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Innovative combination of all sources of information for production traits in Slovenian Brown Swiss

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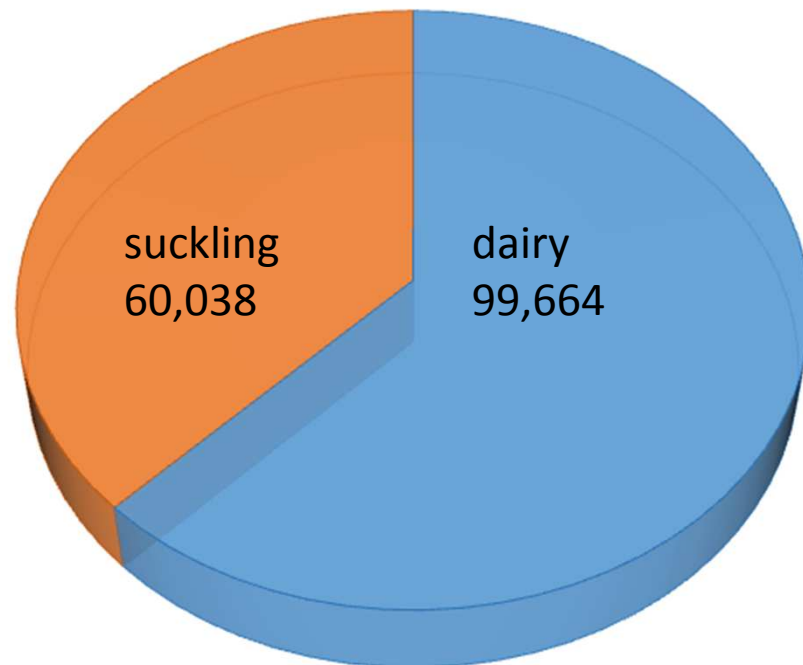
Content

- ✓ Slovenian cattle breeding
- ✓ Current evaluation methods
- ✓ Aim of the study
- ✓ Results
- ✓ Conclusions

