Modeling the Emergence of Epistatic Gene Combinations as a Phenotypic Function of Evolution

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Empirical evidence demonstrates that an organism's phenotypes are often based on multiple interdependent genes, rather than a single gene. When the expression of a phenotype is predicated on a combination of genes, the relationship among the genes is said to be epistatic. While epistasis is well documented, little is known about the dynamics underlying its emergence and evolution. Understanding how natural selection promotes genetic interaction is key to unlocking the mysteries surrounding the evolution of complex phenotypes and how differentiation provides impetus to speciation. This project uses a custom C software program to simulate the evolution of a simple haploid species. To model the progression of epistasis, the program must select and optimize from among patterns and degrees of genetic interdependency. A modified version of Kauffman's NK model is used as the core algorithm, where N represents the number of loci composing the genome of an artificial species, and K the connectivity among loci. Because Kauffman's NK model uses a fixed value K, adjustments are made to allow for a variable K such that natural selection can evolve to an optimum level of genetic interdependency. The results of this project show increasing genetic interdependence over time, implying an evolutionary bias towards greater epistatic complexity as organisms possessing highly connected genomes overcome less connected genomes. An arithmetic basis for major evolutionary jumps is proposed. Finally, the pronounced fitness gradient between a radically differentiated organism and its genetic heritage is offered as a mechanism for speciation.

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