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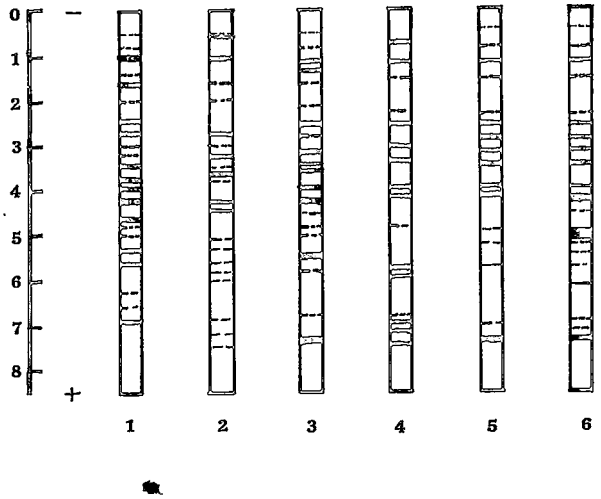

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I. Research Notes

Induced M_1 sterility and mutation frequency in *Triticum aestivum*

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It is now known that M_1 spikes after mutagenic treatments exhibit a range of variation in the degree of sterility. Earlier reports on the effects of M_1 seed fertility on mutation frequency in M_2 (GAUL 1958, 1964, EHRENBERG *et al.* 1961, KIVI 1965, SHARMA and BANSAL 1970) are not consistent. These observations were based on chlorophyll mutation frequency in genus *Hordeum vulgare*. For our present studies, different varieties of bread wheat (*Triticum aestivum*) were used as a test material. The observations were recorded on viable phenotypically detectable mutants. The mutation frequency was calculated on total M_2 population scored. Induced M_1 sterility has been used as an indicator parameter. The results pertaining to fertility and mutation percentage in different sets of treatments and varieties are summarized in Table 1.

The data compiled in Table 1 is taken from different sets of experiments representing the observations of ten different years. From the results an obvious conclusion can be drawn that irrespective of the treatments, dosage effects, varietal response or genotype treatment interaction, the reduced fertility in M_1 generally gives higher mutation frequency in M_2. The cytological studies have indicated that induced cryptic and gross chromosomal changes in M_1 are mainly responsible for the re-patterning of the genetic material and thereby affecting the seed fertility level. GAUL (1961) suggested that the sterility in M_1 spikes, in term of seed setting should serve as an indication of the frequency of chromosome mutations.

If the aim is to maximise the viable mutation rate, then it would be better to restrict to a few effective treatments, which will have limited M_2 population. With the increased sterility the mutation frequency was considerably enhanced, but there was no change in the mutation spectrum. These results should be of interest having practical implications for planning mutation breeding programmes. The fertility range of 50% or less

Table 1. Fertility and mutation percentage in different sets of treatments and varieties

Variety	Pedigree	Treatment	Mean fertility in M_1	Fertility percentage over control	Mutation percentage in M_2
Ridly (E.5722)	Introduction from Australia (Nabawa × Hard Federation) × Gabo	Control	2.40	100.00	0.09
		X-ray 16 Kr	2.39	99.58	2.29
		〃 21 Kr	2.32	96.66	2.77
		r-ray 16 Kr	2.45	102.08	1.28
		〃 chronic	0.92	38.33	13.73
		Fast neutrons, 10 hrs	2.33	97.08	1.64
		32 P 5 μc/seed	1.09	45.41	4.72
		35 S 5 μc/seed	1.03	42.91	4.84
NP 829	NP165 × E.865	Control	2.51	100.00	0.07
		X-ray 16 Kr	2.37	94.42	1.19
		〃 21 Kr	2.26	90.03	1.35
		r-ray 16 Kr	2.33	92.82	2.20
		〃 chronic	1.43	56.97	11.82
		Fast neutrons, 10 hrs.	2.44	97.21	0.53
		32 P 5 μc/seed	1.94	77.29	5.96
		35 S 5 μc/seed	2.06	82.07	5.43
NP 770	Konoso × NP 4	Control	2.42	100.00	0.00
		X-ray 21 Kr	2.37	97.93	1.73
		〃 16 Kr	2.45	101.20	2.20
		r-ray 16 Kr	2.38	98.34	0.77
		〃 chronic	1.03	42.56	19.20
		Fast neutrons 10 hrs.	2.47	102.06	0.75
		32 P 5 μc/seed	1.76	72.72	9.78
		35 S 5 μc/seed	1.75	72.31	7.33
Sharbatal Sonora	Mutant of Sonora-64	Control	3.00	100.00	0.00
		r-ray 20 Kr	2.60	86.67	2.70
		〃 30 Kr	2.60	86.67	2.50
Kalyansona	(Fn × K. 58 × N 10B-N) Gb 55	Control	3.40	100.00	0.00
		r-ray 20 Kr	3.60	105.88	1.60
		〃 30 Kr	2.80	82.35	3.90
Chhoti-Lerma	RR64 (Sib) × HAR	Control	3.10	100.00	0.00
		r-ray 20 Kr	2.70	87.09	0.70
		〃 30 Kr	1.70	54.84	1.40
Safed-Lerma	(Y50 × N-10B) (L-52) LR 3	Control	2.50	100.00	0.00
		r-ray 20 Kr	1.60	64.00	1.80
		〃 30 Kr	1.60	64.00	1.50

can be used as a reliable indicator parameter for selecting the most potent genotype treatment combination.

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Identification of chromosomes carrying a locus for a gene conditioning the production of tyrosinase in wheat grains

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Summary

Using the substitution lines of Chinese Spring (Hope) and Chinese Spring (Timstein) the presence of loci for genes conditioning tyrosinase production in caryopses was identified on 2A of Hope, and 2A and 2D of Timstein. It is suggested to use *Tc* as symbol for these genes.

Introduction

When PIEPER (1922) tried to disinfect wheat seeds that were infected with common bunt, with phenol containing Betanal he observed that after a few hours the seeds turned brown, dark brown or blackish, or remained unchanged. HERMANN (1928) described this phenomenon and heralded its use as a means to identify wheat varieties and to measure varietal purity. An intensive research started in Europe before 1940 (DUTKIEWICZ-MICZYNSKA 1930, FRIEDBERG 1933, LISTOWSKI 1936, MICZYNSKI 1938, PERCIVAL 1934, SNELL and PFUHL 1930, VOSS 1933, 1936, 1938, these publications also refer to literature in Hungarian, Russian, Polish and Ukranian). In Europe the above method is still applied as one of the means to describe varieties (e.g. JONARD 1951, SIMON 1955 and others).

This phenomenon was also described for North America (FRASER and GFELLER 1935, 1936). It seems that at present it is not widely known there, because it is not mentioned

by PETERSON (1965) and QUISENBERRY and REITZ (1967). The same holds true for other continents.

The pigmentation reaction is also identified for other *Triticum* species (HERMANN 1928, FRIEDBERG 1933, BLANCHARD 1953, BHOWAL *et al.* 1969). BLANCHARD described the pigmented grains of *T. durum* as having a greyish appearance which is not found in *T. aestivum.*

Barley seeds (FRIEDBERG 1933, LISTOWSKI 1936, SAWICKI 1955, HÄNSEL 1958) and rye seeds (SCHRÖDER 1932) also turn brown or blackish in the presence of phenol.

