



Advancing Genomic Evaluation for Methane Efficiency in Walloon Holstein Cattle towards Implementation

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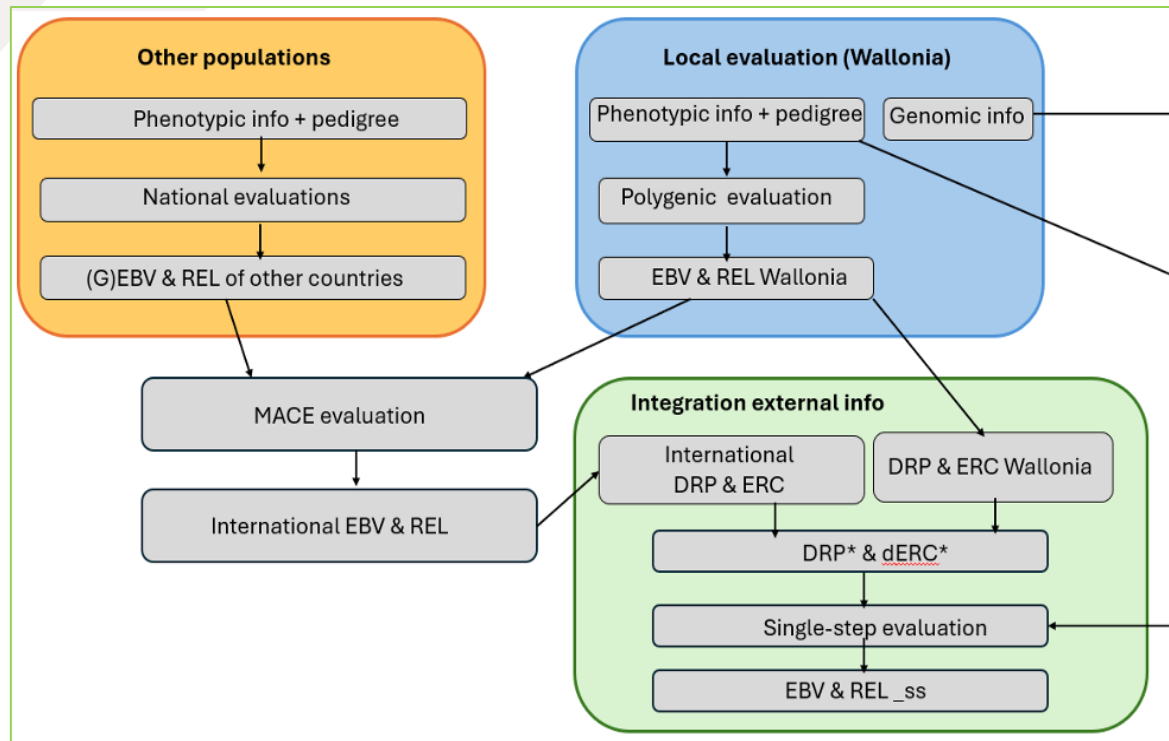
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Introduction



- ▶ Yesterday Katrien Wijnrocx showed:
 - ▶ Novel single-step analysis for currently evaluated traits



Introduction



- ▶ Yesterday Katrien Wijnrocx showed:
 - ▶ Novel single-step analysis for currently evaluated traits
 - ▶ But we are also working on novel traits as reported since several years → CH_4
 - ▶ My presentation last INTERBULL Meeting in Bled in 2024



- ▶ Objectives today:

To illustrate advances towards implementation and publication

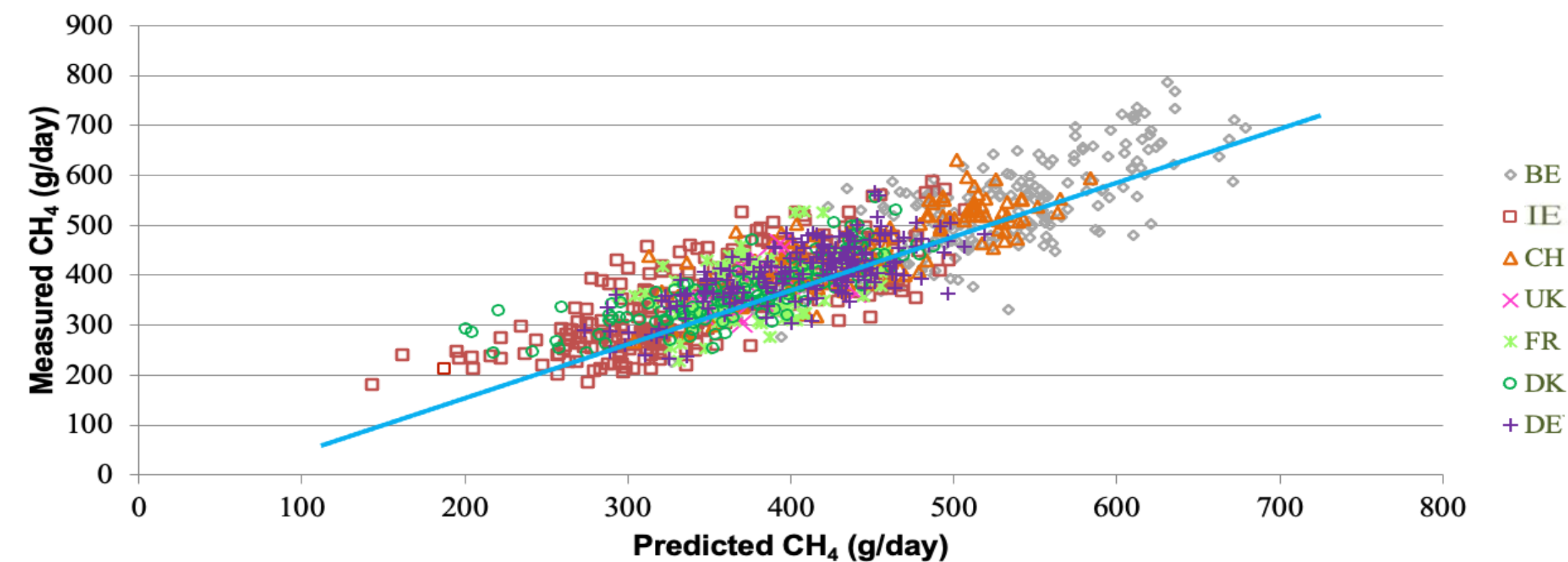
Steps towards genomic evaluation for CH₄



