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# Genetic and environmental variability of quantitative traits in poultry


**Modul no. 4: Precision Livestock Farming**

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Erasmus+ project 2021-1-SK01-KA220-HED-000032068

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## Qualitative characters

- Mendelian traits
- These are traits with a clear distinction between phenotypes, i.e. with clearly distinguishable categories (e.g. coat, presence of horns, ...).
- They are influenced by a small number of large effect genes (major genes, oligogenes).
- The influence of the external environment on a given trait is negligible.
- **P = G**
- They exhibit discrete variability.
- Examples: animal coloration, monogenic genetic disease, etc.

## Quantitative traits

- They are those traits with a continuous development of the property.
- A large number of small effect genes (minor genes, polygenes) are affected.
- The influence of the external environment is involved in different proportions for different traits.
- **P = G + E**
- They show continuous (smooth) variability.
- Examples: performance traits and their production performance, polygenic disease (mastitis) etc.



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# Phenotype value

$$P = G + E$$

P = phenotypic value of animal

G = effect of genotype

E = effect of the environment

+ random environmental effects

Typical complex traits in poultry:

- Body weight
- Abdominal fat
- Egg size
- Egg wight
- Egg thisckness
- Fertility
- Hatchability
- Feed consumption
- …

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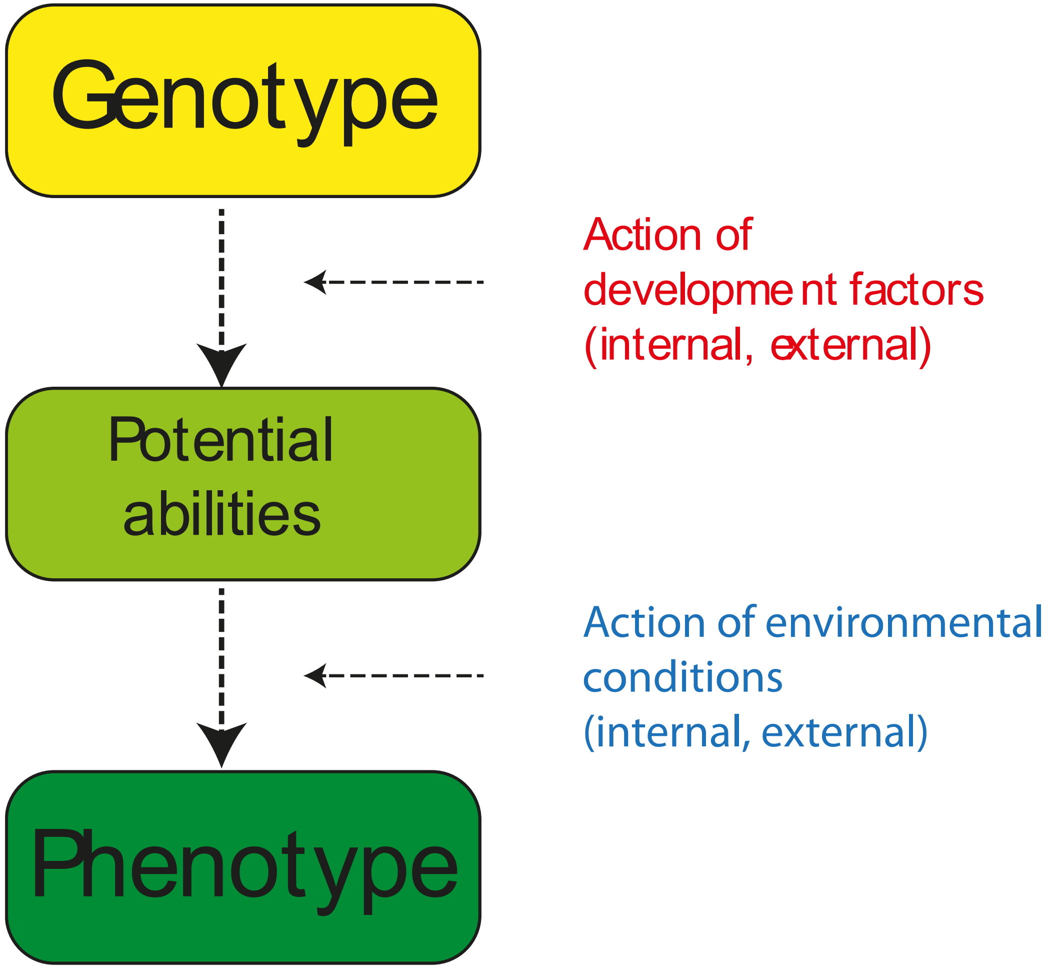
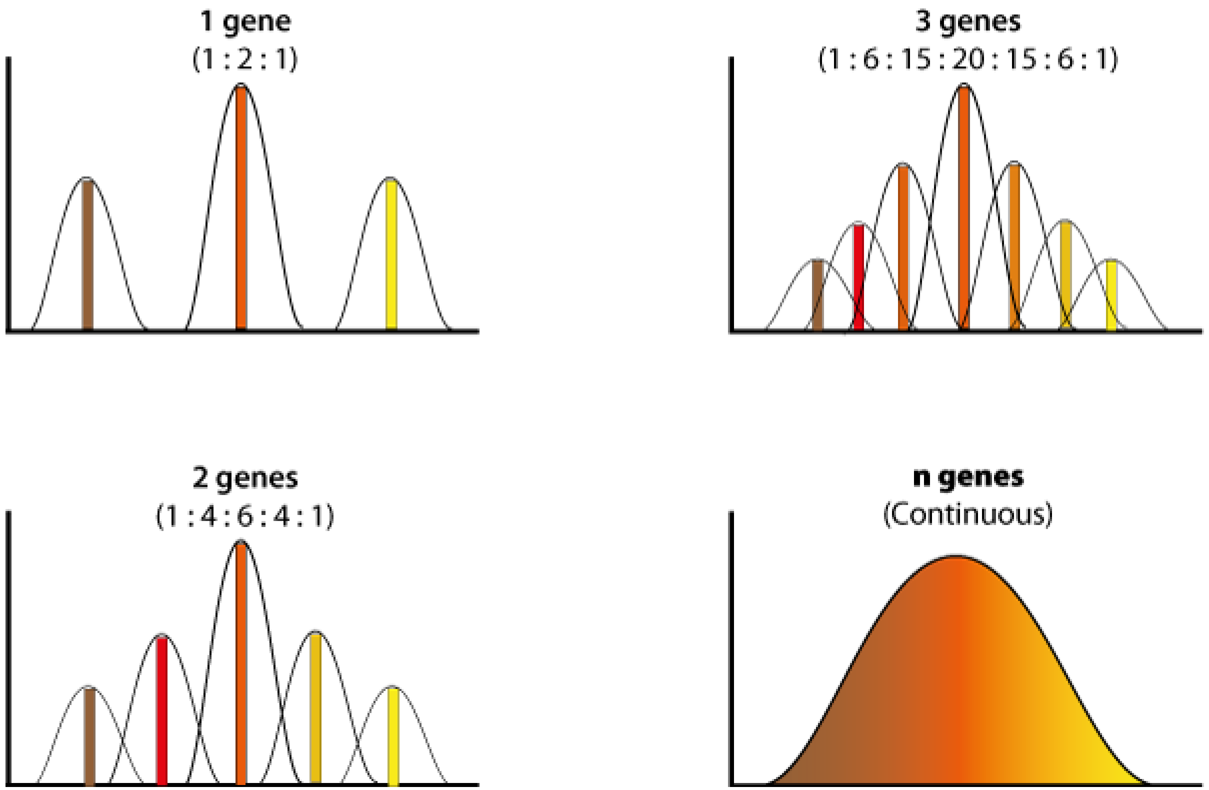
# Relationship between genotype and phenotype



