

INTRODUCTION TO ANIMAL BREEDING

Lecture Nr 2

Genetics of quantitative (multifactorial) traits

What is known about such traits
How they are modeled

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Nature of variation, sources of variation

Genotype and environment

Components of the genetic value

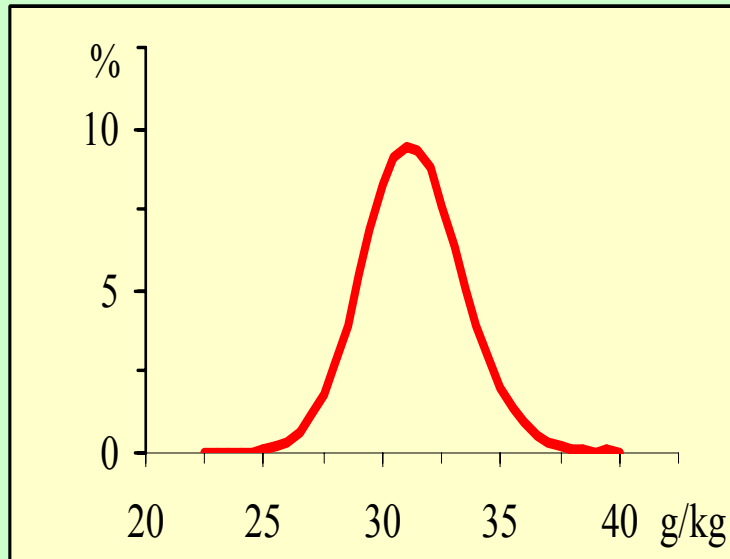
Resemblance between relatives

Summary

