Management of genetic diversity in small populations

Chapter 5

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Introduction

- Goals of live conservation
  - ΔG to meet future market demands (e.g. wrt niche products)
  - Maintain genetic resources / prevent their loss
  - Research opportunities
  - Maintain socio-economic / cultural / historic value
    - Keep rural areas populated
  - Maintain landscape / ecological value
- genetic improvement important to small breeds:
  - Breed needs to be attractive to some breeders
  - genomic selection is option
    - Genomic infra-structure available

Aim

- Use of genomic tools to achieve

these goals of live conservation schemes

A simple, linear model of inheritance / ΔG

- (often used in computer simulations)
- Limited number (1000) of genes have effects
  - Normally or Exponentially or Gamma distributed
- Selection program : fix the good alleles
  - Don’t loose initially rare good alleles (reduces longterm gain)
  - Limit random drift at the genes => allele-freq changes in right direction
  - Genetic drift outside genes is not important for (longterm) gain
- Loss of genetic variance due to selection is rapid
  - Partly remedied by assuming very many genes
  - Does not agree with practical observations
- Linear model only works in the shortterm

A shortterm linear, longterm nonlinear model

- Consider longterm strong selection program (e.g. broilers)
  - During the course of selection various problems occured (ascites; leg-weakness)
  - As pathways under current selection start to perform ‘good’:
  - Selection needs to be directed towards new ‘pathways’ that limit performance
  - Overall genetic variance remains
  - This is due to a nonlinear interactions between pathways
- Conclusion wrt maintaining genetic diversity:
  - We need to maintain genetic diversity everywhere in the genome
    - Because we dont know which set of genes we will be selecting for next
    - Differential weighing of chromosomal regions in diversity management is unnecessary
  - This is enhanced by changes in the breeding goal / management of animals

(non)genomic selection/management

Matrices	EBV estimation	
F-Management	A	G
A	EBV-OC	GEBV-OC
G	XX	GEBV-GOC

- EBV-OC = Pedigree-based selection and pedigree based optimum contrib.
- GEBV-OC = Genomic EBV and pedigree based OC
- GEBV-GOC = GEBV and G matrix based OC

Pedigree versus genomic F

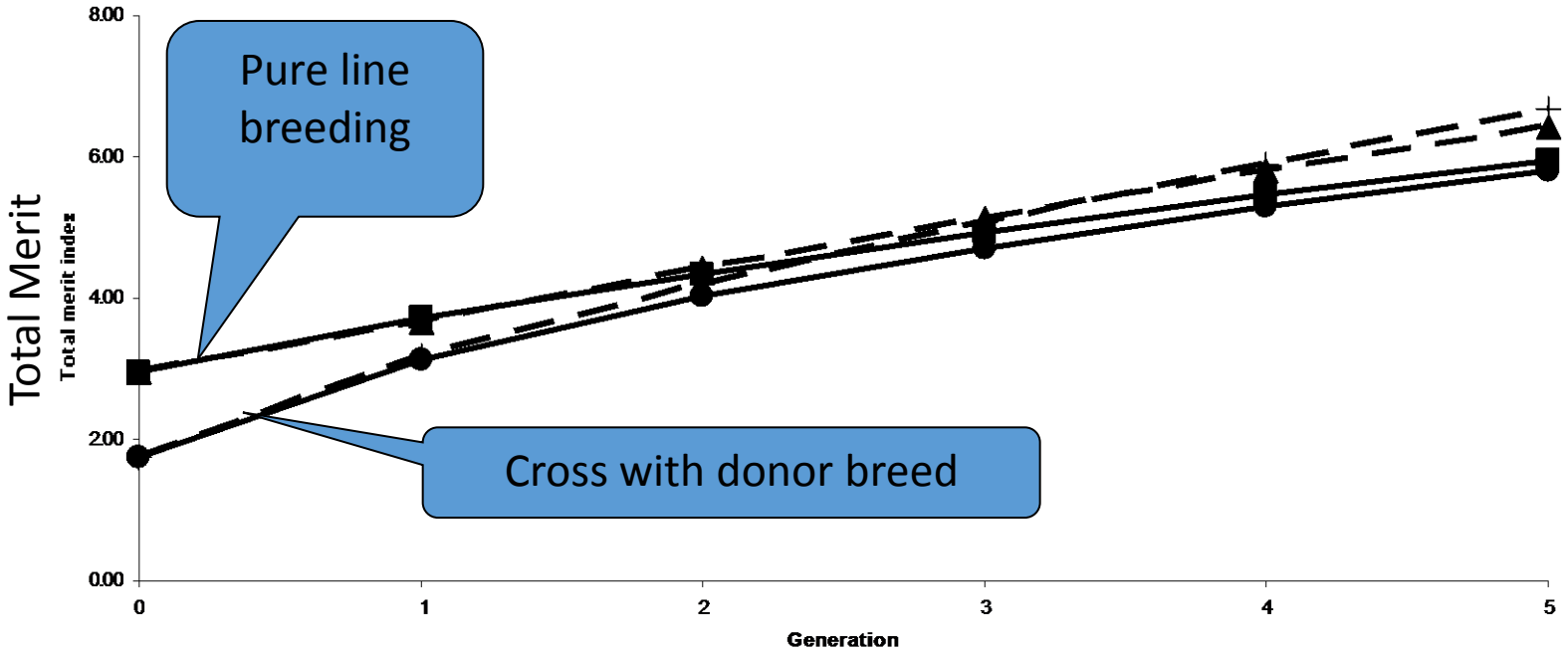
- Breeding schemes cause genetic drift mainly in ‘gene-rich’ regions
  - GEBV concentrate more on gene-rich regions
  - Pedigree-F is defined for unlinked loci
    - These dont exist in finite genome
    - $\Delta F_{Genomic} > \Delta F_{Ped}$
- target rates of inbreeding: mainly based on molecular genetic drift
  - Thus ΔF_{Target} of ½ - 1 % / generation apply to genomic ΔF
  - And ΔF_{Target} for pedigree ΔF should be reduced:
    - E.g. ¼ - ½ % / generation

