

Horizontal Gene Transfer of Protein Domain Architectures

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Abstract: Horizontal gene transfer (HGT) is the process whereby nucleic acids are transmitted from the genome of one species to another without inheritance by descent (i.e. parent to child). Some people believe that there is no prokaryotic tree of life, but in fact a thicket of shared genetic material. It is therefore extremely important to understand HGT, as it is so divergent from assumptions made in some phylogenetic analysis, such as a direct ancestry of homologous proteins. Previous studies have focused on trying to predict precisely which genes have been horizontally transferred and where, based on multiple sequence alignments and searches for a 'footprint' or biochemical signal peculiar to the parent genome. This is very difficult and the signal is quickly lost with evolutionary time. We propose avoiding to attempt prediction of every horizontal transfer event, but to take a global view. We look for proteins comprised of sets of structural-domains (domain architectures, as identified in the SUPERFAMILY database) that show disparity in their deletion rates across the tree of life, requiring an overwhelmingly improbable realisation of events in order for their current distribution in observed genomes. This does not provide concrete identification of individual HGT events, but creates an enriched set of possible contenders, acting as an indicator towards HGT across all organisms. This allows us to make advances towards answering some key questions:

1. Do prokaryotes have an underlying Darwinian tree of life?
2. Is horizontal gene transfer a significant factor in eukaryotic organisms?

Our research suggest an upper bound of 25% for the percentage of domain architectures in bacteria involved in HGT, suggesting that bacteria do indeed possess an underlying Darwinian tree. Furthermore, HGT does not appear to have been a significant contributor to the eukaryote repertoire.

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