



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

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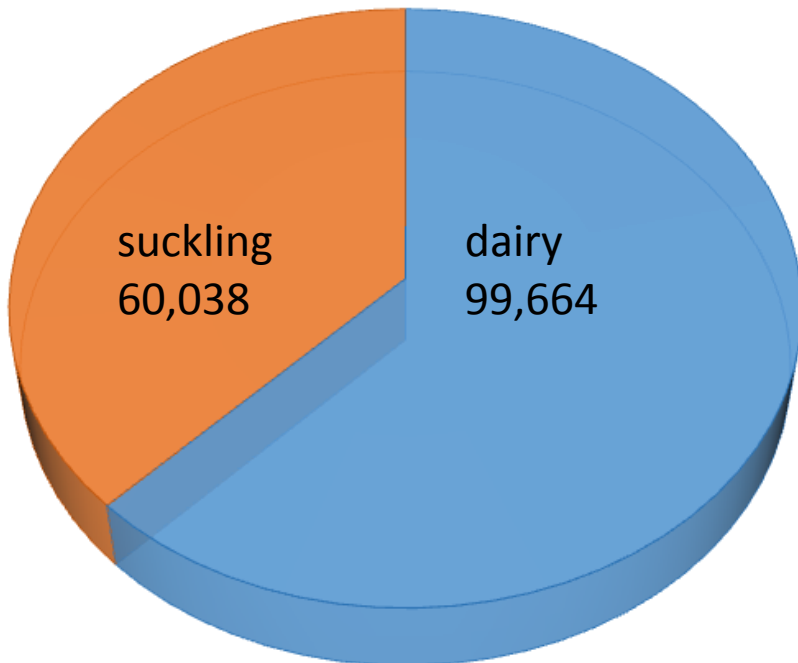
Content

