

Implanting MACE values in national single step genomic evaluation

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Holstein population in Czech

- ▶ 220.000 cows, ~210.000 in recording system
- ▶ Open population, with strong influence of imported bulls
- ▶ Data: 1,3 mil. recorded cows from 1995 (~25 mil. records)
- ▶ Milk production 9.792 kg, calving interval 408 days
- ▶ Usually bigger herds > 200 cows

History of ssGBLUP in Czech Rep.

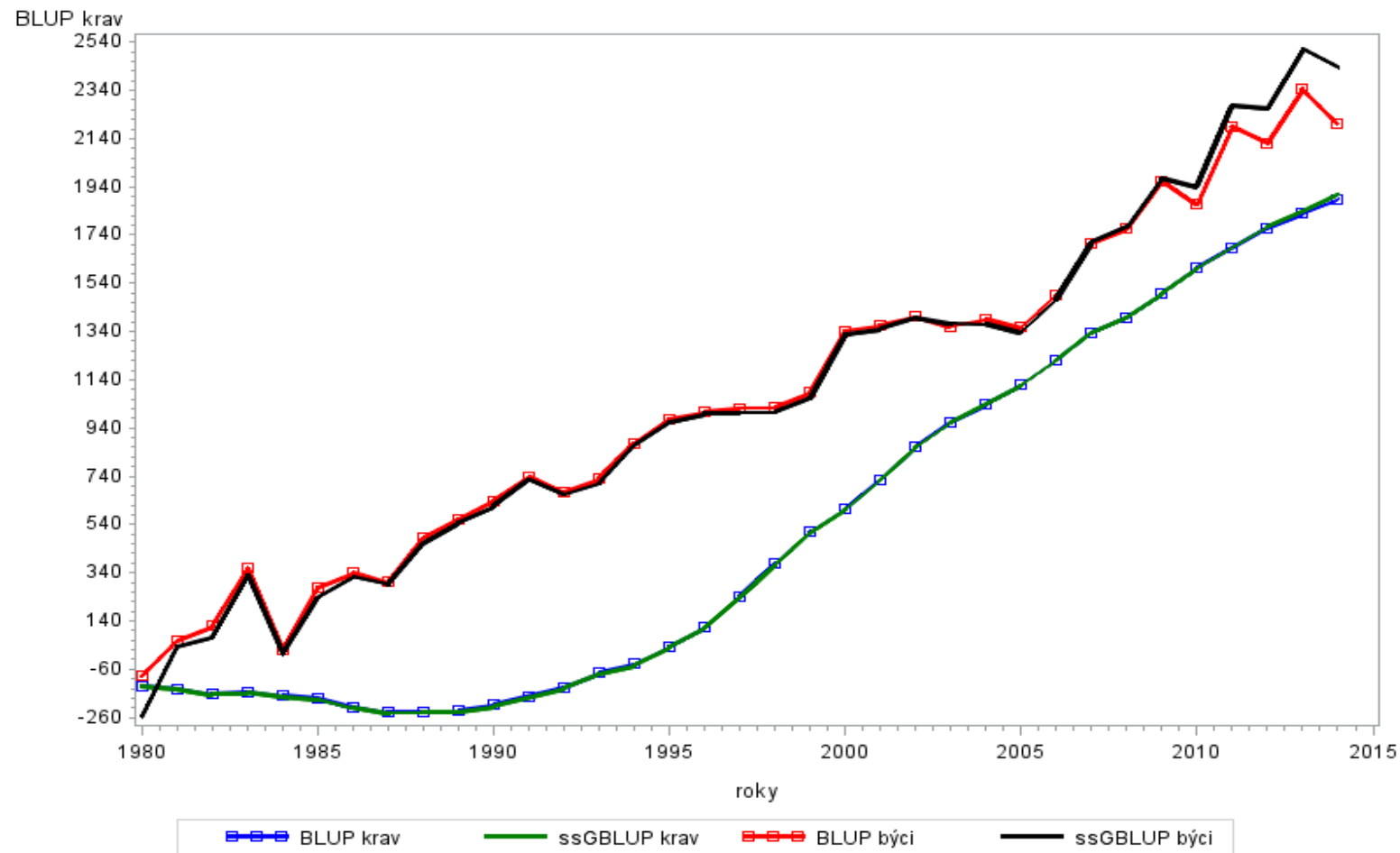
- ▶ 2011 beginning of the ssGBLUP development
- ▶ Own programs based on Misztal and Madsen
- ▶ 2014 first release for production traits, followed by somatic cells
- ▶ 2015 added other traits and genomic index
- ▶ 09/2015 production traits validated by Interbull

