Global Interbull EBV in domestic single step genomic evaluation

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Objective:

Combine for Holstein cattle

domestic database
of production records

Interbull EBV

into one joint evaluation.

Circumstances

Majority of Sires are foreign

↓

Therefore sires in insemination

weak connection

to the domestic population.

But

criterion is the production in domestic condition.

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} x G,
- Proportion of H.

After editing

- 39,904 loci

  1,605 genotyped bulls,

  1,259 in training set,

  140 with   0 daughters in 2008

        and > 50 (average 67) in 2012,

  206 others, with small No. of daughters.

Data
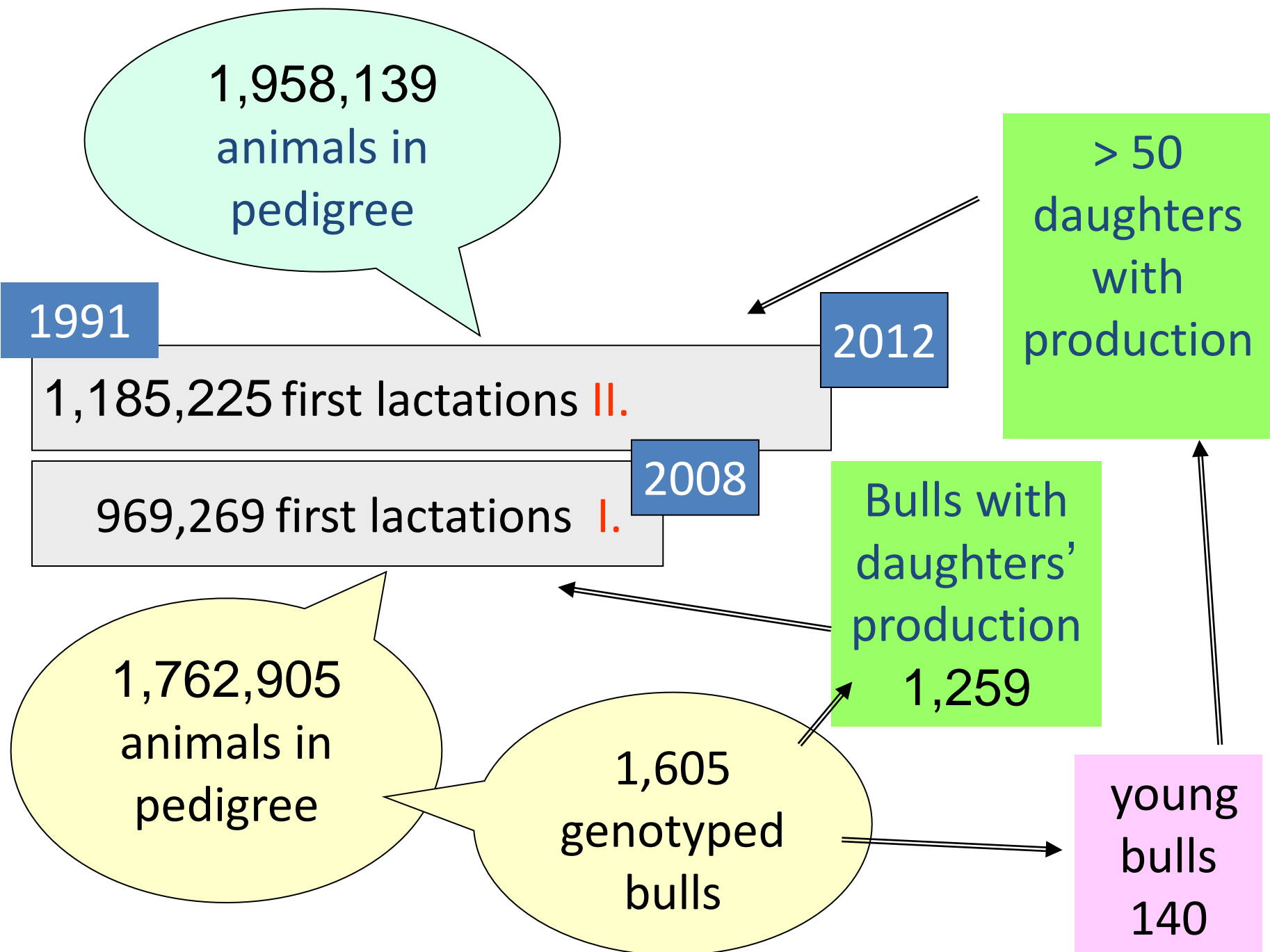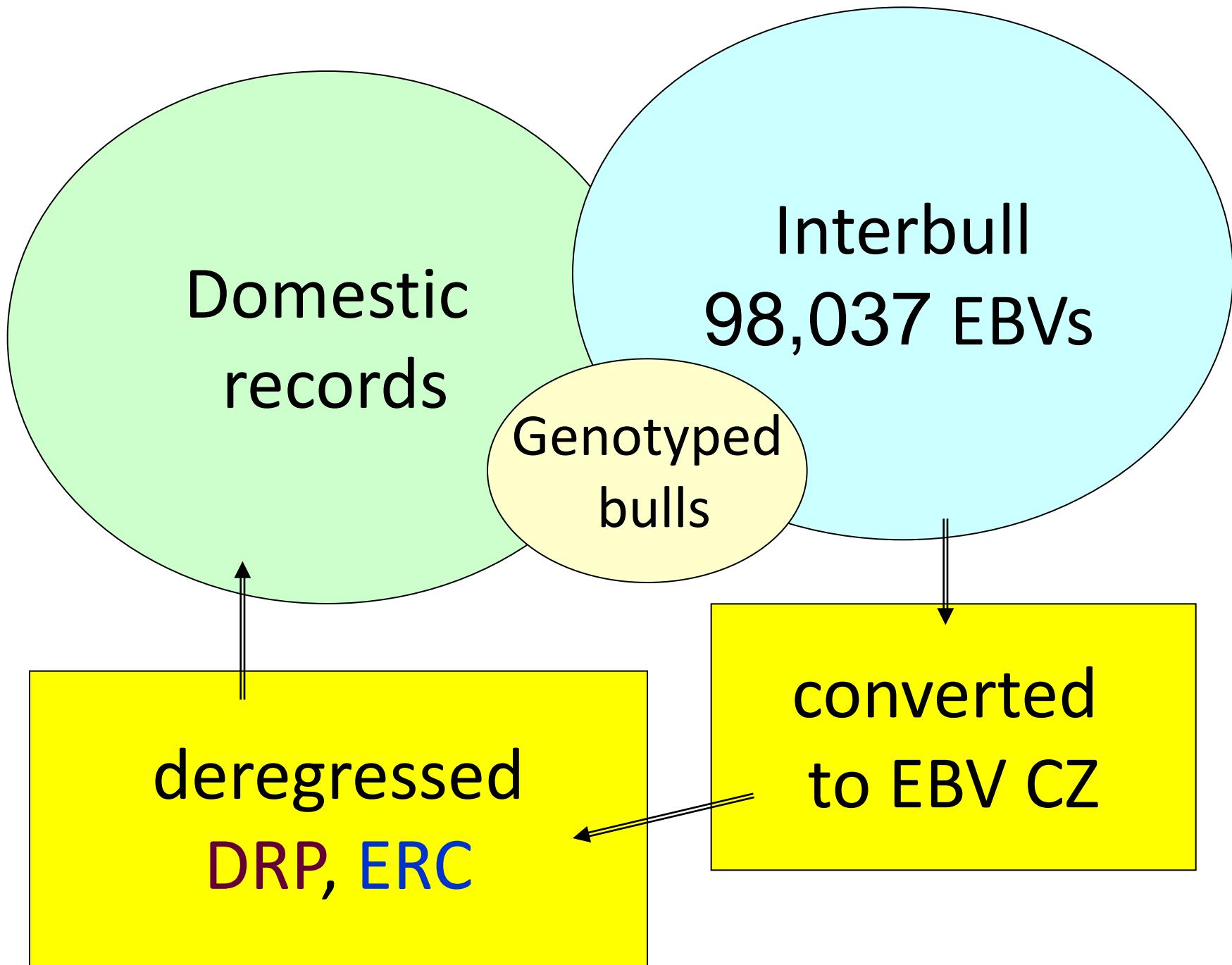
Strategies

Method of prediction	Calculated value	Sources of production		
		Domestic	Interbull	D + I
BLUP	EBV	D-EBV	I-EBV	DI-EBV
Ridge Regression	DGV		rI-DGV	
	GEBV *		rI-GEBV	
GBLUP	DGV		gI-DGV	
	GEBV *		gI-GEBV	
ssGBLUP **	GEBV	D-GEBV	I-GEBV	DI-GEBV

* GEBV = 0.8 DGV + 0.2 D-EBV .