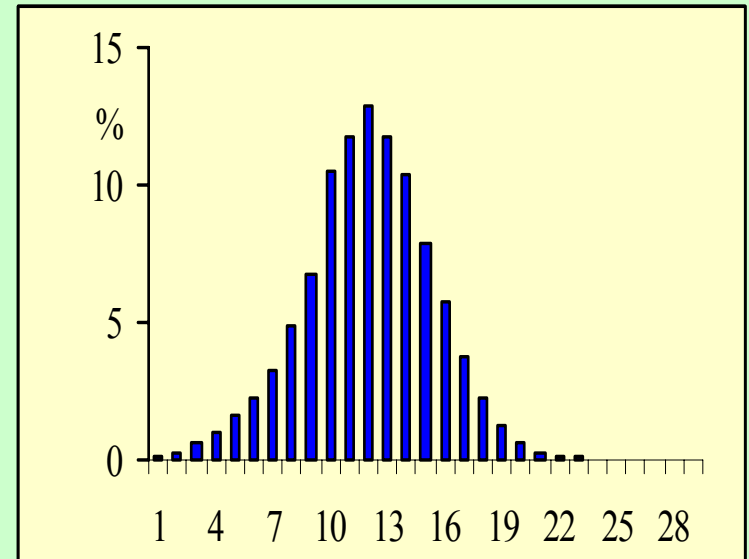


Specificities of quantitative traits

1. Continuous variation



Protein content
Dairy cows



Litter size
Sows

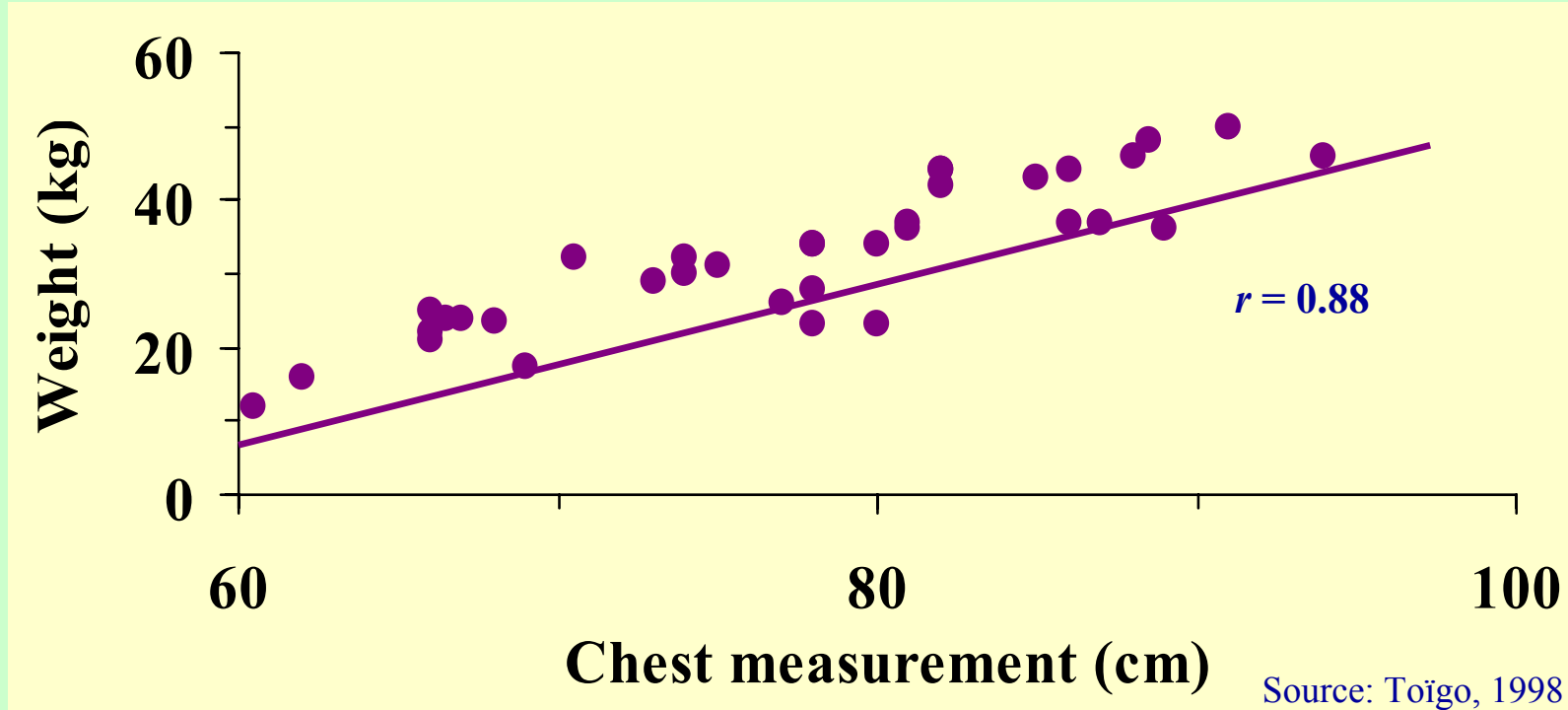
Source: French protocol of performance recording on farm



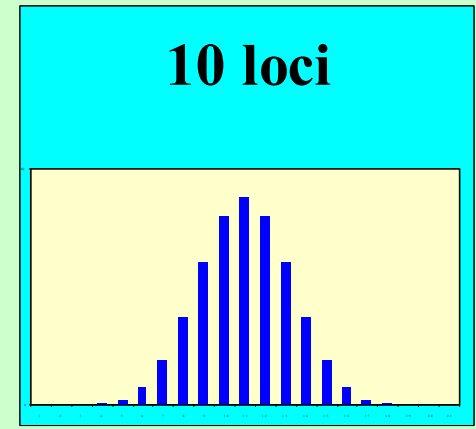
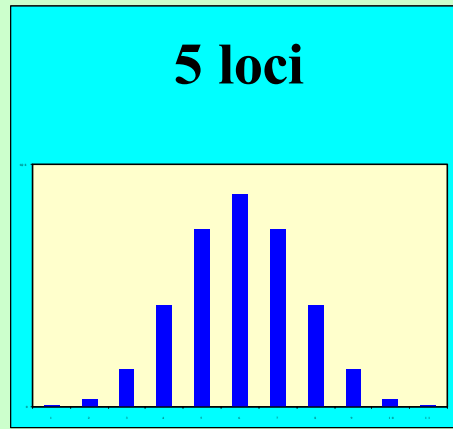
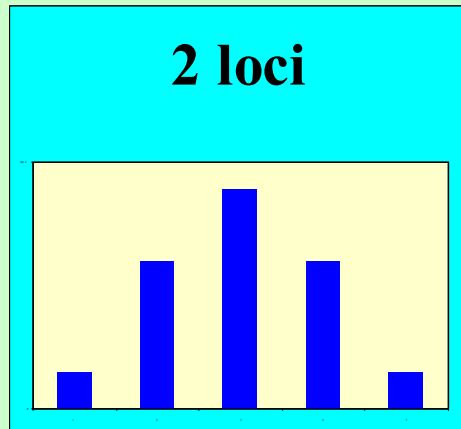
Specificities of quantitative traits