Current status

- ▶ Single step genomic BLUP for Holsteins
- ▶ Official release of young genomic bulls every 2 months
- ▶ Production traits, somatic cells score, Conformation traits, fertility, longevity
- ▶ Of about 4100 genotypes (600 young bulls, 2000 proven bulls, 1000 „proven“ cows, 500 bulls only in pedigrees)
- ▶ Production model: Test day AM with random regression
- ▶ Other models: single traits AM
- ▶ Longevity: Survival Kit, thus genomic Blending-GBLUP
- ▶ Reliability according Misztal 2013

Genetic gain kg milk

Genetický zisk podle BLUP a ssGBLUP hodnocení

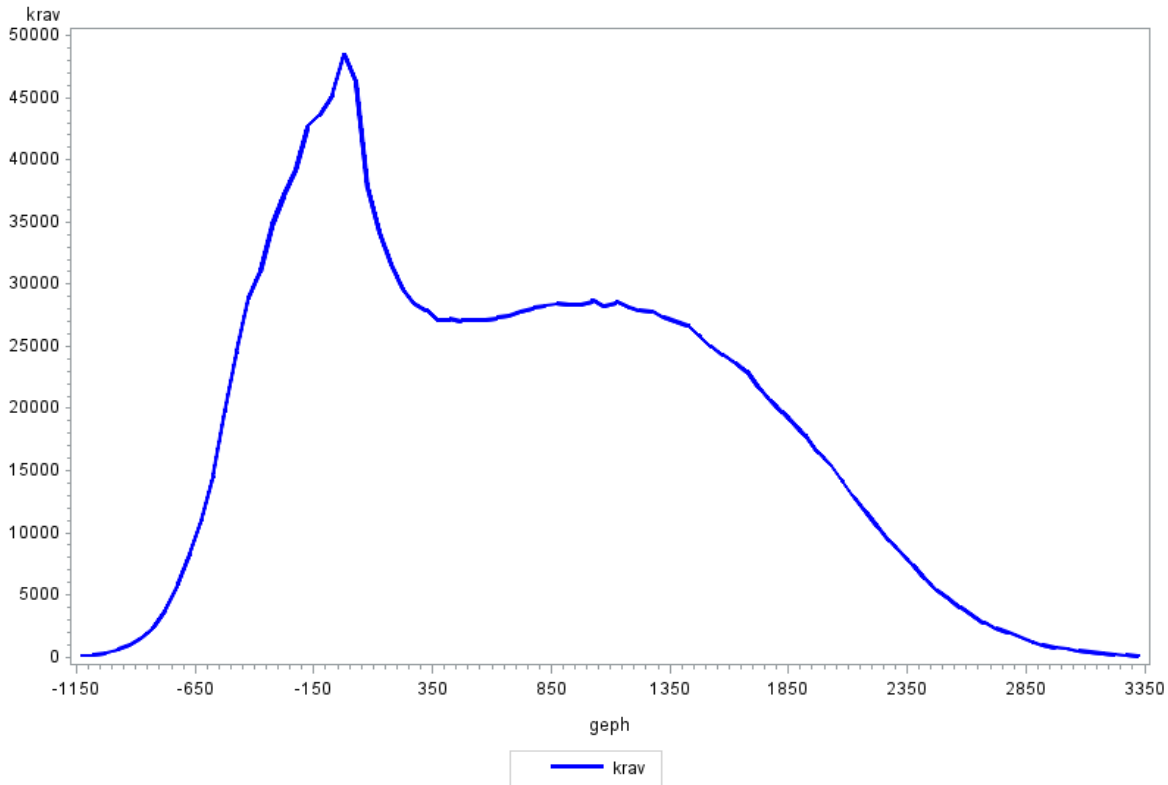


GBVs according groups of animals

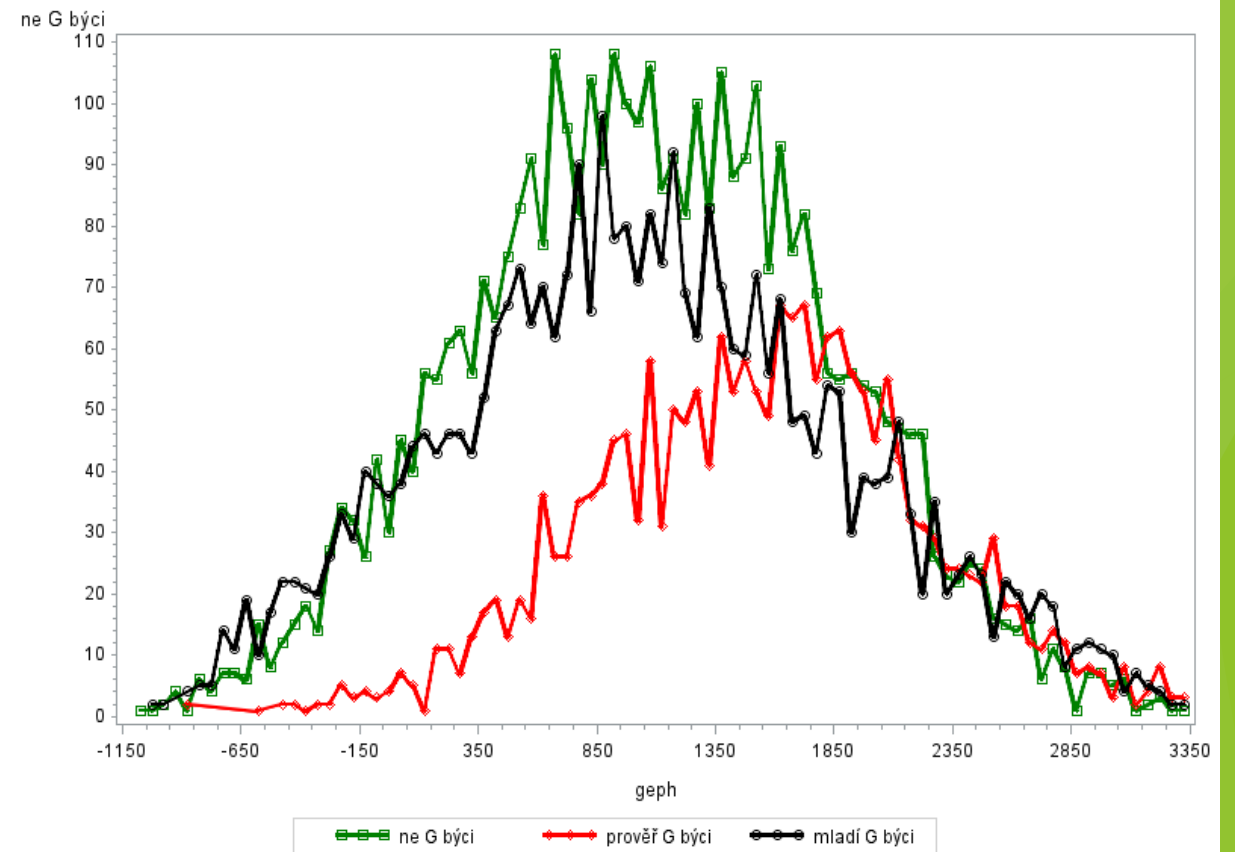
	N	average	s	minimum	maximum	Reliability
cows	1 655 633	699	848	-1 887	4 080	0,573
No-genotyped buls	3 973	1 088	768	-1 160	3 777	0,816
Proven genotyped bulls	2 034	1 541	693	-895	3 694	0,934
Young genotyped animals	3 349	1 070	853	- 1 020	3 500	0,747

