

Evolution: Selectionist View

Introductory article

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The selectionist view of molecular evolution maintains that a large fraction of molecular variation seen in natural populations is due to beneficial mutations.

Copies of the same gene in different individuals of a population usually differ at multiple positions in their deoxyribonucleic acid (DNA) sequence. Similarly, the proteins they encode differ at multiple positions in their amino acid sequence. Mutations, either point mutations or small insertions or deletions, cause these differences. Such mutations fall into three classes. The first class consists of neutral mutations, causing a change in DNA or amino acid sequence that does not affect gene function and thus leaves an organism's fitness unchanged. A second class comprises beneficial mutations, mutations that improve the function of a gene and that increase an organism's fitness. Natural selection will increase the frequency of genes carrying such mutations in a population. A third class consists of deleterious mutations, which adversely affect the function of a gene, decrease the fitness of an organism, and are thus eliminated from populations. For this reason, deleterious mutations do not contribute to observed molecular variation, even though they are usually the most frequent mutations. Neutral or beneficial mutations are thus responsible for observed molecular variation. According to the selectionist view, a sizeable fraction of this variation is due to beneficial mutations. A beneficial mutation can confer a benefit in and by itself, in which case natural selection will cause it to become fixed in the population. Variation observed due to such beneficial alleles is thus transient. It is a snapshot of a mutation's journey to fixation. Other mutations confer benefits only in combination with another allele at the same locus. In this case, natural selection will tend to keep the frequencies of both alleles high, which maximizes the number of organisms with the beneficial allele combination. Such 'balancing selection' will retain variation indefinitely.

Natural selection affects the frequency of beneficial and deleterious mutations and with it those of nearby

neutral mutations, especially in regions of low recombination. Thus, natural selection links the fates of beneficial, deleterious and neutral mutations; this link complicates identification of the causes of molecular variation.

A variety of tests can detect whether neutral or beneficial mutations are responsible for observed variation. Some of them use key predictions of the neutral theory of molecular evolution. One such prediction is that the mean and variance of the number of neutral mutations accumulated in different organismal lineages should be approximately equal. A variance greater than the mean suggests the presence of natural selection. Another test uses the rate S at which synonymous mutations, changes that do not affect a protein's amino acid sequence, accumulate in a gene over time. Such changes are likely to be neutral. The test compares this rate with the rate R of nonsynonymous changes, which affect the amino acid sequence of the encoded protein. A ratio $R:S$ of more than 1 indicates an abundance of beneficial amino acid changes preserved through natural selection.

See also

Darwin and the Idea of Natural Selection
Evolution: Neutralist View
Evolution: Views of

Further Reading

- Gillespie J (1991) *The Causes of Molecular Evolution*. New York: Oxford University Press.
Kimura M (1983) *The Neutral Theory of Molecular Evolution*. Cambridge, UK: Cambridge University Press.
Kreitman M and Akashi H (1995) Molecular evidence for natural selection. *Annual Review of Ecology and Systematics* 26: 403–422.

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