Variation of Nineteen Isozyme Loci in the USDA Soybean Germplasm Collections from China. (C08-palmer151551-Poster)

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Abstract:

To evaluate the genetic variation in soybean (Glycine max (L.) Merr.) within and among provinces of China and to relate genetic differentiation patterns to geographical regions, we determined allozyme variability among 1771 accessions from the USDA germplasm collection. We found a significant correlation between sample size and genetic diversity. Significant differences in allelic frequencies among provinces were found for 18 of 19 loci (mean FST =0.192). Cluster analysis corresponded to three regions (northern, central, and southern), except for province Guangdong. Linear regression via permutation of pairwise FST values on geographical distance was significant, indicating a relatively consistent pattern of differentiation among provinces. These results suggest historical seed movement between provinces has occurred via west to east, vice versa (similar latitude) rather than north to south, vice versa (different latitude). This suggests movement of seeds among similar maturity groups. Crosses between each of these three groups and crosses between these and South Korean and Japanese gene pools should increase genetic variability.

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Presentation Information:

Presentation Date: Wednesday, November 13, 2002
Presentation Time: 4:15-6:00 pm
Poster Board Number: 940

Keywords:

soybean, germplasm, isozyme, China