

Accessing Genetic Information: Technology for Large Scale SNP Genotyping

To enable large-scale SNP genotyping we have combined a multiplexed oligonucleotide ligation-based assay with read-out on miniaturized arrays of universal capture probes. The probes are attached to beads, which are assembled into arrays on the ends of optical fiber bundles. By formatting these miniaturized arrays into a matrix that matches a 96-well microtiter plate, many samples can be processed simultaneously and efficiently in an automated fashion. This combination of technologies provides a novel and versatile system for genetic analysis that has the capacity to match the needs of analysis on a genomic scale. Fundamental aspects of the technology will be reviewed, and the application of these arrays to SNP genotyping will be discussed.

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CV

Mark Chee received his B.Sc. in Biochemistry from the University of New South Wales in 1985 and his Ph.D. in Molecular Biology from the University of Cambridge in 1991. Dr. Chee was a postdoctoral fellow at the Stanford Yeast Genome Center and at Affymax Research Institute. At Affymax, and subsequently at Affymetrix, Dr. Chee contributed to the development of oligonucleotide arrays for the analysis of complex genetic samples. Dr. Chee was a co-founder of Illumina and is currently Vice President of Genomics at Illumina.

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