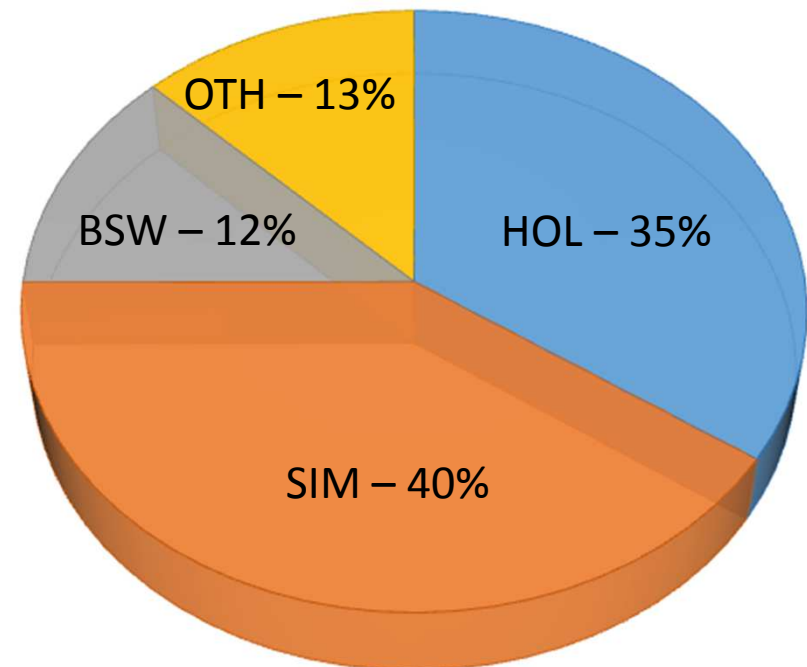
Current Slovenian situation

- ✓ Brown Swiss dairy cattle
- ✓ Small population

Number of cows – 159,702



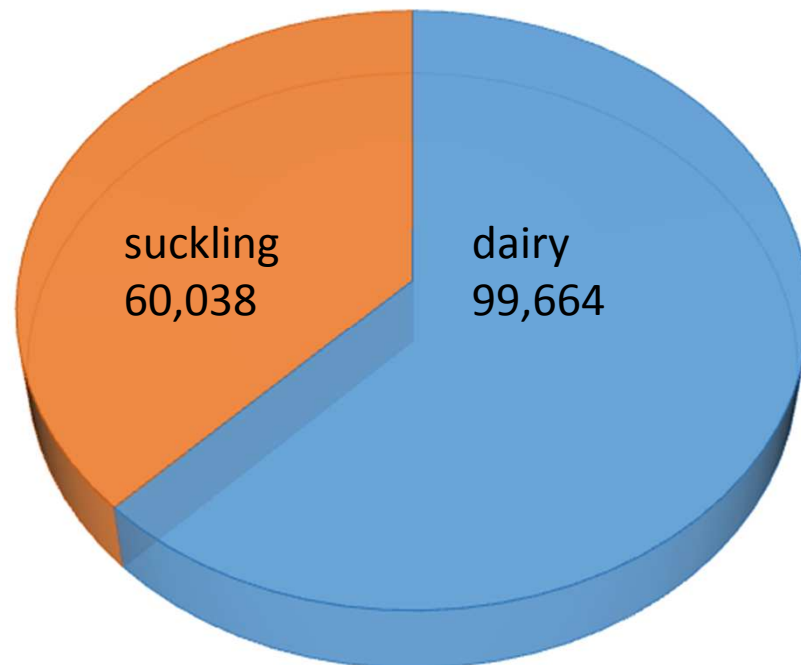
Proportion of dairy cows by breed



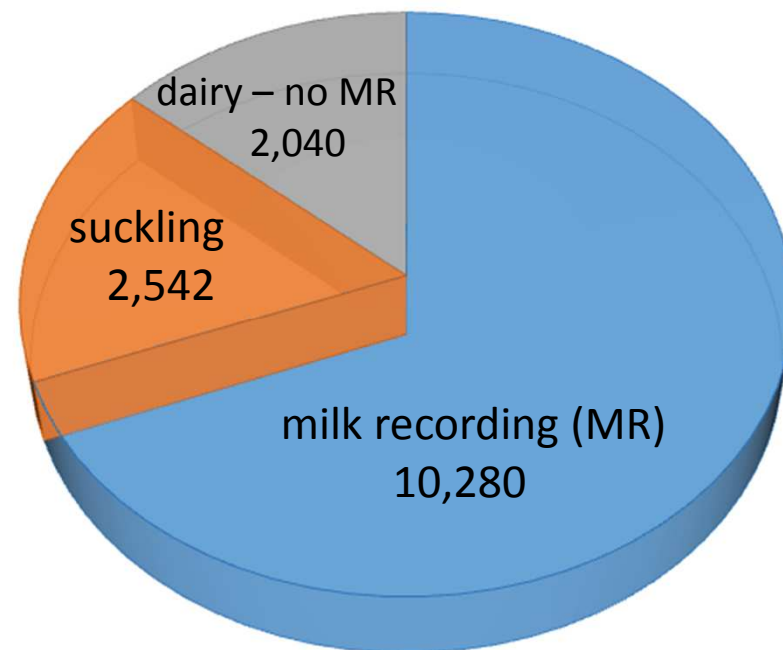
Current Slovenian situation

- ✓ Brown Swiss dairy cattle
- ✓ Small population

Number of cows – 159,702



Number of BSW cows – 14,862



Current Slovenian situation

- ✓ Brown Swiss dairy cattle
- ✓ Small population
 - ✓ Genetic improvement based on its own breeding program supplemented with import from other populations

Evaluation January 2014		Sires	Number	>300 daughters	
TD records	1,286,698	SVN	576	129	22.4%
Cows	56,764	Foreign	180	15	8.3%
Lactations	156,917	Total	756	144	19.0%

