Theoretical and Applied Genetics 41, 100–103 (1971)
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Variability and Covariability for Plant Height, Heading Date, and Seed Weight in Wheat Crosses

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Summary. Variability, covariability, heritability, and expected genetic gains from selection for heading date, plant height, and kernel weight were estimated in progenies derived from six wheat crosses. The crosses differed in the magnitude of the genetic variabilities of their progenies, but all crosses had significant variabilities for all traits. Heritability estimates were calculated by the variance components method. The estimates of heritability were relatively high for all three traits and averaged 86% for heading date, 77% for plant height, and 70% for kernel weight. The presence of significant genetic variabilities and high heritability estimates indicated that selection would be effective for the three traits.

The segregates derived from crosses between medium tall parents showed transgressive segregation that would permit isolation of short-statured types. Transgressive segregation also occurred for heading date and kernel weight.

Heading date and plant height were positively and highly significantly correlated in four crosses out of six. But both plant height and heading date had, in general, low negative correlations with kernel weight which would not preclude the development of short wheats with high kernel weight from these crosses. The association between characters was mostly genetic in cause.

Plant breeding involves three main successive stages: (1) obtaining or creating genetic variability; (2) practising selection to isolate the desired genotypes; and (3) utilization of the selected genotypes to develop superior varieties. Estimates of genetic variance, heritability, and genotypic association among characters can be of valuable use in these three stages.

Heritability percentages have been estimated by different methods for various attributes in wheat such as yield, yield components, heading date, plant height, spike and seed characters, and others (McNeal, 1960; Gandhi et al., 1964; Kronstad and Foote, 1964; Johnson et al., 1966; Schlehuber et al., 1967; Reddi et al., 1969; Lesbock and Amaya, 1969). For the traits studied here, heading date, in general, has the highest heritability values, plant height has intermediate values, and heritability for kernel weight is medium-low.

The associations among the various wheat characters were studied by Schlehuber at al., 1967, Reddi et al., 1969, and Lesbock and Amaya, 1969. In general, heading date was found to be positively correlated with plant height, and both characters were negatively correlated with kernel weight.

In Egypt, plant breeders have imposed selection pressure upon the wheat genetic pool in favour of medium-tall strains, to maintain a reasonable yield of straw which is urgently needed for animal feeding during the summer. However, in recent years, the productiveness of short wheat cultivars under high nitrogen fertilization has attracted the interest of many plant breeders from different countries. But the short cultivars in the world collection are lower in test weight than the medium-tall types. Moreover, segregates from crosses between the Mexican short cultivars and our local ones have exhibited a high frequency of defective plants with firing leaves, a case which was described by Hermsen (1963) as hybrid necrosis. An alternative approach for developing new short cultivars is to search for the desired genotypes in the progenies of crosses among normally-statured parents which might originate from transgressive segregation.

Several years ago, a number of crosses were made between introduced and local wheat cultivars and strains to provide a pool of germplasm for a selection program. Six of these crosses were investigated to: (1) search for short strains in the segregates derived from these crosses; (2) estimate the variability and covariability of plant height, heading date, and kernel weight; (3) calculate the heritabilities of these traits; and (4) predict the genetic advance from selection.

Material and Methods

The experimental populations used in this study were derived from six crosses among several local and introduced common wheat "*Triticum aestivum* L. em. Thell." cultivars and strains. The crosses were as follows:

Cross number 1 "A194-1 × Tosson"
2 "Exchange × No. 43"
3 "Giza 139 × A194-1"
4 "A194-1 × No. 43"
5 "Tosson × Giza 150"
6 "Exchange × Giza 150".

Cross numbers 1 to 6 will be used to refer to crosses in this presentation.

There were differences among the parents for heading date, plant height and kernel weight (Table 1).

