Axiom Soybean Genotyping Array

Whole-genome high-density genotyping for soybeans

The Applied Biosystems™ Axiom™ Soybean Genotyping Array (also called the Axiom SoyaSNP 96-Array Plate) was designed through our Expert Design Program in collaboration with the Korea Research Institute of Bioscience and Biotechnology (KRIBB), the Rural Development Administration, and the National Institute of Crop Science. The single-nucleotide polymorphism (SNP) sequences were provided by Drs. Soon-Chun Jeong, Namshin Kim, and Jung-Kuyng Moon. The array was described by Dr. Jeong from KRIBB at the Plant and Animal Genome Conference, Singapore, 2014 [1].

Soybean is an important source of dietary protein and oil worldwide, but modern breeding practices have resulted in narrow diversity in cultivated soybeans due to underuse of wild soybeans as a breeding resource. With markers from wild and cultivated soybeans, the Axiom array is ideal for genome-wide association studies (GWAS) and high-density genetic mapping [2] to identify important adaptive genes in wild and cultivated soybean germplasm.

The high marker density on the Axiom array avoids underrepresentation of the soybean genome, which is often observed when using other technologies that offer insufficient SNP density or employ markers that exhibit bias toward certain regions of the genome.

The distribution of SNPs mapped to the Williams 82 reference sequence (Wm82.a2.v1) across the 20 chromosomes is superior to any other commercially available soybean SNP array.

Highlights

Content

A total of 180,961 SNPs were selected from across the 20 soybean chromosomes and represent cultivated (*Glycine max*) and wild (*Glycine soja*) soybean accessions.

The number of SNPs is estimated to provide 1 SNP for approximately every 6.1 kb.

- 114,735 SNPs (63.4% of total number of markers) are located in 40,631 genes
- 22,952 SNPs are in 13,259 regions within 5 kb upstream or downstream of genes
- 43,274 SNPs are located in intergenic regions

Diversity

- SNP discovery and validation were completed using a diverse set of 16 soybean accessions from Korean populations and 31 accessions from Chinese populations
- The array performance was evaluated on a diverse set of 228 soybean lines

Applications

Genome structure and complex trait research

- Perform GWAS and fine mapping
- Identify traits of economic importance
- Construct high-resolution genetic maps and detect natural variations in genome structure

Molecular breeding

- Perform association mapping and genomic selection

Population and evolutionary genetics

- Distinguish between populations of different origins
- Distinguish between cultivated and wild populations

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SNP selection

The marker discovery was completed by high-depth sequencing of 16 Korean populations containing 10 cultivated and 6 wild accessions [3], and low-depth sequencing of 31 Chinese populations containing 14 *Glycine max* and 17 *Glycine soja* soybean lines [4]. For each population, the sequences were aligned to the Williams 82 reference sequence. The SNPs were filtered to eliminate SNPs with minor-allele frequency of ≤0.021 and SNPs that had mutations within 40 bp of the high-quality SNPs. Putative SNPs were submitted to calculate *in silico* design scores. The final 180,961 SNPs included 40,136 from the Korean population, 71,930 from the Chinese population, and 68,895 that were common between the two populations (Figure 1).

Results

The performance of the array was evaluated by genotyping 228 soybean lines including high-depth resequenced lines, duplicated DNA samples from different origins, diverse cultivated and wild lines, and multiple F2 and recombinant inbred lines.

The data analysis and clustering were automated using Applied Biosystems™ Genotyping Console™ Software and the SNPolisher™ package. SNPs were filtered according to the Best Practice Supplement to Axiom Genotyping Solution Data Analysis User Guide (P/N 703083). A total of 222 samples passed our best practices workflow, and the results were automatically classified into 6 SNP classes. The concordance rates between SNP calls from PolyHighResolution and off-target variant (OTV) clusters and SNP calls from high-depth genome resequencing among 10 cultivated and 4 wild soybean lines ranged from 94.7 to 99.4%. Today, Applied Biosystems™ Axiom™ Analysis Suite software should be used for analysis following the Best Practices Workflow as described in the Axiom Genotyping Solution Data Analysis Guide (P/N 702961).

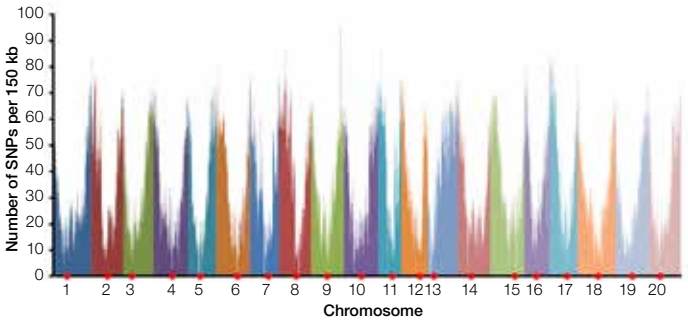

Figure 1. Distribution of the markers across the 20 soybean chromosomes mapped to the Williams 82 reference sequence. Markers on the array are well distributed over the chromosomes, with a higher number in the gene-rich telomeres and fewer in gene-poor centromeric regions.

Ordering information

Product	Description	Cat. No.
Axiom Soybean Genotyping Array	Contains one 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550469
Axiom GeneTitan Consumables Kit	Contains all GeneTitan Multi-Channel Instrument consumables required to process one 96-array plate	901606
Axiom 2.0 Reagent Kit	Includes all reagents (except isopropanol) for processing one 96-array plate	901758

References

1. Lee Y-G et al. (2014) A large Axiom soybean SNP genotyping array: development, validation, and genetic mapping. Plant and Animal Genome Asia Conference, Singapore, abstract P050.
2. Jeong S-C et al. (2014) Fine mapping of QTLs controlling pod dehiscence with a 180K Axiom soybean SNP genotyping array. Molecular and Cellular Biology of the Soybean 15th Biennial Conference, Minneapolis, MN, abstract P074.
3. Chung WH et al. (2014) Population structure and domestication revealed by high-depth resequencing of Korean cultivated and wild soybean genomes. *DNA Res* 21(2):153–167.
4. Lam HM et al. (2010) Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. *Nat Genet* 42(12):1053–1059.

Find out more at **thermofisher.com/microarrays**

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