, Mg, Na, K, P, and protein in case of grain and for former four in case of plant samples following usual laboratory procedures. Free proline was determined in fresh leaves according to the method described by BATES *et al.* (1973).

Results and Discussion

Effect of nature of salinity on germination, 100 grain weight, free proline accumulation and yield of wheat, have been presented in Table 1. The germination was delayed with salinity in general. The maximum delay at first level of salinity was observed with the salinity caused by the mixture of sodium salts. At second level of salinity, germination

Table 1. Effect of type of salinity on germination, 100 grain weight, yield and free proline accumulation in wheat.

Treatments	ECe mmho s/cm	Average delay in germination(days)	100 grain wt. (g)	Yield (g/pot)		Free proline (μ mol e/g fresh wt.)
				Grain	Straw	
Control	3.0	—	5.15	8.2	14.9	14.2
NaCl	7.5	5.25	4.14	6.2	12.0	9.3
	15.0	10.75	3.01	4.7	9.0	5.8
C.D. at 5%	—	—	0.901	1.58	1.81	—
$NaHCO_3$	6.0	4.25	4.35	6.4	12.1	6.2
	12.0	6.75	3.44	4.2	10.3	3.5
C.D. at 5%	—	—	0.271	1.42	2.49	—
Na_2SO_4	6.0	3.75	4.86	8.2	17.7	25.8
	11.5	6.00	4.00	6.8	11.8	31.4
C.D. at 5%	—	—	0.452	1.33	2.49	—
$CaCl_2$	7.0	3.0	5.07	8.6	13.6	24.0
	11.5	5.25	5.18	6.0	10.0	27.0
C.D. at 5%	—	—	N.S.	1.81	1.81	—
$MgCl_2$	7.0	3.50	4.95	8.6	15.1	22.0
	11.5	6.25	5.05	4.7	11.0	26.8
C.D. at 5%	—	—	N.S.	2.03	2.03	—
$CaCl_2$ + $MgCl_2$ +	7.5	3.75	4.70	8.7	15.2	23.0
NaCl	11.5	7.75	3.50	5.5	10.0	25.8
C.D. at 5%	—	—	0.485	1.21	3.512	—
NaCl + Na_2SO_4 + $NaHCO_3$	7.0	6.75	4.68	8.5	14.2	20.0
	11.2	7.25	3.60	6.2	10.5	24.0
C.D. at 5%	—	—	0.679	1.81	2.285	—

N.S.=Non-Signijcant.

delayed by a range of 0-2.5 days depending upon the nature of salt except NaCl where salinity was too high. 100 grain weight decreased significantly with NaCl and $NaHCO_3$ salts even at first level of salinity; tolerance limit of wheat, over control while in other cases reduction was noted at highest levels of salinity. The decline in 100 grain weight may be attributed to decreased photosynthesis and poor utilization of photosynthate in presence of high osmotic pressure in the root zone along with the disturbed inorganic nutrition of plants (Khalil *et al.* 1967).

Table 1 further indicates significant reduction in straw and grain yields at highest level of salinity with all salts. $NaHCO_3$ and NaCl salinities reduced grain yield even at first level of salinity perhaps due to reduction in 100 grain weight. Straw yield increased significantly at 6 mmhos/cm ECe with Na_2SO_4 over control while increase at lower level of salinity with $MgCl_2$ and chlorides of Ca+Mg+Na was not significant. Straw production also declined significantly at first level of salinity caused by $NaHCO_3$ and NaCl. Free proline accumulation (Table 1) also declined with NaCl and more so with NaHCO3 type of salinity. In other cases free proline increased with salinity and attained maximum concentration with Na_2SO_4.

The data presented in Table 2 indicates that except Ca and Mg-salts, calcium and magnesium accumulation in plants declined at first level of salinity over control and due to poor growth of plants at second level of salinity, their accumulation was higher than preceding level. Sodium accumulation increased with all types of sodium salts, their mixture and salinity levels and declined with $CaCl_2$ and $MgCl_2$ salinity at 11.5 mmhos/cm ECe. The salinity caused by the mixture of $CaCl_2+MgCl_2+NaCl$ did not allow sodium to accumulate to the toxic concentration. K content in general decreased with all salts and almost with salinity but there was no much difference between first and second levels of salinity in this respect. K/Na ratio declined with type and amount of salinity. The degree of decrease was distinctly greater with the mixture or individual sodium salt. The critical limit of K/Na ratio with repect to free proline accumulation is 4.1.

The chemical composition of grains presented in Table 3 shows increased content of calcium with $CaCl_2$, slight change with $MgCl_2$ and no change with the salinity caused by the mixture of chlorides of calcium, magnesium and sodium. Salinity caused by sodium salts increased Na and had an antagonistic effect on Ca contents of grains. Mg content in grains increased with $MgCl_2$ and changed slightly in other cases. Grain obtained from sodium salinity were comparatively poor in K content. $NaHCO_3$ salinity at 12 mmhos/cm ECe improved grain content of P. Increased protine content in grain with salinity corroborates the findings of UPRETY (1970) and KUMAR *et al.* (1980)

Present study shows maximum toxic effect of $NaHCO_3$ followed by NaCl salinity even at tolerance limit of wheat. This may be ascribed to the more caustic effect of HCO_3 than Cl ion in addition to absorption and accumulation of Na in the plants at the expense of K and

Table 2. Cations' accumulation in wheat at flowering stage of growth

Treatments	ECe mmho s/cm	Ca %	Mg %	Na %	K %	K/Na ratio
Control	3.0	0.63	0.16	0.42	3.56	8.5
NaCl	7.5	0.53	0.14	0.75	2.78	3.7
	15.0	0.65	0.26	1.25	2.50	2.0
$NaHCO_3$	6.0	0.44	0.12	0.67	2.28	3.4
	12.0	0.54	0.17	1.08	2.25	2.1
Na_2SO_4	6.0	0.53	0.13	0.56	3.32	5.9
	11.5	0.55	0.18	0.83	3.40	4.1
$CaCl_2$	7.0	0.79	0.21	0.40	3.32	8.3
	11.5	0.90	0.26	0.32	2.50	7.8
$MgCl_2$	7.0	0.66	0.21	0.42	3.36	8.0
	11.5	0.68	0.34	0.33	2.31	7.0
$CaCl_2$+ $MgCl_2$+	7.5	0.53	0.16	0.47	3.43	7.3
NaCl	11.5	0.71	0.28	0.50	2.70	5.4
Na_2SO_4+ NaCl+	7.0	0.53	0.14	0.62	3.35	5.4
$NaHCO_3$	11.2	0.60	0.21	0.78	3.20	4.1

Table 3. Composition of wheat grains as affected by salts and salinity.

