

Heritability and Relationships Among Traits for Edamame Production in Two Soybean Populations

George L. Graef, Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, 68583-0915, USA, ggraef1@unl.edu

Jason L. Garst, former M.S. student, Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, 68583-0915

James E. Specht, Department of Agronomy and Horticulture, University of Nebraska, Lincoln, NE, 68583-0915, USA, jspecht1@unl.edu

Introduction and Methods

Soyfood consumption in the US has increased throughout this decade. The trend may be attributed to the heightened health consciousness of Americans (Brar and Carter, 1993). Quality of edamame is a major concern to consumers, while ease of culture and high yield are important to the producer. Although each consumer discriminates the quality of edamame differently, quality requirements can be grouped into five major categories, including appearance, flavor, aroma, texture, and nutritional value (Masuda, 1991). In developing new varieties, plant breeders must consider each of these categories, while retaining a line with good agronomic characteristics and high yield.

The strategy of hybridizing Japanese cultivars with adapted US lines requires large segregating populations to insure a reasonable chance of finding progeny with all the necessary attributes for variety release (Brar and Carter, 1993). It would be helpful in variety development if breeders had some estimate of the relative genetic control and relationship of edamame quality traits. Heritability estimates and relationships among traits are necessary for determining breeding strategies to develop soybean cultivars adapted to US production environments and suitable for edamame use. The objectives of this study were to estimate for two segregating populations of edamame and mature soybeans: (i) the heritability of quality traits and (ii) the genotypic and phenotypic correlations between all pairs of traits.

Two populations of $F_{3:5}$ lines were formed by crossing a high-yielding, adapted variety by two Japanese vegetable-type cultivars. Crosses of U91-3516 X 'Mikawashima', denoted UX704, and U91-3516 X 'Gion Fuuki', denoted UX706, were made in 1993. The line U91-3516 is an experimental line from the University of Nebraska Soybean Breeding program, and is a F_4 -derived line from the cross 'Hamilton' x 'Kenwood'. During the 1994 growing season, the F_3 seeds of each cross were planted at 16 seeds m^{-2} at Lincoln, Nebraska. Individual F_3 plants were harvested according to maturity. A random sample of 75 plants stratified by maturity were chosen from each cross to form each population. The checks included were U91-3516, Mikawashima, Gion Fuuki, 'Saturn', and 'LS 301'.

Edamame Soybean Traits

The $F_{3:5}$ lines and checks for the edamame soybean traits were evaluated during 1995 at Lincoln and Mead, Nebraska in 3 environments. The two environments at the Lincoln Agronomy Farm were planted 28 days apart. Plots were single rows that were 0.91 m long, 0.76 m wide,

and sown at a rate of 35 seeds plot⁻¹. To increase plot uniformity, at approximately V3, each plot was trimmed to 0.61 m and thinned to 16 plants, with alleys 0.91 m wide. Lines in each population and checks were arranged in a randomized complete block design with 2 replications in each environment. Each population was treated as a separate experiment. When the earliest maturing plants of each site reached growth stage R2, the plants were irrigated every 7-12 days. For both populations, notes were taken twice weekly and all data were collected at or after harvest except days to growth stage R1 and R6. Each plot was harvested within 3 days after 50% of the plants had reached growth stage R6 (Fehr and Caviness, 1977)

For the population UX704, traits measured for each plot were: (1) days to R1, (2) days to R6, (3) days from R1 to R6. At harvest, the five center plants of each plot transported to the lab where the pods were manually stripped and the following data collected: (4) Pod length, reported as the average of 5 randomly selected pods; (5) Pod color, the 5 pods that were measured for length were visually given a color rating with a score ranging from 1 (bright green) to 6 (yellow) based on a color chart; (6) number of pods plot⁻¹; (7) average number of pods plant⁻¹, estimated by number of pods plot⁻¹/number plants harvested plot⁻¹; (8) number of 1-seeded pods plot⁻¹; (9) number of 2-seeded pods plot⁻¹; (10) number of 3-seeded pods plot⁻¹; (11) percent of 2- and 3-seeded pods; (12) Green pod weight (reported as grams plot⁻¹); (13) 1-seeded pod weight; (14) 2-seeded pod weight; (15) 3-seeded pod weight; (16) percent of 2- and 3- seeded pod weight; (17) average number of beans pod⁻¹; (18) average number pods 500 g⁻¹, estimated by total number of pods/total weight of pods*500g; (19) fresh 100 seed weight, the weight of 100 seeds shelled from randomly selected pods. For the population UX706, the traits measured for each plot were: (1) days to R1; (2) days to R6; (3) days from R1 to R6. At harvest, a random sample of pods were gathered to measure (4) Pod length; (5) Pod color; (6) fresh seed weight.

