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SNP genotyping with arrays

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Single nucleotide polymorphisms (SNPs) are sequence variants in which two alternate bases occur at one position. The SNP Consortium is developing a dense map of SNPs in the hope that certain variants can be associated with disease states. With hundreds of thousands of SNPs identified, the scoring of these SNPs in patient populations has become the limiting factor. Hirschhorn *et al*. provide a possible solution in the October 24 Proceedings of the National Academy of Sciences by making the existing technique of single-base extension (SBE) a parallel process (*Proc Natl Acad Sci USA* 2000, **97:**12164-12169). The technique begins with target amplification and the annealing of a primer next to a SNP site. A single fluorescently labeled nucleotide is incorporated as the next base; the identity of the fluorescent label identifies the variant base. Hirschhorn *et al*. modify this basic SBE technique by adding generic sequence tags to the primers. Up to 100 of the primer/tag combinations are added to a single sample and, following SBE, annealed to a spotted array of anti-tag oligonucleotides on a glass slide. All the SNP results can be read out simultaneously with an accuracy of approximately 99%. The technique is cheaper than a similar version based on photolithography [http://www.genomebiology.com/resolver.asp?PubMedID=10854416], and more versatile than a version that requires arrays of locus-specific primers.

References

1. Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome.

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4. *Proceedings of the National Academy of Sciences*, [http://www.pnas.org/]

5. A primer-guided nucleotide incorporation assay in the genotyping of apolipoprotein E.

6. Parallel genotyping of human SNPs using generic high-density oligonucleotide tag arrays.

7. A system for specific, high-throughput genotyping by allele-specific primer extension on microarrays.