

GEBV with GMACE correlations in the Czech Republic



Příbyl J.¹, Zavadilová L.¹, **Pešek P.¹**, Šplíchal J.², Bauer J.¹,
Vostrý L.¹, Motyčka J.³, Fulínová D.², Čermák V.², Růžička Z.²,

¹Institute of animal science, Czech Republic

² Czech Moravian Breeding Corporation, Czech Republic

³ Holstein Cattle Breeders Association of the Czech Republic, Czech Republic

2011-2014 – several genomic approaches compared

- RRBLUP
- GBLUP
- Blending ssGBLUP
- ssGBLUP
- ssGBLUP with combination of domestic production + Interbull DRPs

Correlation of GEBV (EBV) prediction 2008 to daughters results (DYD) 2012 for 140 young bulls

- 969,269 1st lactations 1991–2008, 1,762,905 in pedigree
- 1,185,225 1st lactations 1991–2012, in pedigree 1,958,139
- 98 037 INTERBULL EBVs through year 2008
- 1,605 genotyped bulls (1259 already proven in 2008)

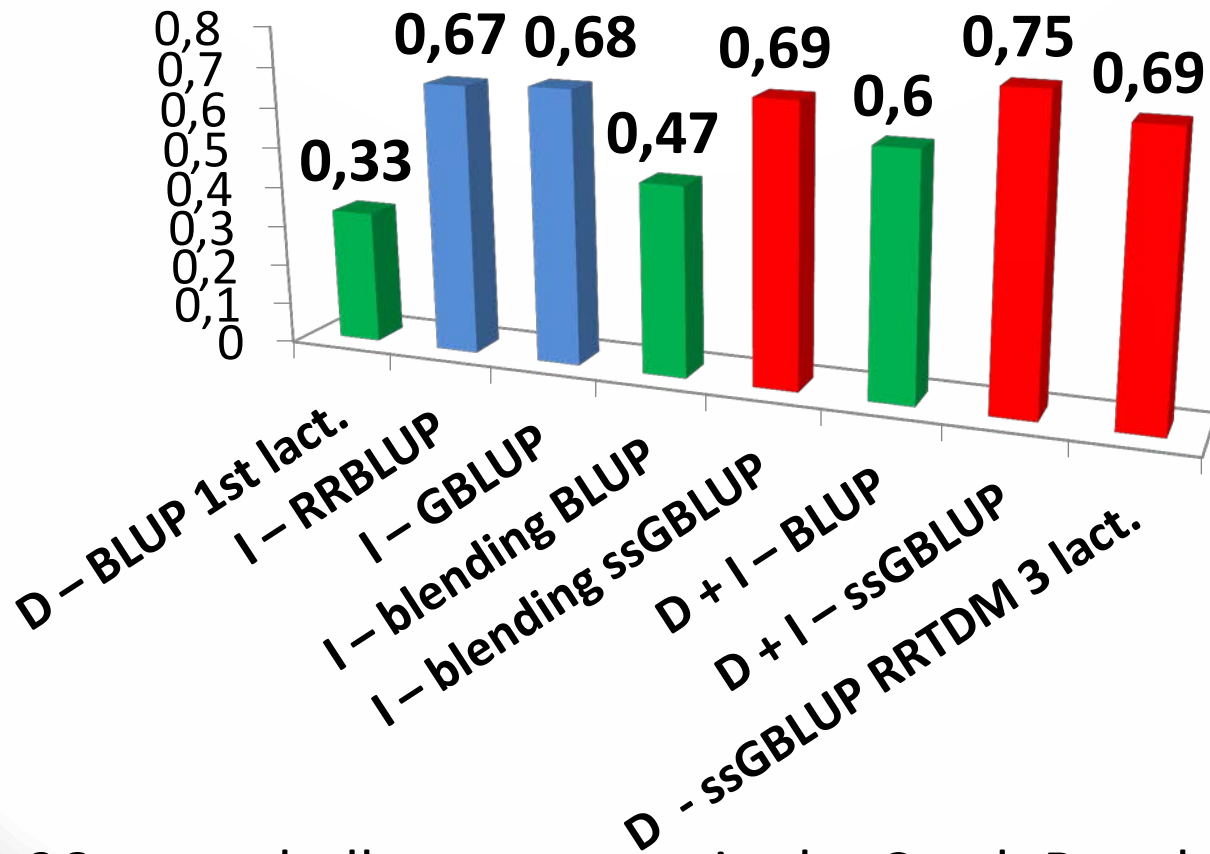
Correlation of GEBV (EBV) prediction 2008 to daughters results (DYD) 2012 for 140 young bulls

