Genomics for conservation of animal genetic resources

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Introduction

- Genome sequence known in livestock species
- (By)product: massive numbers of SNPs
  - available through 2nd generation sequencing techn.
- Dramatic improvement of SNP genotyping
  - ~200$ for 50k SNPs (for cattle: 800k SNPs)
- Future: whole genome sequence for $1000

Aim

- How are we going to use this new technology for conservation of AnGR
- How to manage genetic diversity within breeds
- How are we going to use AnGR

Use of genomics information for conservation of AnGR

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Novelty: across breed relation-matrix

- Estimation:

$$\mathbf{G} = \mathbf{ZZ}'/n$$

where $X_{ij} = (g_{ij}-2p_i)$; $Z_{ij}=X_{ij}/\sqrt{(2p_i(1-p_i))}$

- Accuracy = $n/(n+M_e)$

where M_e is across breed effective no. of segments (Daetwyler et al., 2008)

- In case of sequence data, calculate G:

$$\mathbf{G_{true}} = \frac{\mathbf{XX}'}{\sum 2p_i(1-p_i)}$$

What to do with the **G** matrix?

- Average **G** matrix to across breed kinship matrix, $\mathbf{K_{ab}}$
- Maximise heterozygosity (Eding&Meuwissen,2001)

$$Het = 1 - \mathbf{c}'\mathbf{K_{ab}}\mathbf{c}$$

  - Heterozygosity when interbreeding the breeds
- Maximise MVT (Bennewitz&Meuwissen,2005)

$$MVT = 1 + \mathbf{c}'diag(\mathbf{K_{ab}}) - 2\mathbf{c}'\mathbf{K_{ab}}\mathbf{c}$$

  - Maximimum variance of a hypothetical trait

Alternative due to dense SNP data:

- Maximise across animals (without respect to breed)

$$MVT_{ind} = 1 + \mathbf{c}' diag(\mathbf{G}) - 2\mathbf{c}'\mathbf{G}\mathbf{c}$$

- But this gives no guarantee that number of animals per breed is sufficient to keep Ne ↑
  - – Perhaps extra contraints to maintain Ne or ΔF
- Chooses best animals across breeds
  - – But across breed relationships are probably similar
- When creating just one breed:

$$Het_{ind} = 1 - \mathbf{c}'\mathbf{G}\mathbf{c}$$

How to manage genetic diversity within breeds

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Introduction

- Past: pedigree relations used for ΔF control
  - Measures inbreeding at unlinked, neutral loci
  - Do these exist?

- Currently: more accurate genomic relations
  - optimum contribution selection
    - With genomic control of inbreeding

OC with ΔF constraint 0.005

	ΔG	ΔF-ped	ΔF-genom
ΔFA-TEBV	2.26	0.005	0.007
ΔFA-GEBV	3.08	0.005	0.021
ΔFG-GEBV	1.91	0.004	0.005

Sonesson et al., GSE, 2012

Conclusions within-breed ΔF manag.:

- Traditional selection acts on Mendelian sampling terms (MST)
- Diversity management should constrain Var(MST)
  - OC acts on pedigree inbreeding
- Genomic selection acts on SNPs
- Diversity management should constrain Var(Δq) i.e. variance of freq. change of SNPs
  - G matrix based on SNPs
- If not OC finds 'holes':
  - ways to increase ΔF that are undetected by G or A

How are we going to use AnGR

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A step back: what are future needs of livestock prod.

- Production increase 1%/yr
  - Keep pace with population growth in Europe (~1%/yr)
- Cost-effectiveness up
  - Prices of inputs up
  - Competition with plant products up
    - E.g. plant products in sausages
- Use of waste products as input
- More marginal land (reduced N usage)
- Reduce environmental impact
  - GHG emisions down   (currently 7% of total emissions)
- Animal welfare & health : society more aware

Animal Breeding aims:

- Adapt genetics of animals to these challenges
  - Cost effectiveness
  - Feed efficiency
  - Use of waste products (Gxfeed interactions)
  - GHG emissions down
    - Contribute to general emission reductions
  - Disease resistance up
    - Challenge due to poorer feeds / more marginal conditions
    - Improves also welfare

Animal Breeding Strategies

- Animal breeding
  - important tool to adress these challenges
  - slow process
  - Important due to its accumulation improvements
- Challenges demand rapid changes:
  - Need the fastest animal breeding techniques
    - Breed or cross substitution (use of AnGR)
    - Genomic selection (GS)
    - GS-intogression (combination of GS and AnGR)