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

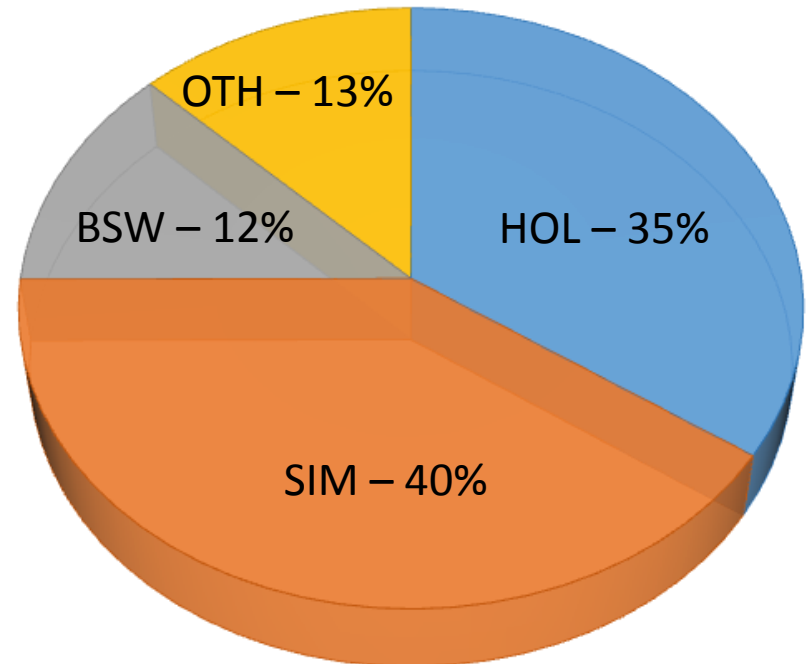
Current Slovenian situation

- ✓ Brown Swiss dairy cattle
- ✓ Small population

Number of cows – 159,702



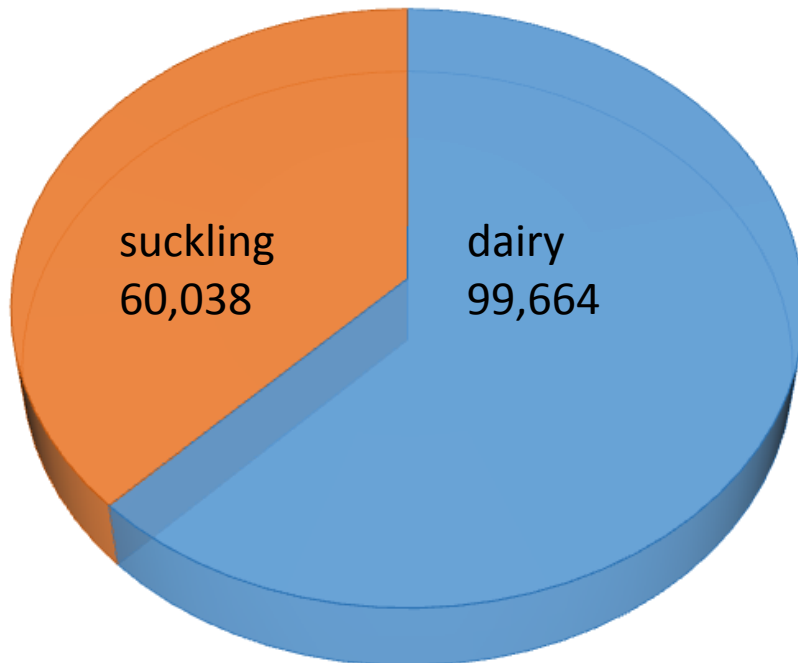
Proportion of dairy cows by breed



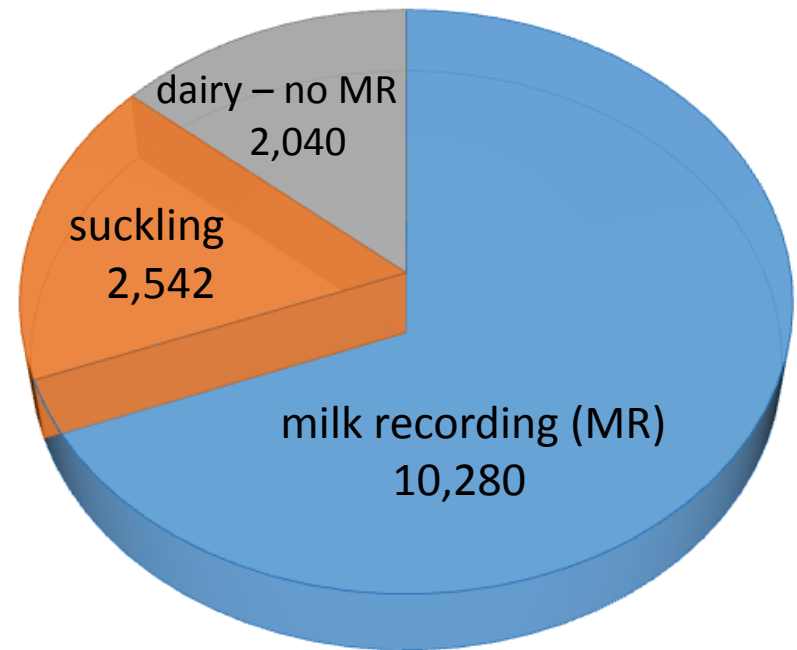
Current Slovenian situation

- ✓ 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

