Defining genetic diversity based on genomic tools

Second chapter in the book:

"Genomic management of animal genetic diversity"

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- **You can not maintain what you can not measure!**

  - ✓ **Degree of endangerment**

    ⇒ **prioritisation**

  - ✓ **Management**

  - ✓ **Monitoring**

    ⇒ **check for success**

- **Keep phenotypic features**

  - ✓ **Morphological** ⇒ **breed standard**
  - ✓ **Productive** ⇒ **profitability**
  - ✓ **Adaptation to particular environment**

$$V_P = V_G + V_E$$

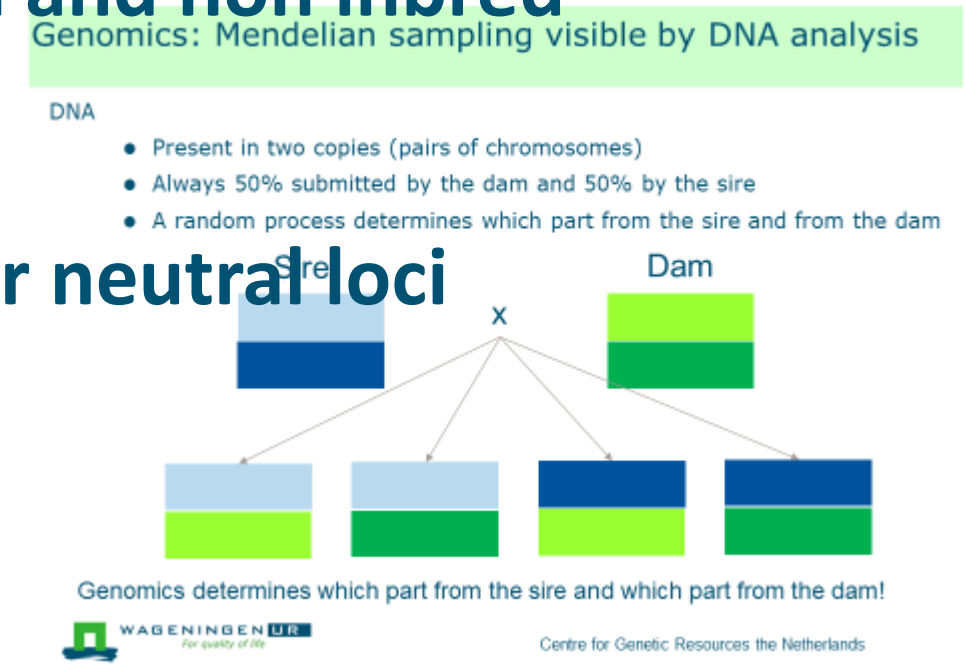
- **Classical approach through the concept of variance**

  - ✓ **Good recording scheme (standardised and accurate)**
    ⇒ **avoid confounding errors with high variability**

- **Look for high levels of phenotypic diversity through high levels of genetic diversity**

PEDIGREES

- **Absent or unreliable**
  - ✓ **Especially between breeds**
    - ⇒ **prioritisation**
- **Assume founders unrelated and non inbred**
- **Average ‘expected’ value for neutral loci**
  - ✓ **No Mendelian sampling**
    - ⇒ **no all sibs are equal**



MOLECULAR INFORMATION

- **Deal with ‘realised’ values**

  - ✓ percentage of polymorphic sites
  - ✓ distribution of allelic frequencies
  - ✓ observed and expected heterozygosity
  - ✓ allelic diversity

  ⇒ detect relevant individuals or populations

- **dense coverage by SNPs**
  - ✓ **every locus in LD with one marker**
    - ⇒ **more precise measure**
  - ✓ **measure non-neutral genetic diversity**
    - ⇒ **account for productivity or fitness**
  - ✓ **separate analysis of particular regions**
    - ⇒ **instead of global picture**
  - ✓ **finer determination of relationships between individuals/breeds**
    - ⇒ **crucial in management**

- **Close SNPs inherited together**
  - ✓ **use haplotype (kinship)**
    - ⇒ **detect selection signatures**
  - ✓ **Runs Of Homozygosity (ROHs)**
    - ⇒ **reflect IBD if they are long enough**
    - ⇒ **but still 'realised' IBD**

' … long stretches of two homologous chromosomes within the same individual that are identical (homozygous for all the loci within) …'