2. Correlation between traits

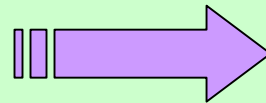
Field data from the Alps Ibex



Sources of continuity



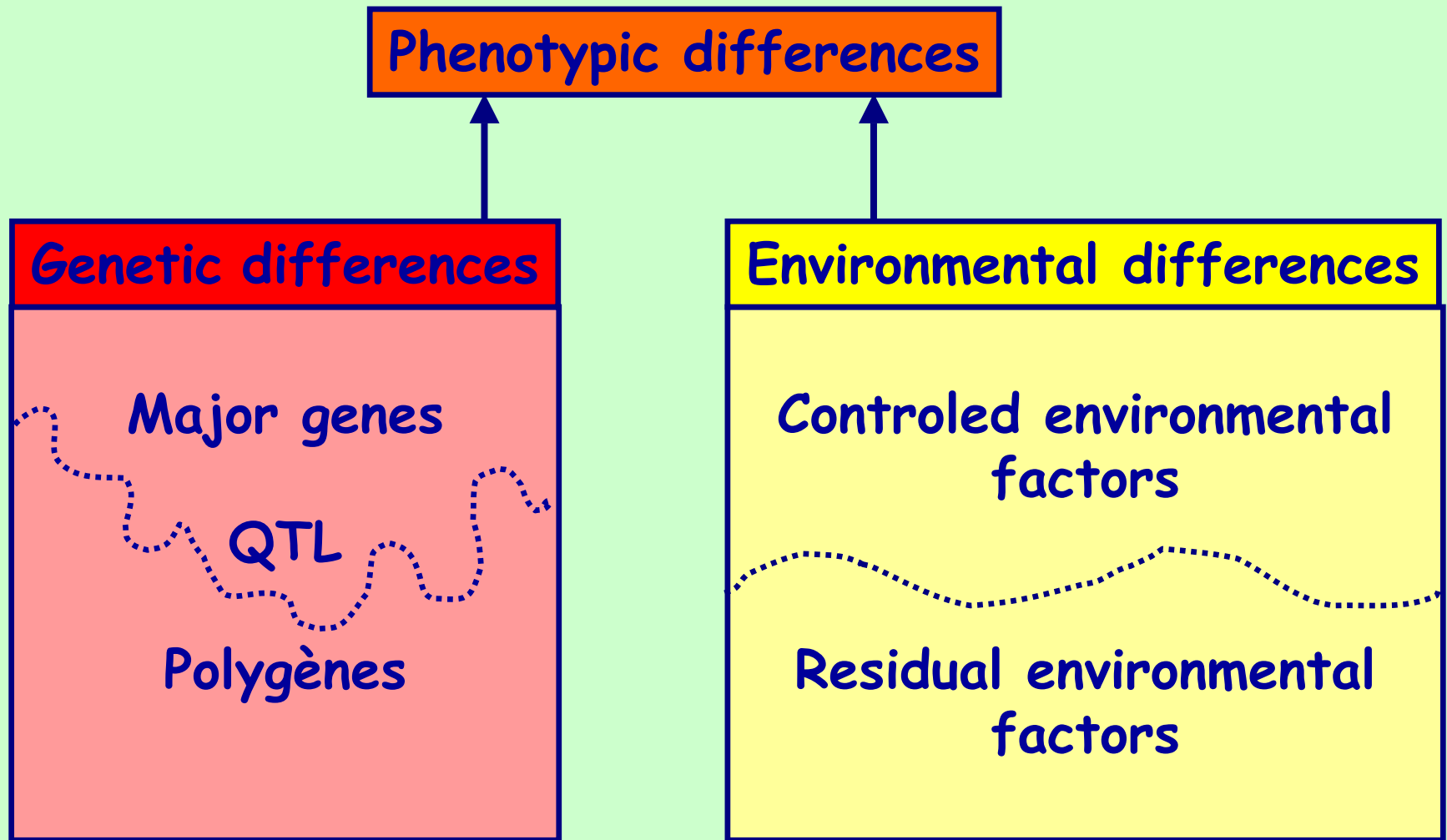
Several loci
Environmental factors



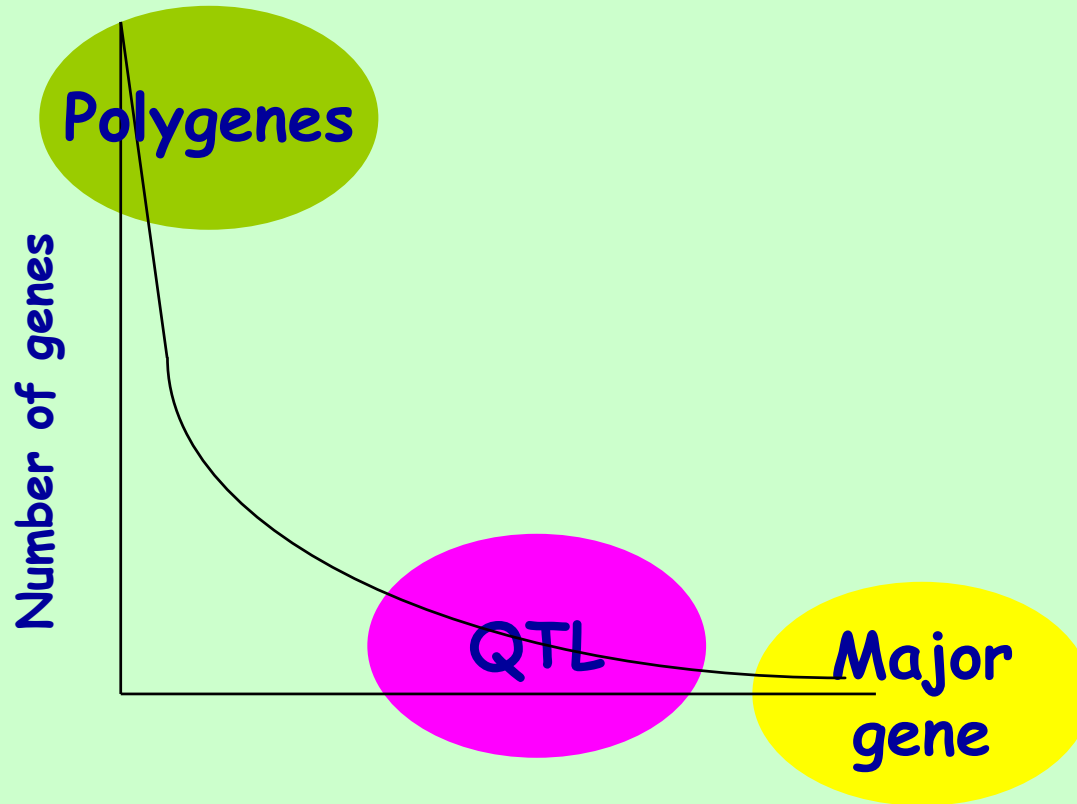
Continuity
Normal distribution
Statistical analysis



Two sources of variation



Genetic sources of variation



Quantitative effect of the gene
(proportion of variance explained by the gene)



Consequences of the number of genes

Crossing experiment with chilli



Photo: INRA - Avignon

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Characterisation of the genotype by its mean value

Photo: INRA



Not so easy to apply
with animals ...

But the general idea
remains:

Value of a genotype
= its (expected)
mean value

Example with wheat
(each variety = a single genotype)



Genotype and residual environment

Performance

$$P \sim N(\mu, \sigma_P^2)$$

If the distribution is not normal:

- Mathematical transformation
- Specific model: thresholds model for discrete traits

(total) Genetic Value

$$G = E(P|\text{genotype}) - E(P)$$

$$G \sim N(0, \sigma_G^2)$$

Deviation of P from $\mu + G$: $E \sim N(0, \sigma_E^2)$

Environnemental (residual) value

$$P = \mu + G + E$$



Means and variances

$$P = \mu + G + E$$

$$E(P) = \mu \ ; \ E(G) = 0 \ ; \ E(E) = 0$$

$$\text{var}(P) = \text{var}(G) + \text{var}(E)$$

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2$$



Takin into account a controled environmental factor

Category 1 \longrightarrow Average effect m_1
Category 2 \longrightarrow Average effect m_2
etc.

