

## GENOTYPIC AND PHENOTYPIC CORRELATIONS IN A SOYBEAN CROSS

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In a plant breeding program, an efficient selection of desired characters in a population is important. Generally, many agronomic characters in a given population are determined by polygenes and quantitatively inherited. In practice, the genetic relationship between two observed characters which are undoubtedly subjected to the environmental influence is difficult to identify.

In recent years, many workers have attempted to understand the genetic relationship between characters in terms of genotypic correlation, and the knowledge thus gained should furnish many important and useful information for the planning of breeding, selection, and interpretation of the result. The genotypic correlation is the result of pleiotropy, linkage of genes(2, 3, 5, 6, 8) and natural or artificial selection(4).

The purposes of this study were to estimate genotypic and phenotypic correlations between all possible pairs of nine characters, and to seek certain characters which may be useful as indicators of certain important agronomic characters.

Weber and Moorthy(10), Johnson *et al.*(5) and Sheth(7) found that in general, the genotypic correlations were higher than the phenotypic correlations. Weiss *et al.*(11) obtained significant positive correlations between maturity and oil content, maturity and low protein content, and high protein content and low oil content. Weber and Moorthy(10) reported the positive genotypic correlations between flowering and maturity, yield and maturity, yield and plant height, yield and seed weight, and negative genotypic correlations between maturity and oil content, and oil content and seed weight. Johnson *et al.*(5) studied the genotypic and phenotypic correlations among 24 characters and concluded that selection based entirely on a long fruiting period, lateness, heavy seed, low protein, high oil and resistance to lodging would be effective in increasing yield. Sheth(7) found the following positive associations among characters; height and maturity, yield and lodging, low protein content and high oil content, and yield and low protein content. Hanson *et al.* (1) also reported high negative correlation between seed yield and protein content.

### MATERIALS AND METHODS

These studies are based on the F<sub>3</sub> and F<sub>4</sub> generations of the cross, Norchief × Harosoy, grown in 1959 and 1960. Sixty four lines were arranged in a randomized block design with two replications for each test. Each plot consisted of a single ten feet row, three feet apart from each other. The center

eight feet section of each row was harvested for yield.

The traits measured on a plot basis were as follows: (a) plant height: length in inches from ground to top of the stem at maturity, (b) lodging index: scored from 1 to 5 with 1 indicating all plants erect and 5 almost all plants down, (c) seed yield: reported in bushels per acre, (d) seed weight: weight in

grams per 100 seeds, (e) flowering: recorded as the number of days from emergence to the date when approximately half of the plants in the row were flowering, (f) fruiting period: number of days from flowering to maturity, (g) maturity: number of days from emergence to the date when approximately 95 percent of the pods were ripe and most of the leaves had dropped, (h) protein and oil content: percentages of protein and oil are expressed on moisture free basis.

Genotypic and phenotypic correlations were calculated from genetic variance and covariance, and phenotypic variance and covariance, respectively as follows;

$$\text{Genotypic correlation } r_g = \frac{\text{COV.}_g \text{ XY}}{\sqrt{\sigma_g^2 X \cdot \sigma_g^2 Y}}$$

where (COV. <sub>g</sub> XY) is the genetic covariance between two traits, (X) and (Y). ( $\sigma_g^2 X$ ) and ( $\sigma_g^2 Y$ ) refer to genetic variance of the character (X) and genetic variance of the character (Y), respectively.

$$\text{Phenotypic correlation } r_{ph} = \frac{\text{COV.}_{ph} \text{ XY}}{\sqrt{\sigma_{ph}^2 X \cdot \sigma_{ph}^2 Y}}$$

where (COV. <sub>ph</sub> XY) is the phenotypic covariance between two traits, (X) and (Y). ( $\sigma_{ph}^2 X$ ) and ( $\sigma_{ph}^2 Y$ ) refer to phenotypic variance of the character (X) and (Y), respectively.

## RESULTS AND DISCUSSION

In general, the genotypic correlations among

characters were slightly higher than the corresponding phenotypic correlations. Similar results in soybean were reported by Johnson *et al.* (5), Weber and Moorthy (10), and Sheth (7), and Weber and Moorthy explained that lower phenotypic correlations are due to the masking or modifying effects of environment on the genetic association between traits.

Genotypic associations varied considerably for most characters in different environments. These variations in genetic correlation may be ascribed to a complicated interaction of genotype and environment, to a sampling error or both.

With a exception, seed yield showed moderately high positive genotypic and phenotypic correlation with plant height and seed weight. Consistently high genetic associations between seed yield and maturity date were observed. The correlation values between oil content and seed yield were too small to be meaningful. With a exception, the seed weight was slightly associated with other traits and the magnitudes of these values were negligible. These relations suggest that effective selection for seed yield without decreasing in oil content can be made by selection for lines possessing lateness, tallness and heavy seeds. Highly significant negative genotypic correlations between seed yield and protein content were obtained. This relationship implies that selection for high yielding lines reduce the probail-

**Table** Genotypic and phenotypic correlation coefficients between important characters for the F<sub>3</sub> and F<sub>4</sub> generations of the cross Norchief × Harosoy.

