

## GENOME EVOLUTION

## Mapping recombination in chimpanzees

Patterns and rates of recombination vary among species, but a fuller understanding of the influence of recombination on genome evolution has been limited by the difficulties in mapping recombination events in many species. A new study in which sequence data is used to generate a fine-scale map of the chimpanzee genome enables a comparison of drivers of recombination between chimpanzees and humans.

Auton *et al.* constructed a high-resolution genetic map based on the genome sequences of ten unrelated western chimpanzees. They validated the mapping strategy by running ten individual human genomes through the same procedures and comparing the results to previous human maps. This showed that a strategy based on ten individual genomes gives sufficient



power to estimate recombination rates and to map recombination hotspots.

The chimpanzee map shows that at the broad (chromosomal or megabase) scale, rates of recombination are similar between chimpanzees and humans. The authors also found genomic features that influence recombination rates. Analysis of chromosomal segments that have inverted orientations in chimpanzees and humans showed that the distance that a sequence is from the telomere has a significant effect on its recombination rate. The most dramatic difference was observed in the comparison of chimpanzee chromosomes 2a and 2b to human chromosome 2: the telomeric chimpanzee regions showed much higher recombination rates than the fused human counterpart.

However, when the authors looked at a finer scale, they did not find shared recombination hotspots between humans and chimpanzees; this is consistent with previous studies of limited genomic regions. In humans and in some other species, a proportion of hotspots contain

binding sites for the zinc finger protein PRDM9. Auton *et al.* show that *PRDM9* sequences in western chimpanzees are highly diverse, but they found no evidence of increased recombination around predicted binding sites for the PRDM9 variants and also did not find other hotspot-enriched motifs in chimpanzees. One of several possible reasons for this difference is that chimpanzee PRDM9 variants bind to a greater variety of sequences than PRDM9 does in humans.

Humans and chimpanzees do share similar recombination rate profiles around genes and CpG islands. These observations suggest that the influence of chromatin structure on recombination may be shared between the species, even if the roles of sequence elements are not.

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**ORIGINAL RESEARCH PAPER** Auton, A. *et al.* Fine-scale chimpanzee genetic map from population sequencing. *Science* 15 March 2012 (doi:10.1126/science.1216872)

**FURTHER READING** Paigen, K. & Petkov, P. Mammalian recombination hot spots: properties, control and evolution. *Nature Rev. Genet.* **11**, 221–233 (2010)