Treatments	ECe mmho s/cm	Ca %	Mg %	K %	Na %	P %	Crude protein %
Control	3.0	0.12	0.11	0.55	0.035	0.23	8.48
NaCl	7.5	0.10	0.11	0.56	0.038	0.24	10.65
	15.0	0.08	0.10	0.37	0.050	0.23	12.35
$NaHCO_3$	6.0	0.11	0.12	0.58	0.040	0.23	10.34
	12.0	0.10	0.12	0.43	0.060	0.31	11.00
Na_2SO_4	6.0	0.11	0.10	0.61	0.036	0.23	11.20
	11.5	0.10	0.11	0.43	0.039	0.28	12.60
$CaCl_2$	7.0	0.14	0.10	0.53	0.018	0.19	9.46
	11.5	0.15	0.10	0.51	0.011	0.22	12.40
$MgCl_2$	7.0	0.11	0.13	0.55	0.025	0.21	9.66
	11.5	0.12	0.14	0.55	0.028	0.23	11.87
$CaCl_2$+ $MgCl_2$+	7.5	0.12	0.11	0.57	0.025	0.26	9.03
NaCl	11.5	0.12	0.11	0.58	0.040	0.21	11.87
NaCl+ $NaHCO_3$+	7.0	0.08	0.12	0.57	0.046	0.24	8.60
Na_2SO_4	11.2	0.07	0.12	0.43	0.053	0.25	11.78

Ca. High sodium with consequent decrease in potassium results into a level of K/Na ratio lower than its critical limit for free proline accumulation. Tissue K/Na ratio under stress conditions is reported to raise salt tolerance of plants through free proline accumulation by CHAUHAN *et al.* (1980) and CHAUHAN & CHAUHAN (1980). An entirely different situation is observed with Na_2SO_4 salinity. Na_2SO_4 appeared comparatively less toxic among sodium salts despite of excess accumulation of Na in tissues probably due to exceptionally high content of free proline. When salinity consists predominantly of monovalent cations and divalent anions ; Na_2SO_4, cation uptake rate exceeds those of anions and ionic balance inside the plants is achieved by synthesis and accumulation of organic acids (CRAM 1976). More accumulation of amino-acids with SO_4 than Cl salinity is reported by STROGNOV (1976) and that of proline in particular by CHAUHAN (1983). Sinificant yield decline even with increase in free proline accumulation at highest level of salinity caused by salts other than $NaHCO_3$ and NaCl may be due to reduced rate of proline accumulation compared to precoding level of salinity (CHAUHAN *et al.* 1980) which is not enough to make osmoregulation adjustments inside the plant in response to low osmotic potential in the root media. It is, therefore, obvious that free proline accumulation in plants under water stress is associated to the salt tolerance of crop (PALFI & JUHASZ 1970 ; CHU *et al.* 1974 ; STOREY & WYNJONES 1980 ; CHAUHAN *et al.* 1980 ; CHAUHAN & CHAUHAN 1980 ; CHAUHAN *et al.* 1983).

From the present investigation it is concluded that $NaHCO_3$ followed by NaCl salinity is more harmful to wheat, than others tested.

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An unrecognized sources of inoculum of wheat stem rust in india

Srikant KULKARNI

Department of Plant Pathology University of Ariicultural Sciences
Dharwad-500 005 (Karnataka State) India.

Wheat in India is generally cultivated as a winter crop. In the Plains and South Indian plateau normally sown in late October or November and harvested in March or April. In South India, the crop matures by February end or early March but in the Northern Plains maturity is between last week of March to middle of April. Sometimes the late sown crops are delayed by a week or two. In Nilgiri and Pulney hills of South India two wheat crops are taken. The winter crop is sown in June and harvested in September. In the northern hills sowing is done a bit earlier than in the plains and crop normally matures by May except at high attitudes (7,000-8,000 ft a.s.l) where it matures by June.

MEHTA (1952) had regarded Central Nepal and Niligri as "the most dangerous foci of infection". He had identified Nilgiri and Pulney hills as foci of infection of black and brown rusts from South India, and also recorded early appearance of black rust in place like Dharwad in the South.

Till recently, it was thought that the primary inoculum of black rust is introduced in the plains from north as well as south. But according to JOSHI *et al* (1971) early appearance of black rust has been recorded in south or Central India in the month of January and February or at times even in December.

It was observed in 1976-77, the stem rust incidence was less in Niligiri and Pulney hills but more in plains of Karnataka. Further more, the incidence of infection was too low throughout southern hills to produce the amount of inoculum required for observed infection. The race distribution determined from collection in Karnataka differed from that found in Southern hills.

Hence, an extensive survey was conducted in Karnataka to locate the focus of infection of stem rust of wheat. The off season survey was conducted during 1980, 1981, and 1982 in Karnataka. It was found that, the farmers grow wheat during off season in the plains of Chikmagalur and Chitradurga districts of Karnataka. They sow right from May to September. This off season wheat is found in patches along with Onion and Coriander. It was found that, there was heavy stem rust infection on off season wheat. The races identified were 21 and 117 A-1 of stem rust. The winter sowing starts from October onwards. Hence, there is a link between off season and normal season crop. The observations suggested a previously unrecognized source of wheat stem rust inoculum in India. Further field survey will investigate the potential of this area as a source wheat stem rust inoculum.

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Influence of tannins on endogenous and GA_3 induced plumule growth in four genetically diverse wheat cultivars

V. KUMAR* and B.D. BAIJAL

Department of Botany, Agra College, Agra, India

The tannins are well known constituents of plant body. Their function is obscure. Treatment with tannins has been reported to inhibit root growth (GRIMM, 1953 ; KLOSA, 1948) and germination (FÖRESTER, 1957). In contrast, there are reports of promoting root growth (KHRISTEVA, 1959), seedling growth (POPOFF, 1931) and germination (FÖRESTER, 1957). Several tannins have been identified as antagonist to GA and IAA induced growth in pea seedlings and cucumber hypocotyl (CORCORAN *et al.* 1972). The authors (KUMAR *et al.* 1981, 1982) reported differential response of four wheat cultivars to applied GA. Further investigation were carried out to study the effect of tannins on endogenous as well as GA induced growth in wheat to find out how tannins affect growth expression and in turn, the drawfism.

Materials and Methods

Seeds of four wheat varieties namely C-306 (tall), Sonalika (single dwarf), Kalyansona (double dwarf) and Moti (triple dwarf) procured from the Division of Genetics, I.A.R.I., New Delhi were used in the present investigation.

The tannins-coumarin and gallic acid were supplied by M/S. E. MERCK, Dermstadt. W. Germany. The sterilized seeds were soaked for 24 hours in tannins solution (0, 10 and 100 ppm) with or without GA_3 (1 ppm). After treatment, the seeds were thoroughly washed to remove adhering solution. The seedlings were raised in dark according to the method described earlier (KUMAR *et al.* 1982). Growth measurement was carried out after 5 days and the data expressed as percentage over control.

Results

GA_3 induced growth : - The gibberellic acid enhanced plumule growth of C-306, Sonalika and Kalyansona. The growth of Moti, the triple dwarf, remained practically unaffected. Tannins and endogenous growth : - The data portrayed in Fig. 1 indicates that contrary to GA induced growth, the C-306 and Kalyansona showed reduction in growth due to both the tannins which increased with the concentration. The reduction was 51% due to gallic acid (100 ppm) and 52% due to coumarin (100 ppm) in the variety C-306. The corresponding reduction was 46% and 38% respectively, in Kalyansona.

