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A better map of the human genome

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Physical and genetic maps of the genome provide complimentary tools for understanding genetic variation and for linkage analysis. The first genetic map of the human genome was generated 15 years ago. In an Advanced Online Publication in Nature Genetics, Augustine Kong and researchers at deCODE genetics in Iceland present the latest genetic map, which has about five times better resolution than existing maps (*Nature Genetics* 10 June 2002, DOI:10.1038/ng917).

Kong *et al.* genotyped over 5,000 microsatellite markers for 146 Icelandic families, representing 1,257 meiotic events. The best previous map contained only 188 genes. Comparison of physical and genetic maps allowed resolution of discrepanciesand deficiencies. The construction of the genetic map benefited from the draft genome sequence when genetic data were sparse. Conversely, the genetic map helps to validate and improve the sequence assembly.

Analysis of both maps allowed calculation of recombination rates. The average recombination rates of the shortest chromosomes (chromosomes 21 and 22) are twice as high as the longest ones (chromosomes 1 and 2), and varied considerably within chromosomal regions. The crossover rates varied from 0.1 to 3 cM per Mb. Recombination rates correlated with GC content, CpG motifs and polyA/polyT stretches. Recombination rates also showed regional variation (recombination 'hot spots') and differed between regions of the maternal and paternal chromosomes. Integrating such high-resolution genetic maps with refined physical maps will aid navigation of the genomic landscape.

References

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