



QUALITAS⁺



Genomic selection in small breeds using multi-breed reference populations

Gábor Mészáros, Solomon Boison,
Birgit Gredler, Hermann Schwarzenbacher,
Theo Meuwissen, Johann Sölkner

Introduction

- Genomic selection – method of choice for genetic improvement of major breeds in many countries
- Large *reference* populations to set up genomic prediction equations to evaluate *test* animals
- But what if the *large* reference sets within breed are not available?

Breeds of interest



Pinzgauer cattle

- Origin: Austria
- Population: 47.000
(7.700 cows)



Tyrol Grey

- Origin: Austria
- Population: 18.000
(3.800 cows)

Data



- Pinzgauer: 220 bulls



- Tyrol Grey: 220 bulls



- Fleckvieh: 6730 bulls



- Brown Swiss: 1415 bulls

Data

- All genotypes from Illumina BovineSNP50 BeadChip (54.001 SNPs)
- Combining single breed data sets and quality control using PLINK
- Quality control conditions:
 - Minor allele frequency: 0.02
 - HWE p-value: 0.00001
 - Missing per SNP: 0.1

Methods

- GEBVs computed with GBLUP using Theo Meuwissen's bayesgg program
- Results: correlations between GEBVs, conventional and deregressed EBVs

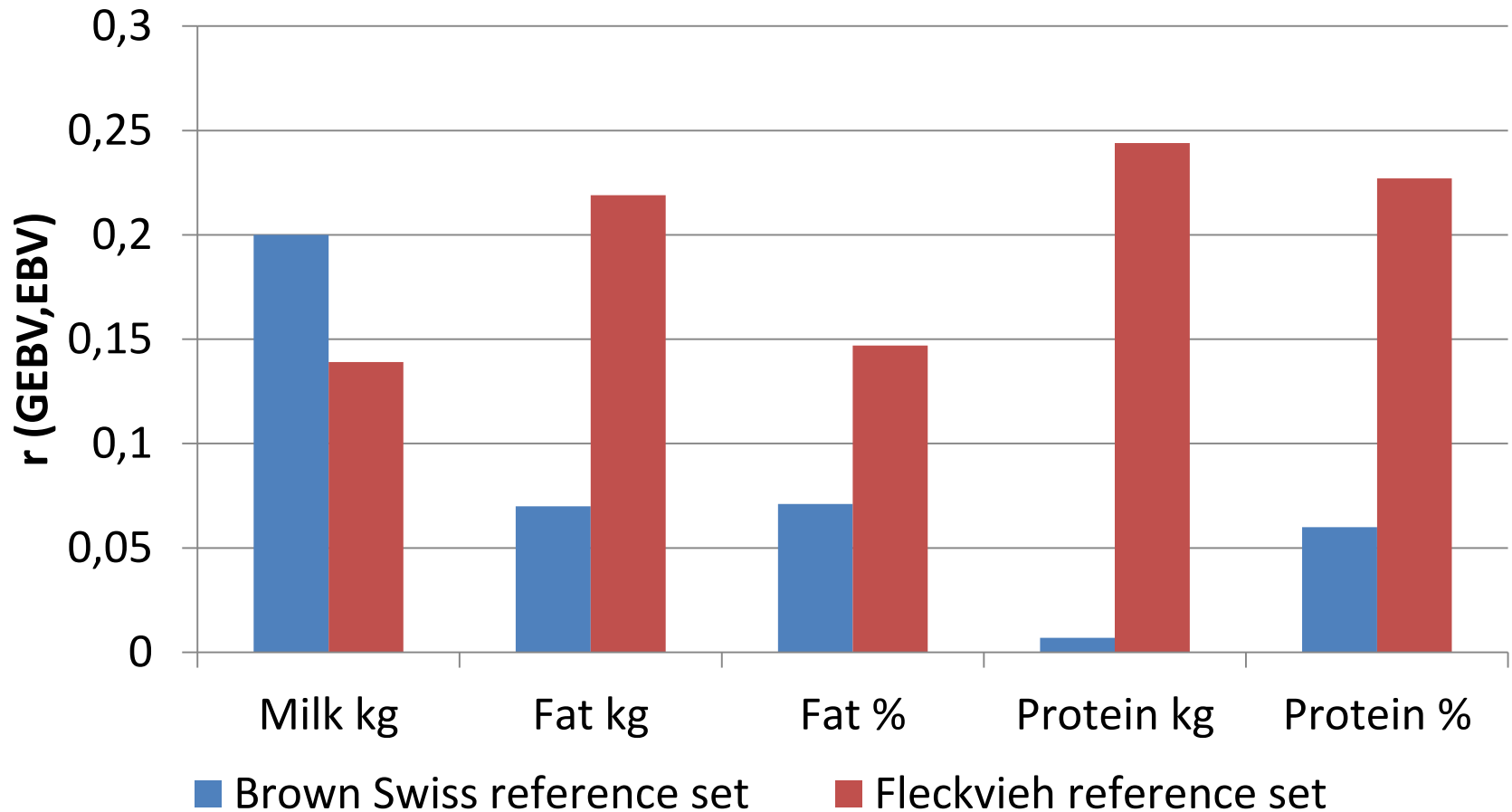
Workflow

- Across breeds scenario
 - Test set: all bulls from the “small” breed
 - Reference set: bulls from the pool data (Fleckvieh, Brown Swiss)
- Multi-breed scenario
 - Test set: ~ 65 youngest bulls from the “small” breed
 - Reference set: the rest of the “small” breed and bulls from the pool data (Fleckvieh, Brown Swiss)
- Conventional vs. deregressed EBVs

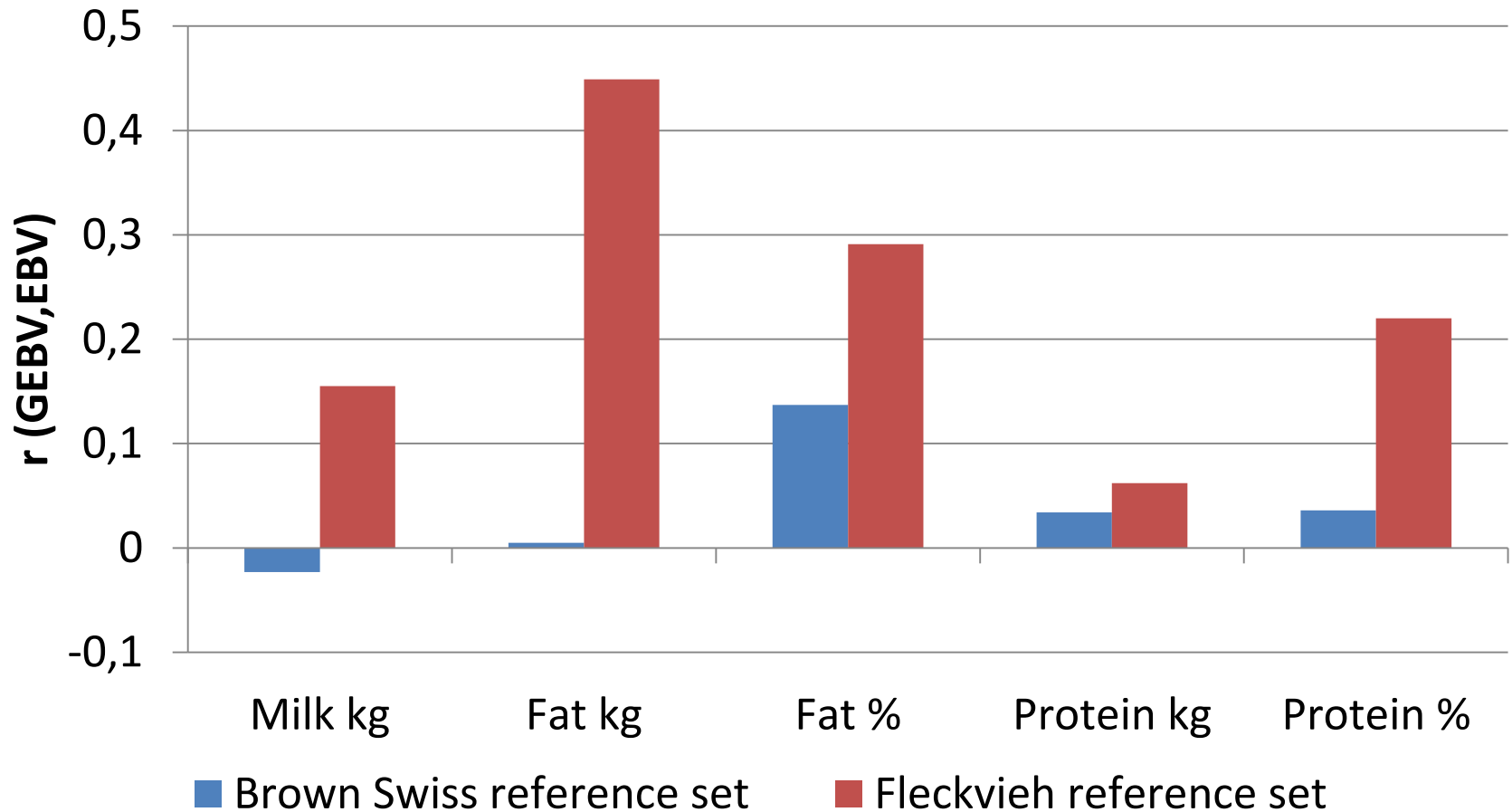
Traits

	h^2
Milk production	0.34
Fat content	0.45
Fat production	0.29
Protein content	0.55
Protein production	0.27

