The data challenge

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Red breed strengths by Bradley Heins, Uni of Minnesota

- Medium sized
- High levels of milk and protein
- Excellent fertility
- Calving ease of dams
- High resistance to mastitis
- Long productive life
- Diversity



How do breeds that are numerically smaller get reliable genomic predictions?





Build your own reference population

- Genotyping large numbers of animals
- Well recorded phenotypes



Multi-breed reference populations

- Irene's talk
- Seems to be promising



International collaboration

- Use genomic breeding values from another country
- Sharing reference populations
- "Interbull" model meta-analysis



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Reliability (R²)



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95% Confidence interval BPI at different reliabilities



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Two traits

- Milk production (heritability ~ 0.3)
- Health or fertility (heritability ~ 0.05)



Progeny testing



80-100 daughters required to get reliabilities >50%

Number of daughters



Selection for clinical mastitis



Genomic selection

- Reference population to predict SNP effects
- Apply SNP effects (prediction equation) to genotyped animals
- Select best animals on genomic breeding values
- Great for difficult to measure or expensive traits



Goddard & Hayes Nat. Rev. Genet. 2009



Genomic reliabilities (calves)	
Protein	76%
Overall type	53%
Fertility	50%
Milking speed	61%

Reliabilities ABVs (7thlactation)78%Protein78%Overall type29%Fertility38%Milking speed37%

1526

Year 2 Year 6/ Year 8 Year 3 Year 5 Year 7/ Year 0 Year 1 Year 4 Yearling Lact 1 Lact 4 Lact 3 Lact 5 Lact7 Calf Lact 2 Lact 6

0

COLLEEN

2199

Genomic selection

- Sources of phenotype data
 - Are the traits available in commercial herds?
 - Data completeness/bias?
- Cost of phenotypes
- Calculating breeding values
 - Heritability
 - Genomic or pedigree relationships?
 - Genomics: female or male reference populations
- Evaluating and monitoring
 - Is genetic improvement being made for these traits?



Reliabilities for research herds and genomic information nucleus



Applying equation of Daetwyler et al. (2008)

Expensive phenotypes

- Examples: feed efficiency, methane emissions, immune response
- Limited number of phenotypes
- What is the most cost-effective reference population?
- Genotype animals with phenotypes (most efficient): use cow reference population
- Develop genomic evaluations, and combine them with evaluations for predictor traits if any



Cost of reference populations



Optimum size and type of reference population

- Ultimately depends on phenotype cost, economic value of trait and heritability
 - See Gonzalez-Recio et al, JDS 97:1-11
- If trait is expensive to measure, it is more efficient to use a research herd reference population
- Problem for expensive traits with low heritability: research herd reference has low accuracy, and information nucleus population cost is very high
- Work on methods to improve reliability important!



Reference populations





International collaboration

- Works well if genotypes are being shared (e.g. European and North American consortia)
- Great for expensive traits (e.g. feed efficiency)
- Methods being developed in situations where genotypes are not shared (e.g. Goddard, Jighly et al)
 - Meta-analysis using SNP effects from each country
 - Being tested in Brown Swiss
 - Potential model for an Interbull service



Using breeding values from other countries

- Beware of genotype by environment interactions
- Different trait definitions etc
- Re-ranking because of feeding system, environment etc. Interbull correlations (protein) between Australia and other countries 0.7-0.8
- Expect reliability in importing country to approximate correlation between countries multiplied by reliability of exporting country



95% Confidence interval



Summary

- Genomic selection relies on high quality phenotypes to develop breeding values
- The size of the reference population required depends on:
 - Heritability
 - Predictor traits
 - Cost of phenotype
- International collaboration can help increase reliability (especially useful for expensive phenotypes)
- Multi-breed genomic reference populations are promising



Tips for numerically small breeds

- Be open to sharing reference populations
- Test genomic predictions from larger populations of the same breed
- Be pro-active in data recording
 - Target new breeding objectives?
- Opportunities for technology to be used to generate much more precise phenotypes
 - Mid-infra-red spectral data from milk-recording



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