The pigmentation is a result of the conversion of phenol (and other phenolic derivatives) into melanin pigments in the presence of tyrosinase (monophenyloxydase) (Voss 1938). This chemical reaction is widely occurring in nature. For wheat seeds the presence of tyrosinase was established by BERTRAND and MUTTERMILCH (1907).

The production of tyrosinase is conditioned in tetraploid wheat by one locus (JOSHI and BANERJEE 1968) and in hexaploid wheat by either one or two loci (FRASER and GFELLER 1936, MICZYNSKI 1938). Tyrosinase production is dominant over no tyrosinase production. JOSHI and BANERJEE (1968) established two dominant alleles. These dominant alleles differ in the speed at which the seeds turn black. This speed might be a result of the production of tyrosinase per unit time, but there may be other causes. It is probably that there are more than two dominant alleles, because different seed samples may show different shades from brown to blackish. The possibility of an additive effect of the two loci should be investigated.

FRASER and GFELLER (1936) symbolized the gene with *Pk*, and Miczynski (1938) with *F.* JOSHI and BANERJEE (1968) used *B.* I propose *Tc* (tyrosinase in caryopsis).

Linkage of this locus was shown to exist with the locus for tyrosinase in glumes (proposed symbol *Tg*) (FRASER and GFELLER 1936, MICZYNSKI 1938). At one time it was believed that there was always repulsion (pigmented grain and white glume, or reversion), but later wheat varieties with genotype *Tc/Tg* were identified.

Material and method

The work was carried out with substitution lines Chinese Spring (Hope), Chinese Spring (Timstein), both made by Dr. E. R. SEARS (SEARS *et al.* 1957) and received from Dr. C. N. LAW. The controls were Chinese Spring-S (ex Dr. SEARS), Chinese Spring-R (ex. Prof. R. RILEY), Hope, Timstein and three standard varieties Cama, Manella and Orca.

Furthermore *T. dicoccum* No. 42, *T. durum* Nos. 73, 74 and 75, Bobin, Gabo and Marquis have been studied. Their origin is given in Table 2.

About 50 seeds of each variety or line were placed in petri dishes and were soaked in tap water for 24 hours at room temperature. After this period the water was removed

and 3 cm^3 1% aqueous solution of phenol was added. Sufficient light was supplied together with room temperature.

After four hours the intensity of the pigmentation of the grains was scored against that of the standard varieties: Cama=9 (blackish), Manella=6 (brownish) and Orca=3 (pale brownish). Difference of one point may be caused by differences in genetic background.

Identification

The result of the work is presented in Table 1. Within both substitution lines the substitutions C.S. (2A-Hope), C.S. (2A-Timstein) and C.S. (2D-Timstein) are conspicuously different from the others and from Chinese Spring lines. These three substitutions have the same score as Hope and Timstein. From these observations it might be con-

Table 1. The pigmentation scores of two Chinese Spring sources, two substitution lines, two donor varieties and three standard varieties

Variety, line	Score	Variety, line	Score
C.S. (Hope)		C.S. (Timstein)	
1A	4	1A	4
1B	4	1B	4
1D	4	1D	3
2A	9	2A	9
2B	4	2B	4
2D	4	2D	8
3A	4	3A	3
3B	4	3B	4
3D	4	3D	4
4A	4	4A	3
4B	3	4B	4
4D	4	4D	4
5A	4	5A	3
5B	4	5B	4
5D	4	5D	4
6A	4	6A	4
6B	5	6B	4
6D	4	6D	4
7A	4	7A	4
7B	4	7B	4
7D	4	7D	4
Chinese Spring-S	3	Cama	9
Chinese Spring-R	4	Manella	6
Hope	8	Orca	3
Timstein	8 (greyish)		

Table 2. The pigmentation scores of the parents and possible parents of Hope and Timstein

Parents	Score
T. dicoccum No. 42, Yaroslav spring emmer, CI 1526	7
T. durum No. 73, Gaza W 277, PI 12518	3
T. durum No. 74, Gaza 277, PI 140959	4
T. durum No. 75, Gaza W 277, PI 189262	3
Bobin	8
Gabo	9
Marquis	8

cluded that 2A and 2D carry a locus for *Tc* and that the allele of *Tc* on 2A of Hope and Timstein and 2D of Timstein has a stronger effect than the alleles of *Tc* of Chinese Spring. It is interesting to observe that these loci of *Tc* are on chromosomes of homeologous group 2. This may point to a possible locus on 2B. BHOWAL *et al.* (1969) reported that the locus of *Tc* is confined to the A-genome. Its presence on 2D of Timstein also points to the D-genome.

A second conclusion is that apparently there is no dosis effect, because the pigmentation of Timstein (two strong alleles) is similar to C.S. (2A-Timstein) and C.S. (2D-Timstein). These substitutions have only one strong allele.

Furthermore the strength of the allele on 2D (Hope) is similar to that of 2D (Chinese Spring). If there is a *Tc*-locus on 2B, the strength of this allele is equal for Hope, Timstein and Chinese Spring.

Parentage of Hope and Timstein:

It is interesting to check the pigmentation of the parents of Hope and Timstein because both varieties derive from a 6x×4x cross. Gabo has been included because this variety is a sister variety of Timstein (KNOTT and ANDERSON 1956, WATSON and STEWART 1916, ZEVEN 1969). The parents are:

Hope—Marquis × *T. dicoccum* Yaroslav

Timstein—Bobin^2 × *T. durum* Gaza.

It is not known whether the tetraploid accessions mentioned in Table 2 are genotypically identical to the plant(s) used as the actual parents.

The pigmentation scores of Yaroslav emmer is 7 and of Marquis 8. Hope may have derived its *Tc*-allele of 2A from either Marquis or Yaroslav. Timstein and Gabo score 8 and 9 respectively, while Bobin has 8 and Gaza-durums 3 or 4. The *Tc*-allele of 2A of Timstein probably comes from Bobin, while that of 2D must have come from this variety.

It is very remarkable that Timstein has the same greyish veil as was observed for *T. durum* accessions (see also BLANCHARD, 1953 in Introduction). Although my Gaza-durums have no such veil Timstein very probably derives this character from its durum parent. No such veil was observed in Gabo.

Conclusion

On 2A of Hope, and on 2A and 2D of Timstein a locus for a gene conditioning the production of tyrosinase in the caryopses has been identified. The allele of this gene has a strong action causing the caryopses to turn blackish after they had been soaked in water for 24 hours and in an aqueous phenol solution for four hours. It is quite likely that a homeologous locus will be found on 2B.

It is proposed to use *Tc* as gene symbol, while the particular genes can be numbered as *Tc*-1 on 2A, *Tc*-2 on 2B and *Tc*-3 on 2D.

