

## Axiom<sup>®</sup> Rice Genotyping Array

Helping the rice research community advance discoveries in rice genetics



Axiom<sup>®</sup> Rice Genotyping Array, the highest density array 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 assay the natural variation of rice varieties worldwide to identify genes underlying important phenotypic traits (e.g., high yields), to understand genetic sources of variation and associated phenotypic changes, and to differentiate varieties for fingerprinting and classification purposes.

Axiom Rice Genotyping Array includes 42,961 markers from GeneChip<sup>®</sup> Rice 44K Genotyping Array<sup>1</sup> and 5,499 markers from a whole-genome SNP array (RICE6K) for genomic breeding in rice.<sup>2</sup>

### Highlights

#### Content

- Backwards compatibility with older data from 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.*<sup>2</sup>

### 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 GeneChip Rice 44K SNP Array were selected from two data sources: SNPs from 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.*<sup>1</sup> The 44,000 markers ensure approximately 1 SNP every 10 kb throughout the 12 chromosomes of rice.

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

### Analysis

The data from Axiom Rice Genotyping Array can be analyzed using Axiom™ Analysis Suite software. SNPs are filtered as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis Users Guide* (P/N 703083).

### References

1. Zhao K., *et al.* Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nature Communications* **2**:467 (2011). doi:10.1038/ncomms1467
2. Yu H., *et al.* A whole-genome SNP array (RICE6K) for genomic breeding in rice. *Plant Biotechnology Journal* **12**(1):28–37 (2014).

### Ordering information

Part number	Description	Details
550625	Axiom® Rice Genotyping Array	Contains one plate with 96 arrays
901606	Axiom® GeneTitan® Consumables Kit	Contains all GeneTitan® Instrument consumables to process one 96-format array plate
901758	Axiom® 2.0 Reagent Kit	Includes all reagents (except isopropanol) to process one Axiom® 96-format array plate

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