- ▶ Breeding goal → trait definition
- ▶ Phenotype → data recording
- ▶ Model → setup and genetic parameter estimation
- ▶ Genomic evaluation system → setup and running of routines
- ▶ Breeding program → reported trait

**Ongoing (slow)
process**

Used MIR equation



CH ₄ Ref. method	n data	n cows	Origin	R ² c	SEC (g/d)	R ² cv	SECV (g/d)
SF ₆ & RC	1,089	299	BE, IE, CH, UK, FR, DK, DE	0.73	53	0.68	57

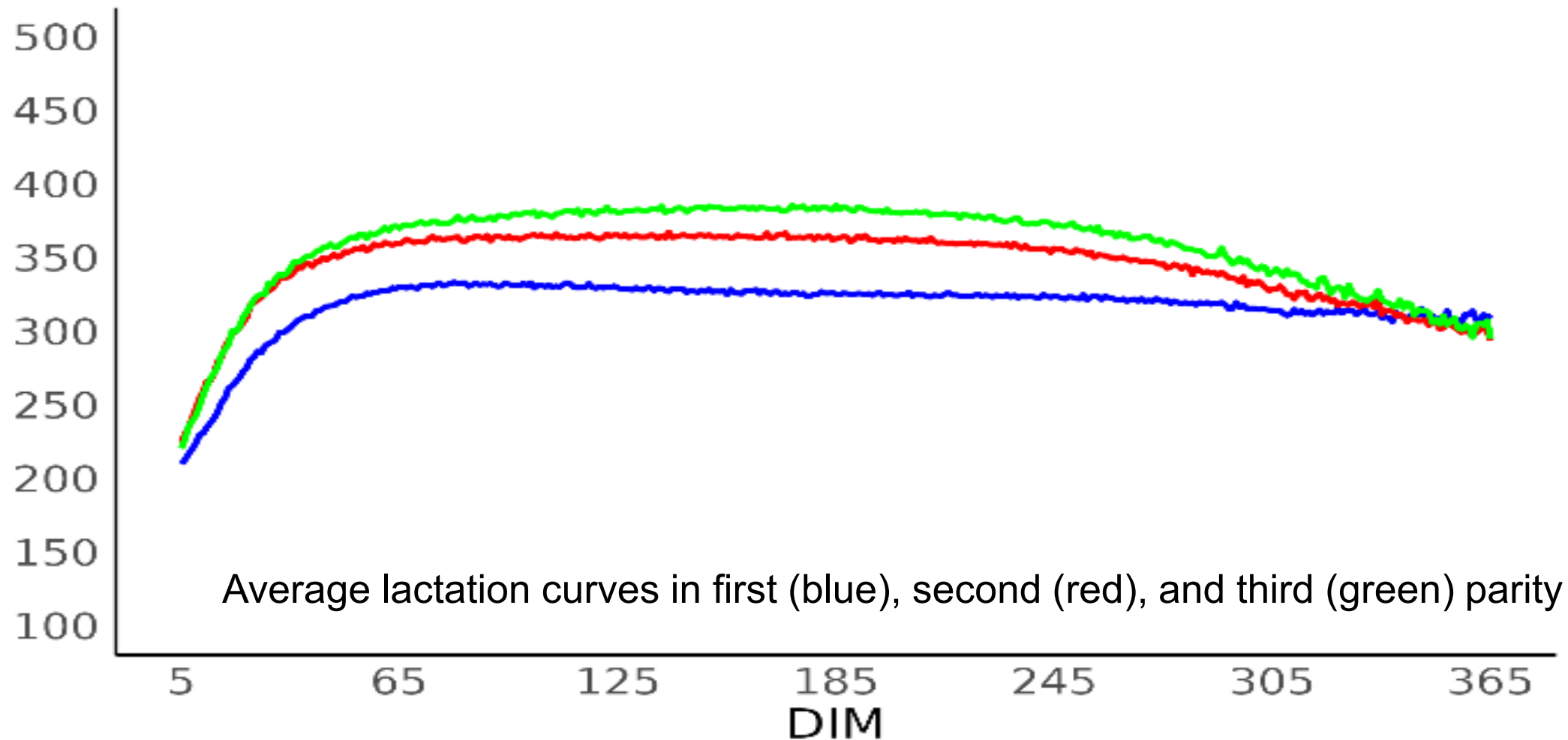
Available MIR-CH₄ (called hereafter PCH₄) data