$$P = \mu + m \oplus G + E$$

The meaning of this " \oplus " is to be questionned



Consequences of the additivity between genotype and environment

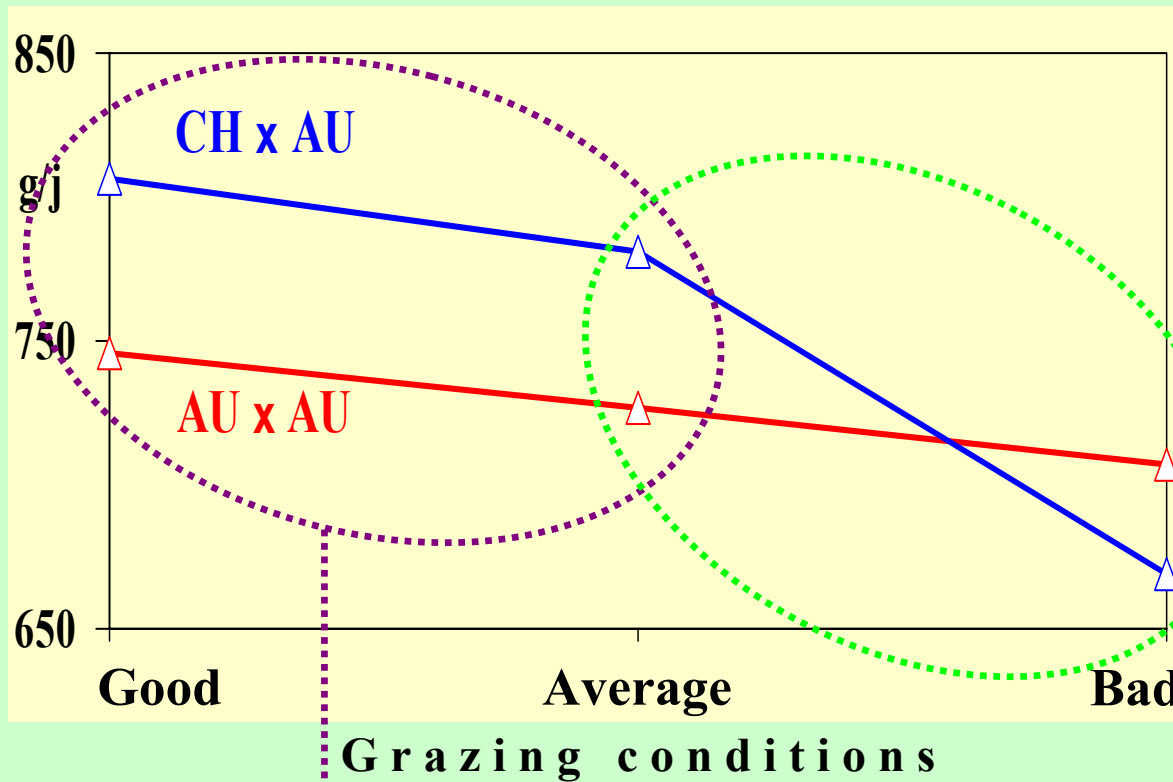
$$P = \mu + m \oplus G + E$$

- 1) The change of environment (m) modifies the performance (P) of each animal by the same quantity
- 2) The differences between genotypes (G) are the same in any environment



Genotype and environment

The example of crossbreeding in beef cattle



Daily growth (g/j)
of calves during
summer grazing
in high altitude pastures

AU x AU: Aubrac calves
CH x AU: crossbred calves
Charolais x Aubrac

Source: Vissac (1971)

Additivity Genotype + Environment

Interaction Genotype x Environment



Nature of variation, sources of variation

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Resemblance between relatives

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How to characterise an allele

The example of the naked neck gene

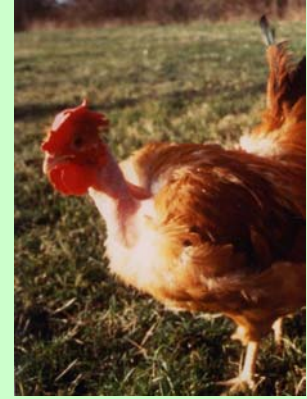


Photo: INRA

| Genotype | + + | + Na | Na Na |
|---|--------|------|-------|
| Plumage weight | normal | - - | - - - |
| Resistance to heat | = | + + | + + + |
| Average egg weight (g) under hot conditions | 46 | 52 | 55 |

Source: Mérat, 1986



How to characterise an allele

The example of the naked neck gene

In a given population, $E(P) = \mu$, according to $f(Na)$

male **Na Na** x females ?

male ?? x females ?

$$\alpha_{Na} = E(P|Na ?) - E(P)$$

Average effect of the Na allele



Components of G

For a single locus

$$G = \underbrace{\alpha_{\text{paternal gene}} + \alpha_{\text{maternal gene}}}_A + \underbrace{\delta_{\text{paternal gene} \times \text{maternal gene}}}_D$$
$$G = A + D$$

