Estimation of non-additive variance components and SNP effects in five dairy cattle breeds

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Milk production traits are affected by many genes, many with a small effect and some with a major effect, thus complex traits.

Complex traits are regulated by complex interplay between multiple genes.

Theoretically, these genes can interact.

Interaction can be explained as non-additive genetic variance (NAGV):

1. same locus interaction (dominance deviation)
2. different loci interaction (epistatic variance)
Non-additive genetic variance (NAGV) is usually omitted in Genomic Selection (GS) and when estimating life-time merit of cows

- GS is based on additive effects of sire
- Especially the case when reference population is made of progeny tested bulls
- But cows with own performances are becoming more popular as a resource of choice for GS
- If NAGV is substantial, it can augment the GRM based solely on the additive genetic variance
Opportunity

Replacement Bulls

Dominance Epistasis

New Traits Previously not analyzed

GS in Medium Populations

Cow Genotyping
Opportunity

- Replacement Bulls
- New Traits Previously not analyzed
- Dominance Epistasis
- GS in Medium Populations
Workflow

GWAS
SNP with Major Effect
Bayesian Methods

genotypes
phenotype

539
539C2
SNPxSNP + GRM

NAGV
Data

**Study animal**
- Approximately 100K dairy cows from five French and Danish populations

**Phenotypes**
- Three milk production traits expressed as yield deviations
- Milk Yield, protein yield and fat yield

**Genotypes**
- Genotyped with 50K Illumina Infinium bead chip
- 7K SNP selected from Whole Genome Sequence
- Imputed to 50K to obtain similar genotype for all cows
(a) Dominance

\[ y = \mu + \sum_{i=1}^{n} x_i a_i + \sum_{i=1}^{n} x d_i d_i + e \]

- Additive SNP substitution effects: \( a_i \sim N(0, I\sigma^2_a) \)
- Dominance deviation: \( d_i \sim N(0, I\sigma^2_d) \)
- Mean
- Vector of phenotypic values
- Genotypes with respect to additive and dominance SNP effects
- Residual term

- Chain=200k, burn=50k, skip=0.5k
- Metropolis-Hastings sampler with acceptance between 0.3 – 0.8
Models

(b) SNP x SNP

\[ Y = 1\mu + A\beta + Wc + \varepsilon \]

- \( \beta \sim \{ N(0, \sigma_{\beta 0}^2) \} \)
- \( c \sim \{ N(0, \sigma_c^2) \} \)
- \( \varepsilon \sim N(0, I\sigma^2) \)

\( \mu \sim \text{uni}[\infty, \infty] \)

\( \pi_{\beta 0}, \pi_{100\beta 0} \sim \text{beta}(10,1) \) and \( \pi_{c0}, \pi_{100c0} \sim \text{beta}(10,1) \)

\( \sigma_{\beta 0}^2, \sigma_{c0}^2, \sigma_{\varepsilon 0}^2 \sim \text{uni}[0, \infty] \)

- Chain=200k, burn=50k, skip=0.5k
- Bernoulli distribution

| \( W_{ij} \) | Locus k |
|---|---|---|
| AA | 1 | 0 | -1 |
| AB | 0 | 0 | 0 |
| BB | -1 | 0 | 1 |
Heritability: Broad and Narrow sense

Heritability (%)

Fat Yield (kg)

Milk Yield (kg)

Protein Yield (kg)

Montbéliarde
Normande
F-Holstein
Danish-Jersey
Nordic-Holstein
Heritability: SNP\times SNP

- Fat Yield (kg)
- Milk Yield (kg)
- Protein Yield (kg)

Heritability (%)

- Montbéliarde
- Normande
- Fr-Holstein
- Danish-Jersey
- Nordic-Holstein

Legend:
- SNP \times SNP
- Additive
SNPxSNP: Allele Substitution Effects
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Summary: Milk yield (Kg) in Holstein
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Conclusion

SNP with major effect including those selected from whole genome sequence explain non-additive variation

This interaction matrix can augment the normal GRM when predicting breeding accuracies

Thank you for your attention
Any questions?