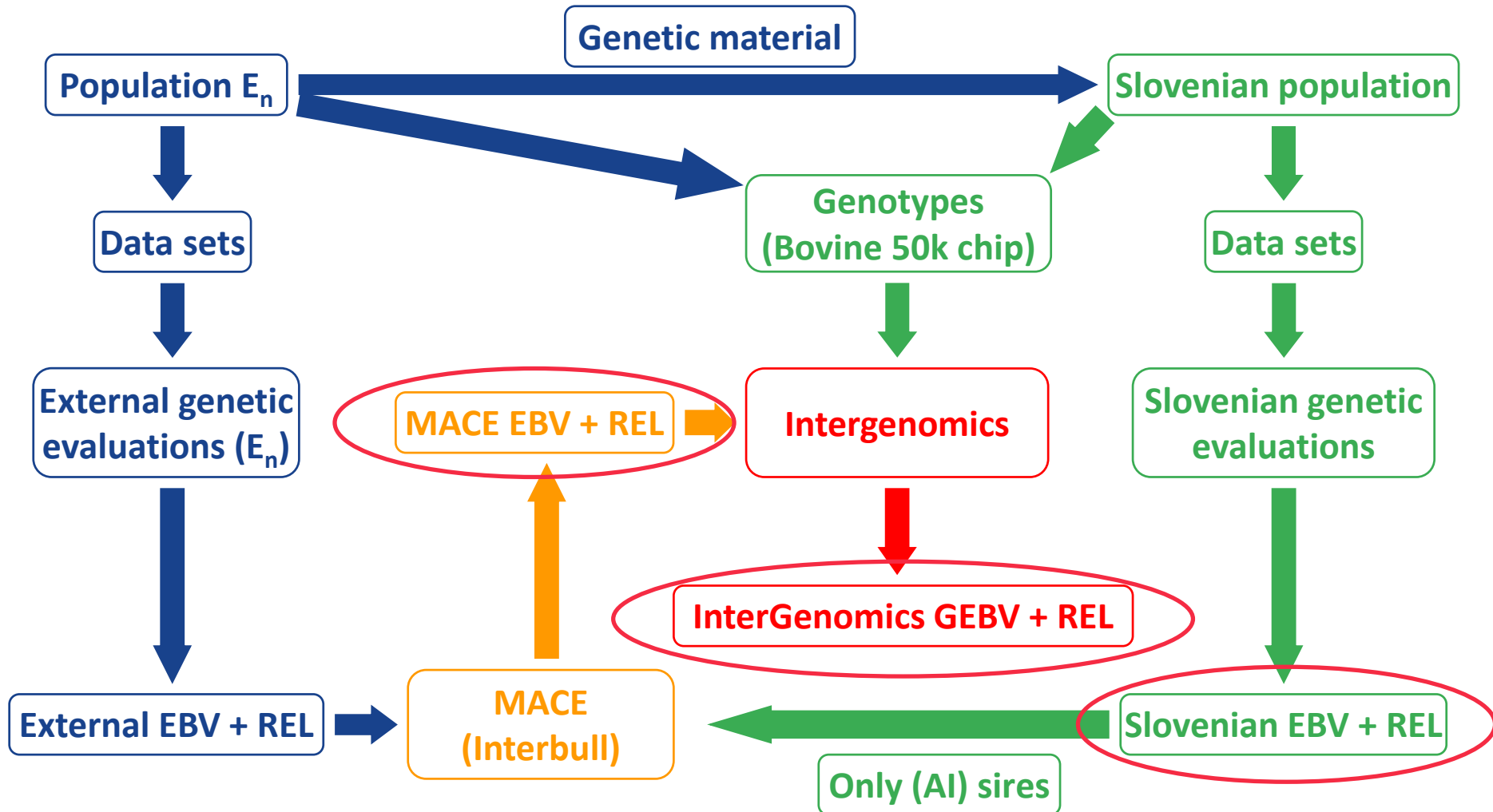
 - ✓ TD model → domestic animals

 - ✓ International

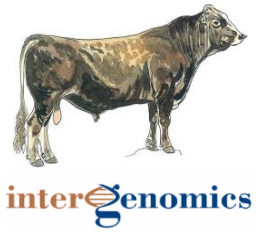
 - ✓ MACE → foreign sires

 - ✓ Intergenomics → young animals

Current BSW evaluations



Aim

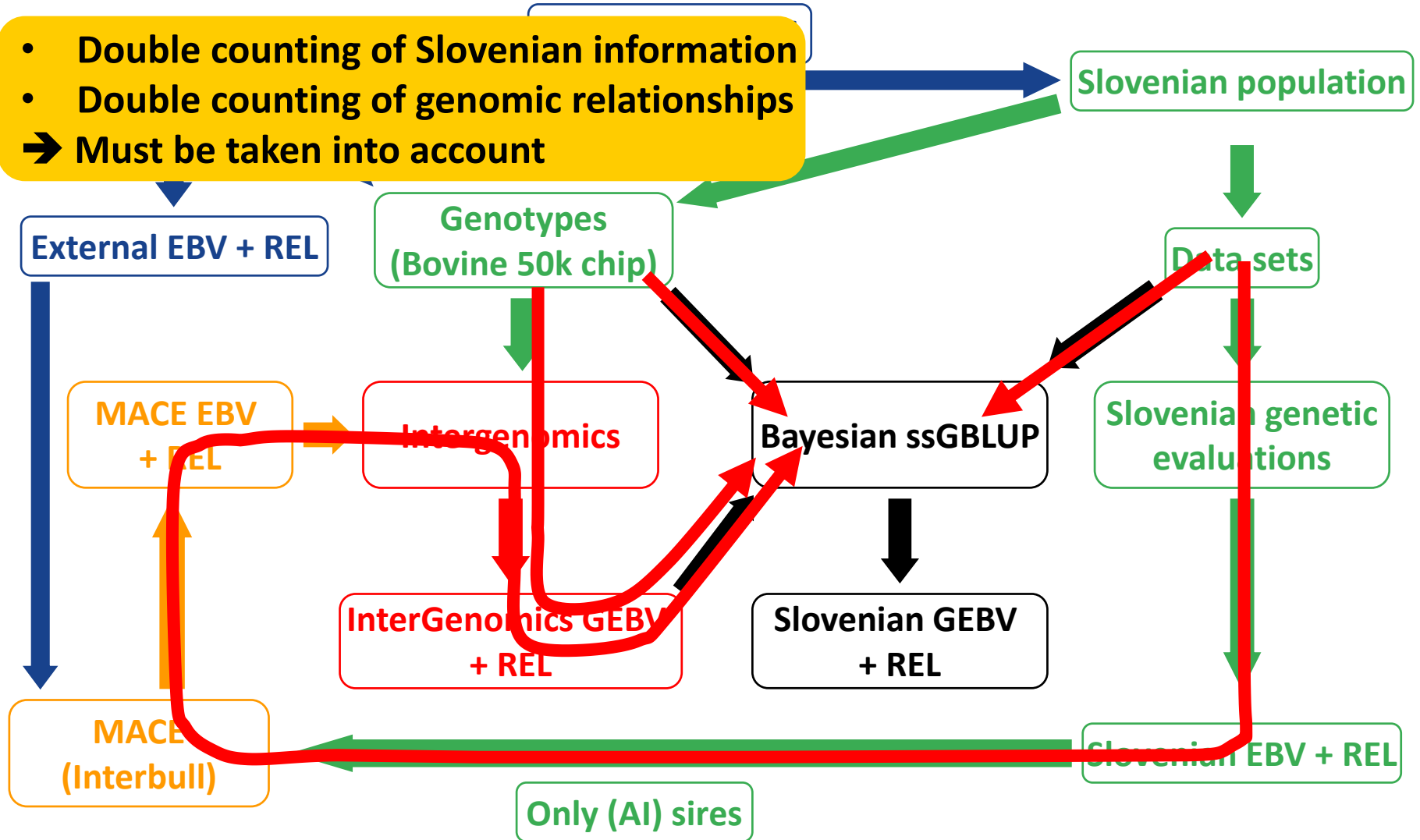


- ✓ Combination of
 - ❑ Pedigree
 - ❑ Slovenian phenotypes
 - ❑ Intergenomics genotypes