Generalisation to a large number of loci

$$G = A + D \quad A \sim \text{N}(0, \sigma_A^2) \quad D \sim \text{N}(0, \sigma_D^2)$$

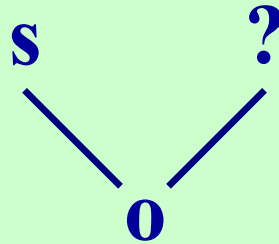
$$\text{var}(G) = \text{var}(A) + \text{var}(D)$$

$$\sigma_G^2 = \sigma_A^2 + \sigma_D^2$$



Transmission from parent to offspring

1. A single parent known



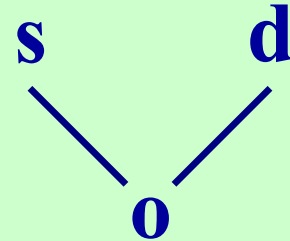
$$E(G_o | s, ?) = \frac{1}{2} A_s$$

$$\text{NB. } E(D_o | s, ?) = E(D) = 0$$



Transmission from parent to offspring

2. Both parents known



$$E(A_o | s, d) = \frac{1}{2} A_s + \frac{1}{2} A_d$$

$$E(G_o | s, d) = \underbrace{\frac{1}{2} A_s + \frac{1}{2} A_d}_{\text{Selection}} + \underbrace{E(D_o | s, d)}_{\text{Crossbreeding}}$$



Heritability: definition

$$P = \mu + G + E = \mu + A + D + E$$

$$\text{var}(P) = \text{var}(A) + \text{var}(D) + \text{var}(E)$$

$$\sigma_P^2 = \sigma_A^2 + \sigma_D^2 + \sigma_E^2$$

$$0 \leq h^2 \leq 1$$

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_D^2 + \sigma_E^2}$$



Nature of variation, sources of variation

Genotype and environment

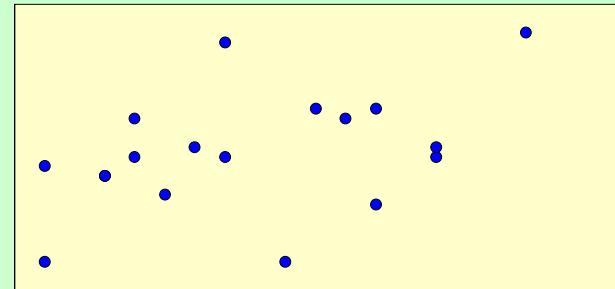
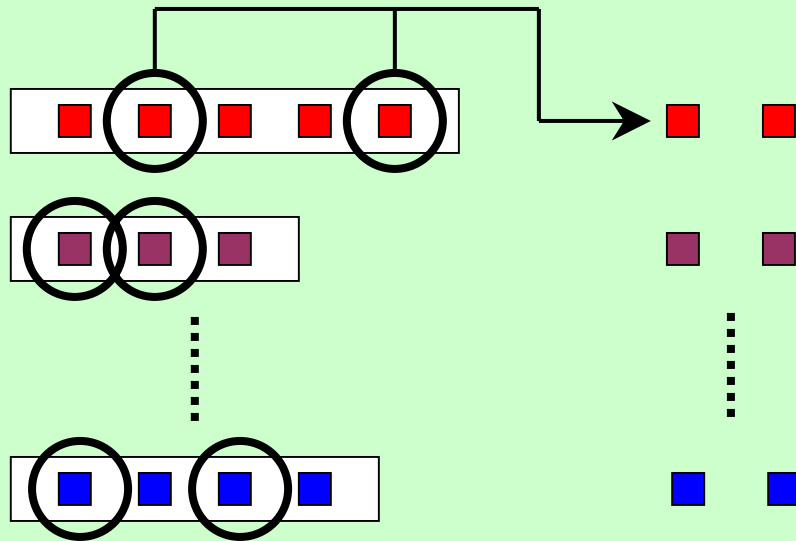
Components of the genetic value

