

For two to many loci there is an additional comp

$$V_{ijkl...} = \mu + BV_{ij} + BV_{kl} + BV_{...} + \dots + \left. \begin{array}{l} \text{Breeding values} \end{array} \right\} \\ + D_{ij} + D_{kl} + \dots + \left. \begin{array}{l} \text{Dominance deviation} \end{array} \right\} \\ + I_{ijkl} + \dots + \left. \begin{array}{l} \text{Epistasis} \end{array} \right\}$$

- Problem: We don't know the number of loci that are important for a given trait.

quantifies interactions between alleles at the same locus.

quantifies interactions between different loci

- Solution: Collect the effects for all loci into three different cumulative effects:

- Cumulative Effect: μ : for the sum of all breeding values from any number of loci
- d : sum of all dominance effect
- i : epistasis effects

Genetic Model: $P = \mu + B + D + I + \dots$