 - ❑ Intergenomics GEBV and GREL

- ✓ 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) |

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

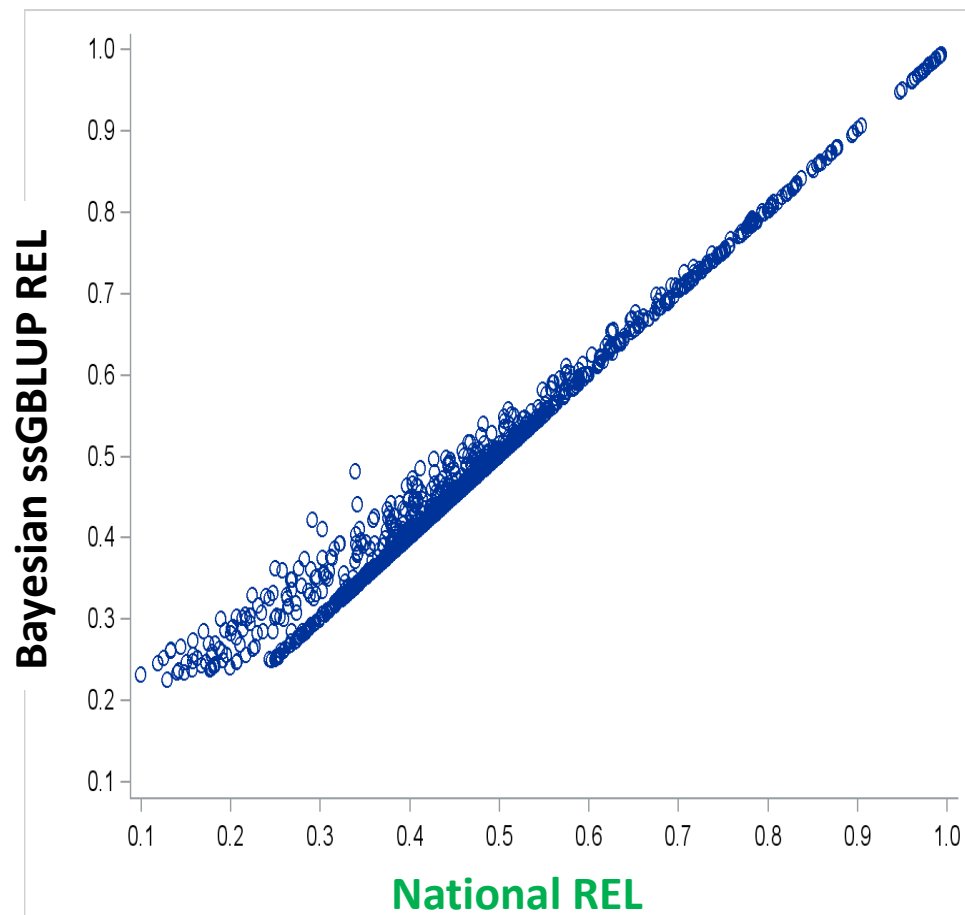
- ✓ Slovenian animals without records and sired by a genotyped InterGenomics sire

| 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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