# The Basis of Polygenic Genetic Variability in quantitative trait

*Crossing heterozygotes and the effect of gene number on phenotypic variability*




Mendelian genetics → Biometric genetics

Population statistical parameters (mean, variance, etc.)



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# Genetic variation

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- Genetic variation refers to the differences in DNA sequences between individuals. These differences can be due to mutations, recombination, or other genetic processes. Genetic variation is the raw material for evolution and is what allows populations to adapt to changing environments.
- Genetic variation is important in animal breeding programs because it provides the raw material for selection. By selecting animals with desirable traits and breeding them together, breeders can increase the frequency of those traits in the population. This can lead to improvements in productivity, health, and other traits that are important for animal production.

# Environmental variability

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## Non-systematic effects

- It affects each individual differently in an unknown direction and of unknown magnitude
- They cannot be corrected
- Introducing "noise" into genetic estimates and predictions
- Residual error

## Systematic effects

- Acts on a group of animals in the same direction and size
- **They can be eliminated by calculation or standardization**
- They are divided into:

  - **internal**: age, litter number, litter order, lactation order, sex, etc.

  - **external**: farm, region, stable, year, season, etc.



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# Environmental variability

- Environmental variability refers to the variation in environmental conditions that can affect the performance of animals.
- Environmental variability can have a significant impact on quantitative traits in poultry. For example, temperature and humidity can affect growth rate and feed efficiency. Other environmental factors such as lighting and stocking density can also affect the performance of poultry.
- Farmers can manage environmental variability in their flocks by providing appropriate housing and management practices. For example, farmers can use ventilation systems to regulate temperature and humidity, provide appropriate lighting conditions, and manage stocking density to reduce stress on the birds.





