Choices in genomic evaluation for small populations

S. Andonov, D.A.L. Lourenco, B.O. Fragomeni, Y. Masuda, I. Pocrnic, S. Tsuruta, and I. Misztal
USCM, Macedonia; UGA, USA
Background

- Small Holstein populations
  - Croatia 40k
  - Macedonia 35K
  - Slovenia 35K
- International trade of genetic material
  - Semen & embryos
  - Pregnant heifers
- Incomplete relationship (lack of deep pedigree)
- National genomic breeding programs - small reference population
- Selection of young animals?
- Progeny testing?
Background

• Choices for small populations are:
  – If data is available include proven bulls/dam into evaluation
    • Pedigree;
    • Phenotypes;
    • Genomic.
  – Become part of other breeding program
  – Participate into consortia.
Background

• Simulation study
• Test different sources of information from connected small ($P_s$) and large population ($P_L$)
• 4 cases
Material

- Large population
  - 2K ♂ and 20K ♀ 20 generations
  - h² = 0.3
  - Replacement sire=0.9; dam=0.3
  - Selection criterion - high EBV,
  - Genotypes for generations 14-20th

- Small population
  - 150 ♂ x 2000 ♀ (Pᵢ 18 g)
  - 2⁰ gen + 100 ♂ (Pᵢ 19 g)
  - h² = 0.3
  - Replacement sire=0.5; dam=0.3
  - Selection criterion - phenotype,
  - Genotypes for 1-3 generations (6000 animals total)
Material

• Genomic
  – 45000 biallelic SNP
  – 29 chromosomes
  – 450 QTLs

• Average of 5 replicates
Small + GEBV_large

<table>
<thead>
<tr>
<th>Category</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phenotype Ps</td>
<td>3166</td>
</tr>
<tr>
<td>Pedigree Ps</td>
<td>22,885</td>
</tr>
<tr>
<td>Genotypes Ps</td>
<td>6000</td>
</tr>
<tr>
<td>GEBV PL sires</td>
<td>4475</td>
</tr>
</tbody>
</table>
Small + Large

Phenotype $P_S + P_L$

Pedigree $P_S + P_L$

Genotype $P_S + P_L$

$P_S P_L$ GEBV

| Phenotype $P_S + P_L$ | 224746 |
| Pedigree $P_S + P_L$ | 425684 |
| Genotypes $P_S + P_L$ | 59558 |
SNP effect * SNP(P_S) = P_{L-SNP} GEBV
Methods

- BLUPF90 family (Misztal et al., 2015)
- Genetic connection between PL and PS ($r_g$) – REML
- Small and Small+Large, Genomic EBV - ssGBLUP
- Small+GEBV_Large - ssGBLUP with external information
- SNP_Large - ssGBLUP extended to calculate SNP effects
- Model:
  \[ y = 1\mu + Za + e \]
  - \( Z \) incidence matrix for the random effect in \( a \).
  - \( a \sim N(0, H\sigma^2_a) \); \( \sigma^2_a \) \( H \) matrix that combines pedigree and genomic relationships
Validation

• Correlation GEBV-TGEBV

• Validate
  – 1000 genotypes of $P_S$ (334 in $3^{rd}$ generation)
  – 3000 genotypes of $P_S$ (1000 in $3^{rd}$ generation)
  – 6000 genotypes of $P_S$ (2000 in $3^{rd}$ generation)

• $r_g = 0.84 \pm 0.019 \ (P_L - P_S)$
Results
Achievements

• Small population stand alone
  • Moderate accuracies
  • Need to increase daughter groups per sire in $P_S$

• Small population + external GEBV of sires
  • slightly improve the accuracy
  • add complexity to the evaluation
Achievements

• Join evaluation of $P_S$ and $P_L$
  The highest accuracies

• SNP effects for $P_L$ to assess GEBV
  Considerably high accuracies
  Constant over replicates
  No need pedigree and performance of $P_S$
  Constrain - prediction of GEBV for animals with SNPs
    all candidates need to be genotyped
Practical implementation

• Small population
  – share genomic in consortia
  – young animals - DGV
  – continue breeding program with GI (verify realization of GEBV)
  – Check genetic gain

• Large population
  – identifying animals with high GEBV and low inbreeding
Thank you!