

Scientists generate the most precise map of genetic recombination ever

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Genetic recombination, the process by which sexually reproducing organisms shuffle their genetic material when producing germ cells, leads to offspring with a new genetic make-up and influences the course of evolution.

In the current issue of *Nature*, researchers at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany, and the EMBL-European Bioinformatics Institute (EMBL-EBI) in Hinxton, UK, present the most precise map of genetic recombination yet. The study sheds light on fundamental questions about genetic shuffling and has implications for the tracking of disease genes and their inheritance.

In order to generate germ cells, sexually reproducing organisms undergo a complex series of cell divisions (meiosis) that includes the shuffling of genetic material inherited from the two parents. Equivalent chromosomes from mother and father pair up and exchange sections of DNA in a process called crossover.

In a different type of recombination, called non-crossover, a small piece of DNA is copied from one chromosome onto the other without reciprocal exchange leading to gene conversion. Non-crossovers are minute events with a subtler effect than the exchange of larger fragments, but both types of recombination can increase genetic diversity and explain why organisms of the same species differ in many ways. Both types of recombination can also act to separate the transmission of neighbouring genes, which are normally inherited

together.

The groups of Lars Steinmetz at EMBL and Wolfgang Huber at EMBL-EBI have produced the most detailed map to date of recombination events in the yeast genome.

“Our map has the highest resolution of recombination events that currently exists for any organism. We can locate crossovers and even hard-to-trace non-crossovers, typically with a precision of about 80 bases. This resolution is 20 times higher than in any existing yeast map and more than 360 times higher than a recent human map,” says Steinmetz.

The map revealed many new insights into the organisation of recombination in yeast. On average over 150 recombination events were observed during a typical meiosis. These events did not occur uniformly across the genome. The recombination rate varied according to location, with events concentrated at so-called hotspots, some of which favoured either crossovers or non-crossovers. The researchers also found evidence for interference between crossovers and non-crossovers - a phenomenon previously only known to occur between crossovers - that makes it unlikely for two recombination events to happen in close proximity.

The fundamental principles of recombination are likely to be shared between yeast and humans. “Our map expands our understanding of crossover and provides a wealth of new information about non-crossovers and gene conversion. It will act as a reference for future research into recombination,” says Richard Bourgon from Huber's group, who developed the statistical methodology for this new type of data.

The insights gained will not only help tackle questions about the basic mechanisms of recombination; they will also have practical implications

for the tracking of disease genes in humans.

Citation: E. Mancera, R. Bourgon, A. Brozzi, W. Huber & L.M. Steinmetz. High-resolution mapping of meiotic crossovers and noncrossovers in yeast. *Nature*, 9 July 2008

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