Unlike the above two varieties, the plumule growth in Sonalika and Moti was enhanced due to the tannins at 10 ppm. The Sonalika displayed greater increase than Moti. Higher

* Present address-Gujarat Agricultural University, Athwa Lines, Surat 395 007, INDIA

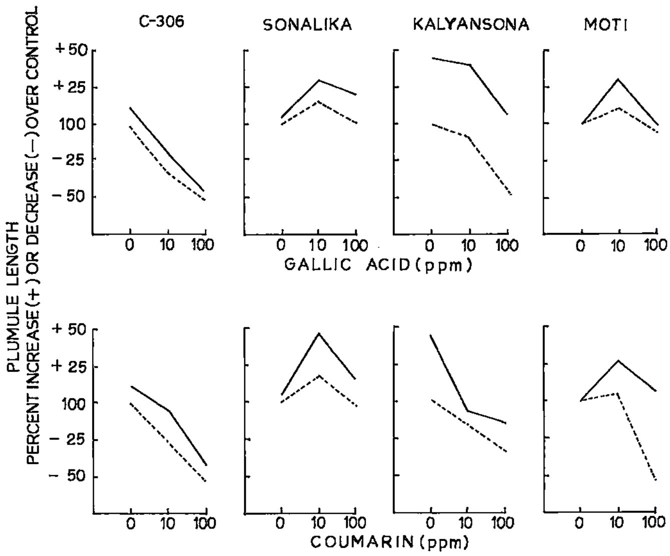

Fig. 1. Effect of tannins-gallic acid and coumarin on endogenous (broken lines) and GA_3 induced plumule growth (continuous lines) in different varieties of wheat.

concentration tended to be inhibitory, particularly of coumarin, more so in the Moti.

Tennins and GA_3 induced growth: - Almost a steep fall in the GA induced growth of the C-306 and Kalyansona was observed due to tannins treatment which proportionately increased with the later's concentration.

In the Sonalika, the GA induced plumule growth was further enhanced by tannins application e.g., the plumule length increased by 6% and 16% due to GA and gallic acid, respectively, a combination of the two (1:10) brought about 30% increase in the same. Similarly, the coumarin also displayed supplimentary effect when coupled with GA_3. The triple dwarf Moti which did not express any effect of GA on plumule growth registered enhancement when supplied with a combination of GA+tannins, over the tannin alone. It recorded nearly 30% and 27% growth with GA+gallic acid and GA+coumarin (1:10) respectively than the gallic acid (11%) or coumarin (6%) alone.

Reversibility of inhibition: - The reversibility of inhibitory effect can be viewed from the fact that inhibition of plumule growth due to tannins was considerably ameliorated and even completely overcome by the induction of GA_3 in the medium. In case of Kalyansona, whereas the reduction due to gallic acid was completely reversed, that by coumarin was partially reversed. Similarly, in Moti, the reduction in growth due coumarin (100 ppm) was restored to normal.

Discussion

Reports on the tannin effecting plant growth and development are often inconsistant. Root growth (Evanari, 1949; Happich *et al.* 1954) and germination (Corcoran, 1970) may be inhibited or enhanced, seedling growth may also be affected (POPOFF, 1931). The plumule growth in the four wheat varieties, undertaken in the present study, was diversely affected by applied tannins. HARADA & NAKAYAMA (1974) observed this phenomenon in certain rice cultivars and ascribed it to endogenous tannin's level.

The gibberellin induced growth was also affected due to tannins application. The finding corraborates that of CORCORAN *et al.* (1972) and GREEN & CORCORAN (1975). They established the tannins as inhibitory to GA induced growth and stressed their role as antagonist to GA action and by increasing the concentration of GA, they could restore the tannin depressed growth. In the present course also, the GA tends to restor (in certain cases it has actually done so) tannin depressed growth. However, the two cases may be different, since this investigation proved tannins to be inhibitory and/or promotory to endogenous growth too, besides GA_3 induced growth. Thus it lent credence to the idea that tannins are involved in the normal control of the plant growth and that both GA and tannins are involved in the same physiological system.

The exact mechanism of inhibition by tannins is still an enigma. PALEG (1965) suggested possible pathways in which GA antagonist could act. GREEN & CORCORAN (1975) pointed out that tannins could act as GA inhibitors by acting as protein inhibitors. But they can not be considered general protein inhibitors, firstly because of protein specificity and secondly, if the inhibition would be there, the GA application would not restore the depressed growth. It was further emphasised that antagonistic action of tannins probably does not involve GA synthesis (GREEN & CORCORAN 1975) which holds true here also, otherwise GA induced growth should not have been affected. Possibility of tannins as competitive inhibitors of GA can also be ruled out because of the dissimilarity in the chemical structure of the two group of substances. There is one possible mechanism 'that is' the tannins could act as an inhibitor of a protein which specifically recognises gibberellins to rander it incapable of promoting growth. But in any case, the exact mechanism of inhibition by tannins is by no means completely understood.

An interesting point emerged out the study was that the triple dwarf Moti which is an insensitive variety to applied GA responded well to tannins and exhibited further enhancement in growth when GA was supplimented with tannins. It appears that tannins application made this variety sensitive to applied GA.

Thus response of the Moti to GA in the presence of tannins seems abstruse. It has been pointed out by the authors (KUMAR 1977; KUMAR & BAIJAL, 1983) that non-responsiveness of this dwarf variety with respect to growth and protease activity involves some natural inhibitor which is probably produced due to altered gene action. GALE & LAW (1976) opined that in certain insensitive dwarf wheat, genes could act via the production of a GA-antagonist which must operate at the active site of GA action and not on the GA molecule itself. STODDART *et al.* (1974) and KOMOTO *et al.* (1973) reported some protein fraction from dwarf peas that selectively binds with biologically active GA's making it inactive.

In the light of foregone discussion, it would appear that the two phenomenon have an unexpected corrollary and it might be possible that tannins action also involves the same fraction of protein which renders GA incapable of its activity. It is likely that in the presence of exogenous tannins, the GA is somehow released free and then both the substances act in their own way. That is probably how proteins are associated with GA and tannins which is turn determine the physiology of dwarfism.

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Genotypic variation in mineral uptake efficiency in wheat mutants under different cultural regimes

A.S. LARIK, H.M.I. HAFIZ* and Y.A. AL-SAHEAL

Department of Crop Production, Gassim College of Agriculture,
King Saud University (Gassim Branch) Saudi Arabia

The genetic improvement of bread wheat, *Triticum aestivum* L. obtained by breeding is due partly to the incorporation of traits which are comparatively easily recognised such as disease resistance and lodging. However, even when these limiting factors are eliminated from the environment the different genotypes display varying response to mineral nutrients, presumably due to their different genetic makeup and physiological superiority (BINGHAM 1967). The mineral uptake capability of a genotype plays an important role in the performance of that particular genotype (RASMUSSON *et al* 1971; SAGGAR *et al* 1974; SIMS & PLACE 1968).

