

B-02

Domestication history and geographical adaptation inferred from a genome-wide polymorphism map of Korean soybeans

*Soon-Chun Jeong*, Korea Research Institute of Bioscience & Biotechnology, Chungbuk, Republic of Korea

Cultivated soybean, *Glycine max* (L.) Merr. represents the world's most important plant source of dietary protein and oil. Despite this essential role in world agriculture, the history of cultivated soybean's domestication from its wild ancestor, *G. soja* Siebold & Zucc., has not been fully resolved. Several previous studies pointed different regions as a center of soybean domestication likely because of sampling bias. In the most cases, accessions collected from the Korean Peninsula were underrepresented, although this region is no doubt a central part of wild soybean distribution. In this study, we aimed to address the origin(s) and diversification of domesticated soybean using a comprehensive geographic collection of soybean samples, which consists of 1957 cultivated and 1079 wild soybeans accessions. Unlike the previous studies, we used the most number of Korean accessions. We genotyped the soybean accessions using the 180k Axiom SoyaSNP array and then used methods to infer the evolutionary history of domesticated soybean. The utility of the data was also evaluated by performing genome-wide association studies of qualitative and quantitative traits.