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Genetic Parameters in Animal Breeding

Modul No. 3: Animal Breeding

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Definition: Genetic Parameters

- Genetic parameters are the values that define the genetic potential and heritability of traits within a population of animals.
- **Heritability** measures the proportion of the total phenotypic variation in a trait that can be attributed to genetic variation.
  - It ranges from 0 to 1.
- **Genetic correlations** quantify the degree to which genes influencing one trait also influence another trait (-1 to +1).
  - Positive genetic correlations indicate that improving one trait will also improve another.
  - Negative genetic correlations indicate a trade-off between traits, wherein improving one trait may decrease another.
- Coefficient of repeatability (r)

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Methods of estimating genetic parameters

- What is necessary to know?
  - Phenotypic values (measured performance)
  - Relationships (determined using pedigree data or genomic data)
- How do we estimate them?
  - We have to use statistical methods, especially linear models (regression analysis, analysis of variance, analysis of covariance...)
  - Estimate the value of genetic and environmental variance

$$s_P^2 = s_G^2 + s_E^2$$

$$s_P^2 = \boxed{s_A^2 + s_D^2 + s_I^2} + \boxed{s_E^2}$$

Statistical methods

- Analysis of variance (ANOVA) – means of square
  - Balanced data
  - Unbalanced data
    - Henderson´s methods (SAS, Harvey, SPSS, …)
- Likelihood methods
  - Maximum likelihood (ML)
  - restricted maximum likelihood (REML)
- Bayesian Methods
  - Monte Carlo, Gibbs Sampling

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Using family performances to estimate heritability

- High heritability
  - **low** variance in families
  - **high** variance between families

- Low heritability
  - **high** variance in families
  - **low** variance between families

Total var = var between families + var within families

Same as *cov* within families

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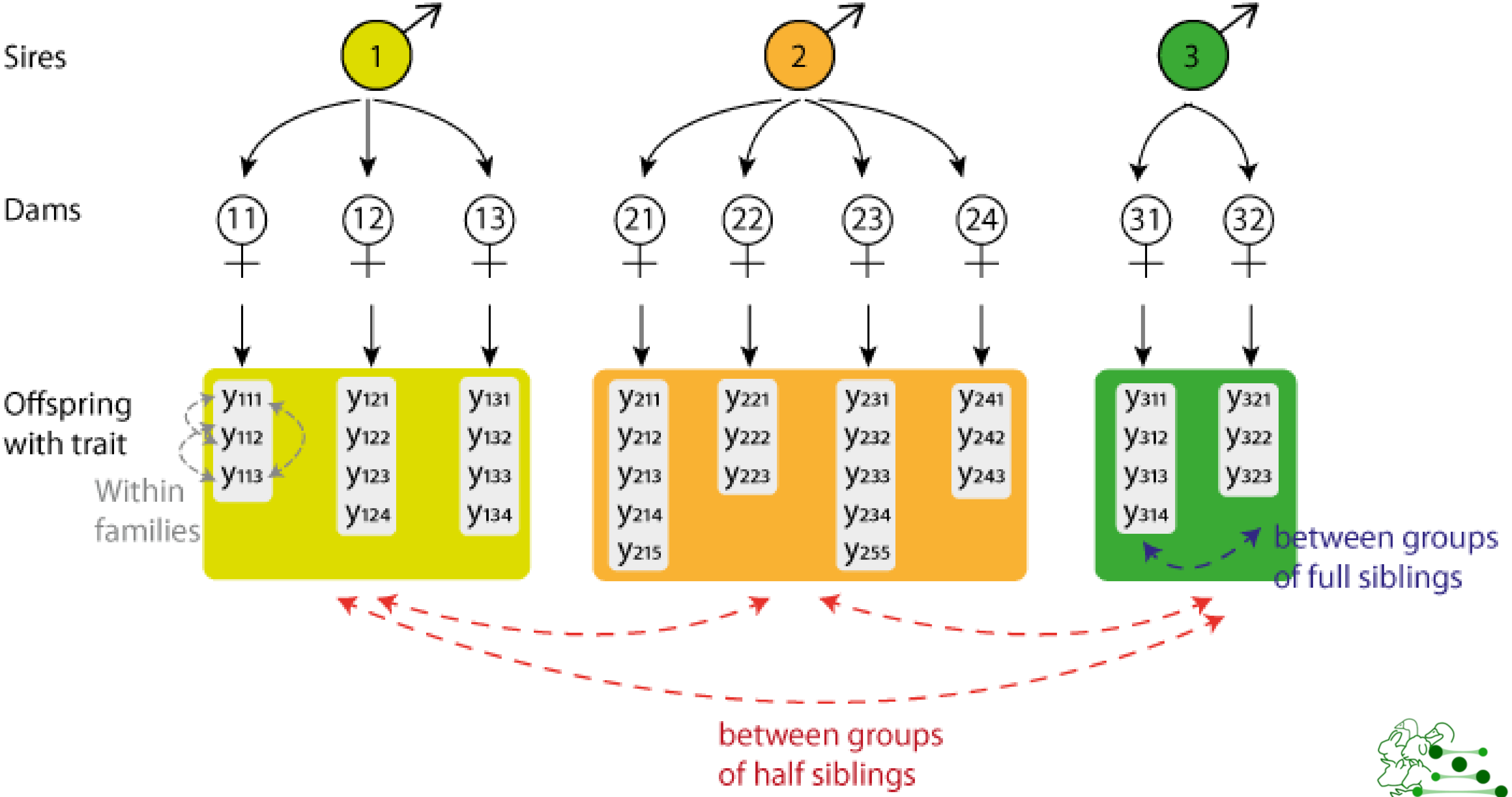
Variation between and within groups of related individuals