The present investigations were undertaken to study the genetic differences in the induced mutants and their mother cultivars with respect to the differential uptake, accumulation, translocation and utilization of N, P, K, Mg, Ca and Na elements at different ontogenetic stages of wheat. Earlier investigations have demonstrated clear differences amongst these mutants, mother cultivar and a commercial variety for many morphological, agronomical and physiological characters (LARIK 1978, 1979; LARIK & HAFIZ 1981, 1983; LARIK *et al* 1984a, b; SIDDIQUI & ARAIN 1974).

Material and Methods

Homogeneous seeds of three cultivars of bread wheat *Triticum aestivum* L. em. Thell ($2n=6x=42=AA\ BB\ DD$) viz., C-591 (Locally bred), Nayab and Indus-66 (Mexican origin) and three phenotypically stable mutants of each variety were grown under field and pot house conditions at the Botanical Garden, Sind Agriculture University, Tando Jam, Pakistan. Seeds of different cultivars were drilled in the beds in five rows 30.5 cm apart and 2 m long at the rate of 100 kg/hectare. The experiment was laidout with randomized complete block design with five replications. The area of main plot was 24×20 m and sub-plot was 2.0×1.5 m.

Earthen pots measuring 22×20 cm were filled with 2.5 kg of air dried soil. Soil was irrigated with 500 ml of tap water one day before sowing. Twelve seeds per pot of 13 genotypes were planted at about 2 cm depth with marked glass rod. The experiment was planned with completely randomized design having five replications. Thus, altogether 195 pots were used i.e. 65 pots for each harvest. Mechanical and chemical analysis of soil is

* Department of Botany, New Campus, Punjab University, Lahore, Pakistan.

Table 1. Chemical and mechanical soil analysis

Soil pH (1:2.5)	T.S.S (1:2.5) $\mu g/ml$	$CaCo_3$ %	Olsen's P $\mu g/g$	Total N %	Water soluble cations				Exchangeable cations			C.E.C meq/100g	Mechanical analysis			Texture
					Ca	Mg	Na	K	Mg	Na	K		Sand	Silt	Clay	
					meq/100g				meq/100g				%			
8.2	392	11	6.5	.07	.470	.025	.092	.091	2.60	.856	.645	12.48	31.5	37	31.5	Loamy

given in Table 1.

Standard dose of NPK fertilizers 54 kg N, 27 kg P_2O_5 and 13.5 kg K_2O per acre were used as mineral nutrients for the crop. Ammonium nitrate, Diammonium phosphate and Potassium hydrogen phosphate were the source of NPK. Full dose of fertilizer was broadcasted and ploughed in the field, before sowing. In pots the amount of mineral nutrients per pot was calculated equivalent to the field rate on soil weight basis. The full dose was applied by thoroughly mixing it in the soil of each pot before irrigating the soil for sowing.

Plant samples for chemical analysis were taken at three different intervals of four weeks and eight weeks after sowing and at maturinty. Samples were dried at 70℃ in an oven and grinded by the sample grinder. One gram from the grinded sample were used for chemical analysis. The samples were digested by H_2SO_4 (5 ml per gm) and H_2O_2 method. The extract was diluted to 100 ml with distilled water and was used for determining the nitrogen, phosphorus, potassium, magnesium, calcium and sodium content in the samples (JACKSON 1958). Total nitrogen was determined by the modified microkjeldahl method. P content was determined Colorimetrically using Bartons Yellow color method on Spectronic-20 at 465 $m\mu$. Ca, K, Na were analysed by Flame photometry using Hangarian Flame Photometer. Mg was determined by the absorption spectrophotometry method with atomic absorption.

Results and Discussion

chemical analysis of plant samples of all the genotypes for mineral uptake efficiency and distribution at various ontogenetic stages of *Triticum aestivum* L. is depicted in Tables 2 to 4. Mutant-37 of Indus-66 displayed significantly ($P \geq .01$) higher uptake of N than all the other genotypes at all sampling dates in both sets of experiments. The N uptake of M-38 of C-591 was significantly higher than its mother cultivar at all sampling dates. In most of the cases Nayab mutants have higher N uptake than their parent and Mexi- Pak. However, Nayab mutant-27 was characterized by low grain N and high straw N content (LARIK *et al* 1984b). This observation indicate that this particular mutant is unable to transfer the absorbed N from shoot to the grain. This physiological function is undoubtedly gene controlled and differences are therefore inherited and gene probably determine not the character of complex, but the total uptake of an element in any specific environment (SINGH & LAMB 1970). Similarly, most of the Indus mutants were higher in N uptake than their parents and Mexi -Pak (Tables 2 to 4). M-27 was consistently higher than parent and Mexi-Pak at all sampling dates. The differential uptake of this mutant suggest that it has a greater uptake

Table 2. Mineral uptake by different wheat genotypes at first and second harvest under field conditions.

Genotype/Pedigree	Mineral uptake in percent											
	First harvest (4 weeks)						Second harvest (8 weeks)					
	N	P	K	Mg	Ca	Na	N	P	K	Mg	Ca	Na
C-591 (Control)	3.08	0.25	4.19	0.21	0.42	0.14	1.68	0.23	2.95	0.129	0.84	0.06
Mutant-7 EMS	2.74	0.33	4.70	0.22	0.42	0.12	1.62	0.29	3.10	0.133	0.80	0.04
Mutant-28 EMS	2.46	0.29	4.36	0.21	0.44	0.08	1.74	0.26	3.03	0.127	0.72	0.04
Mutant-38 EMS	3.36	0.34	5.26	0.22	0.47	0.16	2.13	0.31	3.18	0.137	0.87	0.05
Nayab (Control)	2.24	0.19	3.88	0.16	0.40	0.11	1.51	0.22	2.38	0.112	0.64	0.03
Mutant-6 25 kR	2.80	0.25	4.40	0.20	0.46	0.17	1.71	0.24	2.68	0.124	0.70	0.05
Mutant-22 20 kR	2.58	0.28	4.04	0.19	0.41	0.10	2.10	0.26	2.84	0.131	0.67	0.04
Mutant-27 30 kR	2.69	0.29	4.18	0.21	0.43	0.11	1.90	0.26	2.37	0.119	0.66	0.04
Indus-66 (Control)	2.97	0.22	4.43	0.22	0.52	0.13	1.82	0.26	2.46	0.122	0.77	0.04
Mutant-13 20 kR	2.91	0.28	3.98	0.20	0.39	0.13	1.86	0.29	2.52	0.125	0.72	0.04
Mutant-37 20 kR	3.53	0.29	4.32	0.22	0.40	0.10	2.18	0.29	2.48	0.142	0.64	0.06
Mutant-39 20 kR	3.19	0.23	3.96	0.20	0.43	0.09	1.79	0.19	2.18	0.119	0.62	0.03
Mexi-Pak (Check)	2.74	0.22	4.31	0.22	0.43	0.19	1.71	0.21	2.36	0.128	0.71	0.06
L.S.D. 0.05 =	N.S.	N.S.	N.S.	N.S.	0.06	N.S.	N.S.	0.05	0.36	0.017	0.10	N.S.
L.S.D. 0.01 =	N.S.	N.S.	N.S.	N.S.	0.07	N.S.	N.S.	0.07	0.48	N.S.	0.13	N.S.
S.E. =	0.30	0.03	0.26	0.01	0.02	0.03	0.16	0.02	0.01	0.006	0.03	0.01
C.V. % =	10.50	12.60	6.30	6.30	4.20	26.60	8.40	7.00	4.90	4.90	4.90	23.80

efficiency as a result of either a stronger root system or greater suction pressure. This probably accounts for the greater nitrogen absorption of this mutant. On the contrary, low N content of M-13 of Indus-66 in field experiment and M-28 and 38 of C-591 in pot experiment at maturity indicate the rapid translocation of N to aerial parts. Similar varietal differences in N uptake and utilization have been reported by a number of workers (McNeal *et al* 1966; Gasser & Iordanov 1967; Braun & Fischbeck 1976).

