

Axiom® Wheat HD Genotyping Arrays

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

Axiom® Wheat HD Genotyping Arrays were designed through Affymetrix® Expert Design Program in collaboration with Professor Keith Edwards, Dr. Gary Barker, and Dr. Sacha Allen from the Cereal Functional Genomics Group at the School of Biological Sciences, University of Bristol.

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 sp.*, *Thinopyrum sp.*, *Aegilops sp.*, and rye along with numerous elite hexaploid bread wheat lines and hexaploid landraces selected from the Watkins Collection¹ held at the John Innes Institute were selected and sequenced. SNPs discovered from these sequencing experiments were included on 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:**
 - QTL identification
 - Identification of genetic markers for selecting key traits for use in commercial breeding programs and academic research
 - Development of pre-breeding germplasm

CerealsDB

The CerealsDB website (<http://www.cerealsdb.uk.net/>) is a searchable database that was created by the Functional Genomics group at the University of Bristol, UK, 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

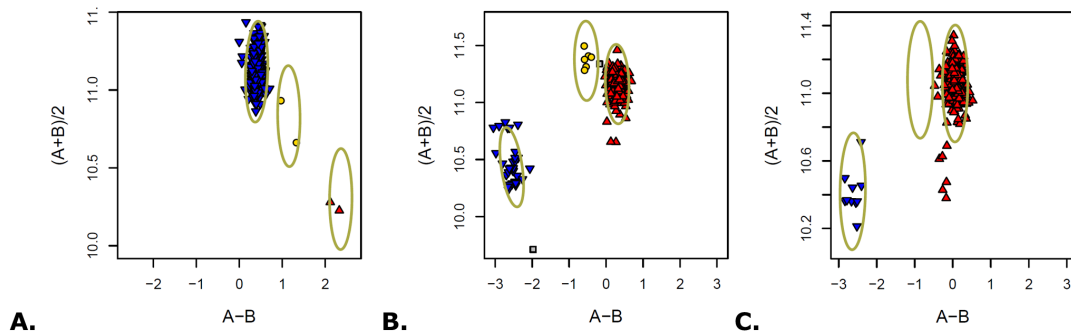
- 48x exome sequencing of 41 global lines, resulting in:
 - ~100,000 SNPs between ten elite cultivars
 - ~290,000 SNPs between elite hexaploid cultivars and nine landraces
 - ~650,000 SNPs between hexaploid wheat and wheat relatives including rye, *Thinopyrum sp.*, *Aegilops sp.*, and *Triticum urartu*.

Experimental results

288 samples were genotyped with Axiom Wheat HD Genotyping Arrays. The data analysis and clustering were automated using Affymetrix' Genotyping Console™ (GTC) Software as per the *Best Practice Supplement to Axiom® Genotyping Solution Data Analysis Users Guide* (P/N 703083), and SNPs were filtered using Affymetrix' SNPolisher™ package.

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: The genotype cluster plots below are examples of polymorphic high-resolution SNPs from Axiom® Wheat HD Genotyping Array. 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.



References

1. <http://www.jic.ac.uk/corporate/media-and-public/historic-grain.htm>
2. http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_download.php
3. http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/axiom_820K_search.php

Ordering information

Part number	Description	Details
550491 550492	Axiom® Wheat HD Genotyping Arrays	Contains two plates with 96 arrays each. Reagents and GeneTitan® MC consumables must be ordered separately. Minimum order 96 samples
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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