Table 1. *Means of parents and means and ranges of crosses for heading date, plant height, and kernel weight*

Parent or cross	Heading date days after Jan. 1	Plant height cm.	Grams per 100 kernels
		Parents	
A194-1	33	110	3.92
Tosson	52	121	3.99
Exchange	50	134	3.75
No. 43	57	132	4.35
Giza 139	43	124	4.89
Giza 150	52	127	3.95
		Crosses	
1	40 (27–57)*	117 (93–142)	3.67 (2.47–4.85)
2	52 (42–72)	133 (99–151)	4.18 (2.99–5.52)
3	42 (29–60)	122 (102–153)	4.12 (3.14–5.02)
4	39 (29–61)	118 (100–135)	3.88 (3.09–4.60)
5	52 (34–61)	125 (103–146)	3.82 (2.83–4.85)
6	52 (42–62)	131 (114–143)	3.73 (3.03–4.34)

* values between parentheses represent the ranges.

In autumn 1968, for each cross a random sample of 50 families (a family is the progeny of an individual F_2 plant), each represented by two lines (a line is the progeny of an individual F_3 plant), was grown in a three-replicate, randomized split-split design at the Agricultural Experiment Station of Alexandria University, Alexandria. Crosses were randomly allocated to the main plots, families within crosses to the sub plots, and lines within families to the sub-sub plots.

For each parent, a sample of eleven families, each represented by two lines, was derived by a similar procedure to that described for the cross populations. Entries of the two parents were randomly allocated among the sub-sub plots of their relevant cross.

For the crosses or the parents, a random sample of 25 seeds from each line was planted in a hill plot in each replicate. Hill plots were spaced one foot apart at right angles.

Data were recorded for each plot as follows:

1. Heading date — number of days after January 1 for 50% of the spikes to be completely emerged from the boots.
2. Plant height — distance in cm from soil surface to the tips of the spikes, excluding the awns.
3. Kernel weight — weight in grams of 100 kernels.

The analysis of variance or covariance was computed for the material of each cross individually. Since the results indicated that the means of squares for the family and line plots among crosses were homogeneous, a pooled error was used for each measured character in each family or line subdivision.

For the calculation of variance components, the subdivisions within crosses (families and lines) were assumed to be random variables as follows:

Source of variation	Estimated mean square
Families	$\sigma_b^2 + l\,\sigma_a^2 + r\,\sigma_l^2 + r\,l\,\sigma_f^2$
Error *a*	$\sigma_b^2 + l\,\sigma_a^2$
Lines *w*/families	$\sigma_b^2 + r\,\sigma_l^2$
Error *b*	σ_b^2

where a and b stand for the errors, r = replicates, l = lines, and f = families.

Heritability on a plot basis was estimated from the variance components as the ratio of:

$$\frac{\sigma_l^2 + \sigma_{f/2}^2}{\sigma_l^2 + \sigma_{f/2}^2 + \sigma_{a/6}^2 + \sigma_{b/3}^2}$$

Expected genetic advance (ΔG) from selection among lines was calculated using the formula proposed by Johnson et al. (1955):

$\Delta G = 2.06$ (genetic coefficient of variability × heritability), assuming selection intensity of 5%. These expected genetic gains might contain a positive bias associated with dominance variability. The extent of this bias would depend upon the degree of dominance, linkage, and nature of gene expression.

Phenotypic and genotypic correlations between attributes were computed according to the methods described by Johnson et al. (1955) as follows:

Phenotypic correlation $(r_p) = M_{12}/\sqrt{(M_1)\,(M_2)}$

where M_{12} is the phenotypic mean product between pairs of characters and M_1 and M_2 are the phenotypic mean squares of the two characters, respectively; and

Genotypic correlations $(r_g) = \sigma_{g_{12}}^2/\sqrt{(\sigma_{g_1}^2)\,(\sigma_{g_2}^2)}$

where $\sigma_{g_{12}}^2$ is the genetic covariance between two characters, and $\sigma_{g_1}^2$ and $\sigma_{g_2}^2$ are genotypic variances of the two characters, respectively.