Mutants with superior P uptake and accumulation were also identified in the present work (Tables 2 to 4). All mutants of Indus-66 had significantly ($P \geq .01$) higher uptake and accumulation of P at all sampling dates than their parent and commercial variety Mexi-Pak. M-38 of C-591 displayed higher P uptake than its mother cultivar at all sampling dates except at second harvest and at maturity in pot condition. Therefore, these mutants can be classified as P-efficient mutants as suggested by Brown (1966), because of their high P uptake capabilities from the growing media. On the other hand, Nayab mutants showed differential response to P uptake. These studies clearly suggest genetic control of P accumulation differences (Barber *et al* 1967; Lyness 1936; Saggar *et al* 1974).

The behaviour of the genotypes for K uptake and accumulation is presented in Tables 2 to 4. Generally the mutant genotypes have displayed improvement in K uptake at different sampling dates under both sets of conditions. Mutant-38 consistently exhibited higher K uptake compared to its mother cultiver at various ontogenetic stages under both conditions.

Table 3. Mineral uptake by different wheat genotypes at first and second harvest under pot conditions.

Genotype/Pedigree	Mineral uptake in percent											
	First harvest (4 weeks)						Second harvest (8 weeks)					
	N	P	K	Mg	Ca	Na	N	P	K	Mg	Ca	Na
C-591 (Control)	3.02	0.40	4.38	0.27	0.28	0.15	1.46	0.32	2.50	0.16	0.24	0.09
Mutant-7 7hr EMS	3.34	0.48	5.20	0.27	0.30	0.13	1.46	0.29	2.67	0.16	0.25	0.10
Mutant-28 7hr EMS	3.64	0.44	4.90	0.24	0.29	0.12	1.62	0.41	2.56	0.15	0.23	0.09
Mutant-38 7hr EMS	3.19	0.54	5.10	0.27	0.28	0.11	1.96	0.30	3.69	0.17	0.29	0.12
Nayab (Control)	2.58	0.46	5.20	0.23	0.28	0.09	1.57	0.25	2.02	0.14	0.18	0.07
Mutant-6 25 kR	2.80	0.42	4.96	0.33	0.27	0.11	2.30	0.28	2.39	0.15	0.21	0.09
Mutant-22 20 kR	2.86	0.42	5.72	0.28	0.30	0.12	1.96	0.35	3.08	0.17	0.24	0.10
Mutant-27 30 kR	3.25	0.55	5.80	0.28	0.30	0.12	1.06	0.33	2.46	0.14	0.20	0.09
Indus-66 (Control)	3.42	0.46	5.94	0.39	0.32	0.11	1.79	0.29	2.18	0.14	0.20	0.08
Mutant-13 20 kR	3.02	0.45	4.65	0.27	0.25	0.10	1.89	0.36	2.47	0.15	0.23	0.10
Mutant-37 20 kR	3.81	0.62	4.14	0.26	0.29	0.11	2.97	0.37	3.02	0.20	0.25	0.10
Mutant-39 20 kR	2.86	0.59	5.04	0.27	0.29	0.11	2.24	0.35	2.29	0.15	0.19	0.09
Mexi-Pak (Check)	2.58	0.50	4.78	0.27	0.27	0.15	1.34	0.32	2.53	0.16	0.23	0.12
L.S.D. 0.05 =	N.S.	N.S.	0.81	N.S.	N.S.	N.S.	N.S.	0.08	0.35	N.S.	0.02	0.02
L.S.D. 0.01 =	N.S.	N.S.	1.08	N.S.	N.S.	N.S.	N.S.	0.11	0.46	N.S.	0.03	0.03
S.E. =	0.41	0.06	0.28	0.03	0.02	0.01	0.43	0.06	0.12	0.01	0.01	0.01
C.V. % =	13.65	13.65	5.85	11.70	5.85	11.70	24.05	9.10	4.55	7.80	3.90	8.45

Nayab mutants had significantly higher K uptake than their parent. The behaviour of M-37 of Indus-66 was not consistent. However, this mutant showed significant deviations than the parent and Mexi-Pak in K uptake potentialities. These results further points to the genotypic differences in K uptake and accumulation as well (CACCO *et al* 1976 ; GORSLINE *et al* 1961 ; KLEESE *et al* 1968, WALKER & SCHILLINGER 1975). These authors suggested that there are wide varietal differences in such genetically determined properties as ion transport and utilization.

As regards the Mg and Ca uptake potential the behaviour of all genotypes was erratic (Tables 2 to 4). However, Nayab mutants displayed greater Mg and Ca uptake at 4 and 8 weeks stage but showed erratic trend in straw at maturity as compared to their parent. This indicates the rapid translocation of Mg and Ca from shoot to the aerial parts. Mutant-13 and 39 had consistently lower Mg and Ca accumulation at 4 and 8 weeks stage than their parent and Mexi-Pak which indicate that these genotypes are unable to absorb as much Mg and Ca as available in the growing media and therefore classified as inefficient genotypes for Mg and Ca uptake and have lower Mg and Ca requirement than their parent. Similar genotypic differences in Mg and Ca uptake and utilization by wheat were reported by MEYERS (1960), KLEESE *et al* (1968) and CLARK (1976).

Na uptake differences among all genetypes were non-significant (Tables 2 to 4). All the genetypes behaved differently at different growth stages. However, most of the mutants

Table 4. Mineral contents in straw at maturity under field and pot conditions.