Parity	No. of records	No. of cows	Mean	SD
(Co)variance component estimation dataset (average 6 subsets)				
1	203,380	30,262	322	67.3
2	162,385	23,932	353	69.9
3	113,551	19,986	367	71.8
All	479,316	34,925	343	69.2
Genomic evaluation dataset				
1	1,935,284	287,511	324	67.0
2	1,528,675	226,132	353	69.9
3	1,081,440	161,234	367	72.1
All	4,545,399	328,290	344	69.2

+ 9,631 genotypes for Holsteins (directly linked to records)

PCH₄ lactation curves

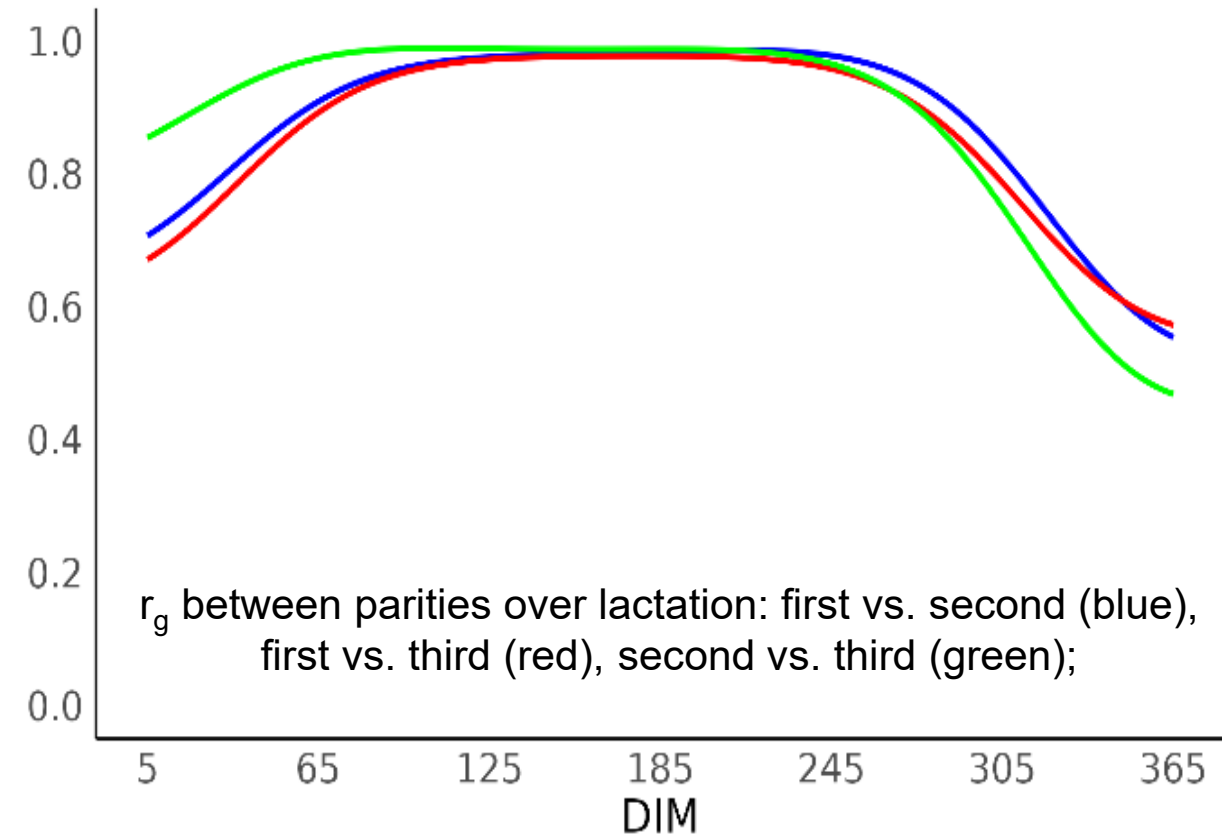
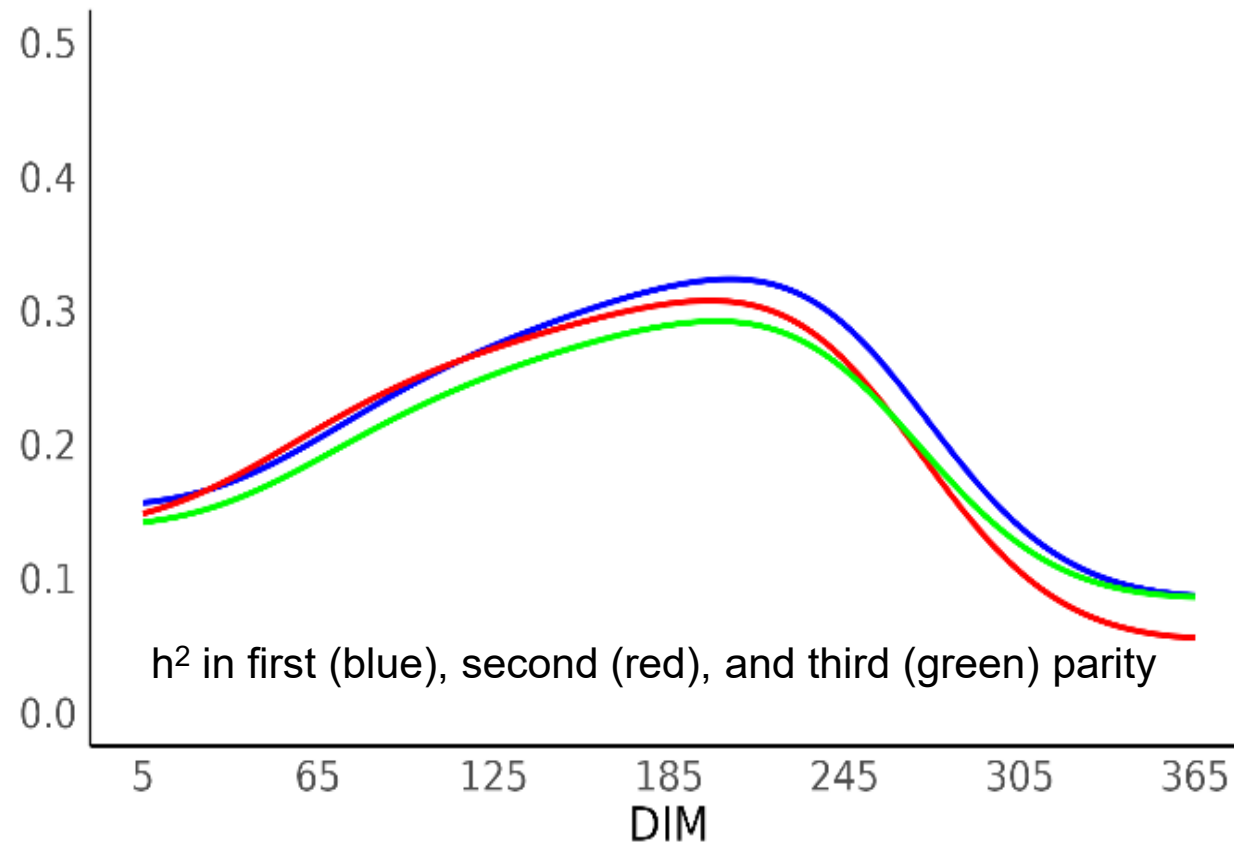


