

Axiom[®] Maize Genotyping Array

High-density genotyping array for maize cultivars grown around the world

Axiom[®] Maize Genotyping Array was designed through Affymetrix[®] Expert Design Program by the AgroClustER Synbreed (funded by the German Ministry of Education and Research, BMBF) through a collaboration led by Prof. Chris-Carolin Schön, Dr. Eva Bauer, and Sandra Unterseer (Technische Universität München, Germany), and Dr. Georg Haberer and Michael Seidel (Helmholtz Zentrum München, Germany). The goal of this project was to develop a high-density (HD) 600,000 maize (*Zea mays* L.) genotyping array to be able to decipher the genetic mechanisms of traits of interest.

Axiom[®] Maize Genotyping Array overcomes specific challenges caused by a high content of repetitive elements, high genomic and structural diversity, and low linkage disequilibrium (LD) in different cultivars. The array interrogates 600,000 carefully selected polymorphic variants to represent the global diversity in the maize genome. The selection strategy used in Axiom Maize Genotyping Array ensures comprehensive representation of all regions of the genome in contrast to the selection strategy utilized in other technologies that exhibit insufficient SNP density or poorly selected markers from lines that are not representative of global diversity.

Axiom Maize Genotyping Array is the only array that offers a very high coverage of polymorphic SNPs.

Highlights

Content:

- 616,201 variants composed of 609,442 SNPs as well as 6,759 small insertion/deletion variants

Marker diversity:

- SNP validation was performed by using a diverse set of European, US, and tropical/semi-tropical lines from various Dent and Flint gene pools

Applications

Complex trait research:

- Genetic diversity analysis
- Association mapping

- Genome-wide analysis and selection
- Haplotype structure in maize varieties
- LD analysis
- QTL fine mapping

Molecular breeding:

- Development of new inbred lines
- Genomic selection

SNP discovery and screening

SNPs discovered through resequencing in a panel of 30 maize inbred lines were selected for a screening experiment to determine true polymorphisms. SNPs from a previously designed maize genotyping array with 50,000 SNPs were included. The screening experiment was carried out on a 1.2 million Axiom[®] myDesign[™] Genotyping Array. The markers were validated in 288 samples of very diverse origin (founder lines, elite lines, hybrids, doubled haploid lines from landraces, Teosinte, trios including two parents and F1) from around the world representing the main maize gene pools.

Since most of the samples were highly inbred, an inbred correction was applied during analysis. The use of tunable parameters such as inbred penalty enabled correct genotype calling of SNPs with only homozygous clusters and lacking heterozygotes in the case of inbreds.

Numerous sequencing studies have found the maize genome to be very highly polymorphic. The presence of nearby polymorphisms may impact the performance of some SNPs. Affymetrix' SNPolisher[™] Analysis Package consists of functions to identify such SNPs and genotype them correctly, for accurate downstream usage.

High-density array

The final high-density panel includes:

- 570,546 SNPs selected from the 1.2 million array
- 48,324 SNPs from a previously designed maize genotyping array

References

1. Ganai M. W., *et.al.* A Large Maize (*Zea mays* L.) SNP Genotyping Array: Development and Germplasm Genotyping, and Genetic Mapping to Compare with the B73 Reference Genome. *PLoS ONE* **6**(12):e28334 (2011) doi:10.1371/journal.pone.0028334

Ordering information

Part number	Product name	Description
550494	Axiom® Maize Genotyping Array Shipping April 1, 2014	Contains one plate with 96 arrays. Reagents and GeneTitan® MC consumables must be quoted separately.
901606	Axiom® GeneTitan® Consumables Kit	Contains all GeneTitan® Instrument consumables required to process one array plate
901758	Axiom® 2.0 Reagent Kit	Includes all reagents (except isopropanol) for processing 96 DNA samples

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