Increasing the goodness-of-fit of genomic prediction model with addition of maternal genomic relationship matrix

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Introduction

- Genomic imprinting has been reported for many economically important traits in livestock such as weight
- GRM relationships do not distinguish between the maternal and paternal origins and ignores parent-of-origin effects such as imprinting
- Progeny gene expression vary based on the parental origin of haplotypes or alleles

Aim

- In this study, we explored the effect of fitting a maternal and/or paternal genomic relationship matrix (GRM), in addition to a regular GRM on REML log-likelihid and variance componenet estimations

Method

- Final weight (600 day) trait for Hereford beef cattle with 2578 genotyped and phenotyped individuals
- Haplotypes were phased using HSPhase 2
- Missing genotypes were imputed using FImpute 2.2
- GRM constructed from all genotypes using vanRaden First Method (2008)
- Paternal and maternal haplotype GRMs constructed using Yang method (2011)
- The variance components were estimated using MTG2 Lee (2016)

Results

Model	LogL	σ^2 $GRM_{Overall}$ (se)	σ^2 $GRM_{Parental}$ (se)	σ^2 e (se)	h^2
G	-8981.65	622.24 (78.46)	-	873.21 (54.47)	0.416
P	-9015.13	-	244.44 (54.88)	1201.55 (49.12)	0.169
M	-9010.51	-	372.99 (63.95)	1038.09 (59.36)	0.264
G+P	-8981.15	593.01 (84.74)	51.17 (55.56)	860.79 (55.91)	0.394
G+M	-8978.11	511.87 (84.74)	159.39 (66.33)	809.73 (59.21)	0.346

G: GRM constructed from all genotypes – vanRaden First Method (2008)
P: GRM constructed from paternal haplotype – Yang (2011)
M: GRM constructed from maternal haplotype – Yang (2011)
G+P: Fitting both **G** and **P**
G+M: Fitting both **G** and **M**

- Combination of regular GRM and maternal GRM simultaneously improved the log-likelihood of the model significantly
- This result could be due to maternal imprinting, however, further research is required to differentiate the maternal genetic effects from the effects of low diversity of paternal haplotypes

References

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