Genotype/Pedigree	Mineral content in percent											
	Field conditions						Pot conditions					
	N	P	K	Mg	Ca	Na	N	P	K	Mg	Ca	Na
C-591 (Control)	0.27	0.061	2.20	0.065	0.788	0.051	0.28	0.03	2.14	0.13	0.91	0.11
Mutant-7 7hr EMS	0.32	0.057	2.38	0.061	0.825	0.048	0.33	0.02	2.13	0.13	1.16	0.12
Mutant-28 7hr EMS	0.41	0.059	2.22	0.069	0.732	0.053	0.26	0.02	2.28	0.12	1.13	0.11
Mutant-38 7hr EMS	0.50	0.069	2.79	0.065	0.915	0.090	0.26	0.02	2.36	0.13	1.20	0.11
Nayab (Control)	0.36	0.067	2.25	0.095	1.031	0.087	0.23	0.03	2.28	0.13	1.12	0.10
Mutant-6 25 kR	0.42	0.101	2.22	0.077	0.859	0.100	0.26	0.02	2.44	0.13	1.11	0.14
Mutant-22 20 kR	0.49	0.069	1.88	0.102	0.745	0.114	0.23	0.02	2.35	0.12	1.09	0.09
Mutant-27 30 kR	0.46	0.066	2.03	0.081	0.774	0.082	0.26	0.03	2.44	0.13	1.08	0.14
Indus-66 (Control)	0.39	0.054	2.23	0.083	0.865	0.091	0.26	0.03	2.54	0.13	1.29	0.17
Mutant-13 20 kR	0.35	0.056	2.11	0.090	0.790	0.101	0.32	0.04	2.59	0.14	1.21	0.15
Mutant-37 20 kR	0.52	0.073	2.40	0.074	0.910	0.075	0.46	0.04	2.65	0.14	1.31	0.16
Mutant-39 20 R	0.42	0.055	2.36	0.087	0.868	0.108	0.28	0.05	2.69	0.13	1.28	0.18
Mexi-Pak (Check)	0.46	0.067	2.16	0.072	0.769	0.120	0.22	0.04	2.05	0.13	1.02	0.14
L.S.D. 0.05 =	0.13	N.S.	0.37	0.021	0.133	N.S.	0.13	N.S.	0.36	N.S.	0.14	0.05
L.S.D. 0.01 =	0.17	N.S.	0.50	0.028	0.177	N.S.	NS	N.S.	0.48	N.S.	0.19	N.S.
S.E. =	0.04	0.013	0.13	0.074	0.05	0.024	0.04	0.02	0.13	0.01	0.05	0.02
C.V. % =	10.50	19.60	5.60	9.80	5.60	28.0	16.25	52.65	5.20	4.49	4.55	13.65

displayed higher Na uptake as different developmental stages as compared to their respective parents. Mexi-Pak was found to be the most efficient variety in Na uptake at all sampling dates. Mutant-38 like all other elements retained its superiority with respect to high amount of Na uptake at different growth stages than all other C-591 genotypes which indicate that M-38 has greater Na uptake efficiency than its parent and M-7 and M-28. All Nayab mutants were higher in Na content than their parent in straw at maturity, whereas C-591 mutants (M-7 and M-28) were inferior to their mother cultivar at all growth stages under both sets of conditions. Gamma irradiated mutants displayed general superiority over EMS -derived mutants.

The results discussed above clearly indicate that mineral uptake from soil is not only influenced by the environmental conditions but to a greater extent by their hereditary potentialities. Similar conclusions about hereditary variations in plant nutrition were drawn earlier (HARVEY 1939; COLLANDER 1941). Based on some elegant experiments BEADLE & TATUM (1959) reported that many nutritional variations among plant varieties are the result of single gene mutation which exerts an influence on the absorption and utilization of mineral nutrients. It is evident from the present results that there is wide genetic variation among the wheat genotypes tested in their absorption, accumulation and translocation of mineral nutrients from the growing media. The genetic differences may reflect the differences in the mechanism of ion transport which is considered to be under genetic control (EPSTEIN &

JEFFERIES 1964; EPSTEIN 1972; CACCO *et al* 1976, LAUCHLI 1976). Therefore, the genetic variants among the genotypes are the possible factors affecting the uptake of mineral nutrients (JENSEN & PETTERSSON 1980) in the present studies.

It is concluded that mineral uptake studies provide guideline for the characterization and breeding of nutritionally efficient genetypes.

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Evaluation of wheat mutants for inproved physiological efficiency

A.S. LARIK, H.M.I. HAFIZ[1] and M.B. KUMBHAR

Department of Plant Breeding and Genetics, Sind Agricultural University, Tandojam, Pakistan

Modern crop improvement approaches involve modification and control of factors which determine crop productivity. The factors dealt with this study are visible plant attributes such as productivity per day, sink capacity (grains per spike, 100-grain weight and yield per plant) and harvest index which contribute to high productivity. Phenotypically stable wheat mutants (Mutant-7, 28, 38, 13 and 39) and their mother cultivars (C-591 and Indus-66) were evaluated for the above physiological parameters.

Productivity per day takes into consideration both plant yield and maturity. Modern agriculture not only strives for high productivity, but also for harvesting a good crop in shorter time so that the net productivity per unit area of land per unit time can be boosted up. Productivity per day was studied in all the mutants and their mother cultivars (Table 1). It may be noted that the major cause of the variation in mother cultivars was the variation in single plant yield rather than the maturity period, the variation observed in mutants arose from an interplay of these two components. A desirable significant shift was observed in the mean of all the mutants. The increase in the mean productivity per day in some of them was substantial. While EMS-derived M-7 showed maximum productivity per day.

In crops like wheat, where grain is the economic end product, the number of grains per plant often becomes a limiting factor in enhancing plant yield even at higher photosynthetic rate. The number of grains per plant, which serves as the sink to receive the translocated photosynthate is, therefore an important criterion in identifyig potential high yielders. Hence the data on these traits (Table 1) clearly indicate that irrespective of the increase 100-grain weight in all the mutants, the increase in yield per plant was invariably associated with the number of grains per spike

Harvest index represents the ratio between the grain yield and total biological yield. In present investigation harvest index was used to evaluate the physiological efficiency of wheat mutants for this useful plant breeding parameter. The alteration in harvest index was manifested in all the mutants with increase in the mean values (Table 1). However, they were not significantly different from their mother cultivrs. Gamma rays originated mutant -39 displayed significant improvemenet in harvest index as compared to its mother cultivar. The physiological cause of variation in harvest index of these mutants is not well understood.

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[1] Department of Botany, New Campus, Punjab University, Lahore, Pakistan.

Table 1. Productivity per day, sink capacity and harvest index of wheat mutants and their mother cultivars

Genotype/Origin	Productivity per day (g)	Grains per spike	Yield per plant (g)	100-grain weight (g)	Harvest index %
C-591 (control)	0.259	36	29.65	2.304	24.01
M- 7 EMS 7hr	0.355	42	39.70**	2.998**	25.82
M-28 EMS 7hr	0.333	43*	37.75**	3.202**	24.41
M-38 EMS 7hr	0.344	54**	39.15**	3.562**	24.44
Indus-6 (control)	0.395	45	42.65	3.001	26.89
M-13 20kR	0.360	59**	39.25	3.265*	26.95
M-39 20kR	0.441	52*	47.95*	3.190	33.36**
L.S.D (.05)* =	0.10	7.00	4.58	0.236	4.70
L.S.D (.01)** =	0.14	10.20	5.40	0.315	6.25
S.E. =	0.04	3.20	1.60	0.083	1.65
C.V. % =	6.50	7.70	3.50	2.800	6.30

However, it seems that lower number of grains per spike was due to accumulation of large amount of carbohydrate in culm has contributed to decreased harvest index (YOSHIDA 1972). For further increase in yield potential of wheat mutants, however, the number of grains per plant is obviously the limiting factor because of the physiological limitation on grain size. From this study, it may be concluded that mutagenesis may offer scope for isolating mutants with increased harvest index. It is possible that the increased grain yield observed in these mutants cound partly have resulted from an increased allocation of dry matter to the grains. It is now widely recognised that the substantial increase attained in the yields of wheat in recent times with the introduction of dwarfing genes is partly due to an increase in the harvest index of these new dwarf varieties (YOSHIDA 1972; JAIN *et al*, 1973). Hence the improvement of plant type associated with higher harvest index in wheat is more likely to be associated with larger spikes carrying more number of grains, high grain weight per ear and high 100-grain weight as well. A similar situation was observed by SIMS (1963) and CHOWDHURY (1978) in Australian grain variety of oats and wheat respectively. EMS -derived mutants displayed high degree of variation for productivity per day (WATSON 1952; ASANA 1968; CHOWDHURY 1978) as compared to gamma rays induced mutants.

