Overview

The international cotton community has made arrangements with Illumina to produce "BeadArray" Panels ("chips") for analysis of cotton SNPs.

- Each array will potentially interrogate up to 90,000 SNPs
  - "BASE CONTENT" will target up to 70,000 public SNPs (on all "chips").
  - "ADD-ON CONTENT"—Clients can potentially add 20,000 private SNPs for client-specific uses.
- Consortium pricing will depend on the number of initial orders, but is expected to range between $65-$78 (USD), excluding shipping, insurance, taxes and processing.

Order Now for Consortium Pricing
Deadline = 2013 Nov. 15
consortiamanager@illumina.com

Background

Plant DNA markers have many applications in breeding and research. Single-nucleotide polymorphisms (SNPs) are the most abundant type of DNA marker and most cost-efficient for most breeding and research applications.

The scale and speed of research on numerous agriculturally important animals and plants increased significantly after public Illumina Infinium assays were developed, facilitating use of highly multiplexed SNP genotyping.

The need for high-throughput marker-based capabilities in cotton motivated a number of researchers to establish large-scale cotton SNP development efforts. They recently formed a Consortium to develop a “Cotton SNP Chip” that could be used globally by public and private breeders, geneticists, and other researchers, and generally enhance cotton genetic analysis, breeding and research. The launch of the chip marks an important step forward for cotton.

Selection of SNPs

SNPs on the Cotton SNP Chip were derived from gene transcripts and genomic DNA of multiple cultivars, genotypes, and species. Not unexpectedly, sequence redundancies exacerbated by the polyploid nature of cotton complicated SNP development. Most of the 70,000 public SNPs that comprise “Base Content” were selected from Consortium SNP populations for which rates of conversion to assays were experimentally determined to be high (~70%+). Since use of SNPs that require two beadtypes per SNP call reduce efficiency of BeadArrays, cotton SNPs were preferentially chosen if amenable to single-bead assays, and their respective assay design prediction scores were high. SNPs were also screened to remove redundancies.

Optimized for Public & Private Uses

The Cotton SNP Chip will follow Illumina’s 24-sample 90k BeadChip format (see image), a configuration that balances expense with the capacity to meet most cotton needs. The 70/20 split between “Base Content” (public) and variable “Add-On Content” (private) aims to meet the combined needs of all users. Most (50,000) of the “Base Content” is devoted to intraspecific SNPs because the Chip will be used extensively for inter-varietal comparisons and other intra-specific applications. Moreover, diversity is low among agronomically elite cottons, so the overall pool of SNPs needs to be large. Most (16,000) of the other 20,000 public SNPs are devoted to other Primary Gene Pool species, i.e., the other AD 52-chromosome species, especially G. barbadense, and to lesser extents, G. tomentosum and G. mustelinum. The remainder (4,000) are devoted to diploid species.

FOR ADDITIONAL INFORMATION:

- See the FAQ Sheet: “International Cotton SNP Genotyping Panel—Frequently Asked Questions”
- For pricing information or quotation: Please contact your account manager or consortiamanager@illumina.com