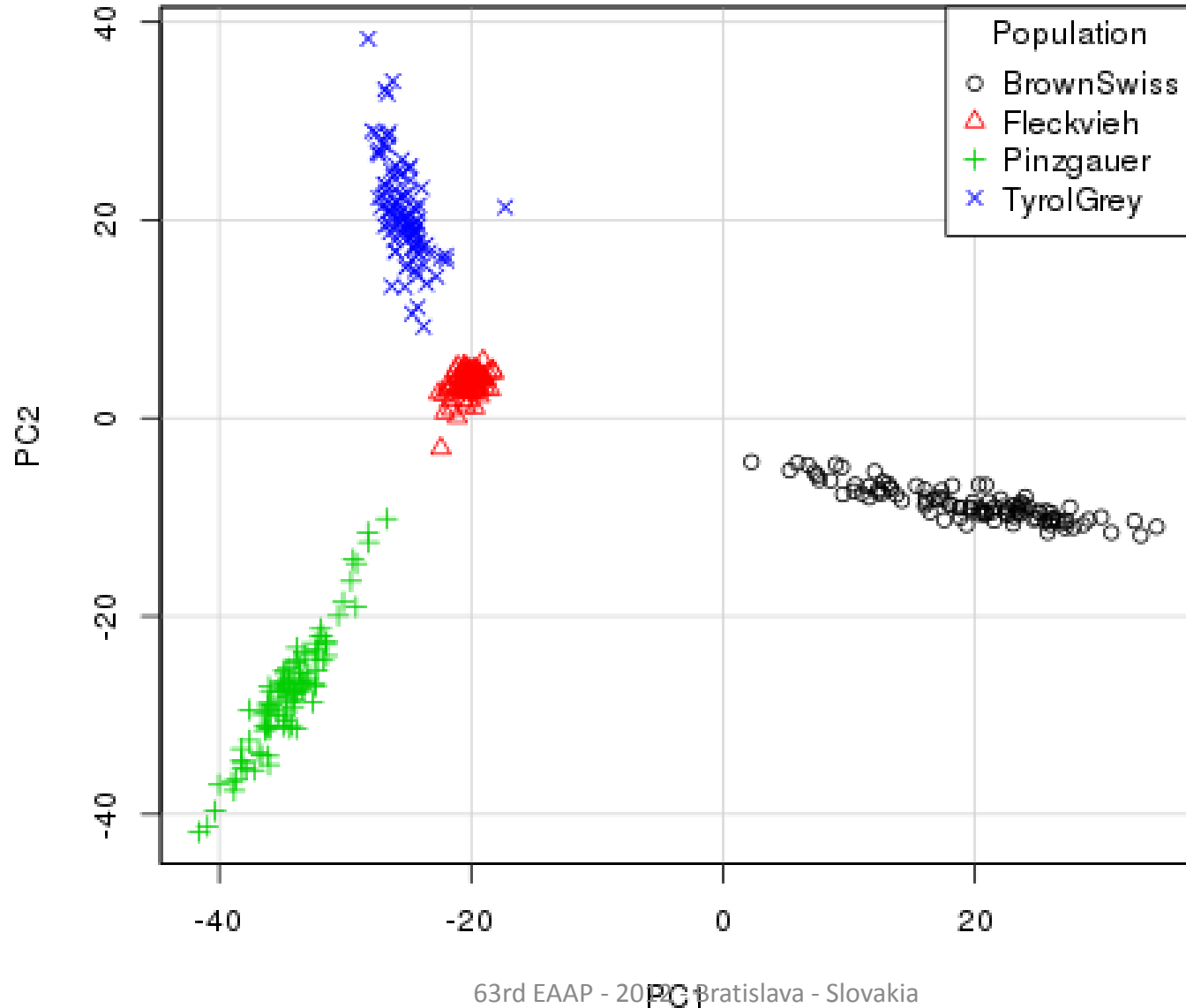
Across breeds scenario – Tyrol Grey



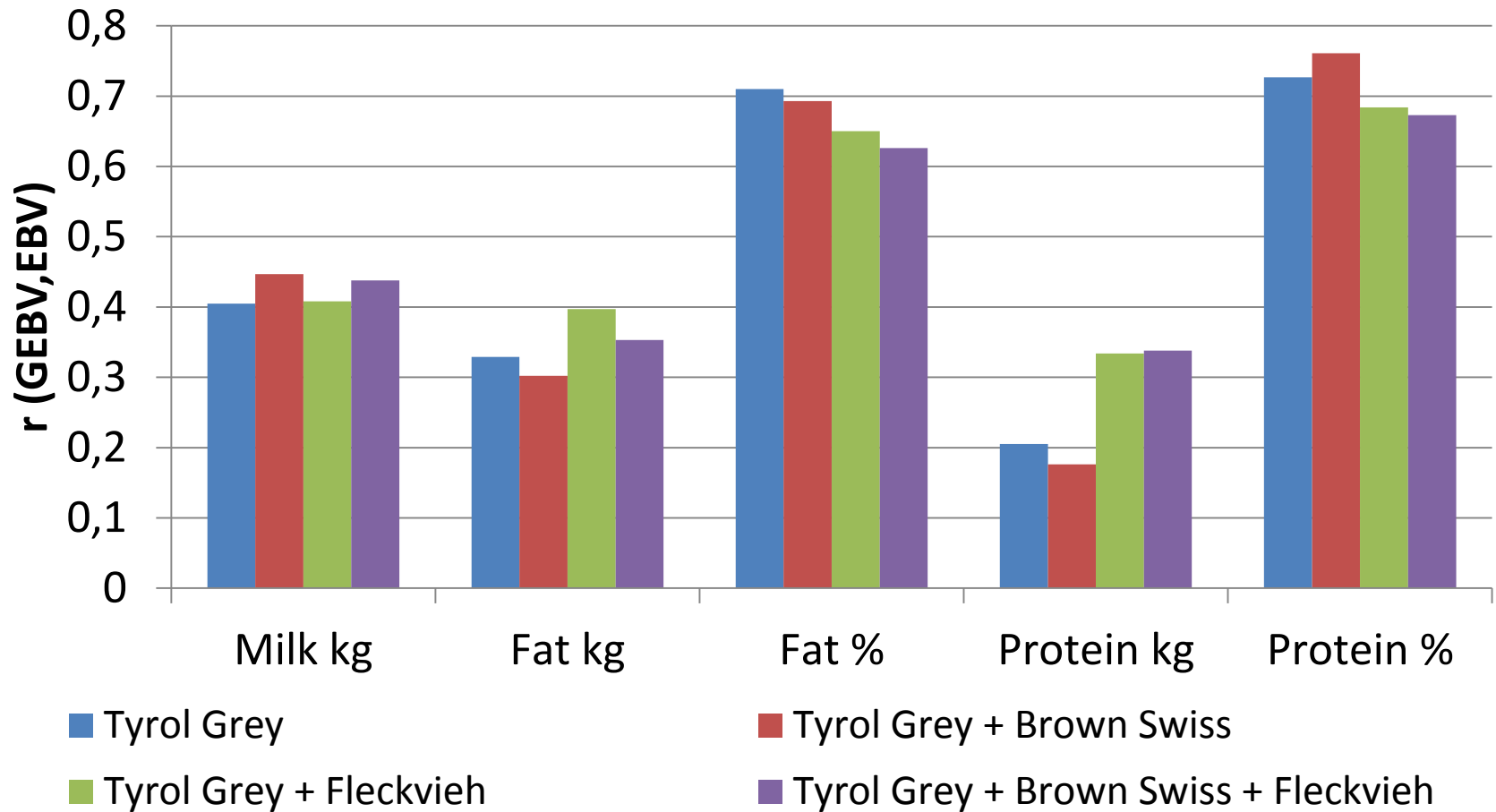
Across breeds scenario – Pinzgauer



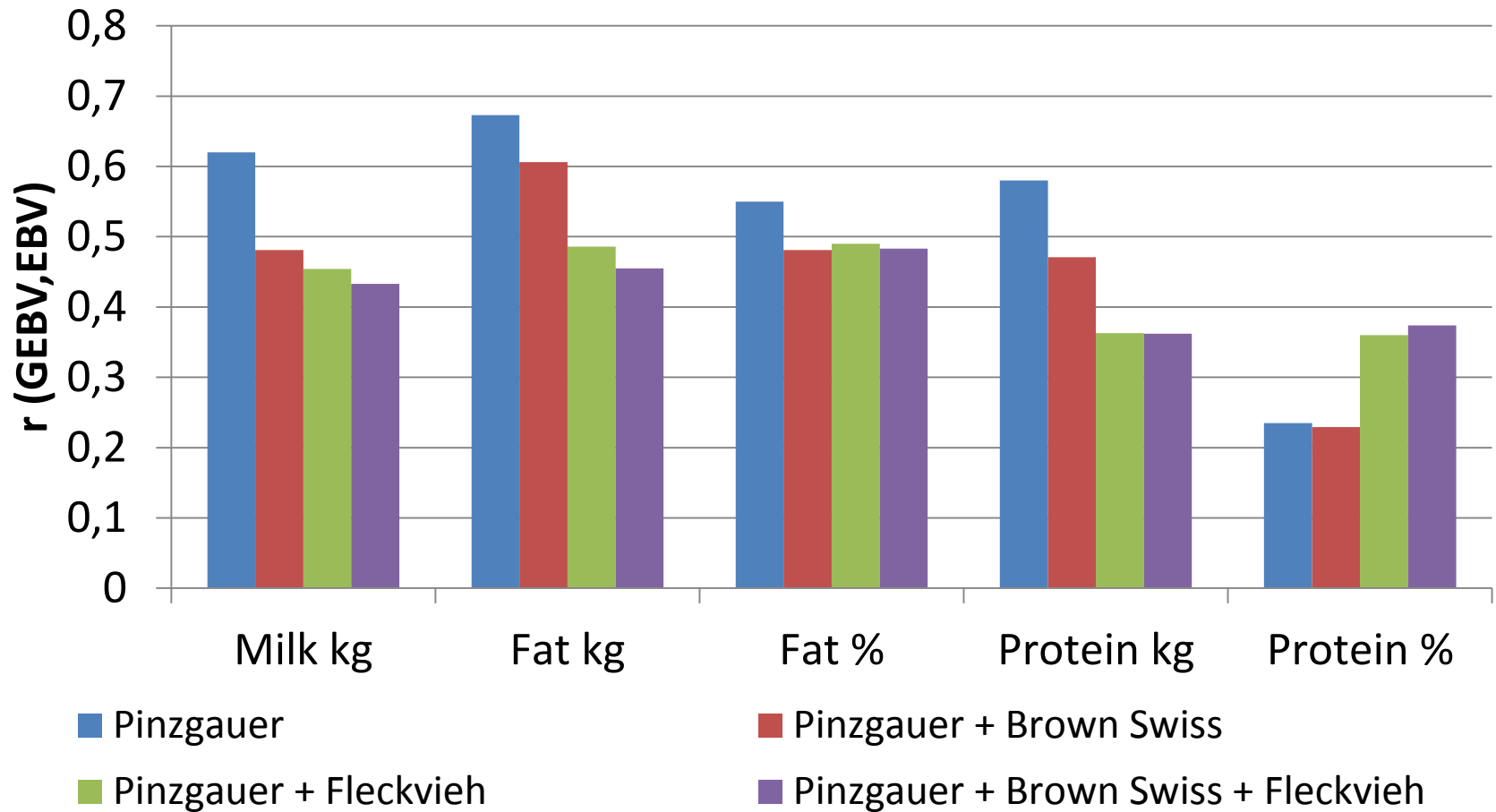
Principal components