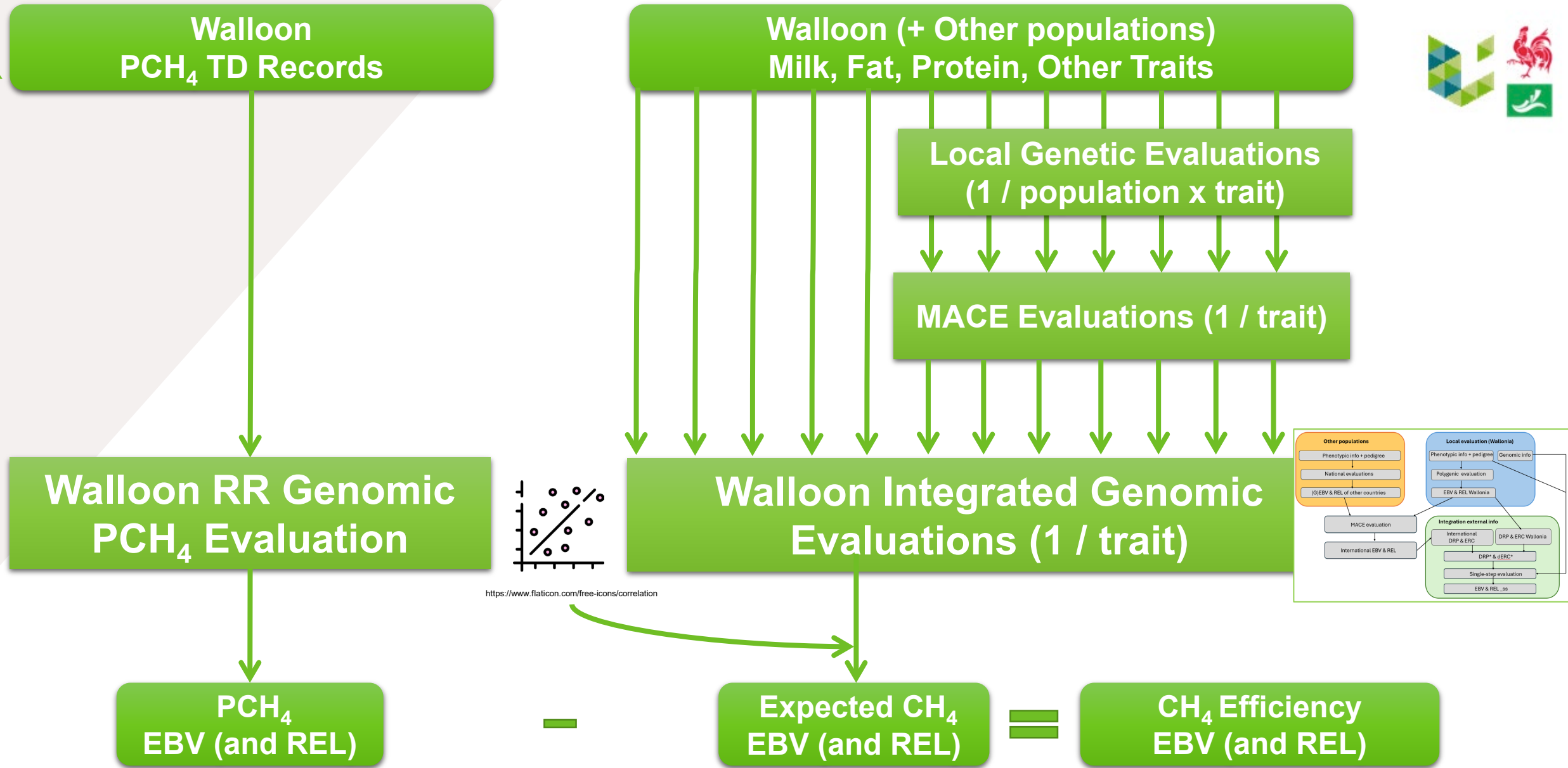
Model → GEBV and GREL for PCH4



- ▶ Multilactation (1-3), random regression test-day model (RRTDM) for CH_4
 - ▶ For organizational efficiency prepared MFP TD files ← PCH_4
 - ▶ IOD – PCG solver
- ▶ GEBV
 - ▶ Average of daily genetic random regression solutions over 305 days and 3 lactations
- ▶ GREL
 - ▶ Pedigree based REL ← exactly same procedure as for production traits (only single-trait)
 - ▶ Then REL → GREL based on Gao et al. (2023) and Ben Zaabza et al. (2022)
 - ▶ Virtually replacing relationship matrix $\mathbf{A}^{-1}$ by $\mathbf{H}^{-1}$ for genotyped animals → extra information
 - ▶ Propagating to non-genotypes animals

Heritability and genetic correlations across lactations





Why residual-based? Is this Methane efficiency?



