Polygenic inheritance

In polygenic inheritance, a trait is inherited **in multiple genes,** each of which has only a small effect on the phenotype. We refer to these genes with a small effect as **minor genes.** Characteristics inherited in this way are usually measurable (e.g. height, weight, ...), which is why the synonymous name **quantitative genetics** is used.

The more complex case, when there are interactions and at the same time **the phenotype is influenced by the external environment**, we denote by the term **multifactorial inheritance**. In this type of inheritance, the polygenic system often interacts with genes of greater effect **- major genes**.

In practice, the terms "polygenic" vs. They often (but not quite correctly) use "multifactorial" inheritance without emphasizing their difference. Multifactorial heredity is simply a principle where the influence of the environmental component and the influence of the genetic component – represented by the polygenic system (as explained below) – are combined.

Genetic principle

Phenotype variance in polygenic inheritance has three main components: **genetic component** (V_G), **environmental component'** *(V_E) and* ***genotype-environment interaction'*** *(V_{GE}).*

$$V_P = V_G + V_E + V_{GE}$$

The ratio of the degree of phenotype variance dependent on genetic factors and environmental factors determines **heritability**.

$$H^2 = \frac{V_G}{V_P}$$

We further divide V_G into variance components caused by the **additive component'** (V_A), the **action of dominance between alleles'** (V_D) and **non-allelic interactions'** (V_I).

For a basic understanding of the principles of polygenic inheritance, we consider a simplified additive model that will help to understand more complex multifactorial interactions.

Additive model of polygenic inheritance

This simplified model assumes an allelic interaction called **semidominance** within the gene. This results in the fact that the value of the phenotype of the heterozygote is the average of the values of the phenotypes of the homozygotes. Furthermore, the non-allelic interaction type **additivity (cumulative)** applies between individual genes. Its consequence is that the effects of individual genes add up. As a result, only the number of dominant and recessive alleles matters, regardless of their position in the genome and their mutual configuration.

Individual alleles are marked with a subscript according to their gene affiliation. Since the phenotype is determined by the number of active alleles, individuals with the genotype $A_1A_1A_2a_2\ a_3a_3$ have the same phenotype as individuals with the genotype $A_1a_1A_2and_2A_3and_3$.

Phenotypic variances in crosses

In the following paragraphs, polygenic inheritance will be explained using the simplified example of population height, where height is inherited by three genes and all environmental influence is excluded. Genotype AAAAAA determines a height of 200 cm and genotype aaaaaa a height of 150 cm. A heterozygote in all genes (AaAaAa) will have the same height as the AAAaaa genotype for the reasons described above.

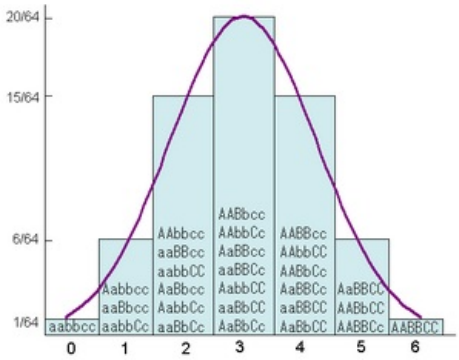
Purely polygenic inheritance is an exception in nature, the phenotype is often influenced by the external environment. Therefore, even phenotypes cannot be included in individual groups with exact size, as assumed in the following text purely according to the genome, but their height is distributed among individual height estimates based on genotype. The graph of the dependence of the number of individuals on the height will not only be columns above certain heights as below, but a curve with peaks in the given places.

Cross

When crossing a dominant and a recessive homozygote, all individuals of the F1 generation have the ***same genotype*** - half of the dominant alleles from one parent and the other half of the recessive alleles from the other parent. (They are heterozygous in all genes – AaAaAa.) Therefore, their phenotype will be a manifestation between the parental phenotypes. When crossing a high P1 population and a small P2 population, each individual of the F1 population will have the same genotype and therefore very little (or, if external influences are completely neglected) variance of the phenotype, since they each have three active alleles. The phenotypic variance of the F1 population can therefore be used to calculate heritability.

Intercross

In an F1 generation cross, the offspring can inherit all possible combinations of alleles in all three genes because both parents have both a dominant and a recessive allele for each gene. Their genotypes will therefore have 0 to 6 active alleles (aaaaaa, Aaaaaa, ..., AAAAAA). Therefore, the variance of the phenotype will also vary between the phenotypes of both parental generations (height 150–200 cm). Phenotypic manifestations in the middle will be represented most often and both extremes least often, the distribution of the phenotype will therefore be according to a **Gaussian curve**.



Parental generation P – two differently tall homozygous generations. Filial generation F1 - one pure heterozygous generation with uniform height. Filial generation F2 – Phenotype divided into hypothetical 7 groups according to genotype (see text). The distribution corresponds to a Gaussian curve.

Polygenic inheritance with threshold effect

[[File:Polygenic inheritance 4.JPG|thumb|300px|Red-marked individuals of the F2 generation of the previous interpretation with five or six active alleles (provided that the prerequisite for height is also a prerequisite for the given disease), i.e. beyond the threshold of the onset of the disease.]] Susceptibility to a genetic defect can be inherited polygenically in such a way that a certain limiting number of recessive alleles cause the disease to develop. In this case we are talking about the **threshold effect of polygenic inheritance'**. If susceptibility to the disease is inherited in three genes, the individual will be affected, for example, with 5 recessive alleles (*Aaaaaa*) and more.

Links

Related Articles

- Multifactorial inheritance
- Allela
- Heritability
- Autosomal dominant and autosomal recessive inheritance
- Nonmendelian inheritance

References

- OTOVÁ, Berta. *Lékařská biologie a genetika I. díl.* 1. edition. Karolinum, 2008. 123 pp. pp. 21–26. ISBN 978-80-246-1594-3.