Method	Correlation	Validated reliability
D - BLUP	0.47	0.29
D - ssGBLUP	0.61	0.48
I - RRBLUP	0.61	0.48
I - GBLUP	0.61	0.47
I - blending BLUP	0.53	0.36
I - blending ssGBLUP	0.65	0.54
D + I - BLUP	0.51	0.34
D + I - ssGBLUP	0.64	0.53

Correlations of GEBVs (EBVs) predicted using different approaches to GMACE

- 1,257,462 1st lactations 1991-2013, 2,314,856 animals in pedigree
- 19,435,367 test-day records of 1,086,267 cows (calved 1995-2013), 2,142,354 animals in pedigree
- 112,880 INTERBULL EBVs
- 2,627 genotyped bulls (2,189 already proven)

Correlations of GEBVs (EBVs) predicted using different approaches to GMACE



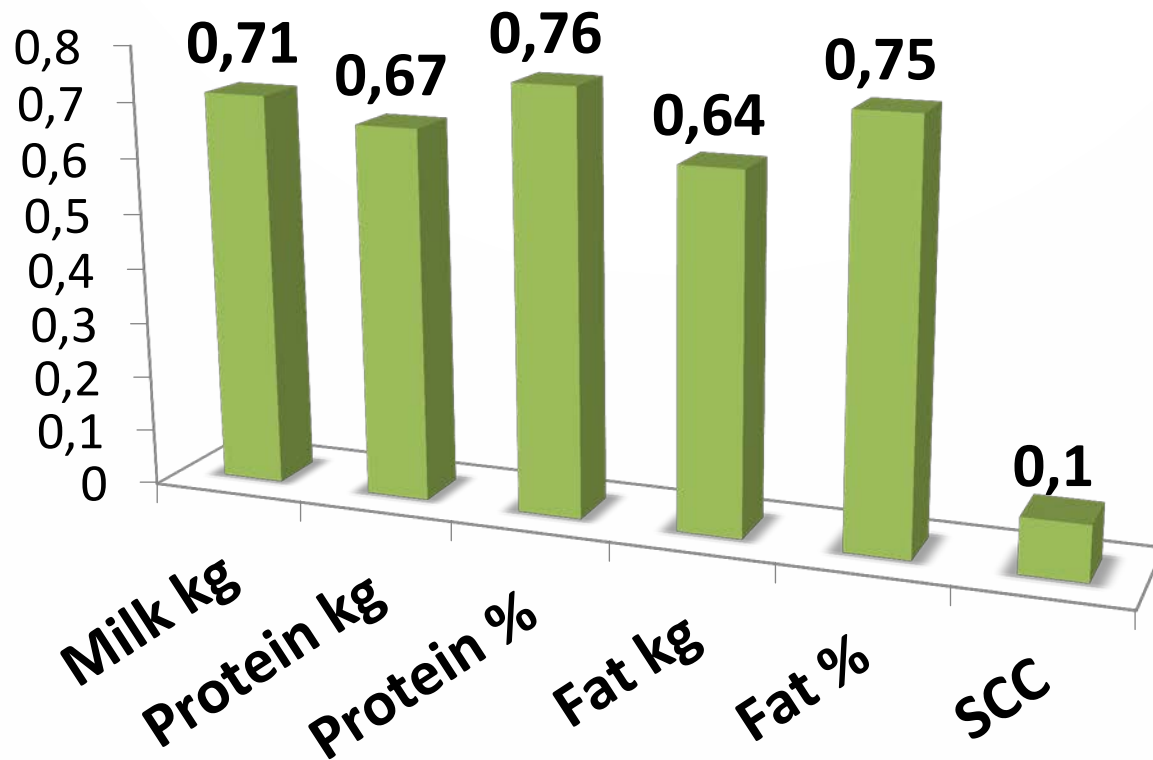
96 young bulls not proven in the Czech Republic