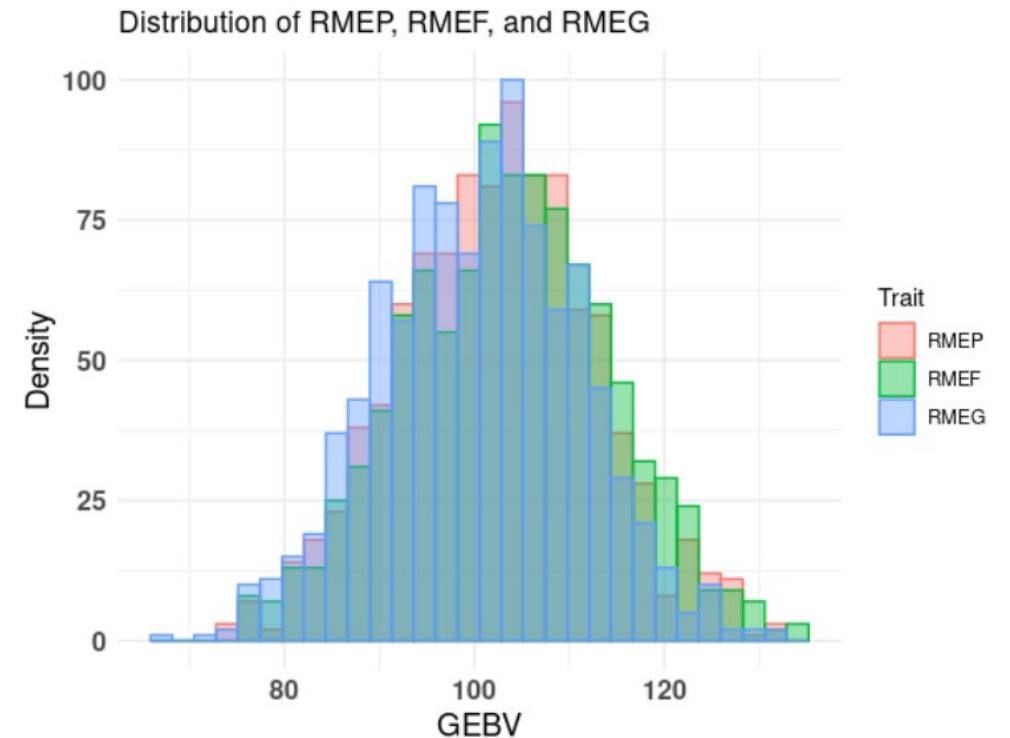
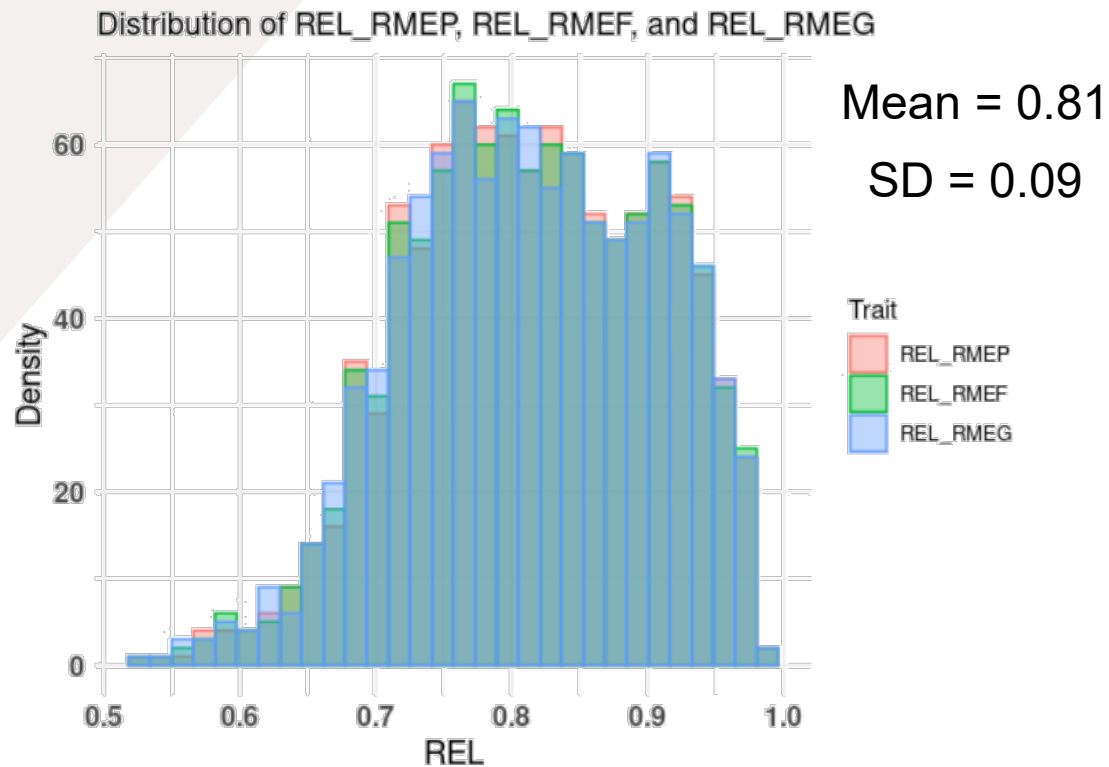
- ▶ Breeding program → reported trait, some options
 - ▶ Full integration index ← missing economic values (except DK)
 - ▶ Restricted gain ← difficulty to optimize
- ▶ Temporary solution
 - ▶ Ranking animals for CH₄ at constant level productive, functional, or economic outcome
- ▶ Leads to residual-based efficiency trait
 - ▶ Can also be interpreted as correcting CH₄ for these levels
 - ▶ We “tested”
 - ▶ Production traits → **RMEP**
 - ▶ Functional traits (Sub-index for functional traits) ← because of the expected negative link → **RMEF**
 - ▶ Economic (Global-)index → **RMEG**
- ▶ RMEP, RMEF, RMEG (more efficient → higher values)
 - ▶ Expressed relatively to all cow born in 2020 with records, their values → mean = 100, SD = 10

