

# New insights into evolution: Why genes appear to move around

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Scientists at Uppsala University have proposed an addition to the theory of evolution that can explain how and why genes move on chromosomes. The hypothesis, called the SNAP Hypothesis, is presented in the scientific journal *PLOS Genetics*.

Life originated on Earth almost 4 billion years ago and diversified into a vast array of species. How did this diversification occur? The Theory of Evolution, together with the discovery of DNA and how it replicates, provide an answer and a mechanism. Mutations in DNA occur from generation to generation, and can be selected if they help individuals to adapt better to their environment. Over time, this has led to the separation of organisms into the different species that now inhabit all ecosystems.

Current theory holds that evolution involves mistakes made when replicating a gene. This explains how genes can mutate over time and acquire new functions. However, a mystery in biology is that the relative locations of genes on [chromosomes](#) also change over time. This is obvious in bacteria, as different species often have the same genes in very different relative locations. Since the [origin of life](#), genes have apparently

been changing location. The questions are, how and why do genes move their relative locations?

Now, scientists at Uppsala University have proposed an addition to the [theory of evolution](#) that can explain how and why genes move on chromosomes. The hypothesis, called the SNAP [hypothesis](#), is based on the observation that tandem duplications of sections of chromosome occur very frequently in bacteria (more than 1 million times more frequently than most mutations). These duplications are lost spontaneously unless they are selected. Selection to maintain a duplication can occur whenever bacteria find themselves in a sub-optimal environment, where having two copies of a particular gene could increase fitness (for example, if the duplicated region includes a gene that increases [growth rate](#) on a poor diet).

Duplications typically contain hundreds of genes, even if only one is selected. The scientists Gerrit Brandis and Diarmaid Hughes argue that mutations can quickly accumulate in the hundreds of non-selected genes, including genes that are normally essential when there is only a single copy in the chromosome. Once two different essential genes are inactivated, one in each copy of the duplication, the duplication can no longer be lost. From this point on, the bacteria will have many genes unnecessarily duplicated, and [mutations](#) to inactivate or delete them will be positively selected because they increase fitness.

Over time, all of the unnecessary duplicated genes may be lost by mutation, but this will happen randomly in each copy of the duplication. By this process of random loss of unnecessary duplicated genes in each copy of the duplication, the relative order of the remaining [genes](#) can be completely changed. The SNAP process can rearrange gene order very rapidly and it may contribute to separating different species.

**More information:** Brandis G, Hughes D. The SNAP hypothesis: Chromosomal rearrangements could emerge from positive Selection during Niche Adaptation. *PLOS Genet* 16(3): e1008615.  
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