Current BSW evaluations

- ✓ Genetic evaluations

- ✓ National

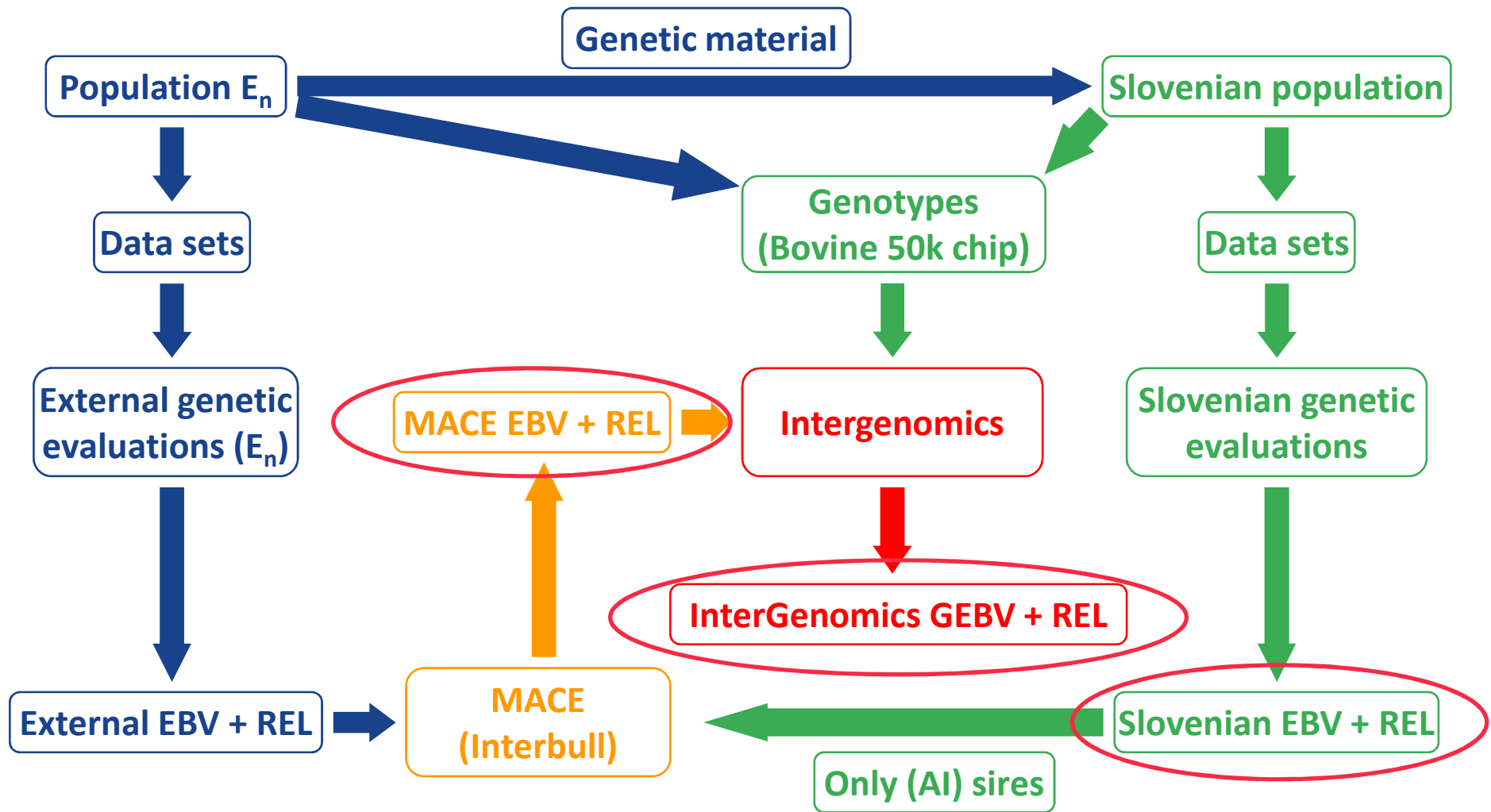
- ✓ TD model → domestic animals

- ✓ International

- ✓ MACE → foreign sires

- ✓ Intergenomics → young animals

Current BSW evaluations



Aim

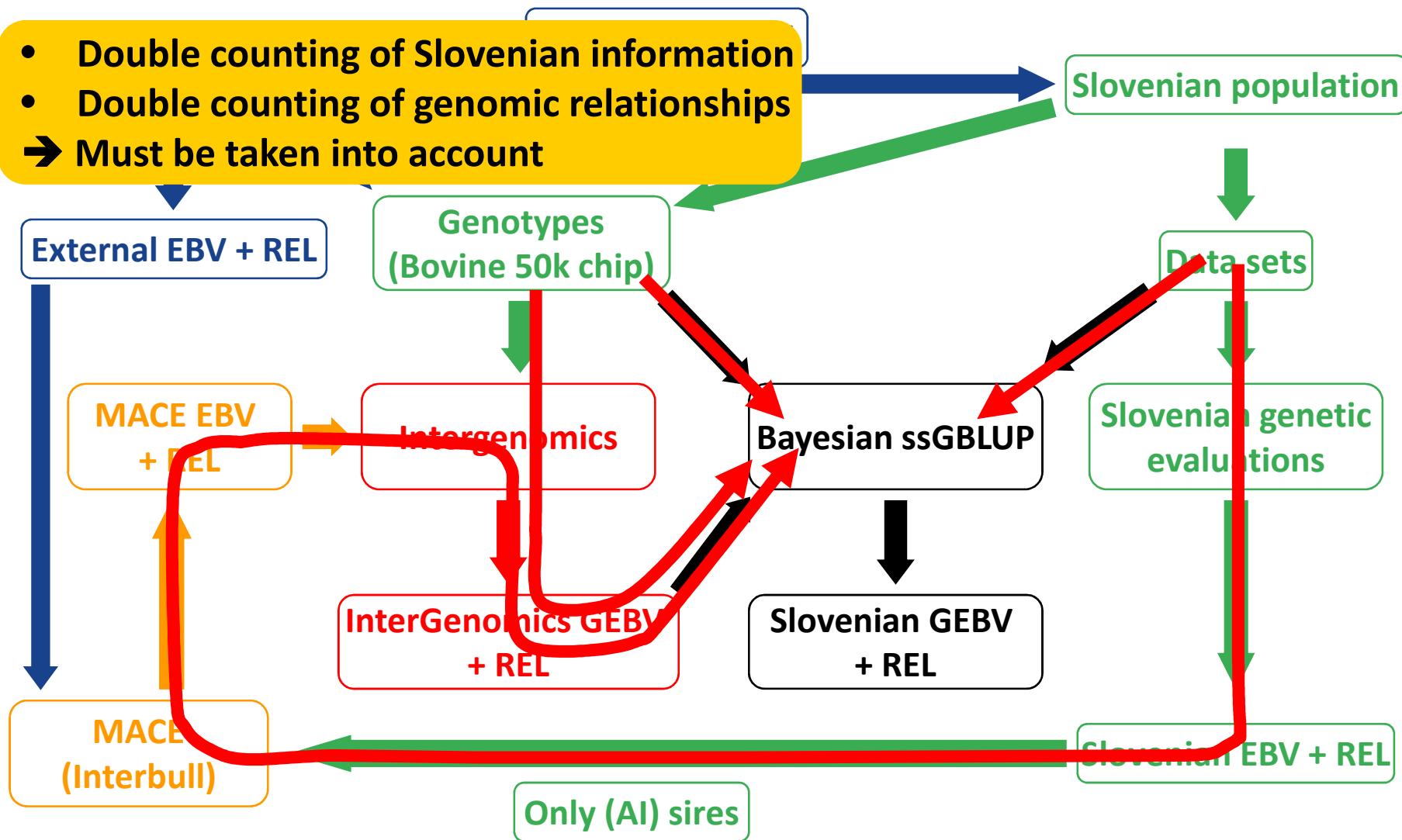


- ✓ Combination of
 - ❑ Pedigree
 - ❑ Slovenian phenotypes
 - ❑ Intergenomics genotypes
 - ❑ Intergenomics GEBV and GREL

- ✓ For milk, fat, and protein yields

Methods

- Double counting of Slovenian information
- Double counting of genomic relationships
- ➔ Must be taken into account



Methods

- ✓ Simultaneous combination of Slovenian phenotypes, InterGenomics genotypes and InterGenomics GEBV and REL
 - ❑ Based on a single-step genomic BLUP (ssGBLUP)
 - ❑ Based on a Bayesian view of linear (mixed) models
 - ❑ Priors constructed from InterGenomics GEBV and REL
- ➔ Only one process
- ➔ Contribution of external information to the estimation of all effects
 - ➔ Propagation to all animals

Data

- ✓ Traits: milk, fat and protein yields
- ✓ Phenotypes (e.g., milk yield)
 - ❑ 1,286,698 records
 - ❑ 56,764 cows
- ✓ 5,852 InterGenomics genotypes
- ✓ 5,852 animals with InterGenomics GEBV and REL
- ✓ Pedigree: 101,522 animals
- ✓ 277 bulls with Slovenian information contributing to InterGenomics evaluations

Results: Rank correlation for milk yield

- ✓ 319 genotyped sires with InterGenomics GEBV and REL and **with** progeny with national records

Evaluations	r^1	REL (SD) ²
InterGenomics	1.00	0.97 (0.02)
National	0.79	0.87 (0.19)
Bayesian ssGBLUP	>0.99	0.97 (0.02)

¹ r = rank correlation between InterGenomics GEBV and national EBV or Bayesian ssGBLUP GEBV

²REL = average reliability (SD in parentheses)