Our choice: **Single step GBLUP**

Benefits:

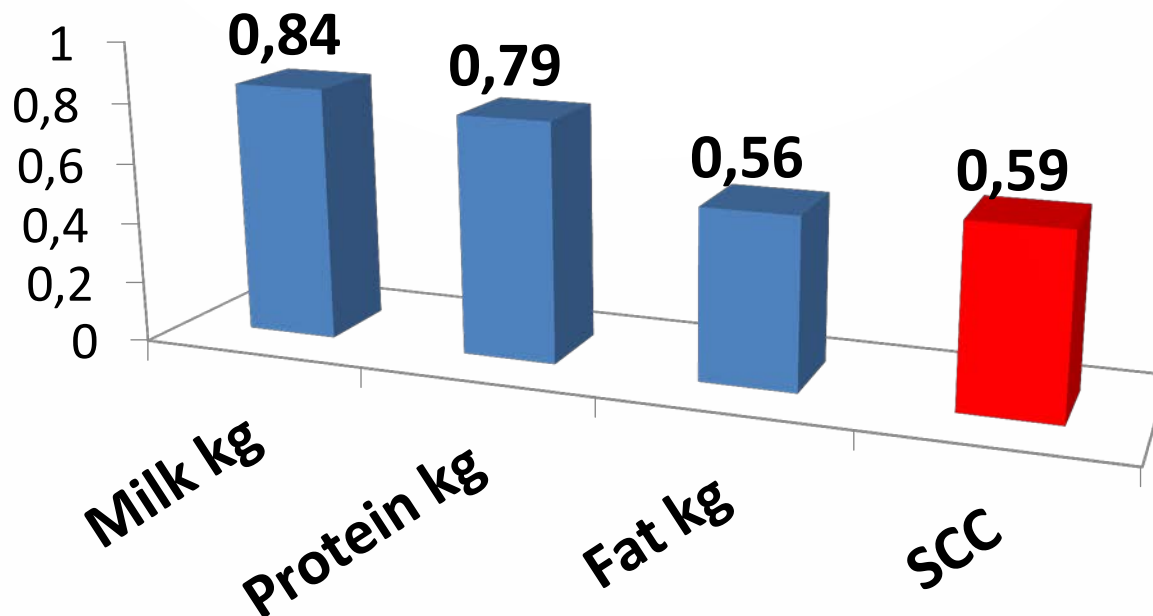
- more accurate yet much simpler than multi-step methods
- avoiding bias in GEBV prediction
- increase of breeding value prediction reliability for ungenotyped animals

Correlations for production traits (RRTDM)

