

**P040**

## **Construction of core collection based on single nucleotide polymorphism analysis in soybean germplasm**

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### **Abstract**

The soybean [*Glycine max* (L.) Merr.] is one of the most important crop resources worldwide as food and forage. It is also important and valuable that to hold crop resources to have high genetic diversities. Recently, a core collection has been constructed in many plants to preserve the genetic resources of various plants. A core collection is small population to represent the genetic diversity of the total collection, and is of strategic importance as they allow the use of a small part of a germplasm collection that is representative of the total collection. Here, we developed the core collection consisting of 816 accessions by using approximately 180,000 (180K) single nucleotide polymorphisms (SNPs) developed in previous study. In addition, we performed genetic diversity and population structure analysis to construct the core collection from entire 4,392 collections. there were excluded sample call rates less than 93% and duplicated samples more than 99.9% according to genotype analysis using 180K SNPs from entire collections. Furthermore, we were also excluded natural hybrid resources which *Glycine max* and *Glycine soja* are mixed in half through population structure analysis. As a result, we are constructed the core collection of genetic diversity that reflects 99% of the entire collections, including 430 cultivated soybeans (*Glycine max*) and 386 wild soybeans (*Glycine soja*). The core collection developed in this study should be to provide useful materials for both soybean breeding programs and genome-wide association studies.

Keywords: *Glycine max*, *Glycine soja*, core collection, SNP

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