Breed or cross substitution

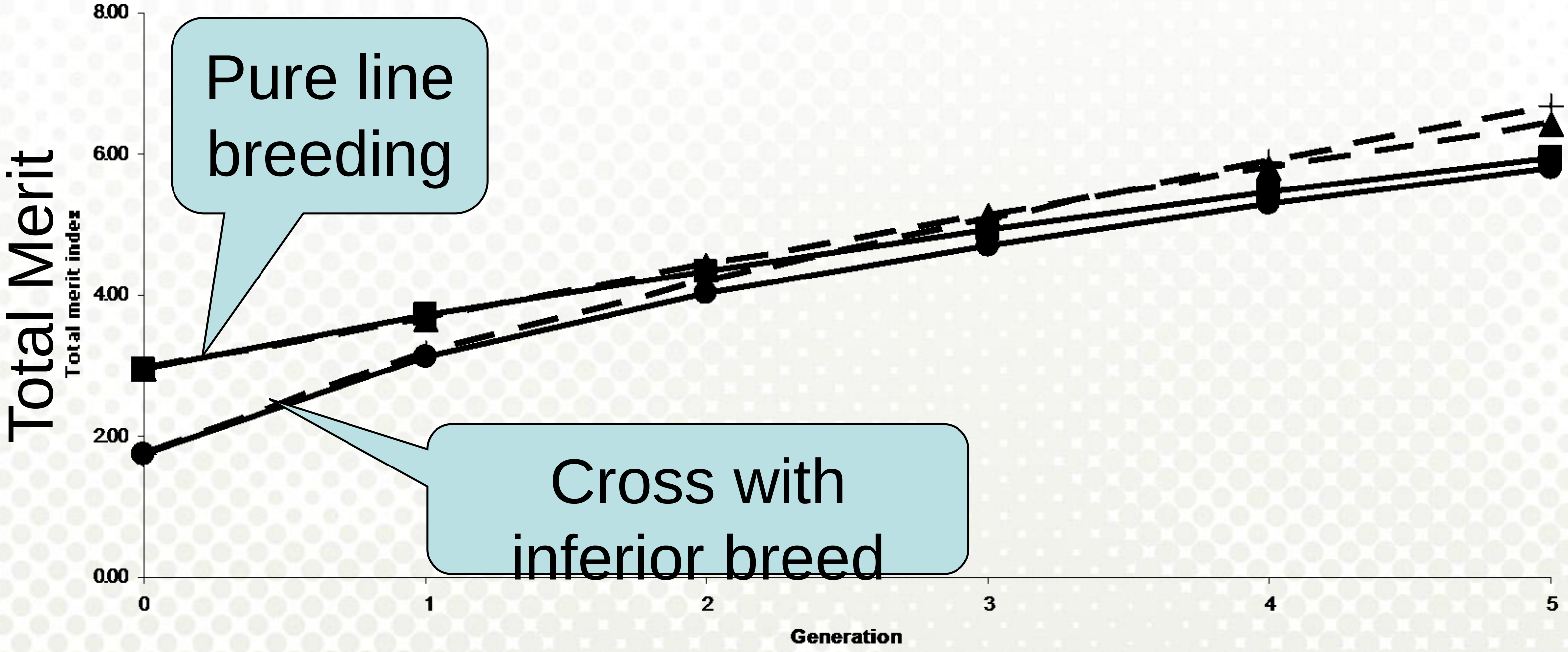
- Requires Animal Genetic Resources (AnGR)
- In view of the challenges:
  - Need efficient low input breeds
  - Utilisation of waste products
  - Use of marginal land
- Many endangered breeds fullfill these requirements
  - Were replaced by high-input / high output breeds
  - May see a come-back (eg. dual purpose cattle)

Genomic selection (GS)

- May speed up ΔG dramatically
  - When generation interval can be reduced
  - When trait cannot be measured on candidate
- Usefull to address GxE issues
  - E.g. production under low-input environment
  - Detect animals suited for low input environment without having record in such an environment