Use small population genetics into comm. breeds: Marker Assisted Introgression

- Assumes trait to be introgressed from ‘small’ to ‘commercial’ breed
- Trait due to 1-2 known QTL (not a complex trait)
- Three steps
  1. Create F1
  2. Backcross to superior breed (maintain good alleles by markers)
  3. After 5 generations: intercross to obtain good alleles in homozygous form
- Manage inbreeding
- If causal mutation known: gene editing may be used
  - Takes one generation

GS-introgression

- Introgression of complex trait(s) from donor breed
- Donor breed better for e.g. disease resistance but inferior for Total Merit



__Tradit. Selection; _ _ _Genomic selection

Odegard et al. 2008

Genomics for ‘breed-recovery’

Problem description:

- Local breed that is no longer fashionable
- Semen of large commercial breed introduced
  - Assume Holstein semen => Holsteinisation
- Breed will be lost (will become Holstein)
  - Diversity will be lost
- How to rescue the breed ?
  - Using genomics
  - Assuming we can manage the selections in part of the breed

OC type of approach

- Minimise:

$$\sum c_i \bar{G}_{i,hol}$$

- c_i is the optimal contribution of the animal
- $\bar{G}_{i,hol}$ is the average genomic relationship of i with the introduced holstein bulls
- Efficiency of Recovery:
  - 1 generation of Holsteinisation: 100%
  - 5 generations of Holsteinisation: 85%

Amador et al. GSE 2013

Conclusions

- Need to maintain genetic diversity everywhere in genome
  - Cannot predict which is the next limiting pathway/trait genes are
  - Differential weighing of diversity not needed / beneficial
- Pedigree vs genomic relationships:
  - Creates 2x2 table of selection methods:
    - A or G for EBV estimation
    - A or G for F management
  - In breeding scheme $\Delta F_{Genomic} > \Delta F_{Pedigree}$:
    - Target rates of inbreeding lower for $\Delta F_{Pedigree}$
    - Difference will depend on selection scheme / genetic architecture

Conclusions (2)

- GS introgression:
  - Tool to introgress complex traits from ‘small’ breeds into a commercial breed
    - Faster than selecting commercial breed for trait
    - Does not require knowledge on QTL positions / limited number of QTL
- Recovery from ‘Holsteinisation’ is possible
  - I.e. situation where local breed is crossed with a fashionable global breed
  - Remarkably efficient if:
    - Holsteinisation lasted for $\leq$ 3 generations
    - Fraction Holstein genes < 30%