Distribution of GBVs - kg milk

Četnosti PH krav ze ssGBLUP hodnocení

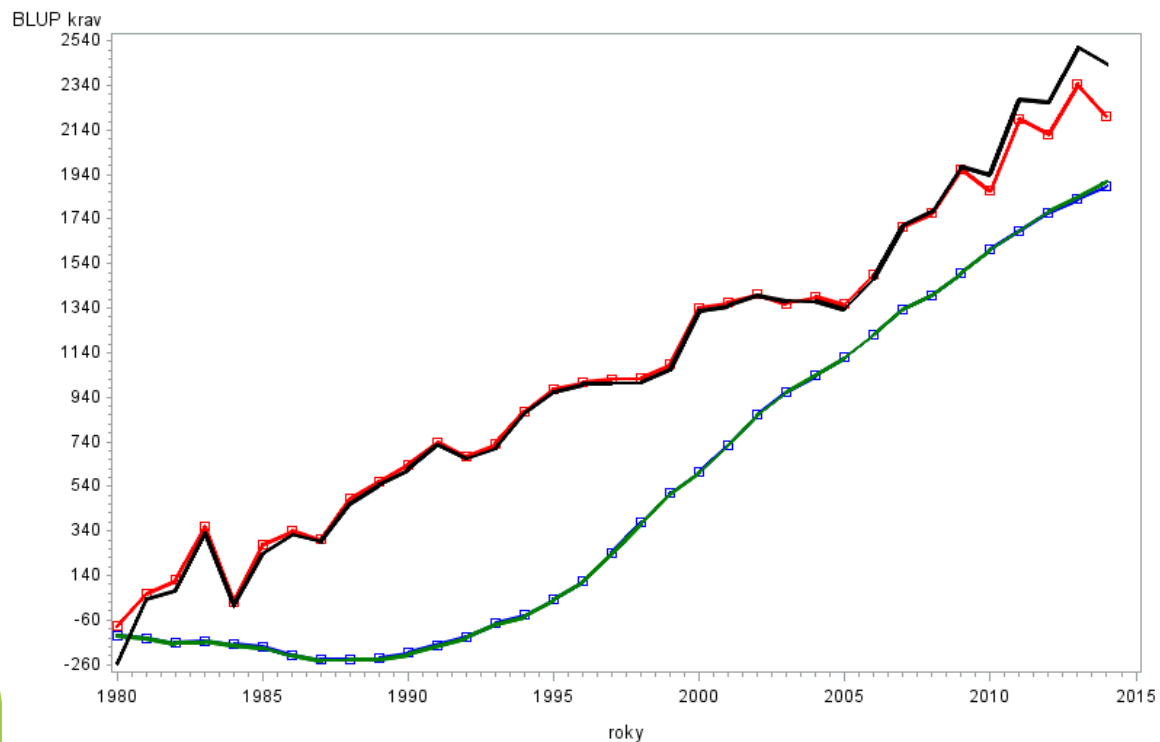


