

Construction of core collection in cultivated soybean germplasm (*Glycine max* L. Merr.) using single nucleotide polymorphism analysis

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[Introduction]

Core collection is a small population to represent the genetic and phenotypic diversity of the entire collection in plant germplasm resources, and is important strategy available as a small part of a germplasm collection to represent of the entire collection. Especially, developing of the core collection in soybean is also important and valuable task as one of the most important crop resources worldwide.

[Materials and Methods]

A total of 2,872 *Glycine max* accessions were collected from the National Agrobiodiversity Center in the Rural Development Administration. The total soybean accessions used in this study originated from China, Japan, Sweden, France, Canada, USA, North Korea, and South Korea, respectively. we performed genetic diversity and population structure analysis to construct a core collection in *Glycine max* germplasm collection consisting of 2,872 accessions by using Axiom 180K SoyaSNP.

[Results and Discussion]

The SNPs of Axiom 180K SoyaSNP array were employed to identify genetic diversity among the total 2,872 accessions from *Glycine max*. population structure analysis was performed using SNP genotyping results from a total 430 core collection accessions and was used the fastSTRUCTURE program. The population used in this study can be divided into 6 groups. A circular phylogenetic tree of the 430 soybean (*Glycine max*) accessions was generated using the neighbor joining method based on the genotyping data by Axiom 180K SoyaSNP. The circular phylogenetic tree showed six large clades. The core collection was extracted by limiting the minor allele frequency of 1% for a total of 2,872 cultivated soybeans. As a result, we extracted the core collection reflecting 99% of 2,872 total collections. Finally, there was developed a core collection consisting of 430 cultivated soybeans. As a result, we developed the cultivated soybean core collection in this study. The core collection developed in this study should be to provide materials useful for both soybean breeding programs and genome-wide association studies.

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