Comparison of genomic selection approaches in Brown Swiss within Intergenomics

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Interbull meeting, Cork

DATA

- 7041 animals genotyped
- 6 countries included: CHE, DEA, FRA, ITA, SVN, USA
- Between 3 and 15 traits by country

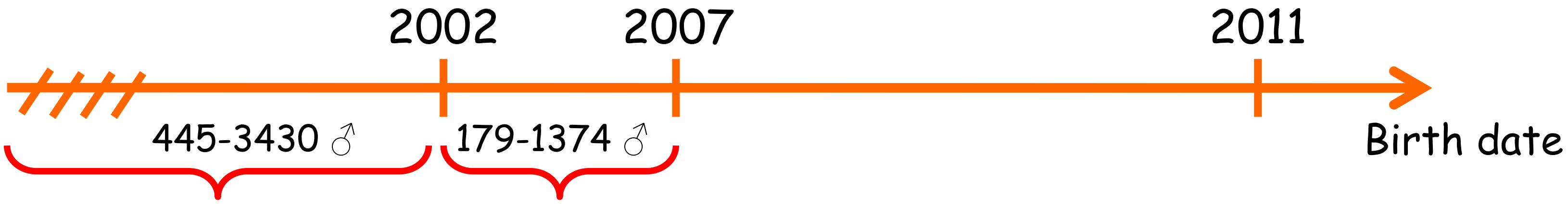
	CHE	DEA	FRA	ITA	SVN	USA
Nb of traits	15	15	13	12	3	15
production	3	3	3	3	3	3
type	9	9	8	7	0	9
functional	3	3	2	2	0	3

- In this study, we focus on
  - 5 countries: CHE, DEA, FRA, ITA and USA
  - 10 common traits (prod:3, func:1 and type:6)

DATA

- Selection of useful animal for genomic selection
  - Animals with genotype and index who belong to a family of at least 4 animals with genotype and index (from 7041 to 4437 animals)
  - Pedigree file contains these animals and their ascendants (from 19570 animals to 12638)
- Data were phased/imputed using Beagle software
- Quality control was applied
  - Maf=1% ; call rate=10% ; HWE=10^{-4}
- Calculation of deregressed proof from index
- Animals of the training population with an EDC<5 are removed from the analysis

DATA



Training pop.
Deregress
proof$_{2007}$

Validation pop.
no performance
in 2007

❯ GEBV$_{2007}$ ⟷ Deregressed proof$_{2011}$

4 methods investigated

- gBLUP with $G = \dfrac{ZZ'}{2\sum p_i\left(1-p_i\right)}$

p >> n problem

- Bayesian LASSO
- Bayes Cπ
- EN : Elastic Net, a penalized regression approach which combines Ridge Regression and LASSO algorithm

$$\hat{\beta} = \arg\min\left\{\sum_{i=1}^{n}\left(Y_i - X_i\beta\right)^2 + \lambda\left(\underbrace{\alpha\sum_j \beta_j^2}_{\boxed{\text{RR}}} + \underbrace{\left(1-\alpha\right)\sum_j\left|\beta_j\right|}_{\boxed{\text{LASSO}}}\right)\right\}$$

Compared to pedigree-based BLUP

4 methods investigated

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- *A polygenic component varying between 10 and 90% was included in the model*
- *Results for the optimal polygenic component proportion are shown for each method and for each trait*

Correlations for production traits

trait	Country scale	Pedigree-based BLUP	gblup	Bayesian Lasso	Bayes Cπ	EN
Fat	CHE	0.416	0.579	0.605	0.607	0.612
	FRA	0.388	0.544	0.584	0.585	0.592
	USA	0.398	0.542	0.591	0.592	0.600
	ITA	0.423	0.582	0.610	0.618	0.616
	DEA	0.427	0.584	0.615	0.624	0.587
Milk	CHE	0.334	0.518	0.561	0.564	0.582
	FRA	0.309	0.476	0.530	0.531	0.550
	USA	0.287	0.450	0.525	0.526	0.551
	ITA	0.343	0.526	0.562	0.562	0.572
	DEA	0.371	0.546	0.579	0.580	0.435
Protein	CHE	0.448	0.575	0.601	0.602	0.603
	FRA	0.385	0.510	0.544	0.545	0.553
	USA	0.382	0.506	0.554	0.555	0.565
	ITA	0.436	0.569	0.593	0.593	0.592
	DEA	0.454	0.590	0.603	0.604	0.626

