Axiom Wheat HD Genotyping Arrays

Whole-genome high-density (HD) genotyping for global hexaploid wheat lines

Applied Biosystems™ Axiom™ Wheat HD Genotyping Arrays were designed through our Expert Design Program with input from Professor Keith Edwards, Dr. Gary Barker, and Dr. Sacha Allen of the Cereal Genomics group at the School of Biological Sciences, University of Bristol, UK.

This is a two-array set designed through a public sector pre-breeding program dedicated to accelerating the genetic improvement of modern wheat varieties.

A collection of wild relatives, including *Triticum, Thinopyrum,* and *Aegilops* species and rye, along with numerous elite hexaploid bread wheat lines and hexaploid landraces selected from the Watkins collection [1] held at the John Innes Institute, were selected and sequenced. SNPs discovered from these sequencing experiments were included on the Axiom Wheat HD Genotyping Arrays.

Highlights
- **Content:** 817,000 SNPs spaced across the wheat genome

- **Diversity:** designed for a variety of global lines including elite cultivars, landraces, synthetic hexaploids, and wheat relatives

Applications
Complex trait research
- Quantitative trait loci (QTL) identification

- Identification of genetic markers for selecting key traits for use in commercial breeding programs and academic research

- Development of pre-breeding germplasm

Array design
CerealsDB
The CerealsDB website (**www.cerealsdb.uk.net/**) is a searchable database that was created by the Cereal Genomics group at the University of Bristol for the purpose of making wheat SNP information available to the public. It is updated regularly and contains:

- **SNP information [2]:** data related to every SNP, including Bristol contig code and 120 bp flanking sequence; flanking sequence and map location are available in the analysis files

- **Variety comparison [3]:** select two or more varieties of wheat to see the SNPs in common or SNPs that are different between them

SNP discovery
**48x exome sequencing of 41 global lines, resulting in:**
- ~100,000 SNPs between 10 elite cultivars

- ~290,000 SNPs between elite hexaploid cultivars and 9 landraces

- ~650,000 SNPs between hexaploid wheat and wheat relatives including *Triticum urartu*, *Thinopyrum* and *Aegilops* species*,* and rye

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Results

The Axiom Wheat HD Genotyping Arrays were used to genotype 288 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), and SNPs were filtered using the Applied Biosystems™ SNPolisher™ package. Today,

Applied Biosystems™ Axiom™ Analysis Suite software should be used for analysis following the Best Practices Workflow as described in the Axiom Genotyping Solution Data Analysis Guide (P/N 702961).

Since the samples had been inbred, an inbred correction (Figure 1) was applied to the screened SNPs during data analysis. This enabled correct genotype calling of SNPs that exhibited only homozygous clusters and lacked heterozygous clusters. Typical genotype cluster plots for wheat SNPs are shown in Figure 1.
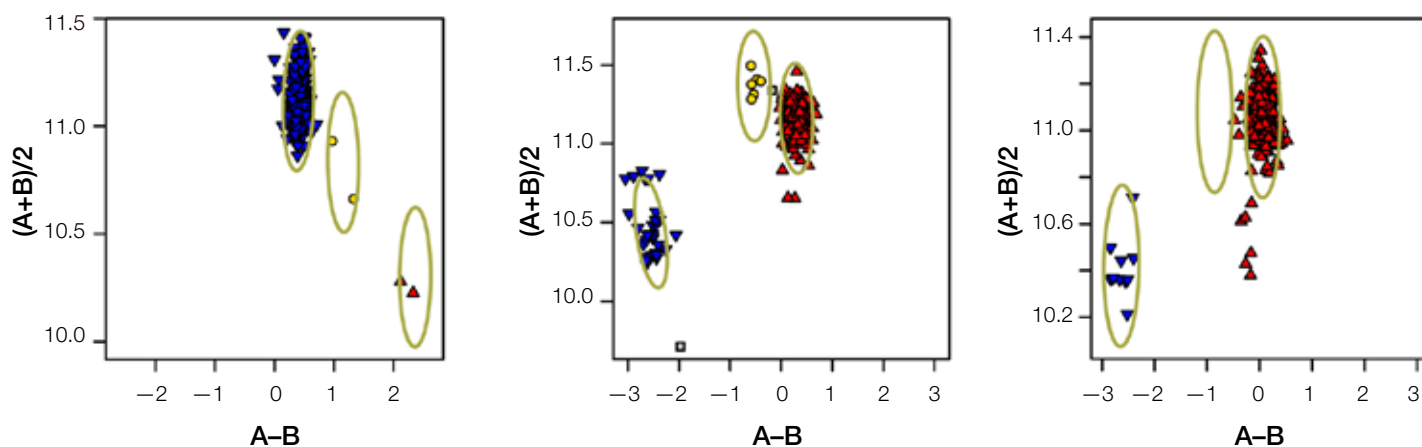
Figure 1. Examples of polymorphic high-resolution SNPs from the Axiom Wheat HD Genotyping Arrays. The genotyping algorithm automatically calls the genotypes without manual intervention. An inbred correction was applied during analysis, thus ensuring correct genotype calls, even in cases when there were few or no examples of the heterozygous cluster.

Ordering information

Product	Description	Cat. No.
Axiom Wheat HD Genotyping Arrays	Contains two 96-array plates; reagents and GeneTitan Multi-Channel Instrument consumables sold separately	550491
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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. John Innes Centre. Germplasm Resources Unit (GRU). https://www.jic.ac.uk/germplasm/
2. CerealsDB. Wheat 820K and 35K Axiom Arrays. http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_download.php
3. CerealsDB. Download the SNPs on the 820K Axiom Array. http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_820K_search.php

Find out more at thermofisher.com/microarrays

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