

Genetic Diversity of Edamame Soybean (*Glycine max* (L.) Merr.)

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Introduction

Edamame [*Glycine max* (L.) Merr.] is the Japanese name for a type of vegetable soybean eaten at the immature R6 stage. Edamame products are becoming increasingly popular in the US and global markets. A major negative agronomic trait, hindering mechanized production, is pod shattering. The East Asian Crop Development lab (EACD) at Washington State University (WSU) has been breeding new edamame lines resistance to pod shatter. Edamame breeding efforts can be more efficient with information on genetic diversity. The objectives of this research were to 1) understand the genetic diversity in edamame soybeans and 2) fingerprint WSU edamame breeding lines.

Methods and Materials

Plant Materials: 131 soybean accessions, including 108 Japanese edamame, 11 Chinese maodou, 8 WSU breeding lines, 2 US edamame and 2 US grain soybeans. Maturity information, testa color, and 100-seed weight were observed and evaluated. DNA was isolated from 2g of fresh leaf tissue from greenhouse grown seedlings. *Genotyping by SSRs:* The Simple Sequence Repeat (SSR) method was employed for fingerprinting. Seventeen SSRs were selected from soybean genetic linkage groups (Cregan et al., 1999). SSRs were amplified by the PCR method and visualized using silver staining on 6% polyacrylamide gels. *Statistical Analysis:* Diversity values for each SSR locus were calculated using the gene diversity index $h = 1 - \sum p_i^2$, where p_i is the frequency of the i^{th} allele at a locus. Genetic diversity was calculated using Jaccard's coefficient. Clustering analysis was constructed using the UPGMA method. Multidimensional scaling analysis was conducted by the MDS procedure of PC SAS.

Results and Discussions

A total 122 bands were detected, and 99 of a total 131 accessions were clearly distinct (Mimura, 2001). Twenty-seven unique alleles were detected among the 108 Japanese edamame and 24 detected among the 11 Chinese maodou. UPGMA clustering analysis created nine clusters and 18 outliers. The large main cluster contained 48 Japanese edamame and a US edamame. Edamame genetic diversity was generally clustered around maturity groups and testa color. The two US grain soybeans and ten Chinese maodou were outliers. The Chinese maodou have unique genetic pools from Japanese edamame in the MDS analysis. All WSU breeding lines were clearly distinct. The genetic diversity among the Japanese edamame cultivars was narrow, compared to Chinese maodou. Japanese edamame and Chinese maodou soybeans may have different genetic pools. Genetic diversity in edamame can be explained by SSRs.

References

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