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Genome sequencing reveals a wide variation of recombination events in eukaryote

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Abstract

Knowledge of the recombination landscape is central to understanding the molecular basis of recombination, population genetically-based inference and genome evolution. Studies have been limited, however, by the density of markers and the accuracy of sequencing. We sequenced many individuals from single meiosis and their parents in *Arabidopsis*, rice, bee and yeast, to close to 100% accuracy with markers ever few hundred bps. We identified large blocks of chromosome that were from either of two parents and so inferred the location of crossover events. Recombination blocks at the level of resolution (>500-kb) are randomly distributed on chromosomes in general. Unexpectedly, smaller recombination blocks (10-500 kb) are not only much more common than the larger blocks but are concentrated as recombination hot-spots. In addition we could identify small (<2kb) gene conversion tracts. We estimate that well over 90% of recombination events are gene conversion events in plants. The rate of alteration of protein sequence owing to gene conversion is over 600 times that owing to mutation. In contrast, only a few events of gene conversion can be observed in bee, suggesting that gene conversion is less important in this anima. Surprisingly, some of small crossovers and gene conversions have occurred at the same position of chromosome in multiple individuals. On the whole, the rates of crossovers and gene conversions vary widely among species. Thus, our results demonstrate that different species have their own profiles of recombination, which could be essential for their haplotype diversity and their adaptation to new environments.

Biography

Dacheng Tian has completed his PhD from University of Newcastle in Australia and postdoctoral studies from University of Chicago. Now he is a professor in Nanjing University in China. He is interested in insertion/deletion genetics (*Nature* 2008), genetic effects of single meiosis by sequencing segregating genomes (*PNAS* 2012), and how the plant R-genes are created, maintained and co-evolved with pathogen (*PNAS,* accepted). He provided the direct evidence for the fitness cost of R-genes (*Nature* 2003). He has published more than 40 papers in reputed journals and serving as an editorial board member of Mol Genet & Genomics.