Hitchhiking Encyclopedia Article

Hitchhiking

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Hitchhiking

Hitchhiking is a term geneticists use to describe a change in allele frequencies within a population that results from a linkage of one **gene** allele to another gene allele that is at a different position (locus). Hitchhiking results in linkage disequilibria that reflects an increase in the frequency of an allele due to its association with anther gene allele that is selectively advantageous (i.e., the pressure of evolutionary **selection** results in an increase in the allele frequency within a population.

When mutations result in the introduction of new alleles into a population, there are usually strong pressures to eliminate such alleles, even if the alleles are favorable. Although new alleles can become widespread within a population, a linkage to another gene allele that is already favorable greatly enhances the spread of the new allele within a population and results in a rapidly increased allele frequency.

Eukaryotic **genome** microsatellite **DNA** exists in many forms (i.e., it is highly polymorphic). Because such microsatellites are co-dominantly inherited, they can be used as markers in tests to determine genetic similarity between organisms (e.g., relational, family, and paternity testing, etc.) or within populations, and as a measure of the closeness of differing populations or **species**. Extremely high **mutation** rates in microsatellite DNA result in the highly observed level of **polymorphism** that, in turn, reflects a high degree of genetic difference or variation. In the absence of strong selection pressures for the microsatellite DNA sequence, then whenever a particular segment of microsatellite DNA becomes linked to a particular gene allele, the microsatellite will generally face the same frequency fate as the allele to which it is linked. If for, example, the allele is subject to selection pressure that results in an increase in it's frequency within a population, the frequency of the selectively neutral microsatellite will also increase. Such microsatellite hitchhiking allows the satellite sequence to be spread widely throughout a population even though it conveys no selective advantage.

Hitchhiking is an important consideration when trying to evaluate the evolution of a genome. Population geneticists study the variation of genes and particular alleles in a population to determine hitchhiking patterns. Evidence of hitchhiking within populations can reveal the selective factors and breeding patterns of that population. Mathematical models are used to predict and to verify the existence of hitchhiking genes or microsatellites.