** Weight for genomic relationship **G** 80 % and pedigree relationship **A22** 20 %.

Size of data for prediction 2008

	Records	Weights ERC	Method
Domestic	969,269	969,269	D- EBV
			D-GEBV
Interbull for genotyped bulls	1,259	57,864	rI- DGV
			rI-GEBV
			gI- DGV
			gI-GEBV
Interbull for all bulls	98,037	785,276	I- EBV
			I-GEBV
D + I all	1,064,912	1,632,668	DI- EBV
			DI-GEBV

Weighted analysis

Ridge Regression

$$y_j = \mu + \Sigma \delta_i \cdot g_i + e_j$$

Fixed effects
μ – contemporary group

Random effects
g_i – locus
δ_i – regression coefficients
e_j – residual

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

Weighted analysis

GBLUP

$$y_j = \mu + an_j + e_j$$

Fixed effects
μ – contemporary group

Random effects
an_j – animal
e_j – residual

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

Weighted analysis

BLUP / ssGBLUP

$$y_{ijkl} = HYS_i + \beta_1 \cdot ca_j + \beta_2 \cdot ca_j^2 + \beta_3 \cdot do_k + \beta_4 \cdot do_k^2 + an_l + e_{ijkl}$$

Fixed effects
HYS – contemporary group
β – regression coefficients
ca_j ; ca_j^2 – curvilinear regression
            on calving age
do_k ; do_k^2 – curvilinear regression
            on days open

Random effects
an_l – animal
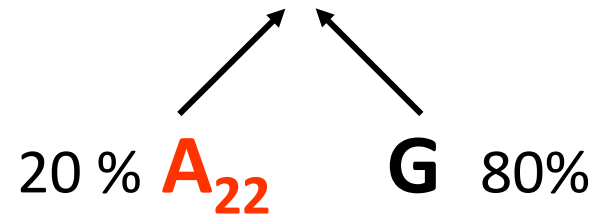**e_{ijkl}** – residual

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

Relationship

Ridge Regression...**I**

BLUP – AM ....**A**

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

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

20 % **A₂₂**   **G** 80%

G – normalised (aver. diag. = 1)

(Forni et al., 2011)

shifted (aver. **G** = aver. **A₂₂**)

(Vitezica et al., 2011)

Programs

- BLUPF90 family of programs

  (Misztal et al., 2002)

- DMU5 module of the DMU software

  (Madsen & Jensen, 2010)

- G-matrix

  (Su & Madsen, 2011)

Verification Procedure

- For the 140 young bulls:

    Correlation:

    > EBV/GEBV/DGV from Data I (2008)
    >
    > X
    >
    > EBV/DYD from Data II (2012)

- **Data I** – using **only pedigree information** and **no progeny information**

- **Data II** – **after progeny testing**.

Results

Difference of young bulls from basis of 2,116 sires with > 60 daughters in 2008

Data 2008	Mean milk kg	Method
Domestic	657	D- EBV
	672	D-GEBV
D + I all	651	DI- EBV
	640	DI-GEBV
Data 2012	629	D- EBV
	630	D-GEBV

Correlation Interbull data 2008

Prediction method 2008	Domestic EBV 2012	Domestic DYD 2012
rI- DGV	0.60	0.57
rI- GEBV	0.67	0.61
gI- DGV	0.59	0.57
gI-GEBV	0.66	0.61
I- EBV	0.62	0.53
I-GEBV	**0.70**	**0.65**

Correlation Domestic + Interbull data 2008

Prediction method 2008	Domestic EBV 2012	Domestic DYD 2012
D- EBV	0.59	0.47
D-GEBV	0.70	0.61
DI- EBV	0.63	0.51
DI-GEBV	**0.73**	**0.64**

