

Alien Genes in Our Genome!!!



Have you ever heard of Horizontal Gene Transfer (HGT)? In essence, the idea is that genes and DNA can be transferred between species in the same environment.^[1] It is well known process for the evolution for unicellular organisms like bacteria in resistance to antibiotics;^[2] nematode worms who have acquired genes from microorganisms and plants; some beetles that gained bacterial genes to produce enzymes for digesting coffee berries and the genome of wasps was found to contain not just DNA from their own species, but also from microbes that live in their guts.

Now a days, the idea that HGT occurs in more complex animals, such as humans, rather than them solely gaining genes directly from ancestors, has been a serious matter of debate and discussion.^[3] If confirmed, this finding would significantly impact theories about the underlying mechanisms of evolution. Traditionally, it was believed that genes were inherited solely from parents, but the process of DNA evolution could prove far more complex than once believed. Most, if not all, animals may have evolved in part due to this transfer of foreign genes, researchers believe.

Well known author Crisp et al^[4] from the University of Cambridge, UK, said: "This is the first study to show how widely horizontal gene transfer (HGT) occurs in animals, including humans, giving rise to tens or hundreds of active 'foreign' genes. Surprisingly, far from being a rare occurrence, it appears that HGT has contributed to the evolution of many, perhaps all, animals and that the process is ongoing, meaning that we may need to re-evaluate how we think about evolution."

The researchers studied the genomes of 12 species of *Drosophila* or fruit fly, four species of nematode worm, and 10 species of primate, including humans. They calculated how well each of their genes aligns to similar genes in other species to estimate how likely they were to be foreign in origin. By comparing with other groups of species, they were able to estimate how long ago the genes were likely to have been acquired.^[4]

It was a matter of surprise that a number of genes, including the ABO blood group gene, were confirmed as having been acquired by vertebrates

through HGT. The majority of the other genes were related to enzymes involved in metabolism.

In humans, 17 previously-reported genes acquired from HGT were confirmed, and 128 additional foreign genes were identified in the human genome that has not previously been reported.^[4] Some of those genes were involved in lipid metabolism, including the breakdown of fatty acids and the formation of glycolipids.^[4] Others were involved in immune responses, including the inflammatory response, immune cell signalling, and antimicrobial responses, while further gene categories include amino-acid metabolism, protein modification and antioxidant activities.^[4]

The team were able to identify the likely class of organisms the transferred genes came from. Bacteria and Protists, another class of microorganisms, were the most common donors in all species studied.^[4] They also identified HGT from viruses, which was responsible for up to 50 more foreign genes in primates.^[4] Some genes were identified as having originated from fungi.^[4] This explains why some previous studies, which only focused on bacteria as the source of HGT, originally rejected the idea that these genes were 'foreign' in origin. The majority of HGT in primates was found to be ancient, occurring sometime between the common ancestor of Chordata and the common ancestor of the primates.

The authors say that their analysis probably underestimates the true extent of HGT in animals and that direct HGT between complex multicellular organisms is also plausible, and already known in some host-parasite relationships.^[4] The study also has potential impacts on genome sequencing more generally. Genome projects frequently remove bacterial sequences from results on the assumption that they are contamination. While screening for contamination is necessary, the potential for bacterial sequences being a genuine part of an animal's genome originating from HGT should not be ignored, say the authors.

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