Genes without templates: Many genes are completely new inventions and not just modified copies of old genes

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(Phys.org) —It is easier to copy something than to develop something new - a principle that was long believed to also apply to the evolution of genes. According to this, evolution copies existing genes and then adapts the copies to new tasks. However, scientists from the Max Planck Institute for Evolutionary Biology in Plön have now revealed that new genes often form from scratch. Their analyses of genes from mice, humans and fish have shown that new genes are shorter than old ones and simpler in structure. These and other differences between young and old genes indicate that completely new genes can also form from previously unread regions of the genome. Moreover, the new genes often use existing regulatory elements from other genes before they create their own.

When scientists decoded the first genes, they made a surprising discovery: similar variants of many genes are found even in very different organisms. This finding can be explained by the fact that evolution uses existing genes and adapts them to varying degrees for new tasks. The copying of genes plays an important role here. Copies are made of a gene and incorporated into the genome. Evolution can then experiment with these copies, while the original can continue to fulfil its function in its unaltered form. Completely new genes are very rare events in this model.

Rafik Neme and Diethard Tautz from the Max Planck Institute for

Evolutionary Biology have now refuted this idea. Based on initial indications of the existence of completely new individual genes, they analysed over 20,000 mouse genes and traced their origins. According to their findings, genes that arose later in evolution are often shorter than those that have been in existence longer. Moreover, younger genes have fewer exons and fewer protein domains. This finding contradicts the accepted view: "If new genes are copies of old ones, a correlation of this kind between length and age would not be expected. However, a young gene needs time to acquire additional exons and introns. Thus, genes become longer with time and consist of numerous exons and introns," explains Rafik Neme from the Max Planck Institute in Plön. Analyses of human, zebrafish and stickleback genes confirm the correlations discovered in the mouse.

The researchers also studied another way in which new genes can arise from existing genes: through a change in the reading frame. The genetic reading frame comprises three consecutive letters of the genetic alphabet. Each of these triplets stands for an amino acid which is translated from the genetic code. If this reading frame is shifted, new triplets arise and the genome is translated into completely different amino acids. "We found several cases, in which genes were overwritten due to such a change in the reading frame," says Neme. An example of this is the Hoxa9 gene – a gene that controls embryonic development. In rodents and primates, this gene uses such an additional alternative reading frame.

According to the findings of the Plön-based researchers, around 60 percent of genes originate from our unicellular ancestors from the early phase of evolution. Large numbers of new genes were added in particular during the advent of fundamental evolutionary innovations: for example, the transition from unicellular to multicellular organisms and the emergence of vertebrates. A particularly high number of new genes also formed after the splitting of the mouse from other rodents.

Interestingly, the scientists only found a few locations on the chromosomes in which newly formed genes accumulate. In fact, they are relatively evenly distributed across the entire genome. One of the few exceptions is a cluster of genes on chromosome 14 which control the activity of neurons, among other things.

New genes thus frequently arise from scratch in the course of evolution. They form in the gene-free sections of the genome, between the old genes. This often necessitates only minimal changes. "For example, genes need elements known as promoters which control their activity. It appears that new genes can appropriate promoters belonging to other genes and use them for their own purposes," explains Diethard Tautz, Head of the Department of Evolutionary Genetics at the Max Planck Institute for Evolutionary Biology.

More information: Neme, R. and Tautz, D. Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution, *BMC Genomics* 2013, 14:117. doi:10.1186/1471-2164-14-117

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