Gene variants may help to distribute the work of evolution between men and women

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Scientists from deCODE genetics today report the discovery of two common, single-letter variants in the sequence of the human genome (SNPs) that regulate one of the principle motors of evolution. Versions of the two SNPs, located on chromosome 4p16, have a genome-wide impact on the rate of recombination - the reshuffling of the genome that occurs in the formation of eggs and sperm.

Recombination is largely responsible for generating human diversity, the novel configurations of the genome that enable the species to adapt and evolve in an ever-changing environment. Yet remarkably, the versions of the SNPs that increase recombination in men decrease it in women, and vice versa.

This highly unusual characteristic may enable the variants to help to maintain a fundamental tension crucial for evolutionary success: promoting the generation of significant diversity within a portion of the population but keeping the pace of this change within certain bounds, maintaining it relatively constant overall and so supporting the stability of the genome and the cohesiveness of the species.

“This is the latest in a series of landmark papers from deCODE in which we have utilized our unique capabilities in human genetics to elucidate some of the key mechanisms driving human evolution,” said Kari Stefansson, CEO of deCODE. “We are also excited that we can now immediately enable individuals to see if they carry such variants, by folding the findings announced today – and others we expect to publish

in the near future – into our deCODEme™ personal genome analysis service."

The deCODE team identified the SNPs through a genome-wide analysis of more than 300,000 SNPs in approximately 20,000 participants in the company's gene discovery programs. The SNPs, referred to as rs3796619 and rs1670533, are within the RNF212 gene, and are estimated to account for approximately 22% of paternal variability in recombination and 6.5% of maternal variability . Little is known about RNF212, though it is a mammalian homolog of a gene called ZHP-3 known to be crucial for the success of recombination in other organisms. The paper, entitled 'Sequence Variants in the RNF212 Gene Associate with Genomewide Recombination Rate,' is published today in the online edition of *Science*.

deCODE has made a number of breakthrough discoveries in the understanding of recombination, fertility and human evolution. In 2002, deCODE published the most detailed recombination map to date of the genome, demonstrating that there are hotspots and coldspots for recombination in all chromosomes, and that these are very different in women and men. This map provided a template for completing the final assembly of the sequence of the human genome.

deCODE scientists then showed that recombination rate varies between families and between women; that recombination rate increases with the age of the mother; and that higher recombination rate correlates with fertility, indicating that evolution appears to place a premium on the generation of human diversity. In 2005, deCODE identified a genetic variant that correlates with higher recombination rate, the first genetic variant ever demonstrated to be under positive evolutionary selection in human populations in real time.

Source: deCODE genetics