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Mapping of the *compactum* gene C on chromosome 2D of wheat

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The *compactum* gene *C* was located on chromosome 2D by UNRAU (1950). MCINTOSH and BAKER (1968) failed to recover any crossover involving *C* when the right arm telocentric 2D of Chinese Spring was combined with 2D of *compactum* variety, Poso, suggesting that the gene is probably located on the left arm of 2D. In the present study, the substitution line, Poso-2D (*CC*), was crossed with Chinese Spring (*cc*) ditelo-2D (left) monotelo-2D (right). F_1 plants without the right arm telocentric (2n=42) ($20_{II}+1$ het_{II}) were selected. These F_1 plants (*Cc*) were selfed as well as used as male parents in testcrosses to Chinese Spring.

Out of 222 F_2 plants, 215 were of *compactum*-type and 7 of *aestivum*-type. Three of the *aestivum*-type plants were studied cytologically and two of them showed $20_{II}+1$ het_{II} (crossovers) at meiosis and the third plant had $20_{II}+t_{II}$ (non-crossover). Since the two plants with an entire 2D showed the *aestivum* phenotype, the *C* gene is located on the left arm of 2D.

The testcross progeny consisted of 177 plants of which 35 were of *aestivum*-type and the remaining 142 of *compactum*-type. Cytological analysis of the *aestivum*-type plants revealed that 31 of them had the paternal telocentric ($20_{II}+1$ het_{II}) and were therefore non-crossovers, while four plants had the entire paternal 2D (21_{II}) and were crossovers. Thus, a crossover value of 2.26% between *C* and centromere was obtained. The data indicates that the *compactum* gene is located on the left (beta) arm of 2D, close to the centromere.

A few *compactum* plants with a crossover telocentric are expected in the population besides the 31 *aestivum*-type plants. However, the crossing over of *C* with the centromere being very low, the number of telocentrics carrying *C* is likely to be small and these would further be subject to competition with the entire 2D. Hence, if the occurrence of *compactum* plants with a crossover telocentric is ignored, the male transmission of telocentric 2D (left) in competition with the entire 2D is 31/177 i.e., 17.5%.

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Preliminary report on variation of chromosome constitution in cultured cells of different lines of Chinese Spring wheat

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In the tissue culture of higher plants, chromosome constitution of callus cells varies in many species and with cultured conditions (FOX 1963, TORREY 1967). In order to study variation of chromosome constitution, more specifically in order to know whether any chromosome increases or decreases at random or whether a particular chromosome does increase or decrease, telocentric chromosomes (SEARS 1954) are very useful materials, because it is easy to detect the loss or increase of the telocentric chromosomes.

The materials used in the experiment were the following five lines: Chinese Spring, nulli-5B tetra-5D, ditelo-5A^{L}, -5B^{L} and -5D, respectively.

Sterilized seeds were placed on agar slant in the test tube, each containing 10 ml of the medium. The medium used in this experiment was RM-64 basal medium (LINSMAIER and SKOOG 1965), to which 3.0 mg/l of 2, 4-D (2, 4-dichlorophenoxy acetic acid) was added. Medium was adjusted to pH 5.8 with 1N-KOH and 1N-HCl before autoclaving.

Calluses which were induced on growing roots of germinating seeds were successively subcultured at intervals of two months on the medium mentioned above. After pretreatment in water at 0°C for 24 hours and fixation in Farmer's fluid, microscopical observation of chromosome numbers were made by Feulgen squash method.

Growth rate and morphology of calluses were about the same in different lines.

Chromosome numbers of callus cells from Chines Spring were almost 2n=42. Nulli-5B tetra-5D and ditelocentric lines produced callus tissues whose chromosome numbers varied greatly from those of Chinese Spring. Chromosome numbers of callus cells from nulli-5B tetra-5D varied from 24 to 86 with the mode at 40 (32%), the majority of the chromosome numbers ranging from 38 to 42 (82%). In the callus cells of ditelo-5A^{L}, their chromosome numbers varied from 27 to 126 with the mode at 42, 52% being 2n=42. In the callus cells of ditelo-5B^{L}, their chromosome numbers varied from 28 to 84 with the mode at 42, 58% being 2n=42. In the callus cells of ditelo-5D, chromosome numbers varied from 35 to 84, 68% being 2n=42.

The fate of the telocentric chromosomes used in the present experiment will be discussed in the separate papers.

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Relative importance of grain yield components in bread wheat (*T. aestivum* L.)

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Introduction

Grain yield is a complex character and is greatly influenced by environmental factors. The plant breeders while formulating selection procedures do not rely directly on it especially in early generations but take into consideration the relative weight age of the ancillary traits such as grain number, spike number etc. One of the earliest method to identify the grain yield components has been the study of correlation coefficients (SIKKA and JAIN 1958, GANDHI *et al.* 1964, VIRK and ANAND 1970) but the technique of path coefficient analysis developed by WRIGHT (1921) and probably used for the first time in plants by DEWERY and LU (1959) has been found more useful as it differentiates specific forces acting directly and indirectly to produce a particular association. This way the relative contributions of component characters (causal factors) are unfolded and can be successfully employed in formulating efficient selection programmes.

Material and methods

The material consisted of 20 populations comprising 11 widely divergent wheat strains, viz., NP 825 and NP 847 from Delhi; C 273, C 303 and C 306 from Punjab; and S 210, S 227, S 354, S 355, S 409 and Mayo-64 from Mexico; and nine F_2 hybrid populations between C 273×S 354, C 273×S 355, C 303×S 409, C 303×S 210, C 303×S 227, C 303×Mayo-64, C 306×S 409, NP 825×C 306 and NP 847×C 303. These twenty populations were grown in a randomized block design with six replications at the Punjab Agricultural University, Ludhiana. Each population was provided a two row 3.5 meters long plot. The row to row and plant to plant spacings were 22.5 and 15.0 cm respectively. The data were collected on ten randomly selected plants from parents and 20 plants of each F_2 population in each replication. The progeny means were used for calculating phenotypic correlations which were partitioned into path coefficients using the technique of DEWERY and LU (1959).

Results and discussion

The spike bearing tillers and 100-grain weight showed a high and positive correlation with each other and also with grain yield (Table 1) while the grain number exhibited

1) Assistant Professor and Associate Professor, respectively.

Table 1. Phenotypic correlation coefficients among different characters

Character	Spikes/plant	100-grain weight (gm)	Grains/spikes
Grain yield (gm)	0.626*	0.815*	−0.380
Spikes/plant		0.712*	−0.765*
100-grain weight (gm)			−0.787*

* Significant at 0.01 level

a negative but non-significant association with grain yield. The correlations reported by SIKKA and JAIN (1958), GANDHI *et al.* (1964), VIRK and ANAND (1970), and VIRK and SINGH (1972) also revealed similar associations. Grain number was negatively associated with other component characters. The correlations thus revealed that selections based on spike number and 100-grain weight could be more rewarding than those on the basis of grain number.