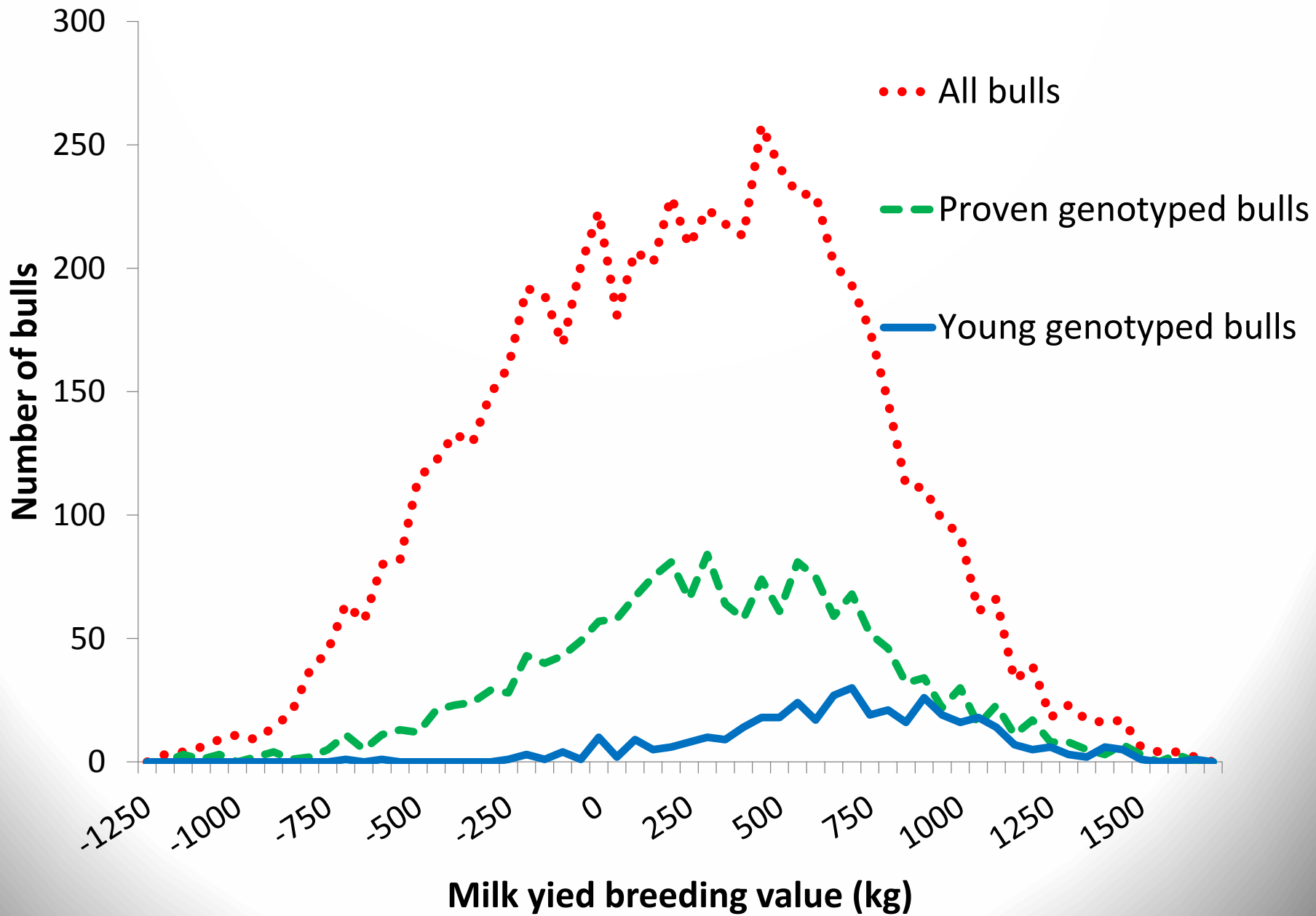


158 young bulls not proven in the Czech Republic