Mature Soybean Traits

To measure traits on the mature seed, the F_{3;5} lines and checks were evaluated during 1995 in two Nebraska environments. The environments were located at the University of Nebraska-Lincoln Agronomy Farm, Lincoln and the Mead ARDC. All agronomic data were collected at or after maturity from each plot. The same traits were measured on both the UX704 and UX706 populations. Maturity was scored as the number of days from September 1 to the date when 95% of the pods had attained a mature color. Lodging was visually rated with a score ranging from 1 (almost all plants erect) to 5 (almost all plants down). Shattering was visually rated with a score ranging from 1 (no shattering) to 5 (over 50% shattered). When the seed moisture content had reached about 10 to 13%, the plants of each plot were manually gathered and threshed with a stationary plant thresher. Seed weight was recorded as grams per 100 seed from 100 randomly selected seeds of each plot. A random sample of whole seeds from each plot was analyzed for protein and oil content using an Infra Tech 1255 Whole Grain Analyzer. All seed traits are reported on a 13% moisture basis.

Data Analysis

The data were analyzed as a randomized complete block (SAS Institute Inc., 1989). Estimates of the phenotypic and genotypic variance were obtained by equating mean squares and cross products to their expectation and solving for the required components. Negative variances were treated as zero. Heritability estimates were made on a line mean basis. Heritabilities based on variance component estimates were calculated for each trait as:

$$\bar{h}^2 = \bar{\sigma}_G^2 / [(\bar{\sigma}_e^2 / rl) + (\bar{\sigma}_{GL}^2 / ll) + \bar{\sigma}_G^2]$$

where $\hat{\sigma}_G^2$ = estimate of the genotypic variance, $\hat{\sigma}_e^2$ = estimate of the error variance, $\hat{\sigma}_{GL}^2$ = estimate of the genotype x environment interaction variance, r = number of replications, and l = number of environments. Although these estimates of heritability are broad sense estimates, they approximate narrow sense heritabilities since additive genetic variance makes up 96% of the total genetic variability by the F₄ generation (Hanson and Weber, 1961). Standard errors of the heritability estimates were estimated using the procedures of Hallauer and Miranda (1981). Analysis of covariance was conducted for each population for all possible pairs of characters. Genotypic and phenotypic correlations were obtained from the appropriate covariance and variance components (Johnson et al, 1955b). Pearson's correlation analysis was used to calculate the correlations between fresh 100-seed weight and mature 100-seed weight, and green pod yield and mature seed yield.

Results

Seed and Pod Development Traits

Genotypes differed significantly for all seed and pod development traits in both populations. Both populations showed significant genotype x environment (G x E) interaction effects for days to R6, days from R1 to R6, and pod color, but not for days to R1 or pod length. A near ideal plant type for edamame should have a R1 date greater than 40 d, pod length of at least 5 cm, and a color score ranging from 1 to 4 (Shanmugasundaram et al., 1991). For the parental genotypes, days to R1 ranged from 46.0 for Gion Fuuki to 49.5 for Mikawashima, and 48.6 for U91-3516. Population means were 52.9 for UX704 and 51.6 for UX706. Both populations had similar values for pod length and pod color that were near ideal values. All of the seed and pod development traits, except days to R6 in population UX706, were similar to the midparent values, indicating that additive genetic effects were more important in determining the population means than non-additive effects. Heritability estimates for all seed and pod development traits exceeded 0.50. Heritability estimates were highest for days to R1 (0.96 ± 0.16 and 0.93 ± 0.16) and were slightly higher than the estimates of 0.84 and 0.89 reported by Johnson et al. (1955a) on an entry mean basis. Heritability estimates of 0.63 for UX704 and 0.77 for UX706 were obtained for days from R1 to R6, which is the fruiting period for edamame soybeans.