Četnosti PH/GEPH býků ze ssGBLUP hodnocení



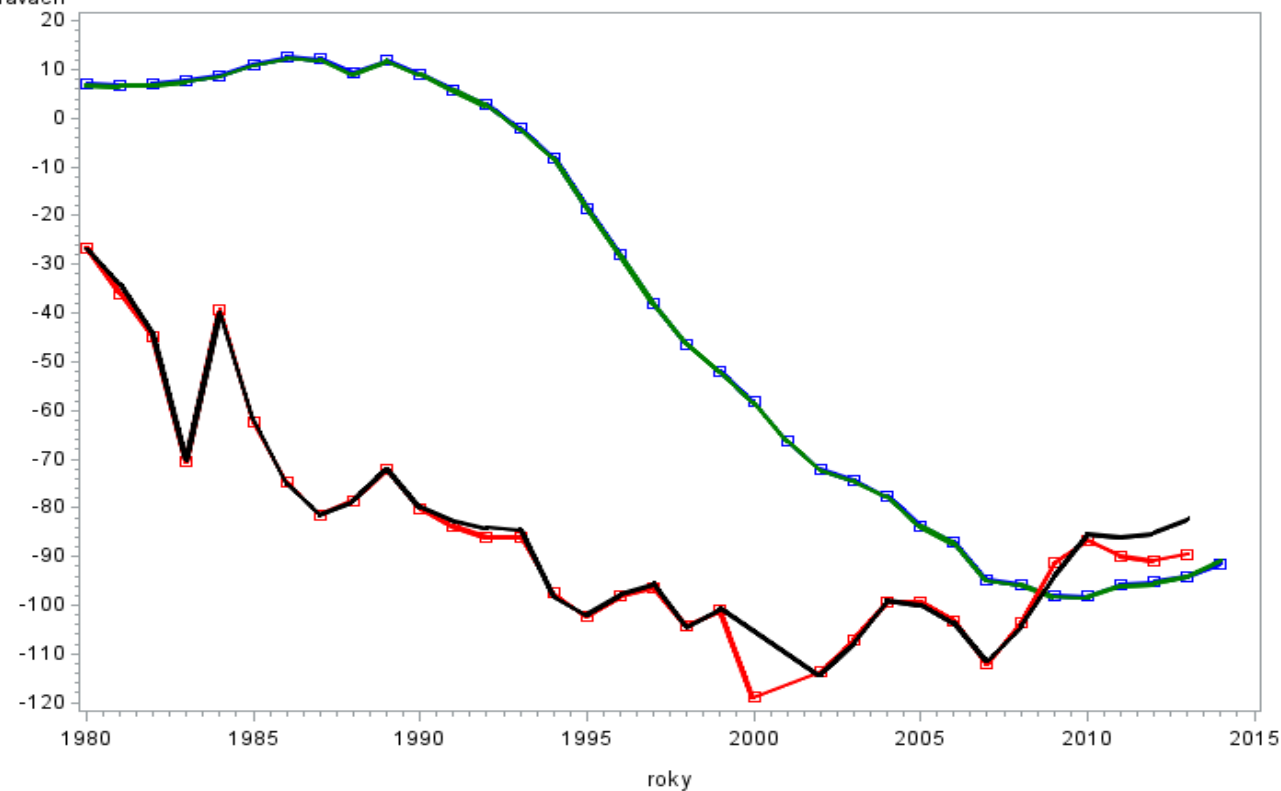
Genetic trend comparsion- milk vs. fertility

