Cotton "SNP CHIP"

Illumina BeadArray™

Order Now for Consortium Pricing

Deadline = 2013 Nov. 15

consortiamanager@illumina.com

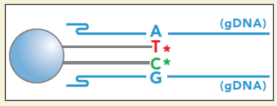
Overview

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.**

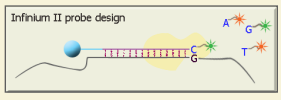
Order by 2013 Nov. 15 to assure availability, and avoid post-deadline price increases.

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 :

"Base Content" Allocations in Cotton SNP BeadArray (2013)

Type	Number	Germplasm	Sequence type	~No. SNPs	Total (~)
Intraspecific	50,000	*G. hirsutum* (Gh), esp. inter-varietal	RNA-seq	25,000	50,000
			gDNA-seq	25,000	
Interspecific (versus Gh)	20,000	Shared among species below	RNA-seq	4,000	
		G. barbadense (Gb)	RNA-seq	3,000	12,000
			gDNA-seq	5,000	
		G. tomentosum	RNA-seq	2,000	5,000
		G. mustelinum	RNA-seq	2,000	5,000
		G. longicalyx	RNA-seq	2,000	2000
		G. armorianum	RNA-seq	2,000	2000
Overall	70,000				

- **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*

SNP-Contributing Laboratories and Groups: Texas A&M AgriLife Research (David M. Stelly, Amanda Hulse, et al.), University of California, Davis (Allen Van Deynze, Hamid Ashrafi, et al.), CSIRO (Iain Wilson, Qianhao Zhu, Danny Llewellyn et al.), BYU (Joshua Udall, Robert Byers et al.), USDA (David Fang, Michael Gore et al.), CSIR-NBRI (Sawir Sawant et al.), and CIRAD (Jean-Marc Lacape. Marc Giband et al.).