Relationships Among Edamame and Mature Traits

Heritability estimates for fresh 100-seed weight averaged 0.62, while mature 100-seed weight averaged 0.81 based on variance component estimates. The heritability estimate for green pod weight was 0.25 for population UX704, while h^2 for mature seed yield was 0.56 for UX704 and 0.79 for UX706. Fresh 100-seed weight was negatively correlated with number of pods plant⁻¹, percent 2- and 3-seeded pods, number of beans pod⁻¹, and average number of pods 500g⁻¹, but was positively correlated with pod length. Green pod weight showed a positive genetic correlation with days to R6 and percent of 2- and 3-seeded pods, but a negative genetic correlation with number of 1-seeded pods. Mature 100-seed weight was positively correlated with fresh 100-seed weight in both populations ($r=0.48$ and $r=0.56$). This indicates that selection on the mature plant should be effective in increasing the fresh-100 seed weight and green pod yield in soybeans. The trait values in both populations were determined mainly by additive effects, but non-additive effects were noted for days to R6, seed oil content, seed protein+oil content, and seed yield. Due to the high labor requirements in testing lines for edamame

characteristics, it is suggested from this study that selection first be made on the mature traits. Once genotypes with large mature seed weight ($>30\text{g } 100\text{-seeds}^{-1}$) and good seed yield are identified, they can be further evaluated for edamame quality traits. Other population structures, such as 3-way or backcross populations, may improve the frequency of lines with desired quality and adaptation.

References

- Brar, G.S. and T.E. Carter, JR. 1993. Soybean *Glycine max* (L) Merrill. p. 427-463. In G. Kalloo and B.O. Bergh (ed.) Genetic improvement of vegetable crops. Pergamon Press Inc., New York.
- Fehr, W.R. and C.E. Caviness. 1977. Stages of soybean development. Iowa State Univ. and Arkansas Agric. Exp. Stn. Spec.Rep. 80.
- Hanson, W.D. and C.R. Weber. 1961. Resolution of genetic variability in self-pollinated species with application to the soybean. *Genetics* 46:1425-1434.
- Hallauer, A.R. and J.B. Miranda. 1981. Quantitative genetics in maize breeding. The Iowa State University Press, Ames, IA.
- Hanson, W.D. and C.R. Weber. 1961. Resolution of genetic variability in self-pollinated species with application to the soybean. *Genetics* 46:1425-1434.
- Johnson, H.W., H.F. Robinson, and R.E. Comstock. 1955a. Estimates of genetic and environmental variability in soybeans. *Agron. J.* 47:314-318.
- Johnson, H.W., H.F. Robinson, and R.E. Comstock. 1955b. Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agron. J.* 47:477-483.
- Konovsky, J., T.A. Lumpkin, and D. McClary. 1994. Edamame: the vegetable soybean. p. 173-181. In A.D. O'Rourke (ed.), *Understanding the Japanese Food and Agrimarket: a multifaceted opportunity*. Hayworth, Binghamton.
- Kwon, S.H. and J.H. Torrie. 1964. Heritability of and interrelationships among traits of two soybean populations. *Crop Sci.* 4:196-198.
- Masuda, R. 1991. Quality requirement and improvement of vegetable soybean. p. 92-102. In S. Shanmugasundaram (ed.) *Vegetable soybean: Research needs for production and quality improvement*. Asian Vegetable Research and Development Center, Taipei, Taiwan.
- SAS Institute Inc. 1989. SAS/STAT® User's Guide, ver. 6, Fourth ed., vol. 2, Cary, NC
- Shanmugasundaram, S., S. Cheng, M. Huang, and M. Yan. 1991. Varietal improvement of vegetable soybean in Taiwan. p. 30-42. In S. Shanmugasundaram (ed.) *Vegetable soybean: Research needs for production and quality improvement*. Asian Vegetable Research and Development Center, Taipei, Taiwan.