Validated reliability
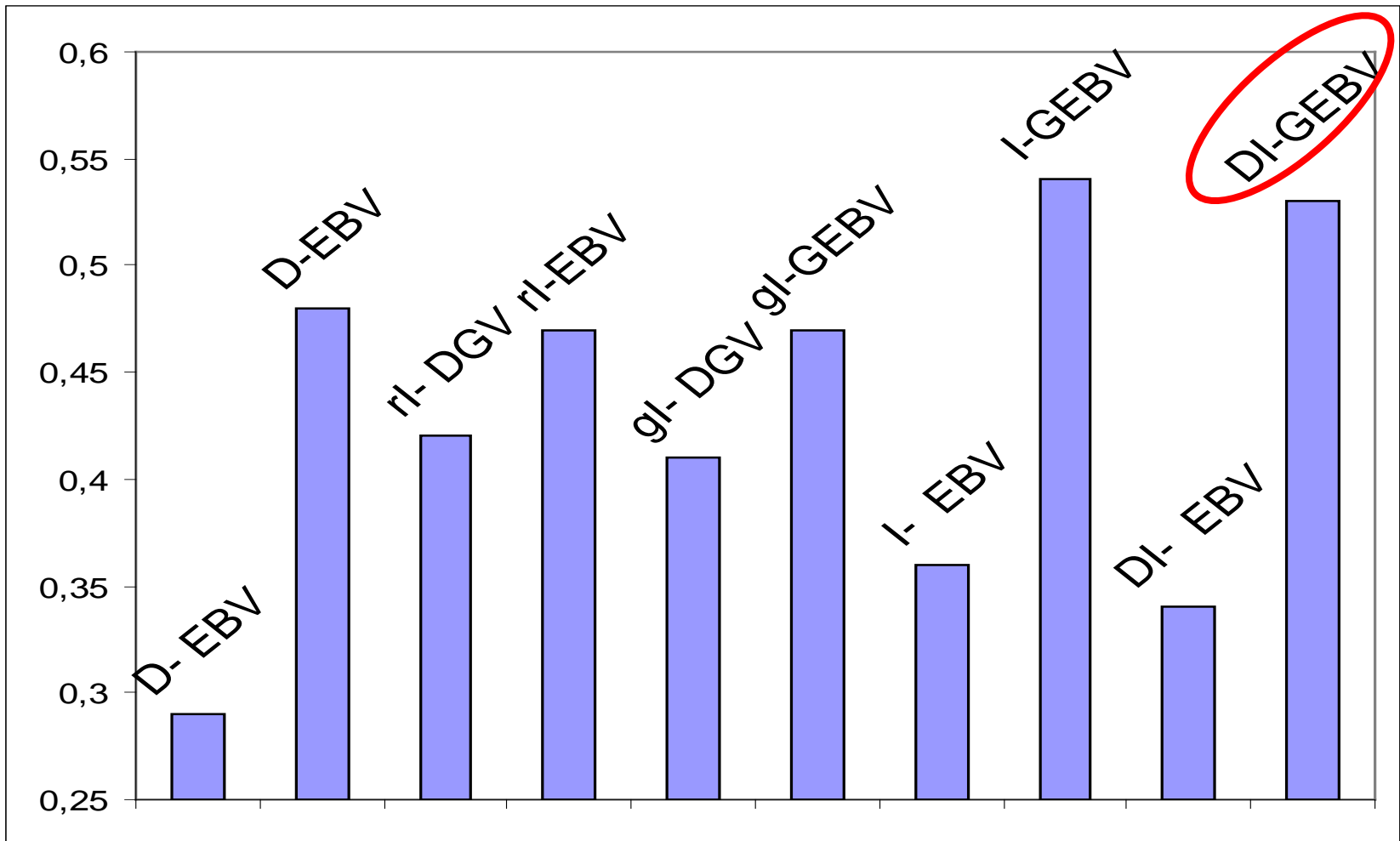
Conclusions

- Combination of domestic and Interbull database improves the prediction of both EBV and GEBV, especially in small populations.

- The DI-GEBV by ssGBLUP was the most suitable method.

Thank you

for your

attention