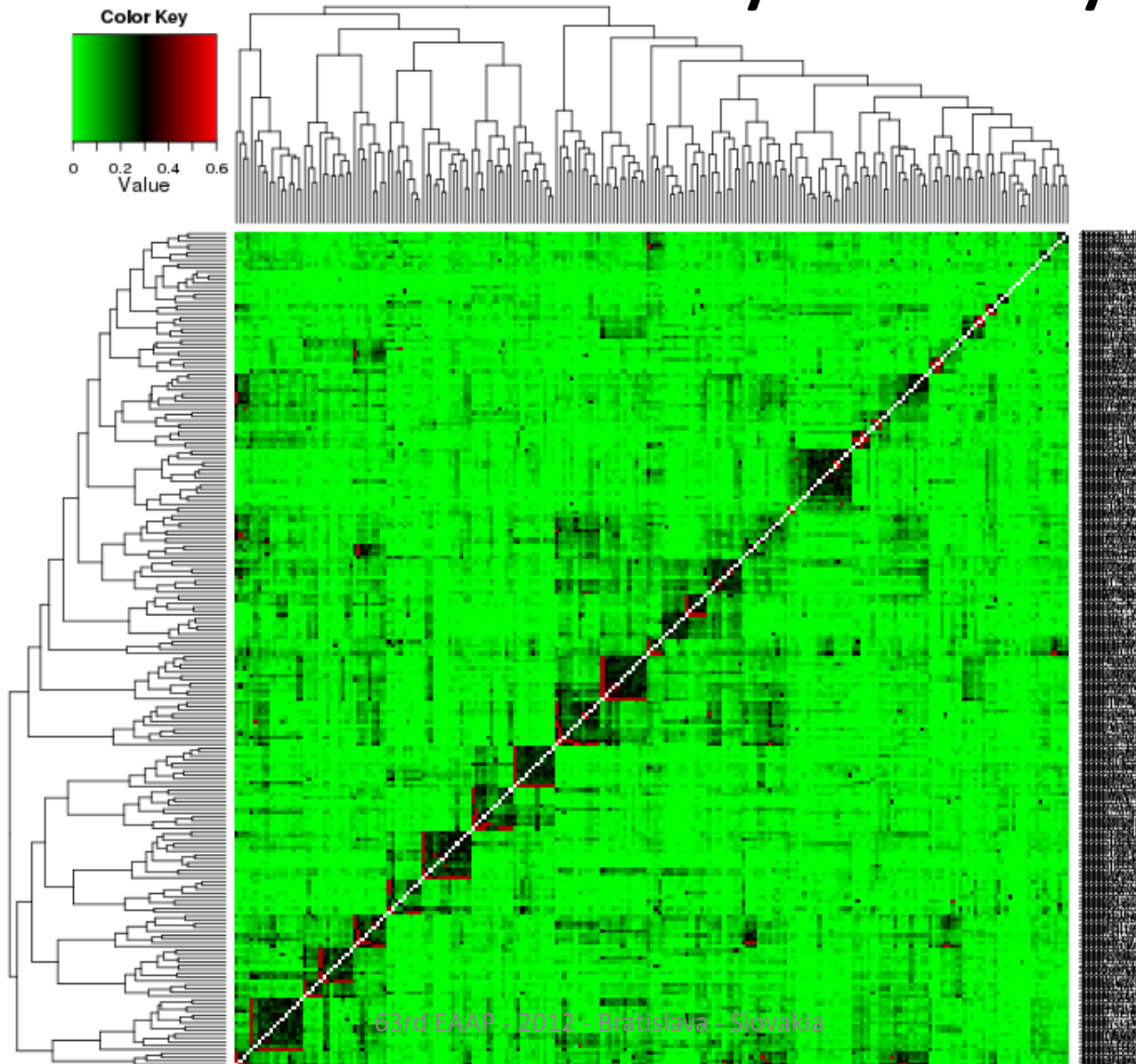
Multi-breed scenario – Tyrol Grey



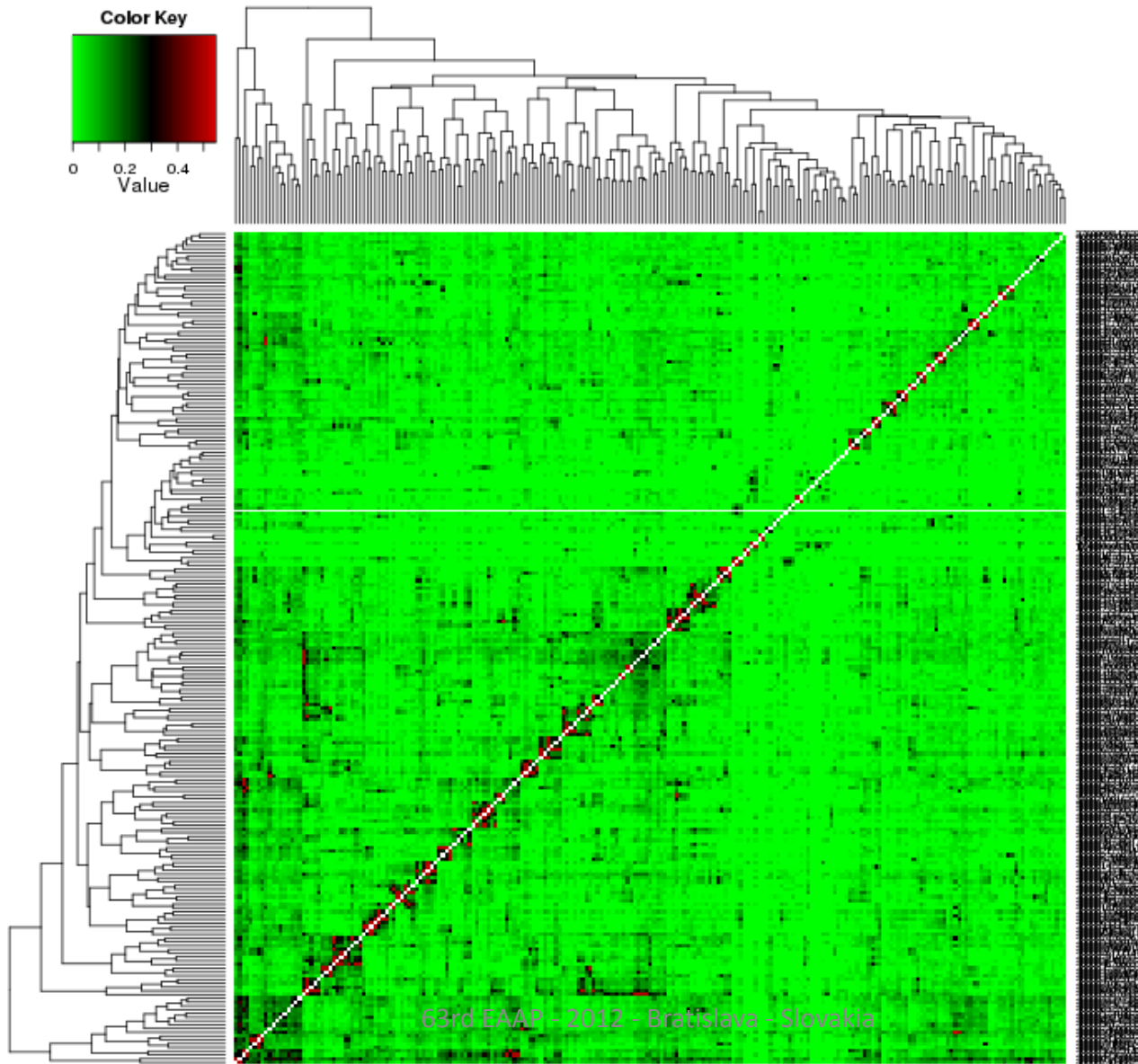
Multi-breed scenario – Pinzgauer



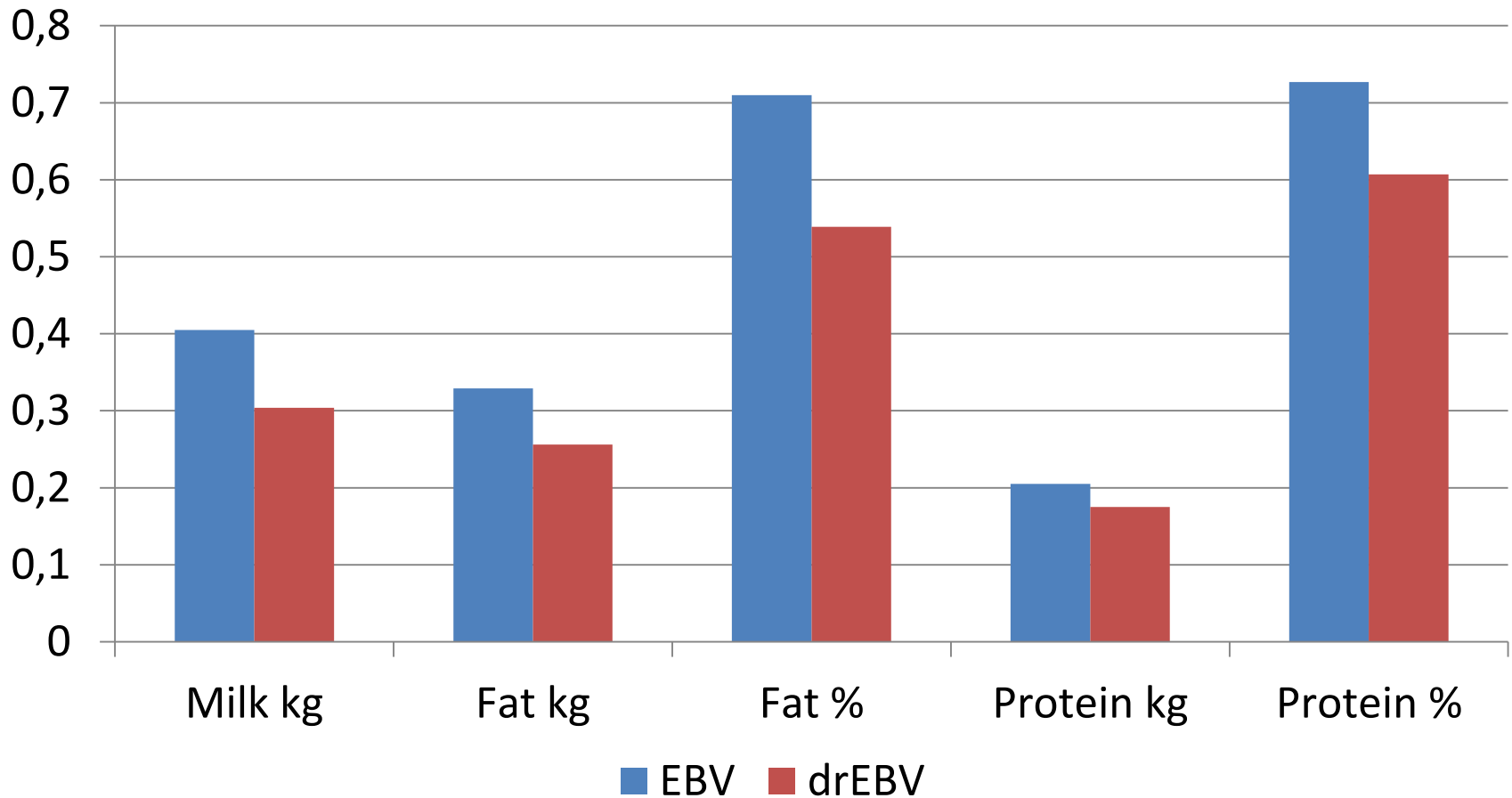
Relatedness – Tyrol Grey