1,020 bulls selected

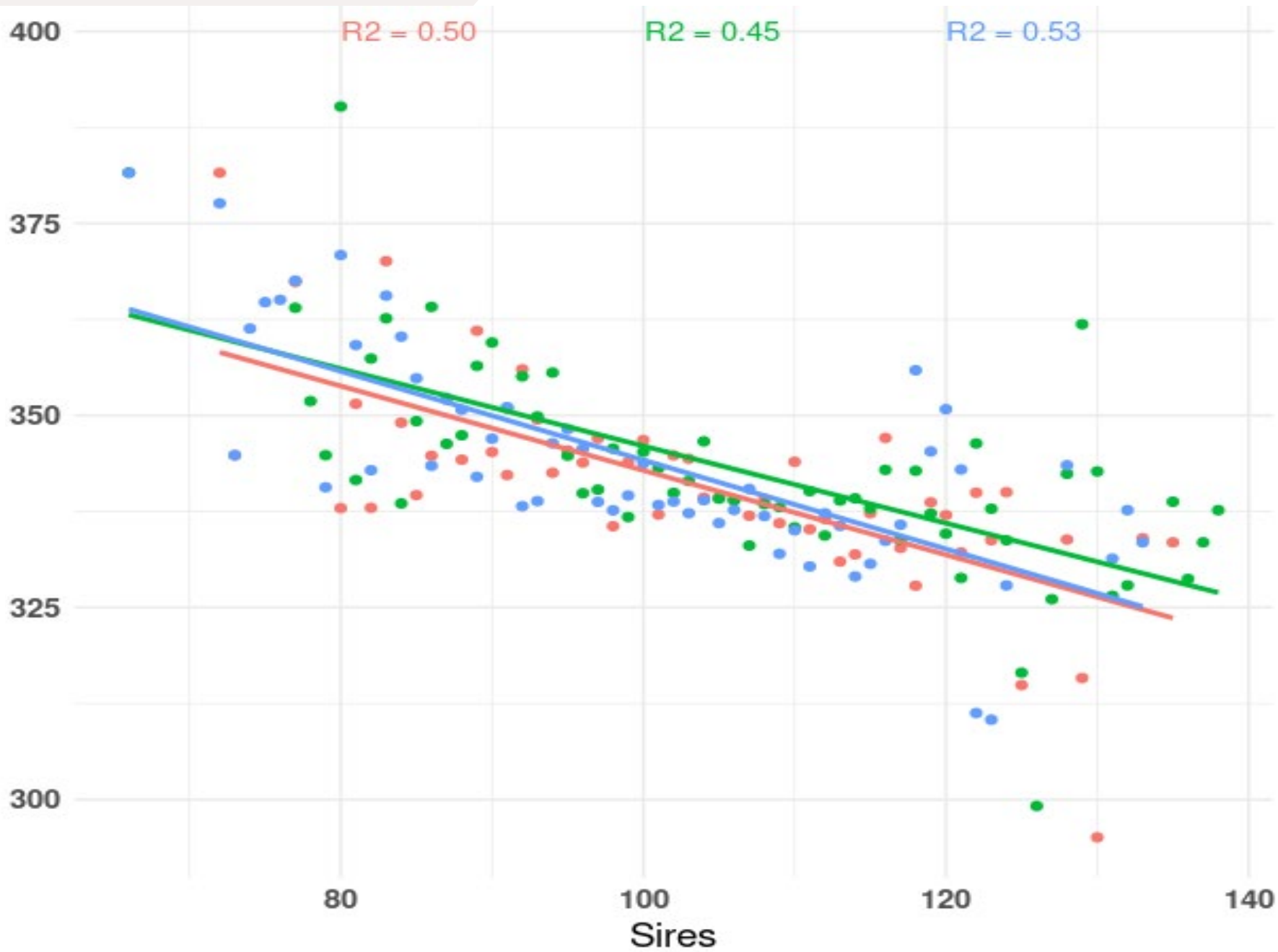
- Reliability ≥ 0.50
- Phenotyped daughters in Belgium ≥ 30



USA	NLD	CAN	DEU	FRA	ITA	BEL	GBR	DNK	CHE	HUN	AUS	AUT	CZE	FIN	IRL
321	187	141	124	98	69	30	22	11	10	2	1	1	1	1	1



Average PCH4(g/d) of daughters



Final question:

Do GEBV based on (PCH₄) MIR-CH₄ represent correctly breath CH₄?