Genetický zisk podle BLUP a ssGBLUP hodnocení



Genetický zisk podle BLUP a ssGBLUP na kravach

BLUP krav na kravach

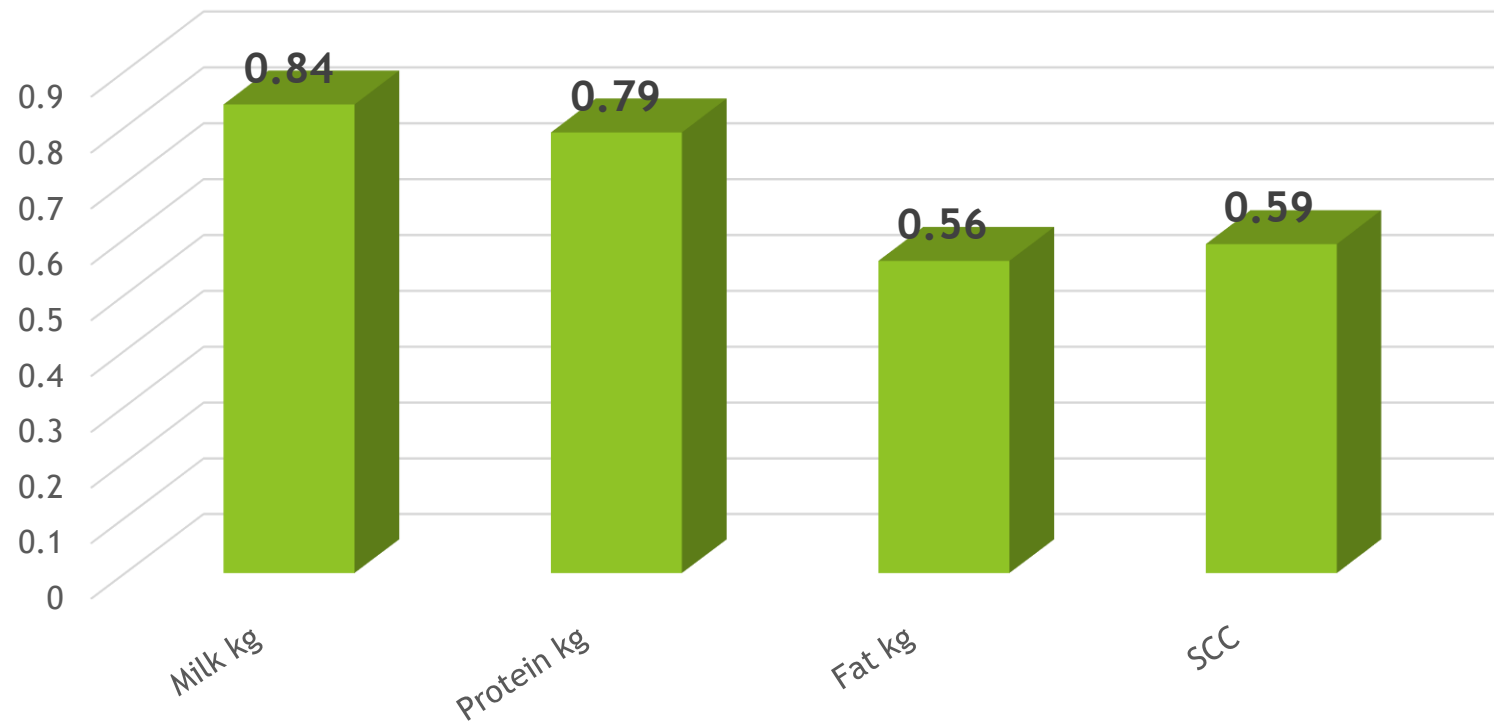


BLUP krav ssGBLUP krav BLUP býci ssGBLUP býci

BLUP krav na kravach ssGBLUP krav na kravach
BLUP býci na kravach ssGBLUP býci na kravach

Problems with ssGBLUP

- ▶ With low number of proven bulls < 1.000 the results we not satisfying
- ▶ Bull proven in MACE does not match with no-daughter genomic estimation



Divergence of model

- ▶ Low density chips are causing overestimating in genomic-relationship matrix especially among siblings.
- ▶ Only non-uniform SNP should be used. Filter by minor allele frequency needed ($> 95\%$)
- ▶ Both cause the iteration process to diverge

“Unrelated” bulls

- ▶ Strong import of foreigner bulls
- ▶ No info from family (female records)
- ▶ Sire (even MGS) has no daughters in CZ yet
- ▶ TOP world bulls can be unrelated to our domestic recording system
- ▶ These bulls are often dragged to the average - thus underperforming

Mace information needed, and better sorted

- ▶ Too many BVs:
- ▶ National evaluation
- ▶ MACE
- ▶ National genomics
- ▶ GMACE

- ▶ => Confused breeders

- ▶ Goal for this year - merging all

1st option

- ▶ We can send ssGBLUP results into MACE
- ▶ Then just merge the results
- ▶ Easy, but probably unfair