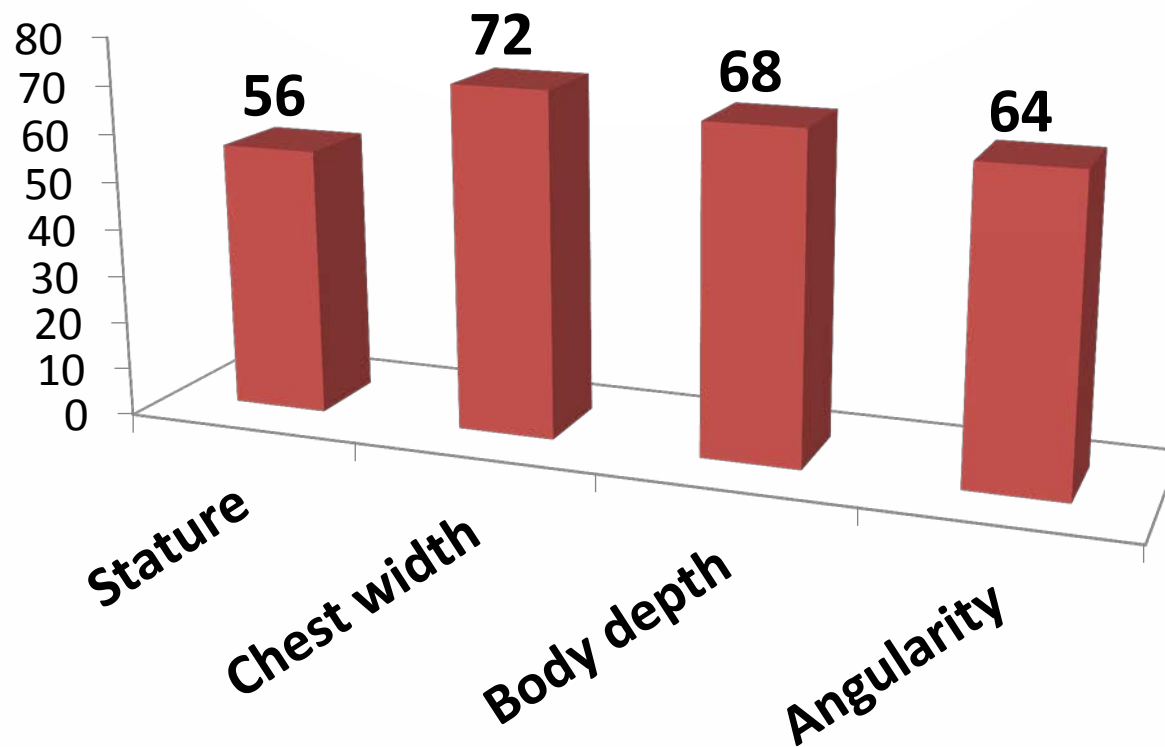
Correlations of GEBV to MACE for production traits (RRTDM)



