Axiom Strawberry Genotyping Array

The world's first expert-designed octoploid strawberry genotyping array to facilitate quantitative trait locus (QTL) discovery and marker-assisted breeding

The Applied Biosystems™ Axiom™ Strawberry Genotyping Array (also called the International Strawberry 90K (IStraw90) Axiom™ Array) was designed through our Expert Design Program in collaboration with the International RosBREED SNP consortium, which is dedicated to the genetic improvement of rosaceous crops.

The array offers genome-wide coverage of polymorphic SNPs across the cultivated garden strawberry hybrid (*Fragaria × ananassa*).

Highlights
- Diverse content: 95,062 SNPs and indels derived from octoploid and diploid cultivars, including:
  – 1,761 multi-allelic SNPs
  – 3,751 SNPs from diploid cultivars; the remaining markers are from octoploid cultivars
- Multiple cultivars: SNP discovery was facilitated with a diverse, worldwide breeding germplasm panel

Applications
- Complex trait research:
  – QTL discovery
  – Identify traits of economic significance

- Molecular breeding:
  – Genome-wide scanning
  – Marker-assisted breeding
- Release of new cultivars:
  – Accelerate and increase efficiency of cultivar development
  – Identify the presence of important markers in the existing strawberry germplasm
  – Identify a germplasm that will perform well in specific growing regions

SNP discovery
SNP discovery was facilitated by sequencing a diverse discovery panel of 9 octoploid cultivars at ≥20x coverage, including:

- Holiday, Korona, and F1 seedlings from the cross Holiday x Korona [1]
- Two likely diploid progenitors, Fragaria mandschurica, F. iinumae
- One known diploid, F. vesca

The sequencing reads were aligned to the *F. vesca* genome sequence.

Marker selection
To address the challenges in genotyping the allo-octoploid strawberry and maximize the number of functional markers, we minimized

sequencing errors and exploited site-specific biological reductions in ploidy. SNPs and indels were chosen based on the following criteria:

- Select markers from cultivars sequenced at 20x coverage to minimize errors from sequencing, misalignments, or erroneous mappings
- Exclude highly repetitive sequences and those containing ambiguities
- Avoid homopolymer and dinucleotide repeat sites when selecting indels
- Include SNPs specific to 1 subgenome
- Achieve reduction in ploidy by targeting subgenome-specific deletions and sites of subgenome-specific sequencing motifs
- Include markers that meet the threshold criteria for predicting reproducibility on the array, based on our in silico design scores

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Based on the cluster properties, 15,000 polymorphic, high-resolution markers were selected to successfully place the SNPs on a genetic map of the hybrid Holiday x Korona. Examples of the different types of cluster plots generated during the analysis are shown in Figure 1.

Results

The Axiom Strawberry Genotyping Array was used to genotype 384 samples. The data analysis and clustering were automated using Applied Biosystems™ Genotyping Console™ Software according to the Best Practice Supplement to Axiom Genotyping Solution Data Analysis User Guide (P/N 703083). SNPs were filtered using the Applied Biosystems™ SNPolisher™ package. Today the Applied Biosystems™ Axiom™ Analysis Suite should be used for analysis following the Best Practices Workflow as described in the Axiom Genotyping Solution Data Analysis Guide (P/N 702961).

Notes about the data analysis

The Axiom Strawberry Genotyping Array requires advanced analysis using functions provided by the SNPolisher R package to filter multi-cluster SNPs (Figure 1D). Additional filters based on reproducibility and inheritance errors are key, and require technical replicates within a genotyping platform and sets of parents and F1 seedlings. Genotyping many varieties together may create multiple clusters during analysis that interfere with each other and/or blend together, compromising the algorithm's ability to correctly call genotypes. Genotype calls are not provided for multi-allelic SNPs.
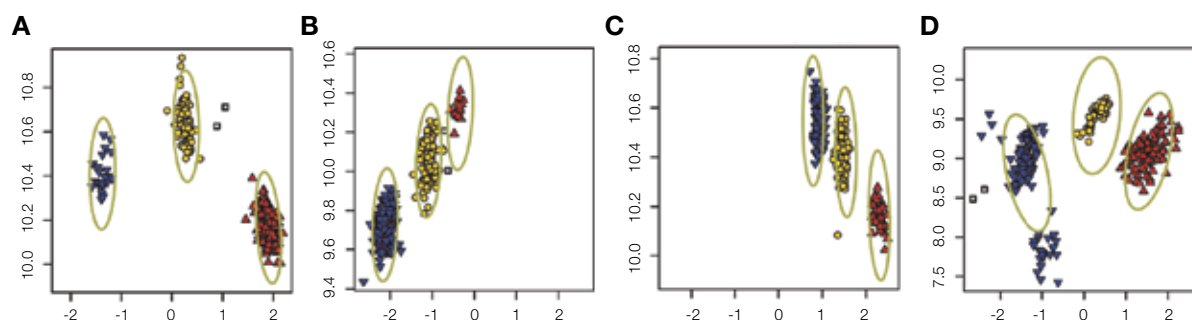

Figure 1. Cluster plots showing patterns observed in the data generated on the Axiom Strawberry Genotyping Array. Plots **A–B** are the result of the ploidy reduction strategies used during array design: **(A)** diploid-like pattern, **(B)** tetraploid-like pattern, and **(C)** octoploid pattern. **D** shows an example of a multicluster, polymorphic, high-resolution genotype.

Ordering information

Product	Description	Cat. No.
Axiom Strawberry Genotyping Array (IStraw90K)	Contains one 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550466
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
Axiom i35 Strawberry Array (384 format)	Contains one 384-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550767
Axiom 2.0 384HT GeneTitan MC Consumables Kit	Contains all GeneTitan Multi-Channel Instrument consumables required to process one Axiom 384-array plate	902234
Axiom 2.0 384HT Reagent Kit	Includes all reagents (except isopropanol) for processing 384 DNA samples	902245
Axiom i35 Strawberry Array (Mini 96 format)	Contains one Mini 96-array plate; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550827
Axiom 2.0 Assay Mini 96 Reagent Kit	Includes all reagents (except isopropanol) for processing samples for two Mini 96-array plates	903013
Axiom 2.0 Assay Mini 96 Manual Target Preparation Consumables Kit	Includes all reagents (except isopropanol) for processing samples for four Mini 96-array plates	902986
Axiom 384HT High-Volume Consumables Kit	Contains all GeneTitan Multi-Channel Instrument consumables required to process samples for five 384-array plates or five Mini 96-array plates	902629

Reference

1. Bassil N (2013) Development and Preliminary Evaluation of the IStraw90 Axiom® Array in Cultivated Strawberry (*Fragaria × ananassa*). Oral presentation: American Society for Horticultural Science.

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

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