Accuracy of genomic prediction for protein yield using different models in Slovenian Brown bulls

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Introduction

- Genomic (SNP) information enables more accurate inference of breeding values (BV) especially for young animals
- Benefits of genomics in small populations are questionable and ways to integrate genomic information into national genetic evaluation are of interest
- **Objective**: to compare the accuracy of progeny and genomically based evaluation of Slovenian Brown bulls for protein yield based on different approaches to utilize genomic information

Material

- Phenotypic data - test-day records (n=1,342,134) used in the routine national evaluation for Brown breed
- 50K SNP genotypes of 183 Slovenian bulls
- DGV for bulls in Slovenian pedigree (n=399) evaluated within InterGenomics

Methods

4 different approaches of utilizing genomic information

⇒ NAT - phenotypic and pedigree information used in the routine national evaluation system

⇒ NATss - single-step methodology utilizing national phenotypic, pedigree, and SNP genotypes

⇒ MT1 - bivariate analysis incorporating genomic information into the national genetic evaluation through DGV as a correlated trait for 183 bulls genotyped in Slovenia

⇒ MT2 - the same as MT1 with the difference that DGV was considered for 399 bulls that appear in the national pedigree

2 datasets

⇓   ⇓

Full = phenotypic data from 1997 to 2011

Reduced = phenotypic data from 2008 to 2011 were removed to exclude progeny data of bulls born after 2004

2 types of accuracies

⇓   ⇓

Theoretical = via average prediction error variance from the reduced analysis

Validation = correlation between breeding values from the full and reduced analysis

Conclusions

- Application of single-step method did not increase validation accuracies due to the limited number of genotyped animals
- However, integration of external genomic evaluations can be done succesfully with bivariate models
- The potential effect of double counting needs to be explored in future

Results

Approach	Accuracy	
	Theoretical	Validation
NAT	0.58	0.56
NATss	0.61	0.54
MT1	0.84	0.87
MT2	0.74	0.72