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# Genetic parameters

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- Most production traits in chickens are quantitative in nature (polygenic inheritance, additive gene action, environmental influence, continuous variability).
- We can use estimation of genetic and environemntal variability to calculate other genetic parameters.
- **Genetic parameters** – They are statistical parameters
  - **heritability, repeatability, genetic correlation, and phenotypic correlation**
- **Genetic parameter estimation** is a **statistical method** used to estimate the genetic parameters of traits in animals
- The estimation of genetic parameters is an important issue in animal breeding.
- Estimating additive genetic and possible non-additive genetic variances contributes to a better understanding of the genetic mechanism.
- Genetic parameters have a significant role in designing a breeding program and are required to evaluate economically important traits

# The central genetic parameters - heritability

- **Heritability** is the proportion of phenotypic variation that is due to genetic variation. It is a measure of **how much of the variation in a trait is due to genetic factors** ~ it is basically an estimate of the genetic structure (variability) in a population

$$h^2 = \frac{V_G}{V_P} = \frac{V_G}{V_G + V_E}$$

- Heritability ranges from 0 to 1
  - with 0 indicating that all variation is due to environmental factors and 1 indicating that all variation is due to genetic factors (unreal extremes!)
  - the data source is measured trait values of individuals in a population
  - Heritability is estimated by comparing the phenotypic variation in a trait to the genetic variation in that trait. This is done by comparing the phenotypic variation in a population to the expected phenotypic variation based on the genetic relationships between individuals in that population.

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| Trait in chicken | Heritability estimate |
|---|---|
| Body weight | 0.39-0.91 |
| Weight gain | 0.11-0.81 |
| Abdominal fat | 0.6-0.90 |
| Egg production | 0.11-0.44 |
| Egg size | 0.4-0.50 |
| Shell thickness | 0.25-0.60 |
| Yolk cholesterol | 0.11-0.25 |
| Fertility | 0.05 |
| Sexual maturity | 0.25-0.39 |
| Feed consumption | 0.39 |
| Feed efficiency | 0.03-0.48 |
| Fasting metabolic rate | 0.23-0.43 |



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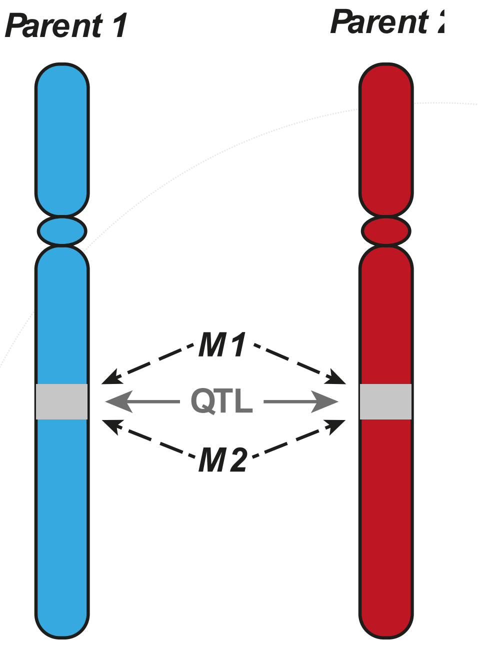
# Genetic Parameter Estimation and Whole Sequencing Analysis

- **Methods for mapping QTL** are actively used in the chicken to identify chromosomal regions contributing to variation in traits related to growth, disease resistance, egg production, behavior, and metabolic parameters.
- However, higher-resolution mapping and better knowledge of the genetic architecture underlying QTL are needed for successful application of this information into breeding programs.

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# Chicken QTLdb

**Top QTL/associations in the database**

| Traits | Number of QTL |
|---|---|
| Body weight | 3,704 |
| Feather pecking | 1,145 |
| Feed conversion ratio | 796 |
| Eggshell effective layer thickness | 784 |
| Eggshell thickness | 774 |
| Egg number | 540 |
| Average daily gain | 418 |
| Feed intake | 411 |
| Egg weight | 393 |
| Body weight gain | 380 |
| Feathering | 372 |
| Earlobe color | 328 |
| Shank length | 282 |
| Comb weight | 276 |
| Feather pigmentation | 251 |
| Abdominal fat weight | 241 |
| Breast muscle weight | 239 |
| Comb height | 199 |
| Carcass weight | 185 |

- As of Apr 25, 2023, there have been 18,411 QTL / eQTL / associations released for public access on the Chicken QTLdb. These data were curated from 386 publications and represent 372 base traits, 115 trait variants, and 39 eQTL genes.
- Chicken QTL Database (animalgenome.org)

