

# Genomic archeology reveals early evolution of sex chromosomes

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A team from Uppsala University, Uppsala, Sweden, is using genomics to shed light on the early evolutionary history of sex chromosomes. The research is published in the April 2011 *Eukaryotic Cell*.

Among other things, the [genome](#) is a place where the distant past can be investigated. Researchers have used it most notably to trace the relationships among species far more accurately than can be done with conventional methods.

[Sex chromosomes](#) in animals are so ancient—in the hundreds of millions of years old—that they retain few traces of the historical events that drove their evolution. But the researchers had found in earlier studies that the mating type chromosomes in the self-fertilizing fungus, *Neurospora tetrasperma*, which are analogous to X and Y in sexually reproducing organisms, have a region of suppressed recombination that is roughly as recent as the split between chimpanzees and hominins—less than six million years old.

Suppressed recombination preserves the genomic landscape, because normally, chromosomes recombine during mating, which shuffles the genes like a deck of cards. But suppressed recombination also interferes with natural selection, by forcing genes to be selected or deselected in packages, like the packages of options on new cars that force you to buy the navigation system, the satellite radio, and the MP3 system if you want the side curtain airbags.

The Uppsala researchers' major discovery is that many preferred codons disappeared from regions of the mating type chromosomes where recombination was suppressed. Codons are the “words” of the genetic code. Different codons code for each of the 20 amino acids used in living systems. They code for amino acids, which are the building blocks of proteins, the molecules that form both most of the structure, and most of the machinery cells. Like words in human language, codons often have synonyms. But “Many organisms studied to date preferentially use a specific set of preferred codons which are believed to promote efficient and accurate protein synthesis,” says corresponding author Hanna Johannesson. Thus, they are known as “preferred codons.”

The suppressed recombination the researchers had found earlier in *N. tetrasperma* is accompanied by the loss of these preferred codons.

Beyond this, “Our study furthers the understanding of factors driving mutational changes in genomes, which is a key issue in medical and natural science,” says Johannesson. “For example, the onset of mutations, and the ability, or inability of organisms to eliminate them from their genome underlie key processes such as the onset of diseases in animals, and the rate of species extinctions. Our study advances the understanding of when and how young regions of suppressed recombination in sex regulating [chromosomes](#) accumulate mutations, and why evolution may fail to remove these harmful changes in an efficient manner.”

**More information:** C. A. Whittle, et al., 2011. Degeneration in Codon Usage within the Region of Suppressed Recombination in the Mating-Type Chromosomes of *Neurospora tetrasperma*. *Eukaryotic Cell*. 10: 594-603

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