The pathways through which the three yield components operate to produce their phenotypic associations with grain yield reveal their direct and indirect contributions (Table 2) and are demonstrated diagramatically. The path coefficient analysis showed that spike number and 100-grain weight having positive and high inter-relationships with grain yield had both high direct and indirect effects through each other. The grain number inspite of its negative but non-significant correlation with grain yield had a high direct effect (0.9843). When the indirect influences of this character were examined,

Table 2. Direct and indirect contributions of three variables towards grain yield in wheat

Character correlated	Path coefficient
Spikes per plant vs. grain yield	
Direct effect of spike number (P_{14})	0.4863
Indirect effect via 100-grain weight ($P_{24}r_{12}$)	0.8651
〃 via grain number ($P_{34}r_{13}$)	−0.7254
Correlation coefficient	0.6260
100-grain weight vs. grain yield	
Direct effect of 100-grain weight (P_{24})	1.2150
Indirect effect via spike number ($P_{34}r_{23}$)	0.3463
〃 via grain number ($P_{14}r_{12}$)	−0.7463
Correlation coefficient	0.8150
Grains/spike vs. grain yield	
Direct effect of grain number (P_{34})	0.9483
Indirect effect via spike number ($P_{14}r_{13}$)	−0.3720
〃 via 100-grain weight ($P_{24}r_{23}$)	−0.9562
Correlation coefficient	−0.3800
Residual effect	0.2560

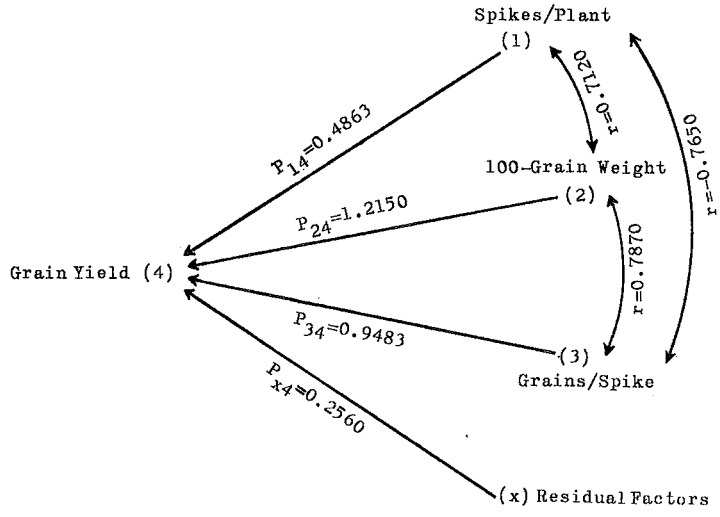

Fig. 1. Diagrammatic representation of factors influencing grain yield in wheat. Double-arrowed lines indicate correlation coefficients and the single-arrowed lines indicate direct path coefficients.

these were found to be negative thus nullifying its direct effect. Hence the selections for high performance for this character will adversely affect the other important variables. Considering the magnitude of direct and indirect contributions, in the material studied, for selection purposes, the effective grain yield components were spikes per plant and 100-grain weight and not the grain number. The results were in agreement with those of VIRK and SINGH (1972) even though the present material included F_2 segregating generations of as many as nine crosses. The inclusion of the segregating populations did not materially alter the inter-relationships of these yield components in wheat.

Summary

The phenotypic correlations in 20 wheat populations consisting of eleven diverse varieties and nine F_2 populations were partitioned to determine the direct and indirect contributions of important yield components viz., spike number, 100-grain weight and grain number towards grain yield. The correlation and path coefficient study gave similar results and it was found that spike number and 100-grain weight showing positive and highly significant correlations with yield had displayed high direct and indirect influences and were the real grain yield components in contrast to grain number.

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Yield components of semi-dwarf and tall spring wheat[1)]

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Abstract

Yield components were evaluated for three semi-dwarf spring wheat (*Triticum aestivum* L. em. THELL) cultivars and two tall cultivars. The average yields of the semi-dwarfs were greater than the average yields of the tall cultivars. Tall cultivars produced equal or larger numbers of spikes per unit area compared with the semi-dwarfs. The semi-dwarfs Pitic 62 and Nadadores 63 consistently had more kernels per spike than the tall cultivars. Numbers of spikelets per spike and kernels per spikelet in Pitic 62 and Nadadores 63 were larger than the same characters in the tall cultivars Chris and Waldron. The semi-dwarf Ciano Sib was consistently greater than all other cultivars for kernel weight.

Introduction

The development of wheat (*Triticum aestivum* L. em. THELL) cultivars with shorter stature have received considerable attention from plant breeders. According to BRIGGLE and VOGEL (1968) most of the semi-dwarf wheats grown in their area of adaptation in the United States have higher yield potential than the standard commercial varieties.

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The greater yield potential of semi-dwarfs has been attributed to their ability to respond to high levels of cultural management, such as nitrogen fertilization, and to their inherent yield potential.

Yield component studies of hard red winter semi-dwarfs by PORTER *et al.* (1964) and JOHNSON, SCHMIDT and MEKASHA (1966) have attributed higher yields to larger numbers of kernels per spike. An evaluation of semi-dwarf spring wheat selections by MCNEAL, BERG and KLAGES (1960) shows that yield and tiller number of the semi-dwarfs were similar to the standard types.

The objectives of this study were to establish the components of yield advantages of semi-dwarf spring wheat cultivars over standard height cultivars and to investigate the stability of these components over environments.

Materials and methods

Two tall cultivars, Chris CI 13751, and Waldron CI 13958, and three semi-dwarf cultivars, Pitic 62 CI 13927, Nadadores 63 CI 13931, and Ciano Sib S 4017 CO 691, were selected from the Colorado spring wheat variety test in 1969 and in 1970 for the yield component study. Irrigated nurseries were grown at Fort Collins, Center, Grand Junction, and Hesperus, Colorado, for this study.

A split-plot design with nitrogen fertilizer levels as main plots and varieties as subplots was used. Each set of three equally spaced nitrogen levels was replicated three times, resulting in a total of 9 replications for varieties. At all locations except Grand Junction, plots were four rows wide with a 30.5 cm spacing between rows. The Grand Junction nurseries were seeded in two-row irrigation beds with a 30.5 cm spacing between rows and 38.1 cm spacing between beds. Plots were either 3.04 or 6.08 m in length, depending upon location. Seeding rates of 68 and 79.5 kg/ha were used in 1969 and 1970, respectively.

Yield was determined by harvesting the two center rows in each plot at maturity, and yield components were measured from the remaining border rows. Spikes per unit area were measured by culm count of one uniform section 0.91 m in length in each plot in 1969 and two 0.91 m sections in each plot in 1970. Kernels per spike, spikelets per spike, and 1,000 kernel weight were determined from a random sample of 30 seed-bearing spikes per plot. Kernels per spikelet were calculated from kernels per spike and spikelets per spike.

Analyses of variance of individual yield components for each location were made. Since unequal variance between locations and years restricted pooled analyses, only means for each characteristic measured for the eight trials are reported.

Results

Agronomic and yield component data are presented in Table 1. In three of the eight location years there was a highly significant yield response to nitrogen treatments. The only cultivar by fertilizer interaction that was significant at the 1% level was kernel weight at Grand Junction in 1970. The general lack of interaction significance indicated that all varieties responded similarly to nitrogen treatment.