73 bulls proven abroad but not in the Czech Republic

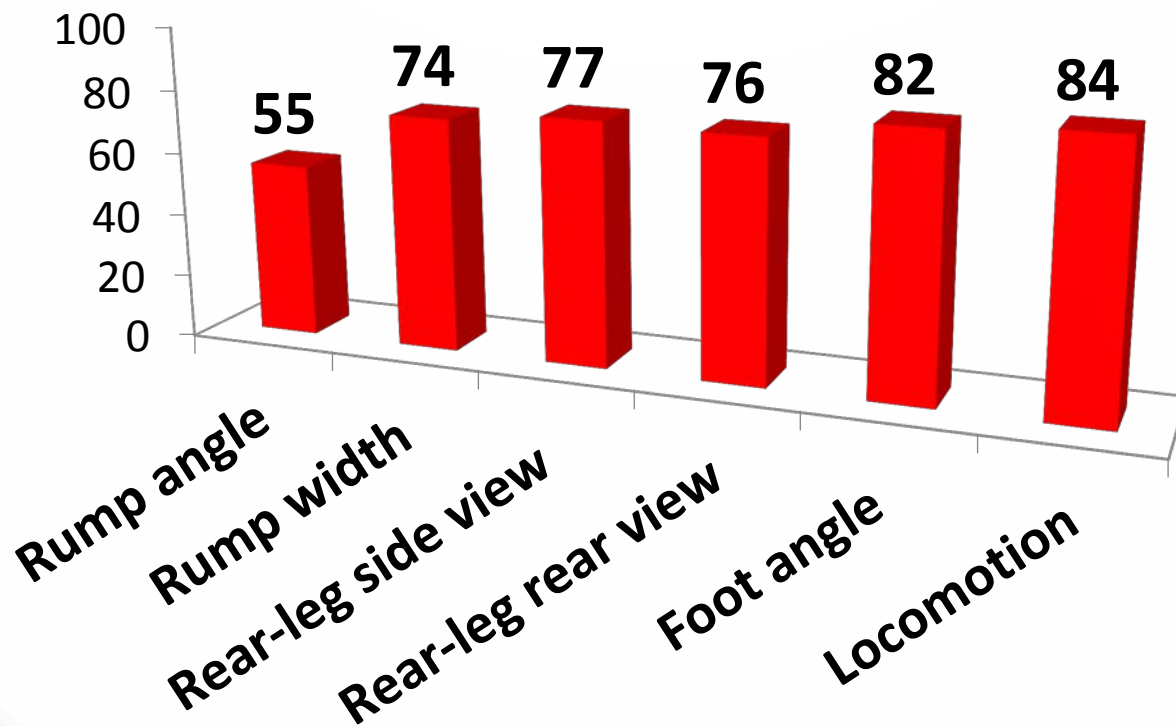


Correlations with GMACE for linear type traits – Body traits



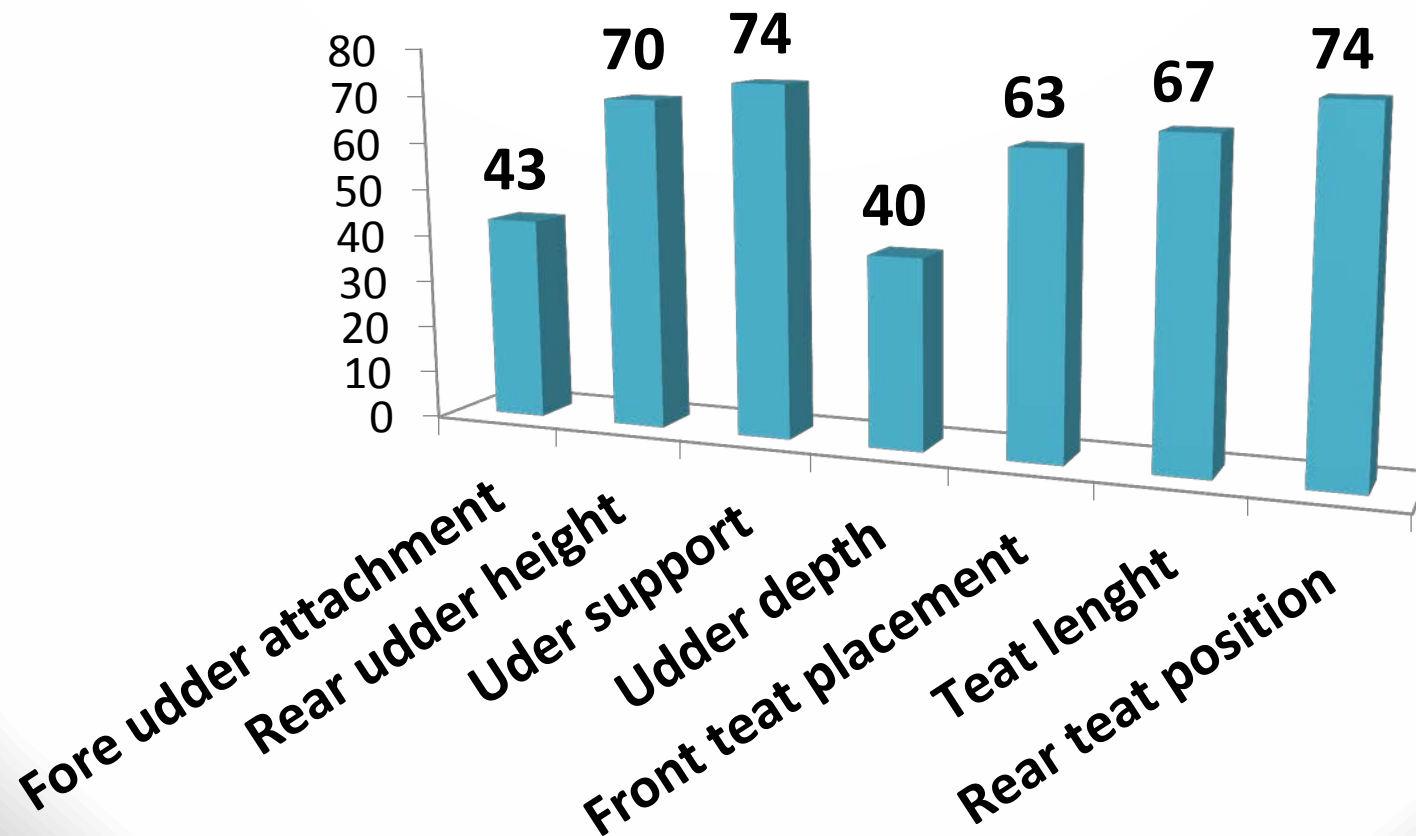
43 young bulls not proven in the Czech Republic