Results and Discussion

Means, Ranges, and Variability

Means of parents and means and ranges of their cross progenies for the characters studied are given in Table 1. A wide range of 24 days for heading date occurred between the earliest and latest parent. For plant height and weight per 100 kernels, differences between the two extreme parents were 24 cm and 1.14 gm., respectively.

The means of heading date or plant height of the cross progenies were, in general, intermediate between the means of their parents. The differences among parents were reflected in their progenies. Wider ranges and higher mean squares (Table 2), and consequently higher variance components (Table 3), for progenies were obtained from crosses between widely

Table 2. *Means of squares of traits from the analyses of variance for progenies of crosses*

Cross	D.F.	Means of squares		
		Heading date	Plant height	Kernel weight
		Families within crosses		
1	49	361.67**	523.08**	0.5884**
2	49	237.44**	314.55**	1.2010**
3	49	365.81**	328.65**	0.7841**
4	49	373.61**	241.35**	0.5037**
5	49	137.02**	149.20**	0.6348**
6	49	109.40**	149.50**	0.4792**
Pooled error	588	12.49	44.26	0.1519
		Lines within families within crosses		
1	50	149.22**	171.80**	0.1805**
2	50	30.96**	82.86**	0.1378**
3	50	127.08**	142.71**	0.2418**
4	50	47.78**	89.64**	0.1944**
5	50	36.12**	94.56**	0.1881**
6	50	20.33**	64.84**	0.1602**
Pooled error	600	9.02	26.80	0.0701

** Exceeds the 1% level of significance

Table 3. *Variance components for traits of families* ($\sigma_{\bar{f}}^{2}$) *and lines* ($\sigma_{\bar{l}}^{2}$) *derived from wheat crosses*

Cross	Heading date		Plant height		Kernel weight	
	$\sigma_{\bar{f}}^{2}$	$\sigma_{\bar{l}}^{2}$	$\sigma_{\bar{f}}^{2}$	$\sigma_{\bar{l}}^{2}$	$\sigma_{\bar{l}}^{2}$	$\sigma_{\bar{f}}^{2}$
1	34.83	47.30	55.64	48.33	0.0544	0.0368
2	33.83	7.31	35.70	18.69	0.1637	0.0226
3	39.21	39.35	28.08	38.64	0.0768	0.0572
4	53.73	12.92	22.38	20.95	0.0379	0.0414
5	16.24	9.03	6.20	22.59	0.0608	0.0393
6	14.27	3.77	11.20	12.68	0.0395	0.0300
Mean	32.00	19.94	26.53	26.98	0.0722	0.0379

different parents than between parents with closer means. For example, the variabilities for heading date or plant height occurring among progenies derived from the two crosses "Tosson × Giza 150" and "Exchange × Giza 150" were relatively lower than those obtained from the other crosses. The parents involved in these two crosses were similar for heading date and plant height.

For kernel weight, the means of the crosses were either intermediate between the two parents or closer to the parent with the lower kernel weight.

All the crosses have shown transgressive segregation for the three traits in both the plus and minus directions. Among the progenies of the crosses there were lines with lower and lines with higher kernel weight than their respective parents. This was also true for heading date and plant height. The occurrence of transgressive segregation for heading date, plant height, and kernel weight would permit the plant breeder to select for extreme types if he desired.

All the mean squares of families or lines for the studied traits were highly significant (Table 2), indicating the presence of genetic variability among the progenies. Study of the relative magnitudes of the genetic variability released in generations has a practical significance when considering the systems of propagation that should be followed during breeding programs. For heading date and kernel weight, the average variation (Table 3) that occurred between families (that represented variability among F_2 plants) was approximately double that estimated for lines within families (variability within F_2 progenies), whereas for plant height, the average genetic variance for families (σ_f^2) was equal to that of lines (σ_l^2). Since two thirds of the available variability for heading date and kernel weight in the F_3 generation could be released among the F_2 progenies, one could maintain a high level of the genetic variability for these two traits if each of the F_2 plants was propagated in bulk for later generations. For plant height, it would be advisable to release the potential latent variability through segregation in a pedigree breeding program that permits selection among and within F_2 progenies. The genetic variance components for lines and families were used to determine the amount of variability among and within F_2 progenies, because they are independent of the magnitude of the other components of variance involved in the mean squares.