Correlations for type traits

trait	Country scale	Pedigree-based BLUP	gblup	Bayesian Lasso	Bayes Cπ	EN
foot angle	CHE	0.369	0.429	0.462	0.559	0.473
	FRA	0.320	0.391	0.418	0.419	0.420
	USA	0.366	0.444	0.456	0.458	0.466
	ITA	0.370	0.418	0.454	0.455	0.454
	DEA	0.380	0.424	0.462	0.462	0.647
Front Teat Length	CHE	0.486	0.616	0.659	0.657	0.656
	FRA	0.465	0.619	0.652	0.659	0.653
	USA	0.466	0.617	0.652	0.657	0.653
	ITA	0.464	0.616	0.653	0.656	0.655
	DEA	0.467	0.617	0.651	0.657	0.556
Rump Angle	CHE	0.418	0.520	0.551	0.555	0.547
	FRA	0.438	0.525	0.557	0.558	0.550
	USA	0.432	0.524	0.552	0.554	0.547
	ITA	0.418	0.516	0.549	0.552	0.544
	DEA	0.441	0.540	0.561	0.563	0.587

Correlations for type traits

trait	Country scale	Pedigree-based BLUP	gblup	Bayesian Lasso	Bayes Cπ	EN
Rear Leg Side View	CHE	0.473	0.555	0.574	0.573	0.569
	FRA	0.419	0.502	0.529	0.528	0.521
	USA	0.401	0.485	0.516	0.516	0.510
	ITA	0.408	0.496	0.520	0.519	0.513
	DEA	0.416	0.494	0.522	0.521	0.528
Rear Udder Height	CHE	0.436	0.506	0.528	0.529	0.508
	FRA	0.345	0.421	0.445	0.444	0.433
	USA	0.427	0.508	0.527	0.527	0.516
	ITA	0.405	0.480	0.497	0.497	0.491
	DEA	0.368	0.464	0.475	0.474	0.551
Stature	CHE	0.407	0.522	0.575	0.579	0.601
	FRA	0.362	0.501	0.576	0.588	0.587
	USA	0.413	0.554	0.605	0.618	0.617
	ITA	0.406	0.553	0.604	0.618	0.613
	DEA	0.364	0.525	0.579	0.593	0.392

Correlations for functional traits

trait	Country scale	Pedigree-based BLUP	gblup	Bayesian Lasso	Bayes Cπ	EN
Direct Longevity	CHE	0.282	0.288	0.293	0.293	0.331
	FRA	0.272	0.297	0.296	0.296	0.316
	USA	0.266	0.314	0.321	0.323	0.345
	ITA	0.312	0.346	0.340	0.341	0.352
	DEA	0.354	0.391	0.363	0.363	0.466

Mean correlation per country

- In Brown Swiss, the contribution of each country to the reference population is very different
    - Mean correlation over the common traits are consequently different according to the country scale
    - Country with a high contribution will convert CD of abroad bulls with a higher accuracy

country scale	mean correlation over the 10 traits using BayesCπ
CHE	0.552
FRA	0.515
USA	0.532
ITA	0.541
DEA	0.544

Mean correlation per method

	mean correlation over the 10 traits	Absolute deviation to 1 of slope of regression
Pedigree-based BLUP	0.393	0.184
GBLUP	0.502	0.182
Bayesian LASSO	0.533	0.110
BayesCπ	0.537	0.109
EN	0.536	0.133

Methods with a polygenic part included

Mean of the polygenic component part over the 5 countries scale

	traits	GBLUP	Blasso	BayesCpi
production	fat	10%	10%	14%
	milk	10%	10%	12%
	protein	10%	18%	22%
type	foot angle	10%	10%	42%
	front teat length	10%	16%	30%
	rump angle	10%	10%	22%
	rear leg side view	14%	24%	20%
	rear udder height	12%	52%	44%
	stature	10%	10%	18%
functional	direct longevity	22%	30%	36%

Validation of the Interbull test

- Number of traits which validate the Interbull test per genomic selection approach
  - Slope of regression between 0.8 and 1.2

country scale	pedigree-based BLUP	GBLUP	BLASSO	Bayes Cpi	EN
CHE	5	7	7	7	7
FRA	6	4	9	9	8
USA	6	7	8	8	6
ITA	7	5	8	8	9
DEU	6	9	8	8	9
mean	6	6.4	8	8	7.8

Conclusions

- Compared to a traditional BLUP, genomic selection allows a gain in correlation between 6.5 and 20.9%
- Bayesian Lasso, Bayes Cπ and EN give the best results with a gain in correlation near 3% compared to GBLUP
- The slope of the regression
  - is closer to 1 with these 3 methods and are improved compared to traditional BLUP
  - More traits validate Interbull test with BLASSO, BayesCπ and EN

Conclusions

- For a same trait, the best correlation is often obtained using the same method whatever the country scale
- The optimal polygenic part is relatively low. Bayes Cπ requires a higher proportion than the 2 other methods
- Short term perspective: QTL detection and genomic selection approaches based on QTL detection (BLUP-QTL)

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