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## Haplotype blocks

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Advances in medicine will undoubtedly be linked to our ability to correlate human genetic variation with disease. In the May 23 ScienceXpress, Gabriel *et al.* report a large-scale analysis of haplotypes in the human genome (*Sciencexpress* 23 May 2002, DOI:10.1126/science.1069424). They characterized haplotype patterns for 51 genomic regions with an average size of 250 kb (covering 13 megabases) from African, European and Asian DNA samples. They genotyped thousands of single nucleotide polymorphisms (SNPs) in 275 individuals by mass spectrometry, and found hundreds of blocks containing only a few haplotypes and low historical recombination rates. The majority of SNP pairs were concordant across population samples. The striking similarity in SNP polymorphisms, recombination sites and haplotypes supports the 'Out of Africa' model for human history. The existence of extensive haplotype blocks will greatly facilitate the study of human variation. This study provides the foundations for construction of a haplotype map of the human genome using common SNP markers, providing insights into human populations and diseases.

## References

- 1. The new genomics: global views of biology.
- 2. ScienceXpress, [http://www.sciencexpress.org]
- 3. The emergence of modern humans.