Table 1. Agronomic and yield component means for five spring wheat cultivars over eight trials

Cultivar	Height (cm)	Yield (kg/ha)	Spikes per 0.91M of row	Kernels per spike	Spikelets per spike	Kernels per spikelet	1000 kernel weight (g)
Chris	103	3689	150.6	31.2	14.2	2.20	32.1
Waldron	97	4133	136.6	31.5	14.6	2.15	36.2
Nadadores 63	82	4919	124.3	40.6	15.6	2.59	37.8
Pitic 62	81	4919	130.1	45.1	15.9	2.81	35.0
Ciano Sib	72	4717	144.9	33.2	14.2	2.34	39.1

Table 2. Ranking of character means for each cultivar in eight trials

Cultivar	Yield		Spikes per area		Kernels per spike		Spikelets per spike		Kernels per spikelet		Kernel weight	
	1~2[1]	3~5	1-2	3~5	1~2	3~5	1~2	3~5	1~2	3~5	1~2	3~5
Chris	0	8	8	0	0	8	0	8	0	8	0	8
Waldron	1	7	2	6	0	8	1	7	0	8	3	5
Nadadores 63	5	3	0	8	8	0	7	1	8	0	6	2
Pitic 62	5	3	1	7	8	0	8	0	8	0	1	7
Ciano Sib	5	3	5	3	0	8	0	8	0	8	6	2

1) Rank group. Example : Chris ranked either 3rd, 4th, or 5th in mean yield in all eight trials.

The semi-dwarfs had higher yield averages than the tall varieties (Table 1). The consistency of relative yield performance over these environments is shown in Table 2 where Chris never ranked first or second in the eight trials and Waldron ranked first or second only once. A wide range of environments was tested as pointed out by the trial means which ranged from 2472 to 6626 kg/ha.

Spikes per unit area were not responsible for cultivar yield differences. Chris consistently had a high mean for this character, but was consistently low in yield. Ciano Sib was high in spikes per unit area and also had a high yield. Both Nadadores and Pitic produced low numbers of spikes per unit area but were high in yield. Trial means ranged from 82 to 204 tillers, indicating environmental response for this character.

Numbers of kernels per spike appeared to account for most of the yield advantage of Pitic and Nadadores. Kernels per spike can be reduced to its two components of spike-

lets per spike (head size) and kernels per spikelet (floret fertility). Pitic 62 and Nadadores 63 consistently had higher values than the other three varieties for both characters. This indicates that high numbers of kernels per spike in the two high yielding semi-dwarfs is a function of both head size and floret fertility. Ciano Sib showed a small advantage over the tall cultivars for kernels per spike and this advantage was attributed almost exclusively to floret fertility.

Kernel weight accounted for a large portion of Ciano Sib's yield advantage over the tall cultivars. This character was also associated with the yield advantage of Waldron over Chris.

Discussion

Yield differences between the tall and semi-dwarf cultivars were explained in two different ways. First, Pitic 62 and Nadadores 63 achieved their yield advantage primarily because of kernels per spike. The advantage in this characteristic was due to both head size and floret fertility. Second, Ciano Sib achieved its improved yield primarily because of high kernel weight. Floret fertility was a contributing factor of lesser importance in this cultivar.

Traditionally, differences in floret fertility have been attributed primarily to environment. This study shows that some genotypes have the ability to produce greater numbers of kernels per spikelet than others over a range of environments. Spikelets per spike are also under rather rigid genetic control as evidenced by the consistency of different values for different cultivars. Kernel weight is somewhat more variable. A commonly desired yield characteristic has been tillering capacity. Our study indicates that low yielding varieties have adequate tillering potential, and tillering did not account for the increased yield in the cultivars measured.

Good consistency of expression for yield components over several environments was observed in this study. This indicates that these characters are under rather rigid genetic control and yield advances should be made through breeding and selection for these characters.

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A simplified method for electrophoretic studies to differentiate wheat cultivars

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Many cultivars within species resemble each other too close to be distinguished by mere morphological descriptions. Many workers have studied isoenzyme patterns in plants by using whole seedling, whole seeds or different plant parts. In order to find out the differences in biochemical level the acrylamide gel electrophoresis by the disc method (DAVIS & ORNSTEIN 1959) has been used here with certain modifications. Many steps were simplified without losing the clarity of protein banding pattern.

Materials and methods

1. 20 embryos of each wheat cultivar. 6 cultivars were used, viz., (1) Chinese Spring, (2) Roter Löwe, (3) Lichtis Früher, (4) Pakistan I, (5) Pakistan II, and (6) Pakistan III.
2. *Solution A:*

   Arcylamide 20.0 gm, Bis 1.2 gm, Water to 100 ml.
   (This makes 5% acrylamide.)

   Solution B:

   Tris 36.6 gm, 1 N HCl 48 ml, water to 100 ml.,
   (pH 8.9~9.0. This is solution A of Davis, 1964.)

   Solution C:

   Ammonium persulfate 0.14 gm in 100 ml. water.

   Tray Buffer:

   Tris Glycine: Tris 6.0 gm, Glycine 28.8 gm, water to 1 litre. (pH 8.3)
   This buffer should be diluted to 10 times when used in trays.

Wheat seeds are soaked in distilled water for 3 hours and the embryos are removed carefully by spearheaded needle. 20 embryos are ground in a small mortar with pestle adding 1 ml. of distilled water. The homogenate is centrifuged at 4,000 rpm. for 25 minutes. Supernatant is taken into another tube and 5 times (in volume) cold ether is added. The homogenate-ether mixture is thoroughly mixed with the aid of pasteur pipette. This mixture is centrifuged for 30 minutes at 10,000 rpm. This procedure removes the lipids which otherwise interfere in forming the clear cut protein bands in

1) The author is a Post Doctoral Fellow of Alexander von Humboldt Stiftung.

the gel. After high centrifugation a white cloudy layer forms separating the homogenate and ether. Using a Pasteur pipette the protein solution is drawn carefully from the extreme bottom of the homogenate. Care should be taken to avoid the white cloudy layer, insoluble debris pellet and ether. The protein solution may be transfered to a small glass vial and kept in desiccator connected to vaccum pump. Ether smell may be cleared after six hours by keeping the vials in desiccator with vaccum. The homogenate contains water soluble proteins.

Preparation of the gel: Only one gel is used. Gel may be prepared by mixing solutions A: B: Water: C in 2: 1: 1: 2 respectively. (20 ml. of the solution is required to fill 10 tubes. The tubes are 10 cm. long having 5 mm. interior diameter.) This mixture is degassed. Then 0.005 ml. of TEMED is added. It is degassed very quickly for a short time once again. The glass tubes, which were fixed in a stand with bottom ends closed, were filled with the solution by means of Pasteur pipette leaving about 1 cm. space on the top. Distilled water is slowly added by means of Pasteur pipette in which a thread is fixed. The thread may be drawn into the Pasteur pipette by vaccum pump. A knot is put to the thread inside the pipette so that it may not slip out during the water is added. The gel surface will not be disturbed by this procedure. The gel sets within 20 minutes. After the gels are set the water may be removed and the tray buffer is added on the top of the gels after one or two changes with the same. Then the protein sample is mixed with one drop of saturated sucrose solution having a few drops of bromophenol blue. (4 or 5 drops of bromophenol blue is added to 10 ml. of saturated sucrose solution). 100 Cmm. of protein solution is found to be necessary. The sample solution may be added by micropipette on the top of the gel through the buffer. Drop of sucrose makes the protein sample seetle down on the gel. Since bromophenol blue is already in sucrose solution it is not necessary to add the indicator once again in the top tray. The remaining procedure is same as described by Davis (1964). 4 m. Amp. per tube was given and electrophoresis was completed in 1 hour 40 minutes.