From present study, there is fairly a good ground to suggest that wheat plant could be reconstructed in terms of high harvest index and better sink capacity and that the mutation breeding can be exploited to evolve mutants with improved physiological efficiency.

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II. Records

CATALOGUE OF GENE SYMBOLS FOR WHEAT 1984 SUPPLEMENT

R.A. McIntosh

Plant Breeding Institute, P.O. Box 180, Castle Hill,
N.S.W., Australia, 2154

A completely revised Catalogue (1983 Edition) will appear in the Proc. of 6th Int. Wheat Genetics Symp., kyoto, Japan. References have been renumbered; henceforth these will be listed numberically rather than alphabetically in Supplements. Please advise corrections and additions for future supplements.

Height

Rht1. Shortim *Rht2* (531). 4x wheat-Malavika (523).

Rht2. Songlen (531). Shortim *Rht 1* (531).

Proteins-Isozymes

1. Alcohol dehydrogenase

Adh-E1	(520).	4ES (520).	v : *E. elongata* (520).
Adh-Ala	(523).		v : Malavika (group durum) (523).
-Alb	(523).		v : Bijaga Yellow (group durum) (523).
Adh-A2	(521).	5AL (521).	v : Chinese Spring (521).
Adh-B2	(521).	5BL (521).	v : Chinese Spring (521).
Adh-D2	(521).	5DL (521).	v : Chinese Spring (521).
Adh-E2	(520).	5EL (520).	v : *E. elongata* (520).
Adh-E3	(520).	6Eβ (520).	v : *E. elongata* (520).

2. Aminopeptidase

Amp-E1	(520).	6Eα (520).	v : *E. elongata* (520).

3. Glutamate oxaloacetate transaminase

Got-E2	(520).	6Eβ (520).	v : *E. elongata* (520).
Got-E3	(520).	3EL (520).	v : *E. elongata* (520).

5. Endopeptidase

Ep-E1	(520).	7EL (520).	v : *E. elongata* (520).

6. Lipoxygenase

Lpx-E1	(520).	4ES (520).	v : *E. elongata* (520).
Lpx-E2	(520).	5EL (520).	v : *E. elongata* (520).

8. Glucose phosphate isomerase

Gpi-E1	(520).	1ES (520).	v : *E. elongata* (520).

10. Hexokinase

Hk-B1	(512).	1BS (512).	v : Chinese Spring (512).

Hk-D1	(512).	1DS (512).	v : Chinese Spring (512).
Hk-B2	(512).	3BS (512).	v : Chinese Spring (512).
Hk-E2	(512).	3Ag (512).	v : Chinese Spring+3Ag (512).

11. Amylase

α-Amylase-In preparation

β-Amylase

β-Amy -A1a	(518).	4Aβ (516, 518).	v : 41 wheats including Chinese Spring (518).
-A1b	(518).	Null allele.	v : 5 wheats (518).
β-Amy -D1a	(518).	4DL (517, 518).	v : 28 wheats including Chinese Spring v : (518).
-D1b	(518).		v : 12 wheats (518).
-D1c	(518).		v : Synthetic hexaploid (518).
-D1d	(518).		v : Azteca (518) ; Ciano 67 (518) ; *T. macha* v : (518).
-D1e	(518).		v : Manella (518) ; Mara (518).
β-Amy -A2a	(518).	5A (518).	v : Chinese Spring (518) ; Glennson (518) ; Highbury (518) ; Lutescens (518) ; Wembley (518) ; C306 (518) ; SD2 (518).
-A2b	(518).		v : 9 wheats (518).
-A2c	(518).		v : *T. macha* (518).
-A2d	(518).		v : Holdfast (518) ; Sappo (518) ; SD1 (518).
-A2e	(518).		v : 24 wheats (518).
β-Amy -B2a	(518).	5BL (518).	v : 45 wheats including Chinese Spring (518).
-B2b	(518).		v : Synthetic hexaploid (518).

12. Esterase

Est-A1	(520).	Est_{A} (522). 3AS (522).	v : Chinese Spring (522).
Est-B1	(520).	Est_{B} (522). 3BS (520, 522).	v : Chinese Spring (522).
Est-D1	(520)	Est_{D} (522). 3DS (520, 522).	v : Chinese Spring (522).
Est-R1	(520).	Est_{R} (522). 3R (522).	v : Imperial rye (522) ; wheat 3A-3R translocation (522).
Est-E1	(520).	3ES (520).	v : *E. elongata* (520).
Est-A2	(528).	6Aβ (524).	v : Chinese Spring (524).
Est-B2	(528).	6BL (524).	v : Chinese Spring (524).
Est-D2	(528).	6Dβ (524).	v : Chinese Spring (524).

13. Triosephosphate isomerase

Tri-A1	(528).	3AS (528).	v : Chinese Spring (528).
Tpi-B1	(528).	3BS (528).	v : Chinese Spring (528).

Tpi-D1 (528). 3DS (528). v: Chinese Spring (528).

Endosperm Storage Proteins

Glutenin. The *Glu-1* gene series is considered homoeoallelic with *Hor3* in barley chromosome 5L (514) and *sec3* in chromosome 1RL (525, 526).

Gliadin. The *Gli-1* gene series is considered homoeoallelic with *Horl* and *Hor2* in barley chromosome 5S (514) and *sec1* in chromosome 1RS (525, 526).

Response to vernalization

Vrn1. v: Diamant II (515); Saratoskaya 29 (515); Shabati Sonora (515). Shortandinka *Vrn4* (515); Takari *Vrn4* (535).

Vrn2. 2B (515). v: Milturum 321 (515); Milturum 553 (515).

Vrn4. 5B (515). v: Pirotrix 28 (515). Shortandinka *Vrn1* (515); Takari *Vrn1* (535).

At end of section add "Gotoh (530) suggested that two genes may determine differences between winter wheats requiring 20 days and 60-65 days of vernalization".

Reaction to *Puccinia graminis*

Sr2. v: Hartog *Sr8 Sr12* (533). Suneca *Sr8 Sr17* (534).

Sr7a. v: French Peace *Sr9a Sr13* (513).

Sr7b. v: Nell *Sr17* (527).

Sr9e. v: SST 16 (529); SST 3R (529); Sunstar.

Sr24. v: SST 23 (529); SST 44=T4R (529); Torres (537).

Sr26. v: Flinders (532); King (538); Takari (535). Bass *Sr36* (536).

Sr36. v: Dipka (529); Flamink (529); Gouritz (529); SST 101 (529).

Reaction to *Puccinia recondita*

Lr1. v: Suneca *Lr13* (534).

