



Axiom Rice Genotyping Array

Helping the rice research community advance discoveries in rice genetics

The Applied Biosystems™ Axiom™ Rice Genotyping Array, one of the highest-density arrays of its kind, enables the rice research community to study genome-wide genetic variation in *Oryza sativa*. With the array's high resolution and superior genomic coverage, researchers can now easily evaluate the natural variation in rice worldwide and identify the genes underlying important phenotypic traits (e.g., high yields). This will further help the rice research community to understand genetic sources of variation and associated phenotypic changes, and to differentiate varieties for fingerprinting and classification purposes.

The Axiom Rice Genotyping Array includes 42,961 markers from the Applied Biosystems™ GeneChip™ Rice 44K Genotyping Array [1] and 5,499 markers from a whole-genome SNP array (RICE6K) for genomic breeding in rice [2].

Highlights

Content

- Backwards compatibility with older data from the GeneChip Rice 44K Genotyping Array
- Detection of common genetic variants within and between the major subpopulations of rice, including *indica*, *aus*, *tropical japonica*, *temperate japonica*, and group V ("aromatic")
- Efficient progeny screening in rice breeding markers identified by Yu et al. [2]

Applications

Complex-trait research

- Flexible and fast identification, and classification of germplasm
- Identification of high-yield variants
- Genome-wide association mapping and tracking of disease genes

Molecular breeding

- Allows for fingerprinting rice germplasm, genotyping bulked segregating pools, checking seed authenticity, and selecting genetic background
- Enables genetic variation analysis of any *O. sativa* strain
- Offers information for polymorphisms between *indica* and *japonica* subspecies as well as varieties within *indica* and *japonica* groups

SNP discovery and selection

The 44,100 SNPs from the GeneChip Rice 44K SNP Array were selected from two data sources: the Oryza SNP Project, an oligomer array-based resequencing effort using Perlegen Sciences technology, and BAC clone Sanger sequencing of wild species from the Oryza Map Alignment Project. A full description of the marker selection process is provided by Zhao et al. [1]. The 44,000 markers ensure approximately 1 SNP for every 10 kb throughout the 12 chromosomes of rice.

The 5,499 markers described by Yu et al. [2] were selected specifically for efficient progeny screening in rice breeding with two considerations: genetic background selection and targeted genotyping. These markers are evenly distributed on the 12 chromosomes, with an average density of 12 SNPs per 1 Mb.

Analysis

The data from the Axiom Rice Genotyping Array can be analyzed using Applied Biosystems™ Axiom™ Analysis Suite software. SNPs are filtered according to the Best Practice Supplement to Axiom Genotyping Solution Data Analysis User Guide (P/N 703083).

Ordering information

| Product | Description | Cat. No. |
|---------------------------------|--|----------|
| Axiom Rice Genotyping Array | Contains one 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately | 550625 |
| 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. Zhao K et al. (2011) Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nat Commun* 2:467.
2. Yu H et al. (2014) A whole-genome SNP array (RICE6K) for genomic breeding in rice. *Plant Biotechnol* 12(1):28–37.

Find out more at thermofisher.com/microarrays