

The Effect of Selection Method on the Association of Yield and Seed Protein with Agronomic Characters in an Interspecific Cross of Soybean

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Introduction

Correlations of seed yield and protein percentage of soybeans (*Glycine max*) were variable. Seed protein content was both positively and negatively associated with maturity (Kwon and Torrie 1964; Weiss et al. 1952). Close relationships between protein content and either plant height or lodging were not reported (Johnson et al. 1955a). In general, high seed yield was associated with low protein percentage (Byth et al. 1969; Hartwig 1969; Hymowitz et al. 1972; Johnson et al. 1955b), although positive correlations between those two traits were also observed among progenies of some crosses (Kwon and Torrie 1964; Weiss et al. 1952). With respect to components of yield, protein content has been positively and negatively associated with number of fruiting nodes per plant and with number of seeds per pod, and has been positively associated with seed size (Fehr and Weber 1968). In two populations, an inverse relationship was reported between protein content and resistance to shattering (Johnson et al. 1955b).

These associations of protein and yield with agronomic traits are primarily in populations derived from cultivars with good agronomic traits. In a diverse cross of *G. max* x *G. soja*, Weber (1950) reported no close association was found between maturity and protein content, while a negative correlation

between these two traits was observed by Malik and Singh (1982). Furthermore, Malik and Singh (1982) reported a positive association between days-to-flowering and protein content. Erickson et al. (1981) obtained the similar conclusion, Wang et al. (1986) reported correlation estimate of -0.455 between seed size and protein content of soybeans (*G. soja*), and Weber (1950) found estimates, averaged over F₂ and F₃-derived lines, of 0.071 and -0.223. Malik and Singh (1982) observed that seed yield was positively related to pods per plant and 100-seed weight. Zhang et al. (1989) showed that seed yield was positively correlated with plant height (0.667), main-stem diameter (0.567), branch number (0.703) and maturity (0.535).

The objectives of this study were to determine the genetic associations of agronomic characters with seed yield and protein, and between seed yield and protein contents content in different selection populations from an interspecific cross of soybeans, *G. max* x *G. soja*, furthermore to determine which selection method would facilitate with the development of high yielding, high protein lines with acceptable agronomic characters.

Materials and Methods

Two varieties, Dongnong 42 and S 17, were used as parents in this study. S 17 is a wild soybean with black and brown seed coat and hilum. Dongnong 42 is a cultivated soybean with large seed, yellow seed coat and hilum, and other good agronomic traits.

The F₁ population was grown in 1993. In 1994, 500 plants in F₂ population was spaced-planted, and five selection methods of generation advance used to sample the F₂ plants, in the order they were performed, as follows:

Picking-Pod Method (PPM): one pod (2 or 3 seeds) was taken from each of the 500 plants to plant the F₃.

5%, 10% and 25% Mass Selection (MSI MSII and MSIII): 25 50 and 125 plants with yellow or green seed coat and hilum, and other desirable traits were selected out of total 500 plants, respectively, and three seeds from each plant were taken to plant the F₃.

Pedigree Selection (PS): from 500 plants, 40 best plants with good

agronomic characters were chosen, and 30 seeds from each plant were picked out to plant the F3 progeny rows.

In F3, the PPM, MSI, MSII and MSIII seeds were bulkily grown, separately, and one pod was harvested from each plant within four methods to form the materials for comparison with those from the PS in F4. For the PS, 40 plants were grown in 40 spaced progeny rows (5m long). Five rows with good traits were chosen, and the plants were harvested individually from each row and characters were measured, then one best individual plant from each row were sorted out. The seeds in each plant were used independently for evaluation in F4.

In F4, the five selections were compared in a randomized complete block design with three replications. The plot consisted of five-4m rows with 0.7 m spacing between rows. Five plants at maturity were harvested out of each row for character measurement. For the PS, only one F3-line with best agronomic characters among 5 lines in F4 test was used for statistical analysis. Field evaluation was conducted at the Experimental Station of Northeast Agricultural University in Harbin.

To determine correlations of seed yield and protein content with agronomic traits, the following data were collected on individual plots: seed yield (based on air dried seed per plant); protein percentage (based on five-gram ground sample of seed and measured by infrared reflectance); maturity (days from emergency to 95% of pods being brown); lodging (based on a scale of 1 to 5 with 1 being erect and 5 being prostrate); seed weight (weight in grams of 100 whole seeds); plant height (measured from the ground to the tip of the main stem in centimeters); node number (included all fruiting and barren nodes); branch number (number of branches); pod shattering based on a scale of 1 to 5 with 1 being 0% shattering and 5 being 50% or more shattering pods per plant (number of pods per plant); seeds per plant (number of seeds per plant).

Analysis of variance were computed for the traits within each selection method. Analysis of covariance within selection method were made between protein percentage and seed yield with each of the other traits. Estimates of genotypic variance and covariance components were obtained by equating mean squares and method-products to their expectations and solving for the required component. Genetic correlations were obtained from their respective variance and covariance component estimates. The following

equation was used to calculate the genetic correlation (r_g): $r_g = \frac{G_{21}G_{12}}{(G_{22}G_{11})}$ Where $G_{21}G_{12}$ = covariance between the additive types of variance for trait 1 and trait 2; $G_{22}G_{11}$ = standard deviations of the additive types of variance for trait 1 and trait 2, respectively.

Results

Means and variance among F4 progenies

Parent and progeny means for ten characters were shown in Table 1. Means of characteristics differed significantly between parents. S17 was small in seed size, late maturity, tall, susceptible to lodging and shattering, high in protein content and low in seed yield. In contrast, Dongnong 42 was large in seed size, short, resistance to lodging and shattering, moderately high in protein percentage and high in seed yield. The diversity among the parents reflected in their progenies.