

Population polymorphisms and their causes

- A **Population** where the gene frequency of the most common allele is less than or equal to **0.99** (99%) is **polymorphic for a given trait** .
- Of course, this stated value is not an objective limit, but was only **determined by agreement**.
- It is most convenient to determine the degree of polymorphism using **heterozygosity**, which is defined as:

$$H = 1 - \sum_{i=1}^m x_i^2$$

where m = number of alleles of the monitored gene and x_i = gene frequency of the i th allele (C-H-W applies: $x_1 + x_2 + \dots + x_m = 1$)

or verbally as the representation of individuals in a population who are heterozygous for a particular locus.

- **Example:** In the population, the allele representation is $p=0.5$ and $q=0.5$.

$$H = 1 - \sum_{i=1}^m x_i^2 = 1 - 0,5^2 - 0,5^2 = 1 - 0,25 - 0,25 = 0,5$$

This is also the maximum that can be achieved. It is true that the larger m and the more unevenly distributed frequency x , the smaller H is.

The minimum would be for $p \rightarrow 1$ and $q \rightarrow 0$ ($H \approx 0$), where the vast majority of homozygotes would be.

- **Heterozygosity** can therefore serve us as a good measure between subpopulations of one population.

Stable polymorphism

- gene frequencies do not change;
- e.g. population in C-H-W equilibrium, or polymorphism maintained by the frequency of heterozygotes, or mutations and back mutations.

Transitive polymorphism

- In a population, when due to selection one allele is gradually replaced by another, as is the case, for example, with selection against homozygotes.

Links

Related Articles

- Castle-Hardy-Weinberg Equilibrium
- Nucleic acid polymorphisms
- Selection
- Population

Source

- ŠTEFÁNEK, Jiří. *Medicína, nemoci, studium na 1. LF UK* [online]. [cit. 11/02/2010]. <<https://www.stefajir.cz/>>.