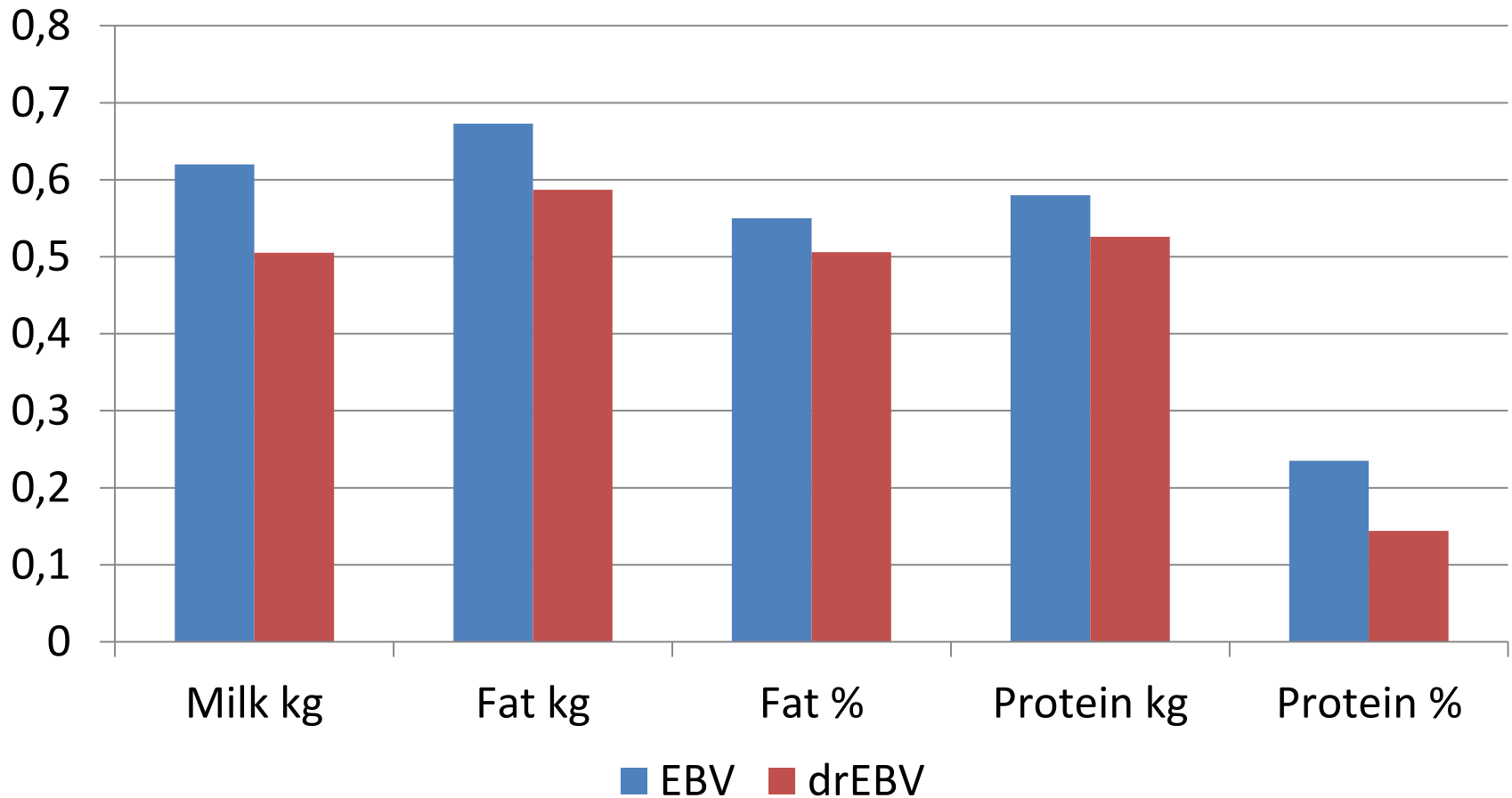
Relatedness - Pinzgauer



EBV vs. drEBV – Tyrol Grey



EBV vs. drEBV – Pinzgauer



Conclusions

- Surprisingly high accuracies using single breeds with small reference sets
- Much larger multi breed reference sets does not increase accuracies

Next steps

- Deregressed instead of conventional breeding values
- Functional traits
- Extension to high density genotypes
- Bayesian alphabet?

Acknowledgements



- Förderverein Biotechnologieforschung;
Rinderbesammungsgenossenschaft Memmingen;
Gesellschaft zur Förderung der Fleckviehzucht in
Niederbayern; Nutztvieh GmbH Miesbach; Rinderunion
Baden-Württemberg eG; Zentrale Arbeitsgemeinschaft
Österreichischer Rinderzüchter; Arbeitsgemeinschaft
Süddeutscher Rinderzucht- und Besamungsorganisationen
- ZuchtData EDV-Dienstleistungen GmbH
- Ana Maria Perez O'Brien, Anamarija Frkonja



QUALITAS⁺



Thanks for your attention!

gabor.meszaros@boku.ac.at