Correlations with GMACE for linear type traits – Feet & Legs



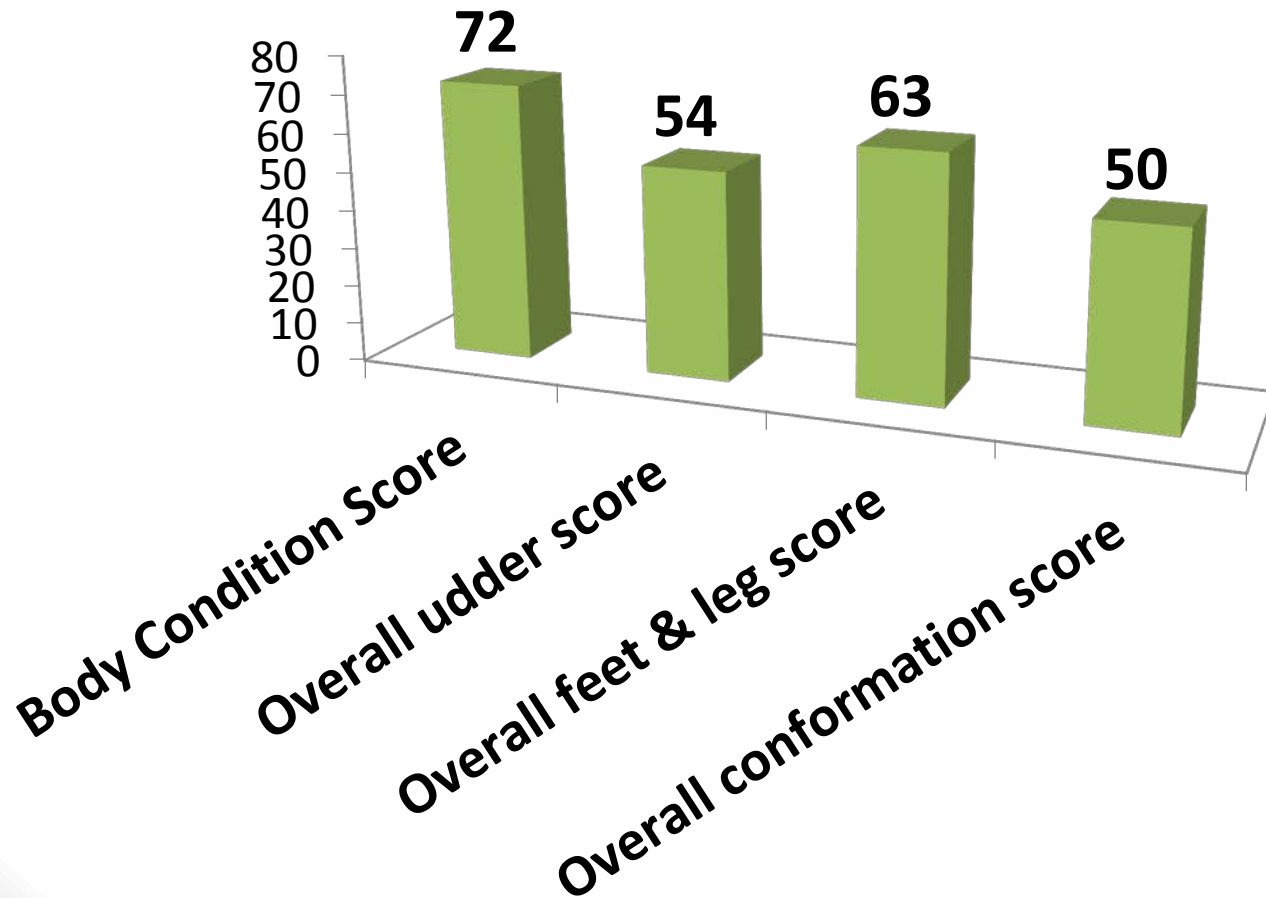
43 young bulls not proven in the Czech Republic