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Analysis of variance – ANOVA

- **Principle**:
    - Detection of important differential effect sources
    - Determine their contribution to the total variance
    - Variance is derived from the sum of squares and degrees of freedom
- Necessary to have individuals in groups with the same degree of relationship
    - Groups of half-siblings by father
    - parents - offspring
- **Covariance between** members of families or groups = component of **variance between groups**
- Decomposition of sum of squares (SS) by sources of variance (animal group) and calculation of mean square (MS)

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Estimation of h^2 in families of half-siblings

- **Variance between families of half-siblings**

  = covariation between half-siblings in groups = $\frac{1}{4} V_A$

- **Variance within families of half-siblings in groups**

  = residual variance = $V_P - \frac{1}{4} V_A = \frac{3}{4} V_A + V_E + V_D$

$$h^2 = \frac{V_A}{V_P} = \frac{4V_S}{V_P}$$

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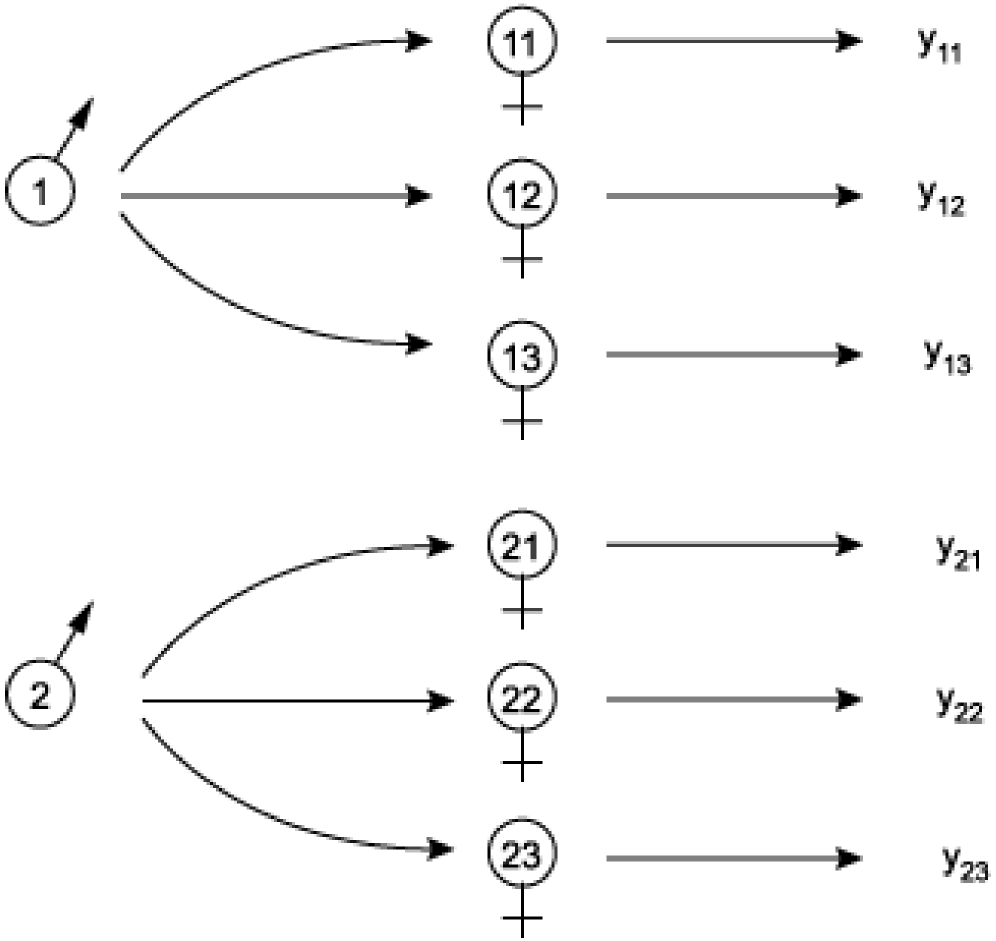
Experimental design for sire model



