

Population genetic load

- there are alleles in the population that **can harm** their carriers
- the effect of these harmful alleles is manifested in the reduction of the relative reproductive capacity of their carriers and from a population point of view represents the genetic burden of the population
- **genetic load** = difference of average relative fertility from relative maximum fertility:

$$L = \frac{w_{max} - w_{prum}}{w_{max}}$$

- can be maintained in the population by a balance between mutations and selection = the so called **mutation load**
- if the load is maintained by the preference of homozygotes = the so-called **segregation load**
- population burden is a linear function of the inbreeding coefficient:

$$L = a + b \cdot F$$

← **a** = load size of non-inbred population (F = 0)

← **b** = size of the burden of the inbred population

- in the genome of an individual, it is expressed using **lethal equivalents** = the number of alleles that kill their carrier in the homozygous constitution
 - the number of lethal equivalents is methodically determined on the basis of a comparison of the mortality of children from consanguineous
 - from studies: for humans: *4 lethal equivalents per individual genome*
- **deleterious equivalents** = various genetic diseases that damage their carriers, but do not show significant changes in fertility
 - it is estimated that there are about 3 – 8 damaging equivalents per individual genome

Links

Related articles

- Coefficient of relatedness
- Coefficient of inbreeding

Sources

- ŠTEFÁNEK, Jiří. *Medicína, nemoci, studium na 1. LF UK* [online]. [cit. 11. 2. 2010]. <<https://www.stefajir.cz/>>.
- PANCZAK, Aleš, et al. *Lékařská biologie a genetika (III. díl)*. 1. edition. Praha : Karolinum, 2013. 146 pp. ISBN 9788024624150.