

Preliminary single-step multi-trait genomic evaluation of Holstein type traits



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MATERIAL AND METHODS :

OBJECTIVE:

To assess the single-step genomic evaluation for 20 linear type traits of Holstein cattle in Czech republic

	No. cows	First calved (years)
Data set (I)	143 208	2005 - 2010
Data set (II)	66 285	2005 – 2007

Training set = 221 sires,
at least 20 first crop daughters calved 2005 – 2007

Illumina Bovine SNP50
were available for 631 sires

Breeding values (BV) were predicted
by multiple-trait animal model:

1. the pedigree-based relationship matrix (A) - traditional (TBV)
2. A augmented by the genomic relationship matrix – genomic (GEBV)

*DMU5 was employed for computation
(Madsen and Jansen, 2008).*

RESULTS:

Correlations TBV I with TBV II or GEBV II for 101 **test** sires,
at least 50 first crop daughters calved 2008 - 2010

Trait	TBV_II	GEBV_II	Trait	TBV_II	GEBV_II
Angularity	0.52	0.51	Bone quality	0.47	0.57 ★
BCS	0.43	0.51 ★	Locomotion	0.28	0.22
Chest width	0.44	0.48 ★	Fore udder attachment	0.11	0.17 ★
Body depth	0.37	0.43 ★	Rear udder height	0.20	0.31 ★
Stature	0.30	0.31 ★	Udder depth	0.10	0.21 ★
Rump angle	0.45	0.49 ★	Rear udder width	0.32	0.39 ★
Rump width	0.46	0.55 ★	Central ligament	0.47	0.51 ★
Rear legs rear view	0.27	0.26	Teat length	0.23	0.32 ★
Rear legs set (side view)	0.51	0.51	Front teat placement	0.42	0.45 ★
Foot angle	0.48	0.46	Rear teat position	0.43	0.43

CONCLUSION:

For 14 linear type traits, genomic breeding values of test sires showed stronger correlation with traditional breeding values obtained using all data than traditional breeding values of test sires did.

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