

# Quantitative Genetics - Multiple Loci

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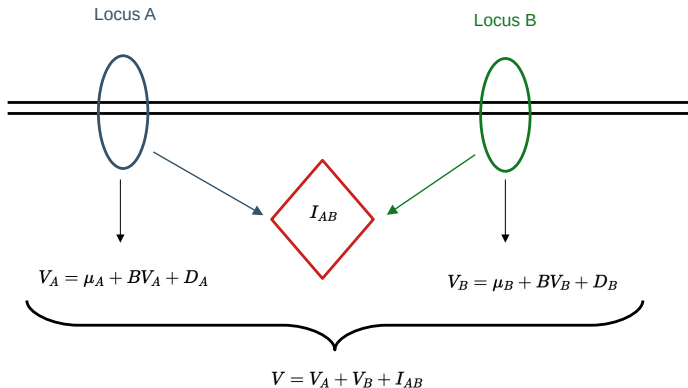
## Two and more Loci

- ▶ Two loci  $A$  and  $B$  having an effect on the same quantitative trait.
- ▶ Additional effect in genetic model: **Interaction** effect (also known as epistasis)
- ▶ Interaction occurs if effect of one locus can have an influence on the effect of the other locus
- ▶ Interaction is quantified by

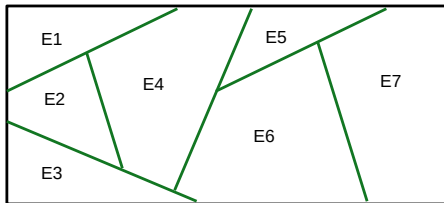
$$I_{AB} = V - V_A - V_B$$

# Influence of Two Loci on Quantitative Trait

## Two Loci Influencing a Quantitative Trait



# Quantify Interaction Effect

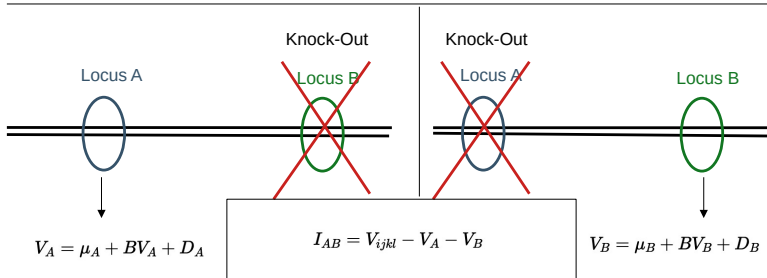


For Animal d with genotype:

$$A_i A_j B_k B_l$$

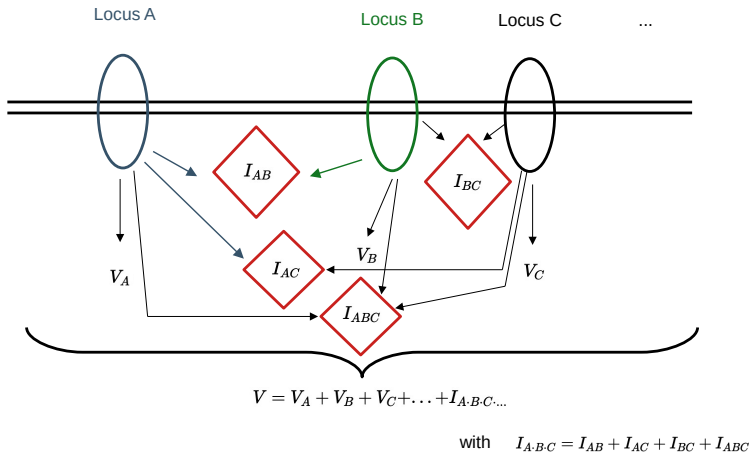
Total Genetic Value  $V_{ijkl}$   
as mean phenotypic value ( $Y$ )  
across different environments  
(E1 to E7):

$$V_{ijkl} = \frac{1}{N} \sum_{m=1}^N Y_{ijklm}$$



# More Than Two Loci

## Many Loci Influencing a Quantitative Trait



# Summary Genetic Model

- ▶ Given genetic model

$$V = V_A + V_B + V_C + \dots + I_{A \cdot B \cdot C \dots}$$

- ▶ Decomposition

$$V = \mu_A + BV_A + D_A + \mu_B + BV_B + D_B + \mu_C + BV_C + D_C + \dots + I_{A \cdot B \cdot C \dots}$$

- ▶ Re-group

$$V = \mu_A + \mu_B + \mu_C + \dots + BV_A + BV_B + BV_C + \dots \\ + D_A + D_B + D_C + \dots + I_{A \cdot B \cdot C \dots}$$

- ▶ Collect

$$V = \mu + BV + D + I_{A \cdot B \cdot C \dots}$$

## Extend to Phenotypes

- ▶ We know from earlier

$$Y = V + E$$

- ▶ Insert decomposition of  $V$

$$Y = \mu + BV + D + I_{A \cdot B \cdot C \dots} + E$$

- ▶ For breeding, only  $BV$  is important

$$Y = \mu + BV + E^*$$

with  $E^* = D + I_{A \cdot B \cdot C \dots} + E$

# Split of Environment

Non-genetic environment is split into

- ▶ known part, corresponding to additional information on animal, like herd, age, sex, ... leads to vector of fixed effects and regression coefficients  $\rightarrow b$
- ▶ unknown part leads to random residual part  $\rightarrow e$



# Model of Phenotypic Observation

Phenotypic observation ( $y_i$ ) of an animal  $i$  can be modelled as

$$y_i = x_i^T \cdot b + u_i + e_i$$

where

- $y_i$  phenotypic observation of animal  $i$
- $x_i$  vector of regression covariates or indicator values for fixed effects
- $b$  vector of unknown fixed effects and unknown regression coefficients
- $u_i$  random breeding value of animal  $i$
- $e_i$  random environmental effects of animal  $i$

# Aggregation over Population

Take all observations from all animals in a given population

$$y = X \cdot b + Z \cdot u + e$$

where

- $y$  vector of phenotypic observations of all animals
- $b$  vector of unknown fixed effects and unknown regression coefficients
- $u$  vector of random breeding values of all animals
- $e$  vector of random environmental effects
- $X$  design matrix with regression covariates or indicator values for fixed effects
- $Z$  design matrix relating breeding values to observations