Resemblance between relatives

Summary



Analysis of the correlation between performances of relatives



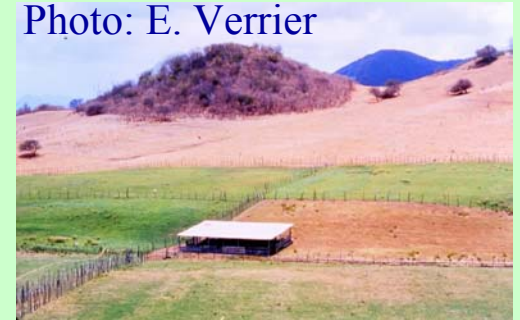
Sample of n sibs couples

The correlation between the performances of relatives depends on:

- The kind of relatives
- The trait

The two sources of resemblance between relatives

Photo: E. Verrier



Shared genes

Shared environment

Covariance between their performances

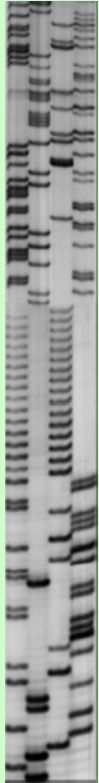
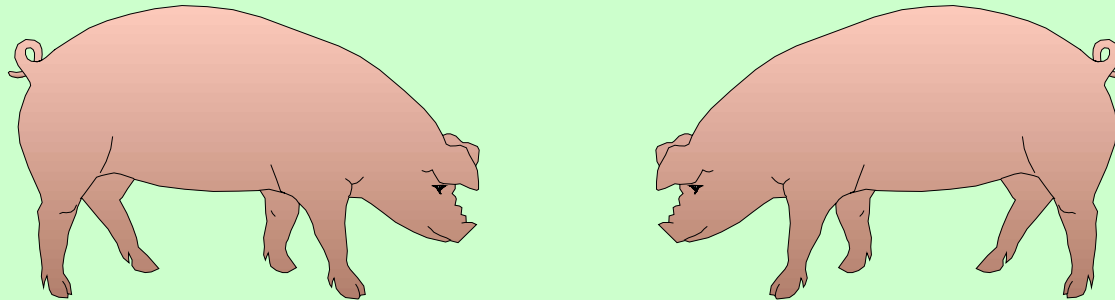
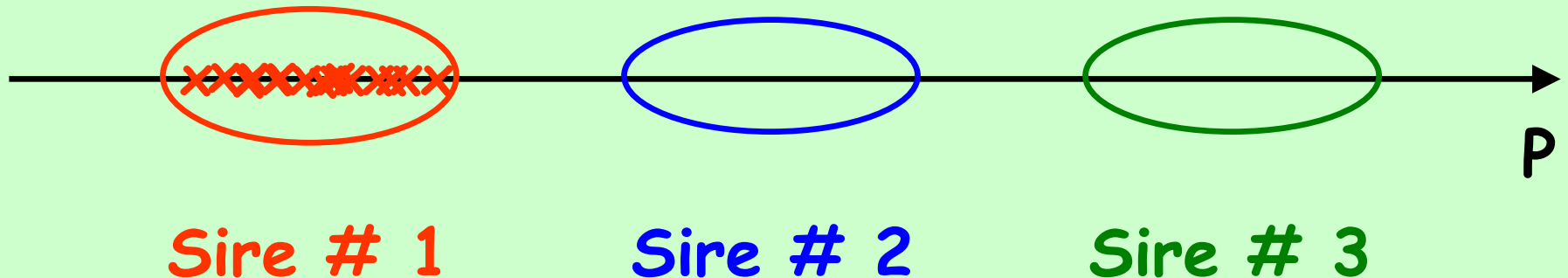


Photo: INRA



Genetic interpretation

The example of paternal half-sibs families



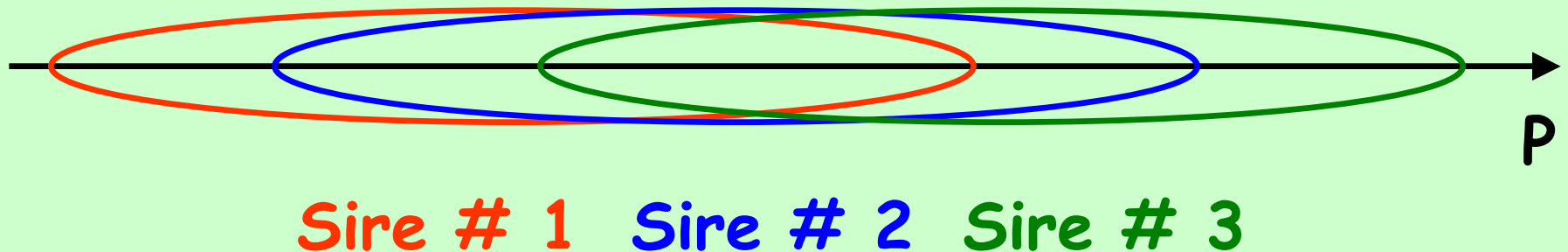
High correlation between half-sibs performances