GS-introgression

- Introgression of 1 trait from ‘inferior’ breed



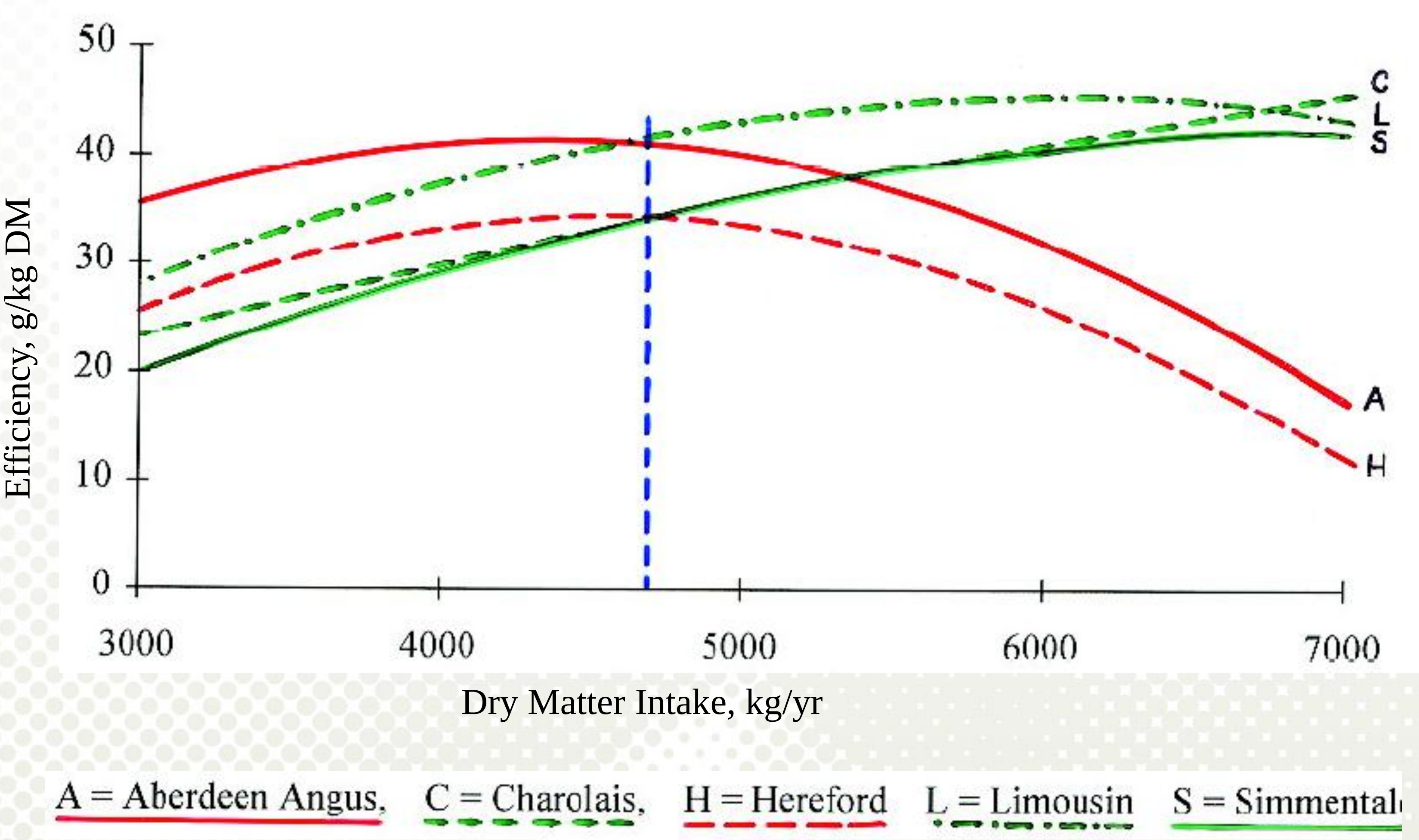
__Tradit. Selection; _ _ _Genomic selection

Odegard et al. 2008

Animal Breeding & adaptation to new env.

- Strategy:
  - adapt animals to the changing (econ) environm.
- Investigate GxE:
  - Feed quality
  - Temperature (other climate changes)
  - Water usage
- Breed comparison with respect to GxE

Biological efficiency of different cattle breeds (Jenkins and Ferrell, 1994)



Conclusions

- Many challenges ahead of livest. prod:
  - Need to redesign the production system
  - Need research to address challenges / new design
  - Incl. changing genetics of animals
- Animal breeding : rapid genetic change
  - Breed/cross substitution : AnGR
  - Genomic selection
  - GS-introgression : get 1 trait out of AnGR

Conclusions (2)

- AnGR important to address the challenges
- Genomics tools are important to:
  - Manage diversity between breeds
  - Manage diversity within breeds
    - essential when selecting for GEBV
  - To transfer traits from ’old’ breed to ’commercial’
    - GS-introgression

A paradigme shift:

- In the past:
  - – Selection for better animals
  - – Problems (due to ΔG) : adapt environm./managem.
    - Inhouse production / antibiotics / better feeds
- In the future:
  - – Environmental changes dictate ΔG changes
  - – AnGR may play important role
    - Provide a means for fast genetic change