



Comprehensive Study on Phenotypic Convergence in Genome Sequences

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DESCRIPTION

A central goal of modern biology is to distinguish between non-functional genetic noise and phenotypically significant changes. At the molecular level, evolutionary processes are largely neutral and stochastic, but natural selection can limit the evolutionary pathways available to the organism. If similar environmental conditions reoccur in divergent lineages, the adaptive response may be similar as well, leading to convergence, or the emergence of similar features in distantly related organisms. Various examples throughout the tree of life demonstrate the prevalence of phenotypic convergence, such as the camera eyes of vertebrates and cephalopods, powered flight of birds and bats, and trap leaves of distantly related carnivorous plants. Because the emergence of such complex traits by neutral evolution is extremely unlikely, phenotypic convergence is regarded as strong evidence for natural selection.

Phenotypic convergence is inextricably linked to molecular events and frequently coincides with detectably elevated levels of convergent molecular changes in gene regulation, gene sequences, gene repertoires, and other biological organization hierarchies. Genome sequences are becoming more widely available for diverse lineages across the entire tree of life, allowing for large-scale exploration of macro evolutionary genotype-phenotype associations. However, because many molecular changes in nature are nearly neutral (that is, they have almost no effect on fitness) and essentially non-functional, false positive convergence in the form of stochastic, non-adaptive, convergent events is especially problematic when conducting a genome-scale search. Furthermore, methodological biases can cause false positives.

A major source of bias occurs in molecular convergence inference because such inference is sensitive to the topology of the phylogenetic tree on which substitution events are placed, whereas alternative methods that do not place substitutions on phylogenetic trees suffer from even higher rates of false positives. Topological mis inference due to technical errors, insufficient data, or biological factors such as introgression, Horizontal Gene Transfer (HGT), paralogy, incomplete lineage sorting, and

within-locus recombination can all produce significant amounts of false convergence signals even when adaptive convergence did not occur.

Importantly, topological errors cause false convergence events that affect both non-synonymous and synonymous substitutions. Positive selection on synonymous substitutions is negligible or not prevalent, so truly adaptive convergence should occur almost exclusively in non-synonymous substitutions (amino acid-changing substitutions). As a result, synonymous convergence may be a reliable reference for estimating the rate of expected non-synonymous convergence due to phylogenetic inference error.

Although it is widely accepted that phenotypes are associated with genotypes, the genetic basis for specific convergent evolved phenotypes may result from distinct, non-convergent genetic changes. These specific cases may occur occasionally as a result of convergent mechanisms, such as the use of similar but not identical amino acids and the use of similar changes at adjacent residues in the protein structure. The accumulation of knowledge about which mutations are repeatedly selected during convergent evolution and which are not may provide insight into the evolvability and constraints that govern organism diversification.

While some evolutionary innovations are unique, many traits evolved in a convergent fashion. Endothermy, hibernation, burrowing, diving, venom injection, electrogenic organs, eusociality, anhydrobiosis, bioluminescence, bio mineralization, plant parasitism, mycoheterotrophy, and multicellularity are all fascinating examples not mentioned above.

Observing similar phenotypes in multiple species in the past led to the theory of evolution by natural selection. The study of protein sequences from various species led to the development of the nearly neutral theory of molecular evolution. Similarly, cross-species genotype-phenotype associations illuminated by molecular convergence analysis, combined with experimental evaluation of mutational effects may lead to new conceptual frameworks on the molecular constraints and adaptive changes that drive phenotypic change among species.

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Semantides, or informational macromolecules, play a unique role in determining the properties of living matter from three perspectives that differ in the magnitude of time required for the processes involved: short-timed biochemical reactions,

medium-timed ontogenetic events, and long-timed evolutionary events. Although the slower processes should be broken down into linked faster processes, if the slower processes are lost, the links between the component faster processes are also lost.