Results: Rank correlation for milk yield

- ✓ 5,533 genotyped sires with InterGenomics GEBV and REL and **without** progeny with national records

Evaluations	r^1	REL (SD) ²
InterGenomics	1.00	0.90 (0.02)
National	0.55	0.17 (0.19)
Bayesian ssGBLUP	>0.99	0.91 (0.02)

¹r = rank correlation between InterGenomics GEBV and national EBV or Bayesian ssGBLUP GEBV

²REL = average reliability (SD in parentheses)

Results: Rank correlation for milk yield

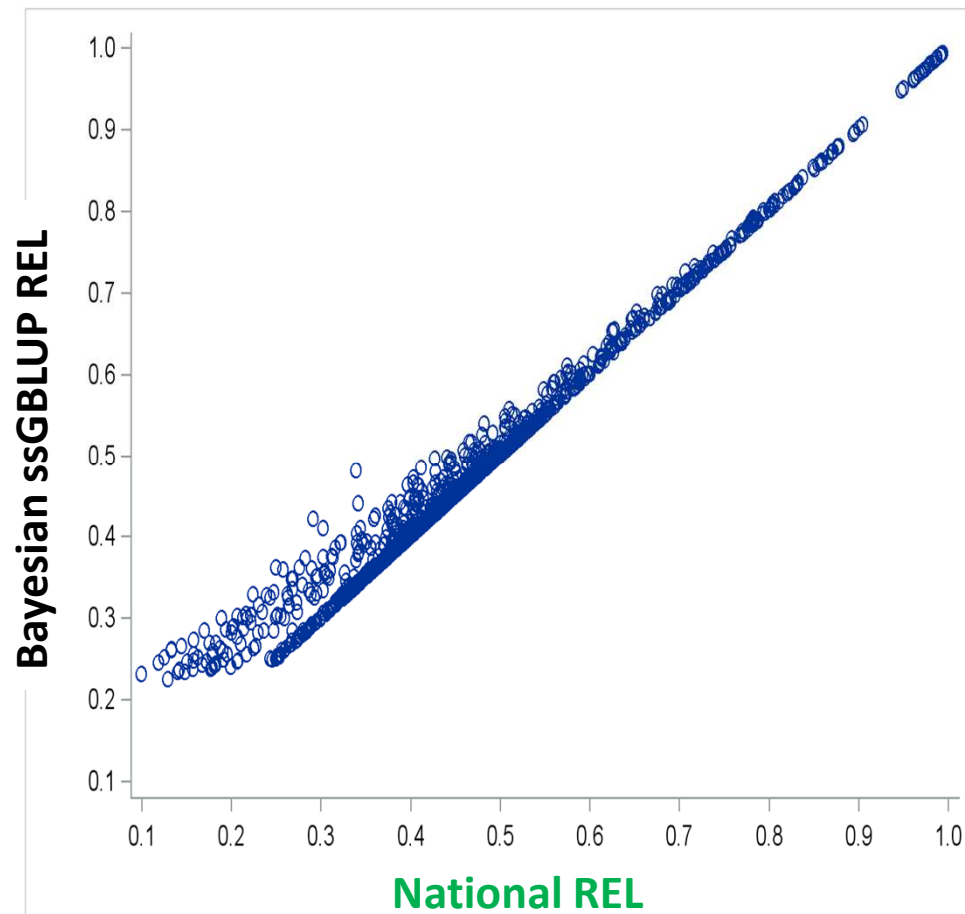
- ✓ Slovenian animals without records and sired by a genotyped InterGenomics sire

Evaluations	Rank correlations ¹		
	REL _s <0.50 N=1,520	0.50<REL _s <0.75 N=348	REL _s >0.75 N=103
National	1.00	1.00	1.00
Bayesian ssGBLUP	0.95	0.99	0.99

¹r = rank correlation between National EBV and Bayesian ssGBLUP GEBV

Results: Reliability for milk yield

- ✓ Slovenian animals without records and sired by a genotyped InterGenomics sire: REL



Conclusions

- ✓ Bayesian approach integrates well InterGenomics GEBV and REL into a ssGBLUP
 - ➔ Recovers large amount of information
 - ➔ Almost the same results for all studied traits
- ✓ Propagation of information
- ✓ Double counting of contributions due to (genomic) relationships and own records avoided
- ✓ More accurate prediction for genotyped animals
- ✓ Availability to consider genotypes of other not InterGenomics evaluated animals (e.g., cows)

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