SNAPSHOOT
ENGINEERED FOR A SAFER TOMORROW

현장을 이해하고, 필요한 솔루션을 연결합니다.

산업안전 · 추락방지 시스템
산업용 소재 · 건축자재
제품 제안부터 공급·시공·설치·교육까지



COMPANY INFORMATION

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TECHNICAL DOCUMENTS

인증서 · 데이터시트 · 기술자료

제품의 규격과 성능, 인증 및 적용 조건을 확인하기 위한 자료입니다.

ABOUT SNAPSHOOT

제품 공급을 넘어, 현장에 맞는 해결책으로

스냅슛은 산업현장의 작업 환경과 요구 조건을 바탕으로
적합한 제품과 시스템을 제안합니다. 현장 실사를 통해 설치 조건을 확인하고,
공급부터 시공·설치 및 사용 교육까지 필요한 과정을 함께합니다.

추락방지 시스템

안전대부착설비 · 수평·수직 라이프라인
레일 시스템 · 리지드 포스트

밀폐공간 진입·구조 솔루션

데빗암 · 삼각대 · 구조용 윈치
윈치 안전블록 · 구조장비

산업안전 보호구

전신형 안전대 · 랜야드 · 안전블록
작업 환경에 맞춘 개인보호구

산업용 소재·건축자재

산업용 테이프 · 접착제 · 기능성 소재
구조용 스크류 · 목조건축 자재

SNAPSHOOT
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홈페이지 바로가기 →
문서 라이브러리 바로가기 →
시공사례 바로가기 →
문의하기 →

본 페이지는 스냅슛의 자료 제공 안내용 표지입니다. 첨부된 인증서 및 기술자료의 발행 주체, 인증 대상과 적용 범위는 해당 원문을 기준으로 확인해 주세요.

DataSheet

affymetrix

Axiom® Strawberry Genotyping Array

The world's first expert-designed octoploid strawberry genotyping array to facilitate Quantitative Trait Loci (QTL) discovery and marker-assisted breeding

Axiom® Strawberry Genotyping Array (also called the International Strawberry 90K (IStraw90) Axiom® Array), was designed through Affymetrix® Expert Design Program in collaboration with the International RosBREED SNP consortium that spans multiple nations, states, and institutions dedicated to 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 derived from diploid cultivars; the remaining markers are derived from octoploid cultivars
- **Multiple cultivars represented:** 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 existing strawberry germplasm
  - Use genetic information to identify 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.
- 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

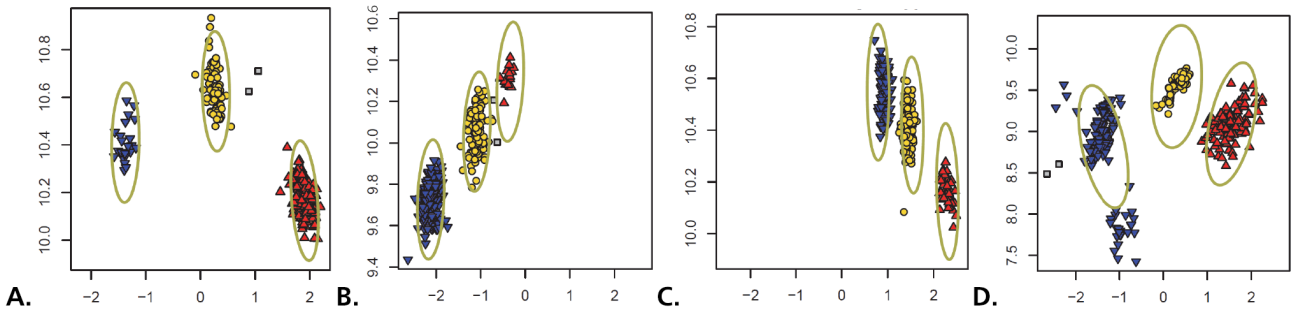
Markers were selected with the goal of addressing the challenges in genotyping the allo-octoploid strawberry genome to maximize the number of functional markers. These goals were achieved by minimizing sequencing errors and exploiting site-specific biological reductions in ploidy. The SNPs and indels were chosen based on the following criteria:

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

Experimental results

384 samples were genotyped with the Axiom Strawberry Genotyping Array. The data analysis and clustering were automated using Affymetrix® Genotyping Console™ Software as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis* (P/N 703083) and SNPs were filtered using the Affymetrix® SNPolisher™ package.

Figure 1: The cluster plots below show patterns that were observed in the data generated on 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 (C) octoploid pattern. Cluster plot (D) shows an example of a multi-cluster polymorphic high-resolution genotype.



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

Notes about the data analysis: Axiom® Strawberry Genotyping Array requires advanced analysis using functions provided by the Affymetrix SNPolisher R package to filter multi-cluster SNPs such as shown in Figure D. Additional filters based on reproducibility and inheritance errors are also key and require genotyping technical replicates and sets of parents and F1 seedlings. Genotyping many different varieties together may create multiple clusters during the analysis that interfere with each other and/or blend the clusters together, compromising the algorithm's ability to correctly call genotypes. Genotype calls are not provided for multi-allelic SNPs.

Reference

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

Ordering information

Part number	Product name	Description
550466	Axiom® Strawberry Genotyping Array (IStraw90K)	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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