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

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

\[ V_P = V_G + V_E \]
- Absent or unreliable
  - Especially between breeds
    - $\Rightarrow$ prioritisation
- Assume founders unrelated and non inbred
- Average ‘expected’ value for neutral loci
  - No Mendelian sampling
    - $\Rightarrow$ no all sibs are equal
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
    $\Rightarrow$ not depending on LD with the SNPs
  - easier to detect rare variants
  - efficient way of detecting SNPs for rare breeds
    $\Rightarrow$ avoid ascertain bias from commercial SNP chips
Partition of diversity within and between breeds

- better description of genetic structure
- prioritisation of breeds

\[ GD = \lambda GD_W + GD_B \]

- \( \lambda = 0 \Rightarrow \) Weitzman
- \( \lambda = 0.5 \Rightarrow \) TGV
- \( \lambda = 1 \Rightarrow \) 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