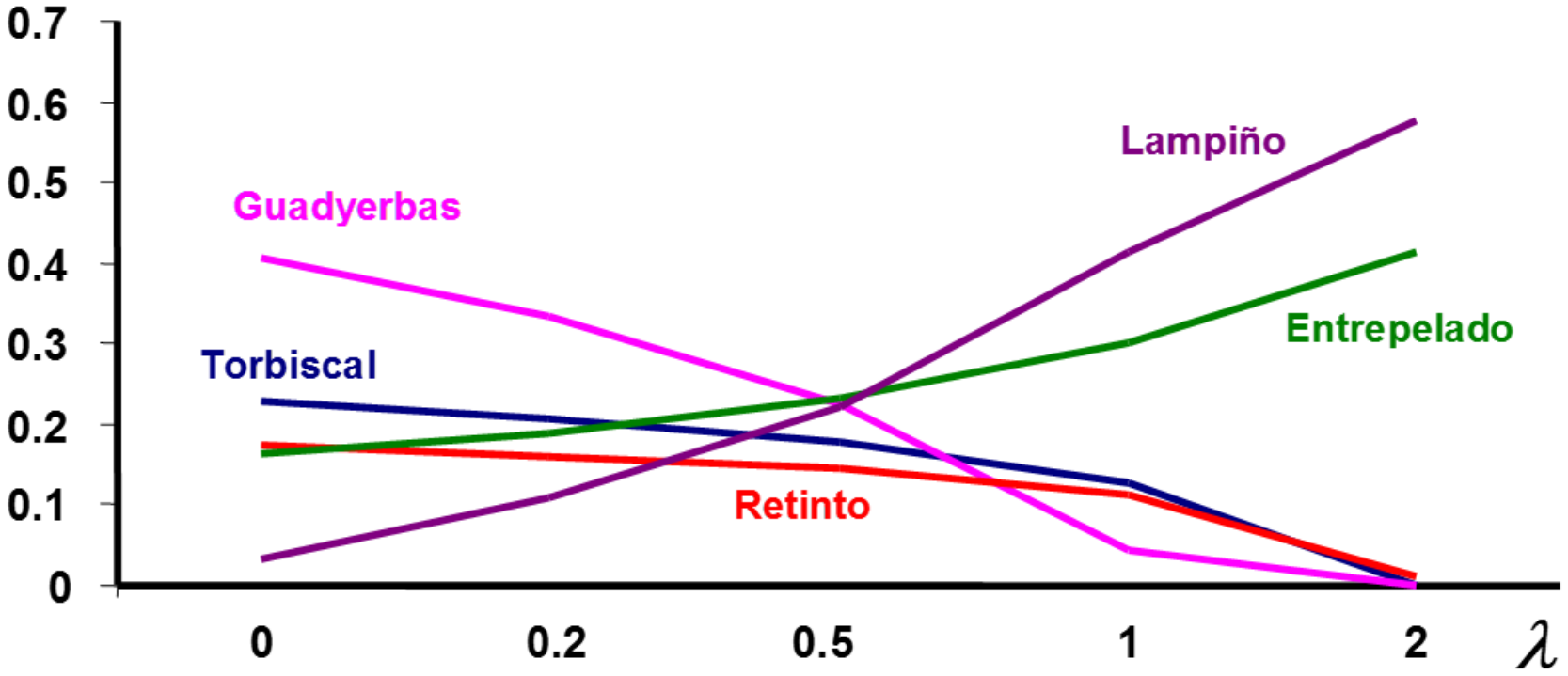
- **whole sequence**
  - ✓ **detect other types of markers, e.g. Copy Number Variants (CNV)**
  - ✓ **causal mutations for important traits are present**
    ⇒ not depending on LD with the SNPs
  - ✓ **easier to detect rare variants**
  - ✓ **efficient way of detecting SNPs for rare breeds**
    ⇒ avoid ascertain bias from commercial SNP chips

➢ Partition of diversity within and between breeds

- ✓ better description of genetic structure
- ✓ prioritisation of breeds

$$GD = \lambda GD_W + GD_B$$

- $\Rightarrow \lambda = 0 \Rightarrow$ Weitzman
- $\Rightarrow \lambda = 0.5 \Rightarrow$ TGV
- $\Rightarrow \lambda = 1 \Rightarrow$ Exp. Het.



- **trait-based adaptive diversity measures**
  - ✓ **excess of variance in genotypic values relative to the variance expected in the absence of selection**
  - ✓ **adaptivity coverage of a set of subpopulations**
  - ✓ **how well the subpopulations could adapt to a large range of environments**