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Human variation

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Analysis of sequence variation provides clues about what makes us different from each other and why we respond differently to disease. In an Advanced Online Publication in Nature Genetics, Reich *et al.* report a genome-wide study of sequence variation in the human genome (*Nature Genetics*, 5 August 2002, doi:10.1038/ng947). They analysed extensive collections of single nucleotide polymorphisms (SNPs) and found evidence for SNP-rich blocks of variation (as long as 100 kb). Further analysis led them to conclude that gene history, rather than differences in local mutation rates, are responsible for this variation. They propose that differences in recombination rates are responsible for local patterns of sequence variation. Reich *et al.* add further evidence for large blocks of linkage disequilibrium in the human genome, a critical feature for future disease-mapping projects.

References

1. A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms.

2. Nature Genetics, [http://www.nature.com/ng/]