Lr13. v: Hartog (533).

Lr24. v: SST 23 (529); SST 44=T4R (529); Torres (537).

Reaction to *Puccinia striiformis*

Yr6. v: Takari (535).

Yr9. Chromosome status not specified: Lyutestsens 15 (519); Shtorm (519); Kromerzhizhskaya (519).

Genetic Linkages

Chromosome 1D:

1DS	*Hk-D1*	Proximal to *Gpi-D1* (512).	

Chromosome 4A:

4Aα	*Rht1*	- *β-Amy-A1*	Independent (518).
	∴ Centromere	- *β-Amy-A1*	>35% (518).
	Gai1/Rht1	- *Adh-A1a*	23.1±4.0% (523).

Chromosome 4D:

4DL	*Rht2*	- β-Amy-D1	Independent (518).
	∴ Centromere	- *β-Amy-D1*	>35% (518).

Chromosome 5A :

5AL β-*Amy-A2-B1* 0.023±0.023 (518).

∴ Gene order β-*Amy-A2-B1-Hn-Q-Vrn1* (518).

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III News

Organization changed in Kihara Institute.

Kihara Institute for Biological Research (Yokohama, Japan) have jointed with Yokohama City University to establish a new university institute for life sciences since April, 1984. Traditional name of Kihara Institute for Biological Research is succeeded, which includes sections of Plant Evolutionary Genetics, Cytogenetics, Cell Biology, and Biotechnology. Dr. Hitoshi Kihara sheated the Director Emeritus, and Dr. Masatake Tanaka was elected as Director of Institute, who has moved from Kyoto University.

Proceedings of 6th IWGS published

The 6th International Wheat Genetics Synposium was successfully held at Kyoto in Nov., 1983. The proceedings of the synposium has been published with the following contents. Anyone who are interested in obtaining it should order to;

Maruzen Co. ltd
P.O. Box5050, Tokyo International
100-31 Japan

with the charge of US$250 ^{00} plus $15 ^{00} for sea mail postage.

Proceedings of 6th International Wheat Genetic Synposium
Ed. by Sadao Sakamoto (Kyoto Univ.)

CONTENTS:

OPENING SESSION

The transfer to wheat of interstitial segments of alien chromosomes By E.R. Sears
Origin and history of "Daruma" - a parental variety of Norin 10 By H. Kihara

SESSION I: EVOLUTION AND SPECIATION

Genome analysis in the genus Triticum By G. Kimber/The nature and origin of wheat Genomes on the data of grain protein immunochemistry and electrophoresis By V.G. Konarex/and 5 papers

SESSION II: INDUCED AND NATURAL VARIATIONS

Utilization of induced variations in wheat improvement By K.A. Siddiqui/and 2 papers

SESSION III: GENETIC RESOURCES IN WHEAT

Semi-wild wheat from Xizang (Tibet) By Q. Shao, C. Li and C. Basang/Genetic resources in diploid wheats: the case for diploid commercial wheats by J.G. Waines/and 4 papers

SESSION IV: ALIEN GENETIC MATERIAL

Broadening the genetic variability of cultivated wheat by utilizing rye chromatin By F. J. Zeller and S.L.K. Hsam/Studies on high protein durum wheat derived from crosses with the wild tetraploid wheat By L. Avivi, A.A. Levy and M. Feldman/Ditelosomic additions of barley chromosomes to wheat By A.K.M.R. Islam/and 7 papers

SESSION V: GENETIC ANALYSIS

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SESSION VI: CYTOGENETICS

A genome restructuring gene in Aegilops longissima By M. Feldman and I. Strauss/Homoeologous group 5 chromosome arm rations in wheat cultivars By R. Morris, T. Taira and J.W. Schmidt/and 8 papers

SESSION VII: BIOCHEMICAL AND MCLECULAR GENETICS

Characterizing and selecting alien genetic material in derives of Wheat-alien species hybrids by analyses of isozyme variation By G.E. Hart and N.A. Tullen/and 4 papers

SESSION VIII: PHYSIOLOGICAL AND ECOLOGICAL GENETICS

Genetic resources of wild emmer wheat: Structure, evolution and application in breeding By E. Nevo/and 6 papers

SEESION IX: CYTOPLASMIC GENETICS

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SESSION X: QUANTITATIVE GENETICS

Quantitative genetic studies in wheat By C.N. Law, J.W. Snape and A.J. Worland/and 2 papers

SESSION XI: TISSUE AND CELL CULTURE

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SESSION XII: BREENING AND BREEDING METHODS INCLUDING HYBRID WHEAT

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SESSION XVI: GENETIC APPROACHES TO PAISING THE YIELD CEILING

Sink-source variation and the pattern of grain filling in Italian wheat varieties By A.

Bianchi, M. Corbellini, M. Pezzali and B. Borghi/Identification and management of major genes monitoring yield and adaptation By A.T. Pugsley/and 2 papers

POSTER SESSION

Triticum longissimum chromosome G ditelosomic addition lines: Production, characterization and utilization By C. Ceoloni/Extra hard kernels associated with semidwarfness By D.R. Sampson/and 28 papers

Published by: Plant Germ-Plasm Institute, Faculty of Agriculture Kyoto University, Kyoto, Japan

Distributed by: Maruzen Co., Ltd., P.O. Box 5050, Tokyo International 100-31, Japan

Catalogue of Aegilops-Triticum germ-plasm preserved in Kyoto Vniv.

A catalogue of Triticum and Aegilops strains maintained in Germplasm Institute, Fuculty of Agriculture, Kyoto University has been published, which is eddited by Dr. Masatake Tanaka, the ex-director of the institute. They are germ-plasm strais collected by Drs. H. Kihara, M. Tanaka and their colleagues for last 50 years, including 2,396 strains of Aegilops, 4,382 strains of Triticum and 83 strains of synthetic species. The list describes the origins of collection localities, and characeristics for each strains.

Anyone who are interested in obtaining it should contact;

Dr. Masatake Tanaka, Kihara Institute for Biological Research Yokohama City University, Mutsukawa 3-122, Minami-ku, Yokohama, , Japan

IV. Editorial Remarks

Announcement for Future Issues

WIS No. 60 will be planned for publication in February, 1985. Manuscripts for this issue are most welcome and accepted any time, not later than December 31, 1984.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics, breeding and cytology of *Triticum, Aegilops, Seeale, 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. Authors peceive 50 reprints of their contributions free of charge. Extra copies are 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 3-11, Minami-ku,
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Back numbers are available by order at cost price.

Acknowledgement

The cost of the present publication has been defrayed partly by the Grant-in-Aid for Publication of Scientific Research Result from the Ministry of Education, Government of Japan and partly by contributions from Kihara Institute for Biological Research. We wish to express our sincere thanks to those organizations. We should also like to express our sincere gratitude for favorable comments regarding WIS Nos. 1~58 and valuable contributions for the present issue. Increased support wolud be appreciated.

The Managing Editor

Explanation of the Figure on the Cover

Ears of sphaerococcum varieties in *T. aestivum* obtained from EMS' treatment. See the text of article by GEORGIEV for the details.

WIS　　No. 59

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