

Pure lining in the USDA Soybean Germplasm Collection

All foreign accessions added to the soybean collection are pure lined. This is a two-year process that will ensure that each accession in the collection is homogeneous and homozygous. In year 1, we plant approximately 50 seeds of each new seed lot and save a remnant sample for long term storage, if possible. During the growing season, we characterize plants within each row for a dozen specific characteristics plus we note any subtle differences that may indicate genetic variation. We harvest a minimum of four plants or as many as needed to sample the diversity present in each row. In year 2, each plant harvested in year 1 is planted in a separate row. We observe and characterize each row as in year 1 looking for diversity within rows and between rows from the same original seed lot. All rows in year 2 that have internal diversity are discarded based on the assumption that these are the result of a recent cross-pollination between accessions within the donor collection or area of origin. We harvest as many individual rows as needed to represent the diversity of each original seed lot. Each harvested row becomes an accession to be added to the collection. All accessions from the original seed lot share a PI number and are differentiated with a letter suffix. Our current collection of introduced soybean has 16,787 accessions that represent 13,751 original introductions. Approximately 15% or 2092 of these introductions have sublines. More than 70% of the heterogeneous seed lots have only two sublines but some have as many as 10.

The process of pure lining germplasm accessions runs counter to traditional germplasm management methods, but our experience strongly indicates that for self-pollinated species pure lining is a superior strategy for maintaining, evaluating, and utilizing genetic diversity. Genetic drift and natural selection will alter heterogeneous accessions unless rigorous control is exerted over population size and harvesting procedures each time the accession is grown. Implementation of such procedures would greatly increase our cost of germplasm maintenance. To test these effects we mixed seeds of near isogenic lines with seed color differences that had no selective advantage (Figure 1) and with presence and absence of pubescence with strong selective effects (Figure 2) and handled these populations as we would our standard seed increase plots. Although the total effects were different in the two mixtures, strong shifts in the population could be noted after only 2 cycles of regeneration. We mixed accessions with different times of maturity and also found major population shifts (Figure 3). It is very difficult to precisely describe heterogeneous accessions, so it is more likely that accidental mixtures by seeds of other accessions will not be noticed and the genetic composition of the accession will be permanently changed. In one study with different seed coat colors (Figure 4), we found a contamination (2 seeds with a black seed coat) in the second year. Instead of removing those seeds, we left them in the sample and this contaminant thrived during the next two cycles. Evaluation of heterogeneous accessions will be, at best, an average of all of the genotypes present and thus will not identify the extreme values that are generally the most useful and must be separated before they can be used as parents. Accurate description, long-term preservation, effective utilization, and precise exchanges are all facilitated with pure line accessions.

Figure 1. Genetic Drift in Clark Seed Color Isolines

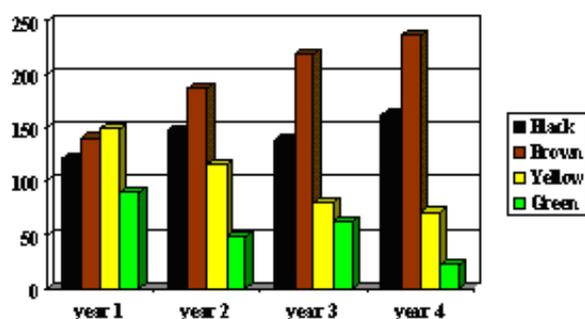


Figure 2. Natural Selection in Clark Pubescence Isolines

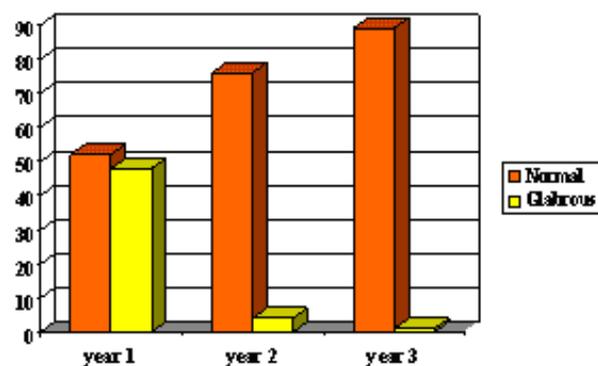


Figure 3. Natural Selection in a Mixed Maturity Accession

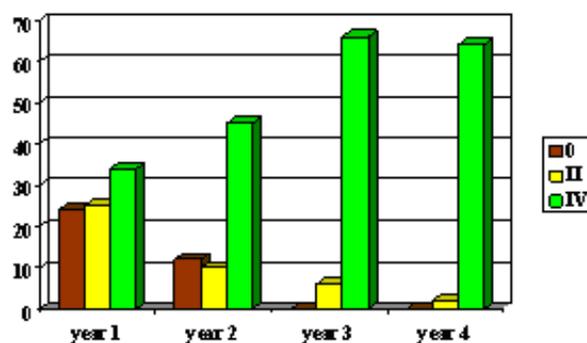


Figure 4. Contamination in Harosoy Seed Color Isolines