The gels are removed with the aid of the fine wire by keeping the tubes in a small trough of water. Gels come out very easily. The gels are fixed in 10% acetic acid for 1 hour in hot water bath (100°C). Proteins will be fixed by this procedure. Staining is done by 0.025% Coomasie blue in 10% acetic acid for 1 hour in hot water bath. Destaining is done in 10% acetic acid for overnight with 2 or 3 changes. The water soluble, Coomasie blue stained protein bands are measured with scale and plotted on millimeter paper. Photographs are made after a few days.

Results and discussion

The present method of gel preparation, electrophoresis, fixing and staining gave good banding pattern of water soluble proteins. Since protein banding pattern in em-

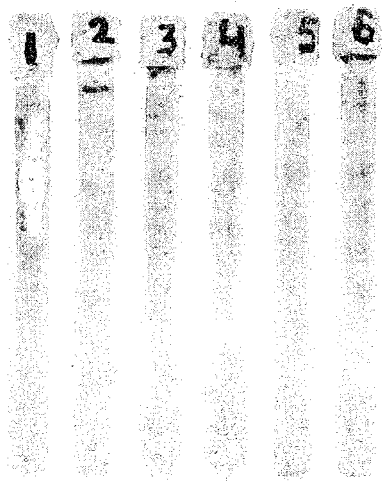

Fig. 1a. Electrophoretic banding pattern of water soluble proteins in different wheat cultivars : 1. Chinese Spring, 2. Roter Löwe, 3. Lichtis Früher, 4. Pakistan I, 5. Pakistan II, 6. Pakistan III

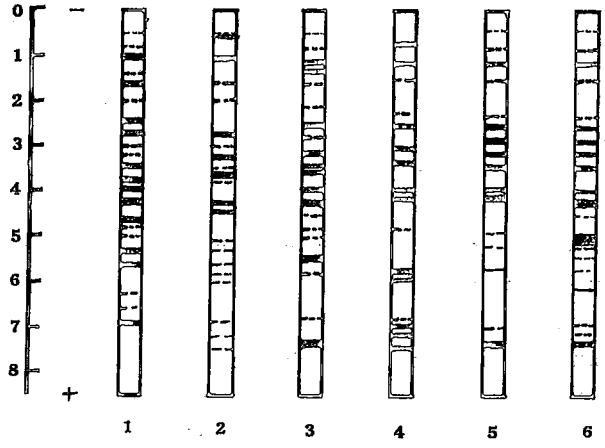

Fig. 1b. Diagramatic representation of the electrophoretic banding pattern of watersoluble proteins in different wheat cultivars : 1. Chinese spring, 2. Roter Löwe, 3. Lichtis Früher, 4. Pakistan I, 5. Pakistan II, 6. Pakistan III
Thick lines indicate major bands and dotted lines indicate minor bands.

bryos will be less affected by environmental conditions embryos are preferred over the whole seed.

In general, more as well as denser bands are present on the upper half of the gel. Up to a maximum of 22 bands could be noticed in chinese spring. Fast moving bands

are less denser as compared to slow moving bands. More positively charged proteins are towards the top. Lichtis Früher has extra bands than Roter Löwe. Pakistan II and III showed different banding pattern over Pakistan I (Fig. 1 a and b).

This method has many advantages:

1. It takes less time in preparing the protein solution which is to be loaded on the polyacrylamide gel.
2. Fixing and staining is completed within 2 hours.
3. It serves as quick method in identifying and also in eliminating duplicate cultivars.

However, this method has one great disadvantage. Since the homogenate is too little, it is very difficult to measure actual protein content we are putting on the gel. Actually how much protein is present in 100 Cmm. of solution is not known. So, the great quantitative differences in the protein composition can be misinterpreted as qualitative differences as the electropheretic mobility of the protein fraction is influenced by the concentration of the protein. Protein estimation by Lowry method is only possible if sufficient quantity of protein solution is available. If some imporvements are made to check the protein content by micro methods this method will be of much use in future.

Acknowledgements

I wish to express may appreciation to Prof. Dr. Gerhard Röbbelen for providing the facilities for this study. I thank Dr. Ove Hall and Dr. Henrik Johansson of the Swedish Seed Association, Svalof, Sweden for going through the manuscript and for their helpful comments. I am also indebted to Alexander von Humboldt Stitfung for the award of fellowship.

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A new interspecific hybrid: *Triticum aestivum* ssp. *vulgare* × *Aegilops ventricosa*

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In order to transfer directly the genes of resistance to eyespot (*Cercosporella herpotrichoides* Fron.) of *Aegilops ventricosa* Tausch., 2n=28, to *Triticum aestivum* ssp. *vulgare* Mac Key, 2n=42, an attempt was made to cross the two species.

As far as is known, this is the first time that such a hybrid has been obtained (Siddiqui and Jones 1967, Knobloch 1968).

In 1970, crosses were made between two cultivars of the common wheat (Moisson, Top) and one semi-dwarf line (Mexique 50×B 21) 2.6.10.3.6.4. as the female parent, and four different strains of *Aegilops ventricosa* as the male parent.

Of the 920 florets of wheat pollinated by *Ae. ventricosa*, four seeds were produced only from the cross (*T. aestivum* cv. Moisson × *Ae. ventricosa ssp. comosa* Coss. and Dur.*).

Two F_1 hybrid plants were subsequently obtained.

They grew quite normally and were intermediate to their parents for most morphological characters, although, in some cases, the traits of one parent were dominant (or epistatic) as recorded in Table 1.

The hybrid plants were pollen sterile with non dehiscent anthers. The seed-setting was rather poor: only twelve seeds were obtained from fourty-two spikes, in a back-cross with *Triticum aestivum* and three seeds have been produced from one hundred and forty-five spikes from free pollination.

Meiotic behaviour of the F_1 hybrids was analysed only at the first metaphase stage

Table 1. Dominant characters coming from *Ae. ventricosa* or *T. aestivum*

Ae. ventricosa	*T. aestivum*
hairiness of the sheath margin	ligule size
spike density	spikelet size
size and shape of rachis internodes	glume asymmetry
firmness, roughness and nervation of rachis internodes	type of disarticulation of the rachis
roughness and nervation of the outer surface of the glumes	
firmness of the glumes	
toughness of spikelets and rachis internodes	

* Kindly supplied by Dr. H. Kihara (his assession No. 1 coming from the Cornell University).