	1*	Seed <sub>1</sub> yield				Seed weight			
		59A	60A	60B	Comb.	59A	60A	60B	Comb.
Plant	G 2*	0.54	0.23	0.19	0.39	-0.06	-0.01	0.02	0.01
height	P	0.41	0.19	0.23	0.33	0.04	0.14	0.06	0.03
Lodging	G	0.23	0.09	0.15	9.26	-0.18	0.11	-0.05	0.00
index	P	0.26	0.21	0.10	0.24	-0.10	0.21	0.03	0.02
Flowering	G	0.84	0.19	0.02	0.64	-0.11	0.07	-0.07	0.09
	P	0.54	0.27	0.03	0.45	-0.13	0.02	-0.05	-0.08
Fruiting	G	0.75	0.38	0.33	0.22	-0.48	0.22	-0.35	0.05
period	P	0.10	0.15	0.14	0.17	-0.03	0.24	0.61	0.06
Maturity	G	0.58	0.52	0.20	0.51	-0.01	0.12	-0.17	0.04
	P	0.40	0.29	0.08	0.48	-0.90	0.26	0.04	0.05
Protein	G	-0.73	-0.36	-0.62	-0.76	-0.08	0.14	-0.08	-0.06

## Genotypic and Phenotypic Correlations in a Soybean Cross

content	P	-0.35	-0.21	-0.29	-0.49	-0.01	0.15	-0.07	-0.03
Oil	G	0.17	0.39	-0.28	-0.09	-0.06	0.09	-0.07	-0.03
content	P	0.03	0.13	0.16	-0.05	0.03	-0.02	-0.10	-0.04
Seed	G	0.01	0.40	0.95	0.41				
weight	P	0.09	0.22	0.42	0.32				
		Maturity				Protein content			
Plant	G	0.37	0.30	0.27	0.37	-0.08	-0.09	0.17	-0.64
height	P	0.31	0.31	0.22	0.33	-0.06	-0.06	-0.25	0.07
Lodging	G	0.41	-0.12	0.87	0.62	-0.09	-0.17	-0.28	-0.02
index	P	0.36	0.05	0.72	0.58	-0.01	-0.04	-0.15	-0.05
Flowering	G	0.62	0.58	0.62	0.62	-0.38	-0.34	-0.44	-0.27
	P	0.42	0.41	0.48	0.55	-0.33	-0.22	-0.22	-0.26
Fruiting	G	0.79	0.91	0.87	0.88	0.23	-0.01	-0.60	-0.24
period	P	0.81	0.89	0.83	0.86	0.15	-0.45	-0.29	-0.18
Oil	G	-0.21	-0.45	-0.46	-0.37	-0.71	-0.59	-0.13	-0.55
content	P	-0.20	-0.22	-0.40	-0.33	-0.56	-0.44	0.03	-0.40
Protein	G	-0.03	-0.17	-0.70	-0.33				
content	P	-0.05	-0.15	-0.37	-0.28				

1\* Abbreviations 59A, 60A, 60B and Comb. refer to plants grown at location A in 1959, location A in 1960, location B in 1960 and computed for combined data of all three environments, respectively.

2\* G and P refer to genotypic and phenotypic correlation coefficient, respectively.

ities of finding high protein genotypes. Similarly negative association between this characters was reported by Hanson *et al.* (1), and they pointed out that this association may not apply under all environments and if nitrogen is not a limiting factor and if other physiological restrictions are not present, then it could be possible to select for a high yielding bean with high protein content. Weber(9) showed that protein percentage was not particularly strongly correlated with any other character. However, since the correlation is not perfect it may be possible to combine high yield with high protein content.

The maturity date was strongly associated with all other agronomic characters in this study. Genotypic and phenotypic correlation between maturity and fruiting period were consistently high in all environments. The possible explanation of these results is that the two traits might be controlled in part by the same set of genes and or they might have a similar physiological response to the environments.

Negative association between protein and oil con-

tent in this study was in good agreement with many other workers(1, 4, 7, 9). These results indicate that the simultaneous selection of high oil and protein in the same genotype is difficult. Oil content showed a relatively high negative genetic correlation with maturity date. Genotypic and phenotypic correlations between maturity and flowering, and fruiting period were considerably high and consistent in different environments. These results suggest that selection for high oil content may be effective by selecting plants which are early flowering, short in fruiting period, early in maturity date and low in protein content.

### SUMMARY

The F<sub>3</sub> and F<sub>4</sub> generations of a soybean cross, Norchief × Harosoy, were grown in replicated trials in 1959 and 1960. Genotypic and phenotypic correlations among all possible pairs of nine characters were calculated.

In general, genotypic correlations were higher than the corresponding phenotypic correlation. The

genotypic correlations between seed yield and other agronomic characters indicated that seed yield was genetically associated with late flowering, late maturity, long fruiting period, larger seed and low protein content. High oil content was associated with early flowering, early maturity and low protein content.

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