Axiom Rose Genotyping Array

Accelerate quantitative trait loci (QTL) discovery and haplotype-assisted selection in tetraploid cut rose and garden rose cultivars

The Applied Biosystems™ Axiom™ Rose Genotyping Array (WagRhSNP Axiom Array) was designed through our Expert Design Program in collaboration with Wageningen UR Plant Breeding, Wageningen, The Netherlands, and the Institute for Plant Genetics, Leibnitz University, Hannover, Germany.

The array offers a total of 68,893 SNPs selected from tetraploid cut rose and garden rose cultivars [1].

Applications

Complex trait research

- Polyploid linkage maps
- Identification of multi-SNP haplotypes in progenies and breeding material
- QTL analysis for discovery of marker haplotypes associated with important phenotypic traits such as disease resistance

Molecular breeding

- Enable haplotype-assisted selection and haplotype-informed choice of crossing parents
- Accelerate and increase efficiency of cultivar development

SNP discovery

SNP discovery [2] was facilitated by transcriptome sequencing of flowers and leaves of the parents of two segregating F1 populations and several garden rose cultivars.

SNP discovery and selection included the following steps:

- *De novo* assembly of each parent
- Assembly of a consensus transcriptome
- Mapping reads of each parent against the consensus transcriptome
- Identification of reliable SNPs, i.e., with sufficient read depth for the minor allele and 35 bp flanking sequence without SNPs
- Transcripts aligned to the Genome Database for Rosaceae for annotation to avoid splicing sites
- SNP identification performed using QualitySNP (**bioinformatics.nl/tools/snpweb/**)

A total of 68,983 SNPs were selected for inclusion on the Axiom Rose Genotyping Array.

Results

A total of 672 samples were genotyped with the Axiom Rose Genotyping Array [3]. These included:

- 96 samples representing two tetraploid mapping populations
- 96 samples representing the tetraploid cut rose population K5
- 96 samples representing tetraploid garden roses
- 384 samples across 13 species varying in ploidy from diploid (2N) to pentaploid (5N)

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The Axiom Rose Genotyping Array requires advanced analysis using fitTetra, an R package for assigning auto-tetraploid genotype scores [4]. The genotyping software fitTetra enables automated genotype calling in tetraploid species, which results in the scoring of the five alternative genotypes (aaaa, baaa, bbaa, bbba, and bbbb; nulliplex to quadruplex) (Figures 1 and 2).

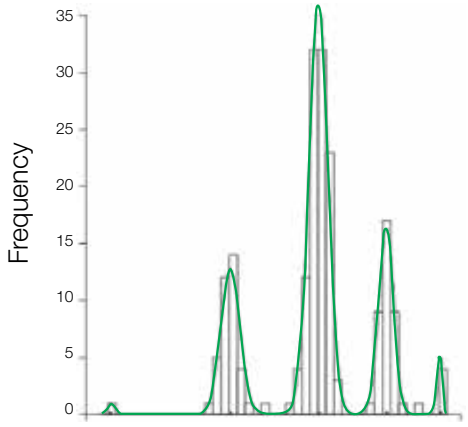

Figure 1. Graphical output using fitTetra showing the histogram of the measured ratios of the two signals: (allele a)/(allele a + allele b), with the model that is fitted to the observed ratios superimposed as a green outline.

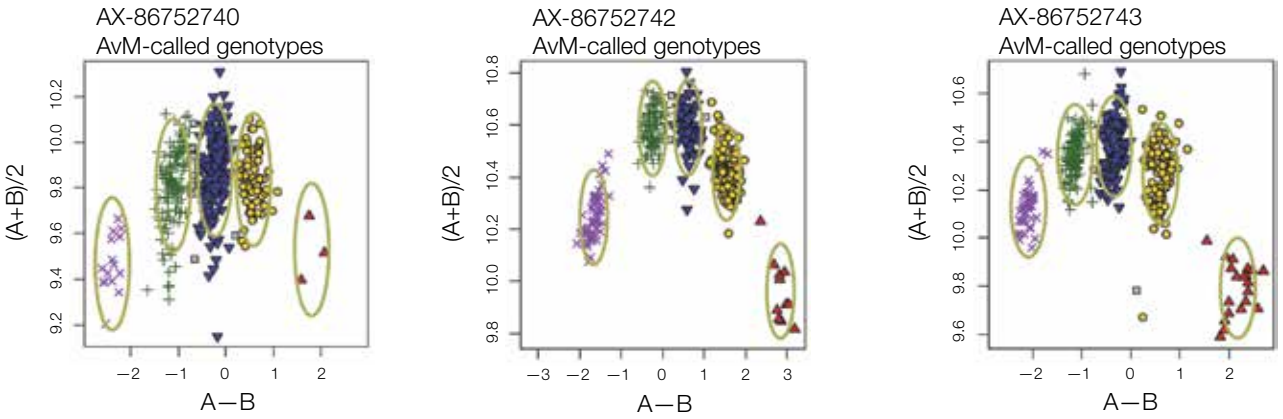

Figure 2. Cluster plots showing patterns that were observed in the data generated on the Axiom Rose Genotyping Array. Rose is an auto-tetraploid plant and typically exhibits five genotype clusters.

Ordering information

Product	Description	Cat. No.
Axiom Rose Genotyping Array	Contains one 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550450
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. Koning-Boucoiran et al. (2012) The mode of inheritance in tetraploid cut roses. *Theor Appl Genet* 125(3):591–607.
2. Smulders M et al. (2012) Towards a large Axiom® Genotyping Array for tetraploid rose. *Conference Next Generation Plant Breeding,* poster.
3. Smulders M (2013) Genetic analysis of tetraploid F1 rose populations based on the Rose Axiom® SNP Array. *The VI International Symposium on Rose Research and Cultivation,* oral presentation.
4. Voorrips RE, Gort G, Vosman B (2011) Genotype calling in tetraploid species from bi-allelic marker data using mixture models. *BMC Bioinformatics* 12:172.

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

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