Variance between families of half-siblings = covariation between half-siblings in groups

$$\mathbf{cov}_{(sibs)} = \mathbf{cov}(y_{ij}, y_{ik}) =$$
$$= \sigma^2_S$$

$$4\sigma^2_S = \sigma^2_A$$

This can be estimated by ANOVA

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Sire model – 1 way ANOVA

- Estimation based on correlation of half-siblings

$$\mathbf{y_{ij} = \mu + a_i + e_{ij}}$$

$$V_S = \sigma_S^2 = \tfrac{1}{4}\sigma_A^2 \qquad \sigma_y^2 = \sigma_S^2 + \sigma_e^2$$

$$V_e = \sigma_e^2 = \tfrac{3}{4}\sigma_A^2 + \sigma_E^2$$

- the assumption that fathers and mothers are unrelated, randomly mated, without selection
- balanced design: *p* sires are mated with *n* dams ⇒ 1 offspring

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Sire model – ANOVA table

Source of variability	Df	SS	MS	E(MS)
Between families (between fathers)	**p – 1**	$SS_S = \sum_{i=1}^{p} n_i(\bar{y}_i - \bar{y})^2$	$MS_S = \frac{SS_S}{(p-1)}$	$\sigma_e^2 + n_0\sigma_g^2$
Within families (rezidual)	**n – p**	$SS_e = \sum_{i=1}^{p}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_i)^2$	$MS_e = \frac{SS_e}{(n-p)}$	σ_e^2
Total	**n – 1**	$SS_c = \sum_{i=1}^{p}\sum_{j=1}^{n_i}(y_{ij} - \bar{y})^2$	$MS_c = \frac{SS_c}{(n-1)}$	

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$$MS_e \doteq \sigma_e^2$$

$$MS_a = \sigma_e^2 + n_0\sigma_g^2 = MS_e + n_0\boxed{\sigma_g^2}$$

$$n_0 = \frac{n - \left(\sum n_i^2 / n\right)}{n-1}$$

$$\sigma_g^2 = \frac{MS_a - MS_e}{n_0}$$

Intraclass correlation coefficient

$$\rho = r_i = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

$$\boxed{h^2 = 4\rho = 4\frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} = 4\frac{\sigma_g^2}{\sigma_P^2}}$$

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Finalization of the calculation

- estimation of the coefficient of heritability
- Estimation of standard error of h^2

$$se_{h^2} = 4.s_\rho = 4.\sqrt{\frac{2.(n-1)(1-\rho)^2\left(1+(n_0-1)\rho\right)^2}{n_0(n_0-p)(p-1)}}$$

$$h^2 \pm se_{h^2}$$

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Importance of Heritability

- High heritability indicates that phenotypic variability of trait in population is largely influenced by genetic variability.
- Breeding programs can focus on traits with high heritability to achieve faster genetic progress (genetic gain).

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Conclusion

- Understanding genetic parameters is crucial for effective animal breeding.
- Heritability, genetic correlations, and advancements like GWAS and genomic selection enable the targeted improvement of traits for increased productivity and profitability in animal agriculture.

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Partners:

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Thank you for your attention!

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