Table 2. Mean meiotic pairing at the first metaphase

Name	Number of cells observed	Univalents		Bivalents						Number of chas/cell	% of pollen stainable
		range	mean	total		open		closed			
				range	mean	range	mean	range	mean		
Ae. ventricosa	50	—	0	—	14	0~6	2.02	8~14	11.98	25.98	98.0
F_1*	200	20~33	24.94	1~7	5.03	1~6	3.71	0~4	1.32	6.35	1.5
T. aestivum	50	0~ 2	0.08	20~21	20.96	0~4	1.94	17~21	19.02	39.98	97.0

For the F_1, meiotic chromosome pairing was analysed in two plants (100 PMC in each).
* One cell with $(20_I+6_{II}+1_{III})$.

and the mean pairing behaviour observed was compared to those of the parents, as shown in Table 2.

Taking into consideration the genome formulation of the parents established by KIHARA and others, the genomic constitution of the F_1 hybrids might be A B D D M^v, and the mean value of meiotic pairing about 7_{II} D+21_I A B D M^v. Considering the hypothesis proposed by KIHARA (1949) of a partial homology between the D and M^v genomes some deviations, with the occurence of trivalents instead of bivalents, and less than twenty one univalents could be expected.

In fact, as shown in Tables 2 and 3, in the material under investigation, a little less than two genomes (mean 5.03_{II}, 1 to 7, mostly open)are able to associate as bivalents and might imply the common D genomes. Meanwhile the other chromosomes (univalents) might belong to the A B M^v genomes. A comparison with the nearly asyndetic meiotic pairing reported by SIMONET (1952) in the F_1 hybrids, with A B D M^v genomes, involving *Ae. ventricosa* and some tetraploid wheat species, supports these results.

Table 3. Meiotic configurations of F_1 PMC's at the first metaphase (%)

PMC's	1_{II}	2_{II}	3_{II}	4_{II}	5_{II}	6_{II}	7_{II}
%	0.5	4.5	7	19	29.5	27.5	11.5

Consequently, these observations raise certain problems concerning the genomic constitution of *Ae. ventricosa.*

Firstly, if it is assumed that the bivalents observed are D associations, it may be concluded that no close homology exists between the D and M^v genomes. However, considering that in the (*T. aestivum*×*Ae. ventricosa*) hybrid, the genetic system from chromosomes 5B and 3D must be effective and restrict pairing to homologous chromosomes, our observations do not weaken the KIHARA hypothesis. The D and M^v genomes might be homeologous to the same degree as the A and B genomes. Only the cross of *Ae. ventricosa* with the mono 5B of *T. aestivum*, unsuccessfull until now, might confirm this.

Secondly, the relationships between the D genomes of *T. aestivum* and *Ae. ventricosa* do not seem as close as in the case of *T. aestivum* and *Aegilops squarrosa* (RILEY and CHAPMAN 1960), or *Aegilops cylindrica* (ASPIAZU and LACADENA 1970).

In fact, in the hybrid (*T. aestivum* × *Ae. squarrosa*) with A B D D genomes, RILEY and CHAPMAN observed usually 7_{II}, mostly closed, while in the present investigation only 5_{II}, mostly open, were formed. Likewise, in the F_1 hybrids between *T. aestivum* and *Ae. cylindrica* with A B D D C genomes, studied by ASPIAZU and LACADENA, the meiotic pairing is rather complicated but the mean number of bivalents is 7.17 and there are some multivalents.

It is of interest to note that SIDDIQUI and JONES (1967), in a study of (*Aegilops ventricosa* × *Triticum dicoccum*) × *T. aestivum* hybrids demonstrated also that the D genome of *Ae. ventricosa* is not completely homologous with the D genome of *Ae. squarrosa* or *T. aestivum*. However, the pairing observed by these authors is more incomplete than ours.

In the present status, the transfer of genes from the M^v genome of *Ae. ventricosa* to common wheat remains difficult by the normal processes of recombination, and the differenciation of the D genome of this species, as illustrated by some lack of pairing with the D genome of wheat, could make introgression into wheat more difficult than from *Ae. squarrosa*.

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Cytoplasmic-genic type of male sterility in *Secale montanum* Guss.

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Introduction

The possibilities for efficient utilization of hybrid vigor in cultivated rye have long time been considered to be limited because of lack of feasible cytoplasmic-genic male sterility system. At least one well documented case of cytoplasmic male sterility influenced in its expression by nuclear genes has been reported in past (Putt 1954). But this source has eventually been lost. More recently some suggestive evidence of cytoplasmic-genic interaction for male sterility in cultivated rye has been presented independently by Zdrilko (1969) and Geiger and Schnell (1970).

The purpose of this paper is to report the development of male sterility controlled by cytoplasmic-genic interaction in wild mountain rye.

Material and method

Secale cereale, cv. Smolickie and perennial *Secale montanum*, KH66–30 were chosen as parental stocks to be used in a systematic search for cytoplasmic male sterility. Pollination with bulk pollen was practiced during the course of crossing and subsequent backcrossing of these two stocks. All other crosses reported in this paper were made between individual clones. Plants were scored for male sterility-male fertility expression on the basis of both visual inspection of spikes at the time of anthesis and microscopic examination of squashed anthers. Those plants having thin indehiscent anthers containing unstainable, if any, pollen grains were classified male sterile. Plants with dehiscing anthers, irrespectively of the amount of fertile pollen grains shed, were considered to be male fertile.

Results and discussion

In 1966, Smolickie rye cultivar was crossed reciprocally with wild strain KH66–30. Each of the two F_1's was then crossed back twice to the male parent of the original cross giving rise to the substitution Bc_2 families, Smolickie$\times$KH66–30^3 and KH66–30$\times$Smolickie^3. Plants of these Bc_2 families resembled quite closely the recurrent parents. The Bc_2, KH66–30$\times$Smolickie^3 plants appeared to be uniformly male and female fertile. Six of the 7 Bc_2, Smolickie$\times$KH66–30^3 plants were completely pollen sterile but set seed freely and 1 plant was fully fertile. The male fertile plant and one of the male steriles, hereafter referred to as MF 70/7–1 and MS 70/8–1 respectively, were chosen to establish clones

for further studies.

The male sterile stock reported herein was derived from interspecific cross, such that considerable part of *S. montanum* germ plasm had been placed in the cytoplasm of *S. cereale*. Furthermore, pollen sterility difference in reciprocal crosses was apparent. It seemed reasonable to hypothesize, therefore, that the male sterility expression resulted from the interaction of *cereale* cytoplasm with nuclear genes of *montanum*.

In order to test this assumption it was necessary at first to have male fertile clones with known genotypes in both *cereale* and *montanum* cytoplasm. The determination of genetic constitution of the clones in question was initiated by crossing MS 70/8–1 × MF 70/7–1. Two of the male fertile F_1 segregates from this cross were then intercrossed and simultaneously crossed back to the sterile parent. All the sibcross and testcross progenies segregated into male fertile and male sterile plants in ratios expected for monogenic inheritance (Table 1). It was concluded that the MS 70/8–1 clone behaved as single gene recessive and that male fertility was restored in the MF 70/7–1 clone by a single dominant allele. Three male fertile clones of *S. montanum*, designated KH66–30–2, KH66–30–4 and KH66–30–5 were also crossed to MS 70/8–1 in an effort to determine their genotypes with respect to the male sterility locus. Two appeared to be heterozygous, and one appeared to be homozygous recessive (Table 2).