Large differences between families
due to the effect of the different sires

→ Large genetic differences → High value of h^2

Genetic interpretation

The example of paternal half-sibs families



Little correlation between half-sibs performances

Small differences between families
due to the effect of the different sires

→ Small genetic differences → Low value of h^2



Covariance between (total) genetic values

$$G = A + D$$

$$\text{Cov}(G_i, G_j) = \text{Cov}(A_i, A_j) + \text{Cov}(D_i, D_j)$$

Dépend de la probabilité de partager, dans un locus donné

An allele

A pair of alleles

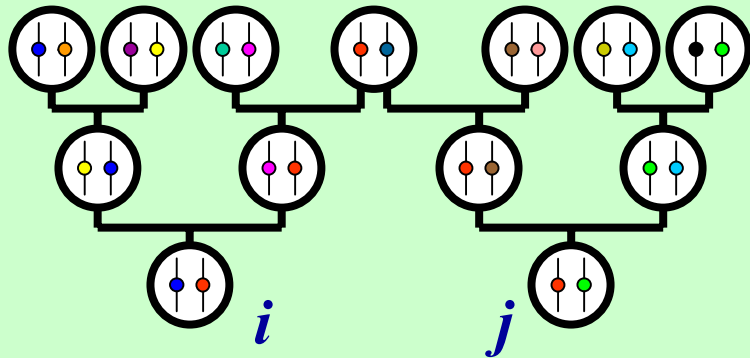
Probabilities for the genes to be identical by descent



Measurement of the kinship between individuals

The coefficient of kinship (Φ) between two animals, i et j , is defined for an autosomal neutral locus, with no mutation

Φ_{ij} = Probability that a gene drawn at random in i and a gene drawn at random in j are identical by descent, i.e. came from the Mendelian duplication of the same ancestral gene



$$\begin{aligned}\Phi_{i,j} &= 1/32 \\ &= 3.125\%\end{aligned}$$

To see details

<http://www.inapg.fr/dsa/uvf/GP/GPintro.htm>



Coefficient of kinship:

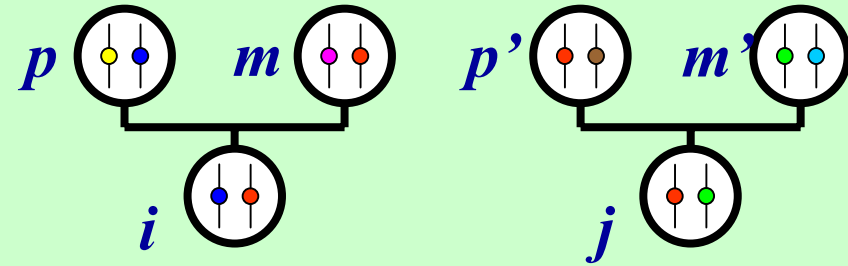
Some usual values of the

| Kind of relatives | Coefficient of kinship |
|--|-------------------------------|
| With no common ancestor | 0 % |
| With a single common grand-grand-parent | 0.8 % |
| With a single common grand-parent | 3.125 % |
| Cousins (2 common grand parents) | 6.25 % |
| Double cousins (4 common grand-parents) | 12.5 % |
| Half sibs (a single common parent) | |
| Full sibss (2 common parents) | 25 % |
| Parent-offspring | |



Covariance between the components of the genetic values of relatives

$$G = A + D$$



$$\text{cov}(A_i, A_j) = 2\Phi_{ij}\sigma_A^2$$

$$\text{cov}(D_i, D_j) = (\Phi_{pp'}\Phi_{mm'} + \Phi_{mp'}\Phi_{pm'})\sigma_D^2$$

$$\text{cov}(G_i, G_j) = \text{cov}(A_i, A_j) + \text{cov}(D_i, D_j)$$



Summary

Quantitative traits are jointly governed by

- a few known genes and an unknown number of unknown genes
- known and unknown environmental factors

Necessity of modeling the effects of these different sources of variation: $P = \mu + m + A + D + E$

A key-concept is the heritability of a trait:

$$h^2 = \text{var}(A)/\text{var}(P)$$

A key-issue is the resemblance between relatives

