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Commentary

Origin of Genetic Variation about the Evolution of Life

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DESCRIPTION

Deoxyribonucleic acid (DNA), the genetic material, contains information about the evolution of life. DNA sequences can be used to infer organism relationships as well as the times of divergence. DNA sequences are used by anthropological geneticists to infer the evolutionary history of humans and their primate relatives. We go over the fundamental methodology used to infer these relationships. The anthropological genetic evidence for modern human origins is then examined. We conclude that modern humans evolved recently in Africa and then colonized the rest of the world within the last 50,000 years, largely replacing previous human groups. Modern humans most likely exchanged genes with Neanderthals before or during their exodus from Africa. From 1930 to 1950, researchers in genetics, zoology, botany, and paleontology joined Darwin's theory of evolution by natural selection with Mendelian genetics to form the modern theory of evolutionary change. They demonstrated that this formulation accurately described the variation and diversity of both living and extinct animals and plants, and they explained why competing theories, such as neo-Lamarckism and simple mutationism, were insufficient or simply false. The modem theory can be summarized in its simplest form as follows. Changes in the genetic constitution of a population of organisms or a group of populations of a species constitute elementary evolutionary change.

Changes in one or more phenotypic characteristics may result from these genetic changes. Genetic change is based on variation caused by DNA sequence mutation and/or recombination. The most basic evolutionary process is an increase in the frequency of a mutation, or set of mutations, within a population, followed by a decrease in the frequency of previously common alleles. The frequency of previously common alleles has decreased. Random genetic drift and various forms of natural selection are the primary causes of such frequency changes. Such changes in one or more characteristics accumulate over time, resulting in potentially indefinite divergence of a lineage from the ancestral state. Different populations of a species may remain similar due to gene flow and possibly uniform selection, but they can diverge (become different from one another) due to differences in mutation, drift, and/or selection. Some of their genetic differences can create biological barriers to gene exchange, resulting in speciation: the formation of different biological species from their common ancestor. The specifics of these processes in any given population are determined by many aspects of the physical and biological environment, as well as existing features of the population resulting from its previous evolutionary history. Single base-pair alterations to insertions, deletions, and rearrangements of genetic material, as well as changes in ploidy, are all examples of mutational changes in DNA sequences (the number of sets of chromosomes). "Selectively neutral" mutations have no effect on "fitness" (survival and/or reproduction). Synonymous mutations in protein-coding regions (those that do not change the amino acid sequence) and mutations in pseudogenes and other seemingly non-functional regions are examples of these. Non-synonymous mutations in coding regions and regulatory sequence mutations are more likely to have an impact on fitness. The rate of mutation (usually on the order of 10-9 per base pair per gamete) is usually too low to significantly drive allele frequency change within a population, but it can determine the rate of DNA sequence change over time and influence the level of genetic variation within a population. It is unclear whether the availability of suitable mutations frequently constrains the rates and directions of phenotypic evolution. There is no known mechanism by which the environment can direct the mutational process in beneficial directions; mutation is therefore random in terms of utility. Measured against the range of variation, most of the many loci appear to have small effects, while a few appear to have fairly large effects. The additive Genetic Variation (VA), one component of VG, is important for natural selection evolution because it expresses the correlation between the phenotypes of parents and their offspring. This component is due to the "additive" effects of alleles, or the phenotypic effect of each allelic substitution averaged across all genetic backgrounds in which it occurs.VA is determined by the number of loci involved in the character, the evenness of allele frequencies at each locus, and the average magnitude of the phenotypic effect of different alleles. The ratio VA/Vp is referred to as a trait's "heritability" (in the narrow sense); it is only valid for the population and environment in which it was estimated, because other populations may have different allele frequencies orenvironments (which affect V1).

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