Correlations with GMACE for linear type traits - Udder



43 young bulls not proven in the Czech Republic

Correlations with GMACE for linear type traits – overall characteristics



43 young bulls not proven in the Czech Republic

Conclusion

Single-step Genomic Evaluation

as the best approach for the Czech Republic

- The stronger correlation with GMACE
compared to multi-step approaches
- Medium to high correlations with GMACE
for production traits as well as linear
type traits

Thank You for Your attention

Additional notes

Weighted analysis

$$\text{ERC} = \delta (\text{rel}/(1-\text{rel}))$$

$$\delta = ((1-h^2)/ h^2)$$

Weighted analysis

Ridge Regression

$$\text{DRP}_j = \mu + \sum \delta_i \cdot g_{ij} + e_j$$

Fixed effects

μ – common constant

Random effects

g_{ij} – genotype of j-th bull in i-th locus

δ_i – regression coefficient

e_j – residual

Heritability (h^2) = 0.25; Weight = ERC

Weighted analysis

GBLUP

$$\text{DRP}_j = \mu + \text{an}_j + \text{e}_j$$

Fixed effects

μ – common constant

Random effects

an_j – animal

e_j – residual

Heritability (h^2) = 0.25; Weight = ERC

BLUP / ssGBLUP, lactation model

$$\text{milk}_{ijkl} = \text{HYS}_i + \beta_1 \cdot \text{ca}_k + \beta_2 \cdot \text{ca}_k^2 + \beta_3 \cdot \text{do}_l + \beta_4 \cdot \text{do}_l^2 \\ + \text{an}_j + \mathbf{e}_{ijkl}$$

Fixed effects

HYS – contemporary group

β – regression coefficients

ca_k ; ca_k^2 – curvilinear regression
on calving age

do_l ; do_l^2 – curvilinear regression
on days open

Random effects

an_j – animal

\mathbf{e}_{ijkl} – residual

Heritability (h^2) = 0.25;

ssGBLUP, RR-TDM, 3 lactations

$$y_{ijn} = \text{HTD}_{in} + f_{fg,n} + f_{pe,n} + f_{an,n} + e_{ijn} \quad ,$$

y_{ijn} = test-day record of milk yield of cow in lactation $n < 1, 2, 3 >$;

HTD_{in} = herd-test-day contemporary group i within a herd in lactation n (fixed effect);

$f_{fg,n}$ = average LP of lactation curve according to groups of cows within management classes of systematic environment (Zavadilová et al., 2005b) (fixed effect);

$f_{pe,n}$ = permanent environmental within lactation LP of lactation curve of cows, random effect with covariance matrix (Zavadilová et al., 2005a);

$f_{an,n}$ = genetic within lactation LP of lactation curve of animal, random effect with covariance matrix;

e_{ijn} = random residual of test day records within lactation n , reflecting changes of variability along the course of lactation.

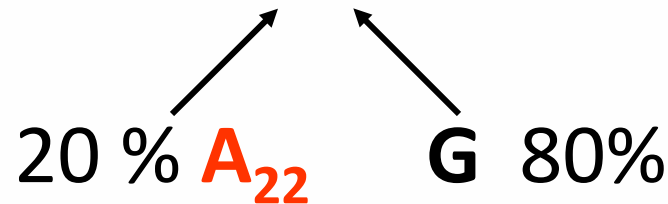
Relationship

Ridge Regression...I

BLUP – AM**A**

GBLUP.....**G** (*VanRaden 2008*)

ssGBLUP.....**H** (*Legarra et al., 2009*)



G – normalised (aver. diag. = 1)

(*Forni et al., 2011*)

shifted (aver. **G** = aver. **A₂₂**)

(*Vitezica et al., 2011*)

SNP editing:

- MAF,
- G-score,
- No. of loci per bull,
- No. of bulls per locus,
- Big error of prediction of old bulls
in training set,
- Big discrepancy of relationship $A_{22} \times G$,
- Proportion of H.