

**P010** Non-recombining segments in the human genome as phylogeographic tools

**Stéphane J. Ballereau, Patricia Balaesque  
and Mark A. Jobling**

*Department of Genetics, University of Leicester, University  
Road, Leicester LE1 7RH, UK*

The HapMap project is revealing genome-wide haplotype structure for African, European and East Asian population samples, and allows us to seek haplotype blocks in which historical recombination is absent. Our aim is to develop novel and informative phylogeographic SNP- and microsatellite-defined autosomal and X-chromosomal haplotypes, and use these in global and regional population studies. We have identified blocks for which there is no evidence of recombination in any of the HapMap samples, and are investigating the influence of SNP density on the interpretation of recombination history. SNP-based phylogenies have been constructed, and rooted using chimpanzee sequences, to allow a comparison of tree topologies and the population distributions of branches on a genome-wide scale. We plan to use microsatellite diversity within the HapMap samples to estimate time-to-most-recent-common-ancestor for haplotypes.