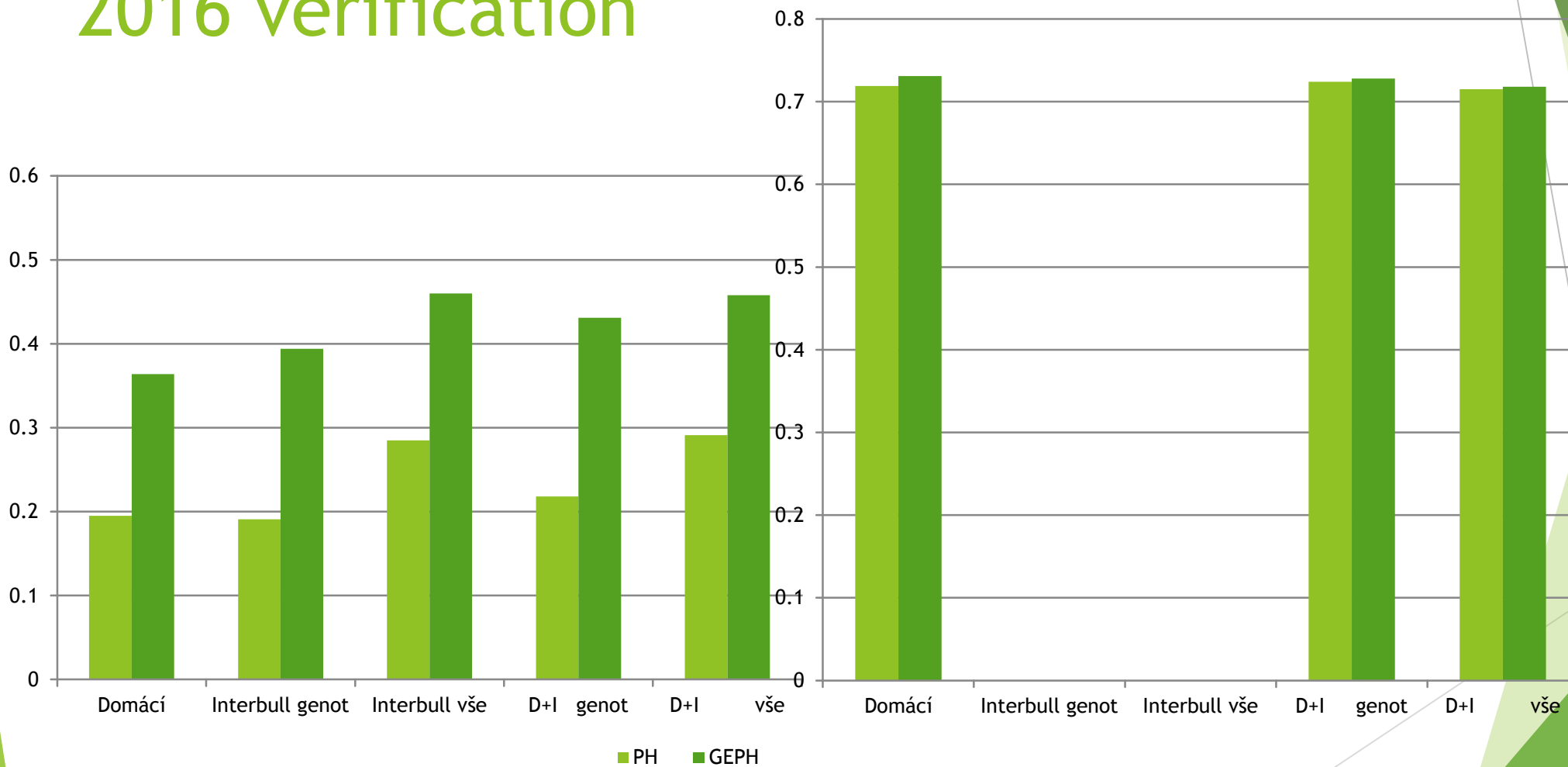
2nd option

- ▶ Using Mace as a input into domestic ssGBLUP aside records
- ▶ More difficult
- ▶ Problem with double counting of daughters

MACE as input to ssGBLUP

- ▶ Deregreded EBVs from MACE (Liu, 2014)
- ▶ Converted into test day records
- ▶ Selection index used for approximation of weights for each pseudo-record
- ▶ Added into one additional HYS aside domestic TD records

Validated reliability 2012 prediction vs. 2016 verification



Y.Bulls 2012 / 2016 >20 daughters (75 avg.)

domestic heifers 24.146 in 2012 / 3 lactations in 2016

Conclusion

- ▶ ssGBLUP is efficient for our population
- ▶ MACE values can be used for improvement for bulls with foreign pedigrees
- ▶ Simplifying of publications for ordinary farmer and his cows