Heritability

Heritability (on a plot basis) was estimated from the variance components. The genetic variance components for lines (σ_l^2) and families (σ_f^2) were assumed to be available for the breeder when testing F_3-derived progenies. In general, heritability percentages (Table 4) were high in crosses and characters. The highest heritability estimates in all crosses were obtained for heading date, followed by plant height and then kernel weight. Average heritabilities for heading date, plant height, and kernel weight were 86, 77, and 70%, respectively. These high values were similar to heritabilities estimated in wheat by Kronstad and Foote, 1964, Johnson et al., 1966, Schlehuber et al., 1967, Reddi et al., 1969, and Lesbock and Amaya, 1969. The fact that these characters exhibited high genetic variabilities and high heritabilities would make selection effective in populations such as those tested in this study.

Table 4. *Heritability percentages and expected gains from selection for three traits in wheat*

Cross	Heritability percentages			Expected gains		
	Heading date	Plant height	Kernel weight	Heading* date	Plant* height	Kernel weight
1	94	88	68	−16	−14	12
2	85	78	78	− 9	− 8	14
3	93	84	76	−15	−11	14
4	90	76	67	−12	− 9	11
5	80	71	70	− 8	− 7	12
6	72	64	60	− 6	− 5	10
Mean	86	77	70	−11	− 9	12

* Selection for early heading and for short types.

Expected Genetic Advance

Expectations of genetic advance (assuming selection intensity of 5%) for the three agronomic traits were calculated according to the formula presented by Johnson et al. (1955). Selection was for early heading and short plants. Selection was expected to be effective for heading date, plant height and kernel weight. The expected gains for early types from the six crosses ranged from 6 to 16 days, with an average of 11 days (Table 4). For plant height, expected gains expressed as percentages of the means ranged from 5 to 14%, with an average of 9%. For kernel weight, values ranged from 10 to 14%. Cross 6 had the lowest expected gains because it has the lowest variabilities and heritability estimates for all characters.

Selection for early heading types was expected to be associated with shortness since both traits were

Table 5. *Phenotypic (r_p) and genotypic (r_g) correlations among traits of progenies derived from six wheat crosses*

Cross	No.	Heading date and plant height		Plant height and kernel weight		Heading date and kernel weight	
		Lines	Families	Lines	Families	Lines	Families
C_1	r_p	0.65**	0.67**	–0.01	–0.03	0.19	–0.21
	r_g	0.75	0.75	–0.27	–0.05	0.26	–0.23
C_2	r_p	0.13	0.33*	–0.40*	–0.15	–0.33*	–0.29
	r_g	0.23	0.39	–0.72	–0.16	–0.72	–0.27
C_3	r_p	0.59*	0.79**	–0.18	0.27	–0.27	0.14
	r_g	0.64	0.85	–0.20	0.33	–0.26	0.12
C_4	r_p	0.76**	0.69**	–0.06	–0.01	–0.13	–0.25
	r_g	0.87	0.90	–0.08	–0.13	–0.15	–0.36
C_5	r_p	0.22	0.33*	0.09	0.07	–0.13	–0.07
	r_g	0.30	0.43	0.13	0.11	–0.14	–0.09
C_6	r_p	0.78**	0.22	–0.04	0.20	–0.38*	–0.18
	r_g	1.01	0.36	–0.06	0.19	–0.47	–0.30
Mean	r_p	0.52**	0.51**	–0.10	0.06	–0.18	–0.14
	r_g	0.63	0.61	–0.20	0.05	–0.25	–0.19

* Exceeds the 5% level of significance
** Exceeds the 1% level of significance

correlated (Table 5). But selection for either early heading or shortness would not lead to lower kernel weight because kernel weight was, in general, genetically independent from heading date and plant height.