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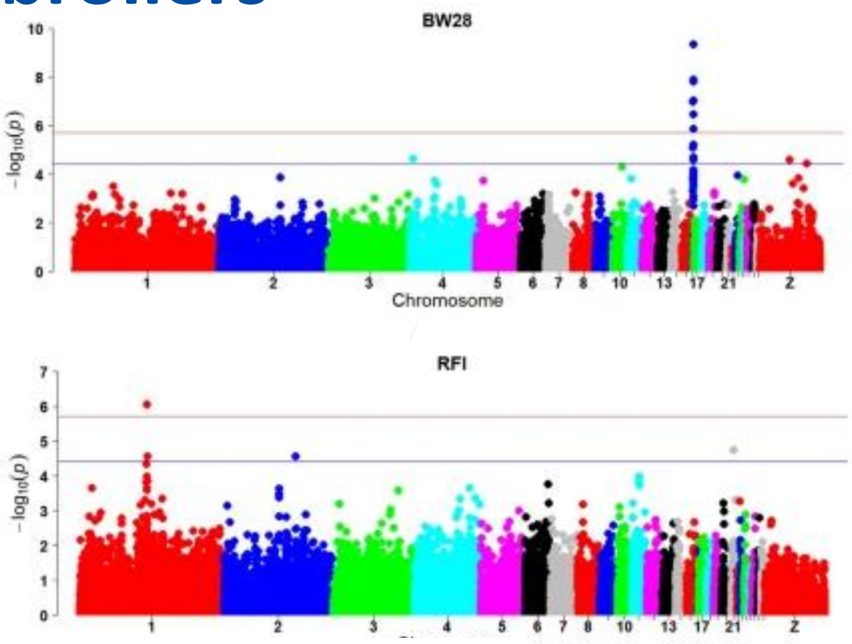
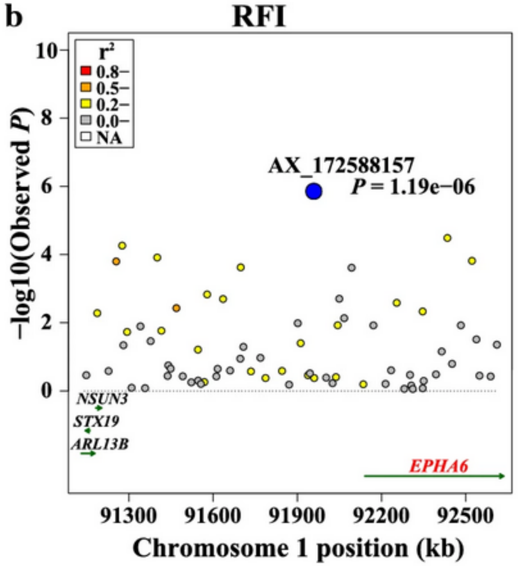
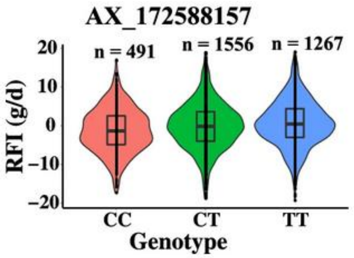
# Example of Identification of QTL regions and candidate genes for growth and feed efficiency in broilers

- estimate genetic parameters and identify QTL for feed efficiency in purebred broilers using a genome-wide association study.
- Broilers were genotyped using **55 K single nucleotide polymorphism (SNP) array**.
- **Estimates of genomic heritability** for seven growth and feed efficiency traits, including body weight at 28 days of age (BW28), BW42, average daily feed intake (ADFI), RFI, and RFI adjusted for weight of abdominal fat (RFIa), ranged from **0.12 to 0.26**.
- A region on **chromosome 16** (2.34–2.66 Mb) was associated with both BW28 and BW42, and the most significant SNP in this region accounted for 7.6% of the genetic variance of BW28.
- on **chromosome 1** (91.27–92.43 Mb) was associated with RFI and ADFI, and contains the *NSUN3* and *EPHA6* as candidate genes. The most significant SNP in this region, accounted for 4.4% of the genetic variance of RFI.
- *NSUN3*, *EPHA6*, and *AGK* were identified as the most likely candidate genes for these QTL. These genes are involved in mitochondrial function and behavioral regulation.
- These results contribute to the identification of candidate genes and variants for growth and feed efficiency in poultry.

https://doi.org/10.1186/s12711-021-00608-3



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# Thank you for your attention!

*This presentation has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no.* ***2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation - Inovácia obsahu a štruktúry študijných programov v oblasti manažmentu živočíšnych genetických a potravinových zdrojov s využitím digitalizácie"****. The European Commission support for the production of this presentation does not constitute an endorsement of the contents which reflects the views only of the authors, and the Commission cannot be held responsible for any use which may be made of the information contained therein.*

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