Table 1. Segregation data from progenies of sibcrosses and testcrosses

Family No.	Pedigree	Segregation, MF : MS		P*
		obs.	exp.	
70093	MS 70/8–1 × MF 70/7–1	41 : 36	1 : 1	0.70∼0.50
71107	MS 70/8–1 × 70093	25 : 32	1 : 1	0.50∼0.30
71108	MS 70/8–1 × 70093	27 : 37	1 : 1	0.30∼0.20
71104	70093 × 70093	15 : 9	3 : 1	0.30∼0.20
71105	70093 × 70093	17 : 9	3 : 1	0.50∼0.30

* Chi-square probability

Table 2. Results from the test for the presence of male sterility genes in clones of *S. montanum*

Family No.	Pedigree	Number of plants		$X^2_{1:1}$	P
		MF	MS		
71098	MS 70/8–1 × KH 66–30–2	0	50	—	—
71099	MS 70/8–1 × KH 66–30–4	29	22	0.96	0.50∼0.30
71100	MS 70/8–1 × KH 66–30–5	23	32	1.47	0.30∼0.20

The test of cytoplasmic-genic interaction associated with the male sterility was provided by 1) crossing reciprocally the MF 70/7–1 clone with KH66–30–2, KH66–30–4 and KH66–30–5 clones, 2) intercrossing the KH66–30–2, KH66–30–4 and KH66–30–5

clones, and 3) scoring the resulting progenies for the presence or absence of male sterility. The cytoplasmic effect hypothesis required only the progenies of crosses involving MF 70/7-1 as the female parent to be segregating for male fertile and male sterile plants, and progenies of the other crosses to be entirely male fertile. As is shown in Table 3, the actual observations were in accord with the expectations of the assumption tested.

Table 3. Results from the test for cytoplasmic effect

Family No.	Pedigree	Cytoplasm*	Segregation, MF : MS		P**
			obs.	exp.	
71092	KH 66-30-2×MF 70/7-1	N × S	30 : 0	1 : 0	—
71093	KH 66-30-4× 〃	〃	39 : 0	1 : 0	—
71094	KH 66-30-5× 〃	〃	39 : 0	1 : 0	—
71095	MF 70/7-1 ×KH 66-30-2	S × N	14 : 18	1 : 1	0.50～0.30
71096	〃 ×KH 66-30-4	〃	30 : 9	3 : 1	0.90～0.70
71097	〃 ×KH 66-30-5	〃	31 : 8	3 : 1	0.70～0.50
71101	KH 66-30-2×KH 66-30-4	N × N	19 : 0	1 : 0	—
71102	〃 ×HK 66-30-5	〃	20 : 0	1 : 0	—
71103	KH 66-30-4× 〃	〃	19 : 0	1 : 0	—

* Cytoplasms of *S. montanum* and *S. cereale* are presumed to be normal (N) and sterile (S), respectively.

** Chi-square probability.

The necessary conclusions from these results are that *S. cereale* has a cytoplasm capable of inducing male sterility to certain *S. montanum* genotypes and that the sterilizability of the genotypes is due to a single recessive gene which is without apparent effect on sterility in *montanum* cytoplasm. Any alternative explanation possible seems to be less reliable. It should perhaps be mentioned here that *S. kuprijanovi* also contains the recessive gene(s) causing male sterility when homozygous in *cereale* cytoplasm.

Much is yet to be learned about the genetics of fertility restoration in *cereale* cytoplasm. Preliminary evidence indicates, however, that the major genes for fertility restoration are dominant and the number of the genes probably is relatively few. It seems reasonable to assume that, at least in some instances, complete pollen fertility may be due to a single dominant gene, plus modifiers. It appears that modifiers can affect the degree of fertility restoration, for none of the segregating progenies studied was completely free of nearly sterile and nearly fertile segregates. The possibility that there are more than two alleles at the *Rf* locus is not excluded, however.

The potential hindrances to using the (*cereale*)—*S. montanum* source of cytoplasmic male sterility in a program for commercial production of hybrid rye varieties are apparent. However, one should not dismiss the possibility of practical use of this stock on the basis of theoretical consideration alone.

Summary

A case of cytoplasmic pollen sterility in wild rye is reported. The male sterility expression is due to the interaction of homozygous recessive gene(s) from *S. montanum* with the cytoplasm of *S. cereale*. Apparently this is the first published report of difference between cytoplasm of *Secale* species with regard to their effect on pollen sterility.

Literature cited

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II. News

Barley Genetics Newsletter

Barley Genetics Newsletter (BGN), an international communication medium in barley genetics, was established in 1971 with the publication of volume 1 (209 pages). BGN Vol. 2 (215 pages) was published recently at the Department of Agronomy, Colorado State University, Fort Collins, Colorado. It includes: Special notices, Research notes, Genetic and cytological techniques, Reports from Coordinators, Current linkage maps, List of genetic stocks, Description of genetic stocks, Letters to the editors, Corrections of barley genetics literature and the Mailing list. Publication of the newsletter was supported by the National Science Foundation, U.S.A. and by contributions from Denmark, Germany and Sweden. Editorial Committee Members are T. E. HAUS (Colorado), R. T. RAMAGE (Arizona) and T. TSUCHIYA (Colorado). Libraries of Land Grand Colleges and Universities receive a copy automatically. Contributors to the newsletter and persons requestiong a copy are on the mailing list.

BGN, Vol. 2 as well as Vol. 1 are still available, free of charge. Libraries or persons interested in receiving a copy should write to:

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III. Editorial Remarks

Announcement for future issues

WIS No. 36 will be planned for publication in March 1973. Manuscripts for this issue are accepted any time, not later than January 31, 1972.

WIS is open to all contributions regarding methods, materials and stocks, ideas and research results related to genetics and cytology of *Triticum, Aegiolops, Secale, Haynaldia* and related genera. Manuscripts should be typewriten in English, and submitted with duplicates. One article should not exceed five printed pages, including one textfigure (smaller than 7×7 cm^2). Lists of stocks are exempted from this page limit. Authors receive 50 reprints of their contributions free of charge. Extra copies are printed by order at cost prince. Communications regarding editorial matters should be addressed to:

Kosuke YAMASHITA
Wheat Information Service
Kihara Institute for Biological Research
Yokohama, Japan

Raise of Membership Fee

Due to the economic situations, the yearly Membership Fee is raised up to ¥700 for foreign member and ¥500 for Japanese member from the fiscal year beginning April 1973. The money should be paid by the Foreign Postal Money Order, othersiwe considerable loss is caused due to the bank charges. Back numbers are available.

Acknowledgement

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The Managing Editor

Explanation of the Figure on the Cover

Fig. 1b. Diagramatic representation of the electrophoretic banding pattern of water soluble proteins in different wheat cultivars: 1. Chinese spring, 2. Roter Löwe, 3. Lichtis Früher, 4. Pakistan I, 5. Pakistan II, 6. Pakistan III. Thick lines indicate major bands and dotted lines indicate minor bands; by A. Sudharsan RAJ (cf. pp. 18~21, present issue of WIS)