Phenotypic and Genotypic Correlations

Coefficients of correlation among heading date, plant height, and kernel weight are shown in Table 5. Genotypic correlations were similar in sign and slightly higher in magnitude than phenotypic correlations in the six crosses. Therefore the significant phenotypic associations between characters were primarily due to genetic causes. Also, correlations were similar in value and sign whether measured from means of families or lines within families. This might indicate that the type of association between characters is due to a pleiotropic effect rather than linkage between genes affecting different characters. Of course, this conclusion may be criticized in that the self-pollination mechanism is apt to fix blocks of genes, because of the limited chances for breaking linkage compared with the random-mating system prevailing in open-pollinated crops which allows for breaking linkage in successive generations.

Except for two cases, all the phenotypic correlations between heading date and plant height were significant and positive. Average phenotypic and genotypic correlations were 0.52 and 0.63, respectively. Similar values were reported by Schlehuber et al. (1967) and Lesbock and Amaya (1969). The present data and that of others suggest that selection of early heading types might result in a population with plant height shorter than the unselected population mean.

Phenotypic correlations between kernel weight and either plant height or heading date were low and insignificant in most cases. This means that within each cross there is no strong genetic association that would prevent selection for early heading types with heavy kernel weight. Furthermore, the short-statured strains that could be isolated from the transgressive segregates, produced from crosses among normally-statured cultivars, are not necessarily associated with low kernel weight. In previous work (Johnson et al., 1966; Reddi et al., 1969), the short culm was associated with low kernel weight in wheat crosses involving short cultivars. Such an association would preclude developing short types with high kernel weight. The genetic interrelationships in the present materials would not put a limitation on breeding for short cultivars with high kernel weight. Of course, the germplasm of the parent materials used here did not include any short cultivar.

Literature

1. Gahndi, S. M., Sanghi, A. K., Nathawat, K. S., Bhatnagar, M. P.: Genotypic variability and correlation coefficients relating to grain yield and a few other quantitative characters in Indian wheats. Ind. J. Gen. and Plant Breed. **24**, 1–8 (1964). — 2. Hermsen, J. G.: Hybrid necrosis as a problem for the wheat breeder. Euphytica **12**, 1–16 (1963). — 3. Johnson, H. W., Robinson, H. F., Comstock, R. E.: Estimates of genetic and environmental variability in soybeans. Agron. J. **47**, 314–318 (1955). — 4. Johnson, V. A., Biever, K. J., Haunold, A., Schmidt, J. W.: Inheritance of plant height, yield of grains, and other plant and seed characteristics in a cross of hard red winter wheat, *Triticum aestivum* L. Crop Sci. **6**, 336–338 (1966). — 5. Kronstad, W. E., Foote, W. H.: General and specific combining ability estimates in winter wheat (*Triticum aestivum* Vill., Host). Crop Sci. **4**, 616–619 (1964). — 6. Lesbock, K. L., Amaya, A.: Variation and covariation of agronomic traits in durum wheat. Crop Sci. **9**, 372 to 375 (1969). — 7. McNeal, F. H.: Yield components in a Lemhi × Thatcher wheat cross. Agron. J. **52**, 348–349 (1960). — 8. Reddi, M. V., Henye, E. G., Liang, G. H. L.: Heritabilities and interrelationships of shortness and other agronomic characters in F_3 and F_4 generations of two wheat crosses (*Triticum aestivum* L. em. Thell.). Crop Sci. **9**, 222–225 (1969). — 9. Schlehuber, A. M., Abbott, D. C., Jackson, B. R., Curtis, B. C.: Correlated inheritance of maturity and quality factors in a hard red winter wheat cross. Crop Sci. **7**, 13–16 (1967).

Received August 25, 1970

Communicated by Å. Gustafsson
and W. Seyffert

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