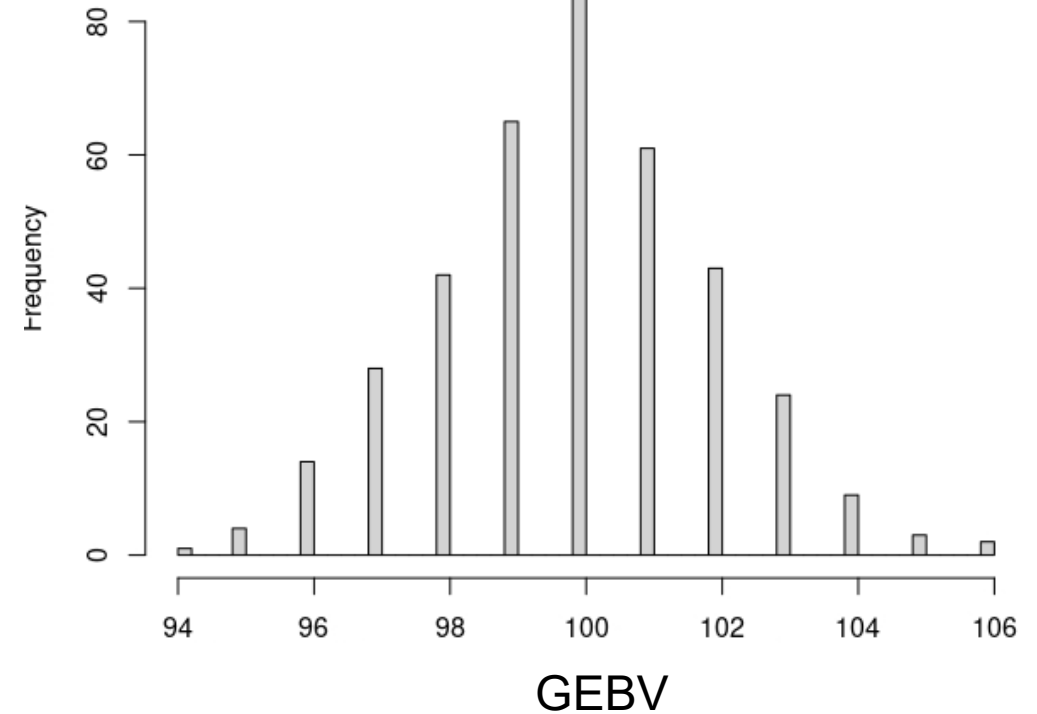
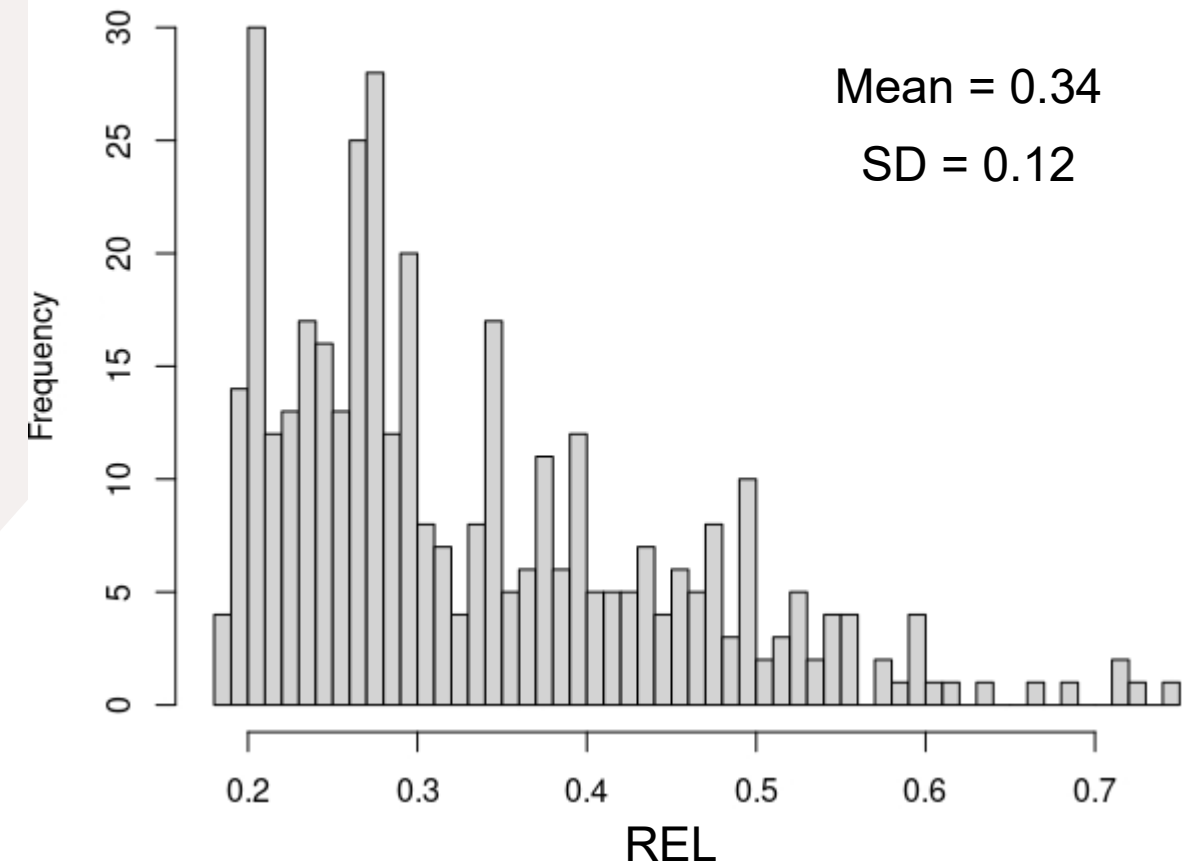
- ▶ Some other countries start to produce GEBV
 - ▶ Public access to limited information ← we are interested to develop here further collaborations
- ▶ Two countries
 - ▶ Country A based on sniffers and Greenfeed
 - ▶ Country B based on sniffers
- ▶ For both limited data, also few bulls reliable enough for comparisons

Country A



- ▶ 382 bulls in common to our 1,020 bulls

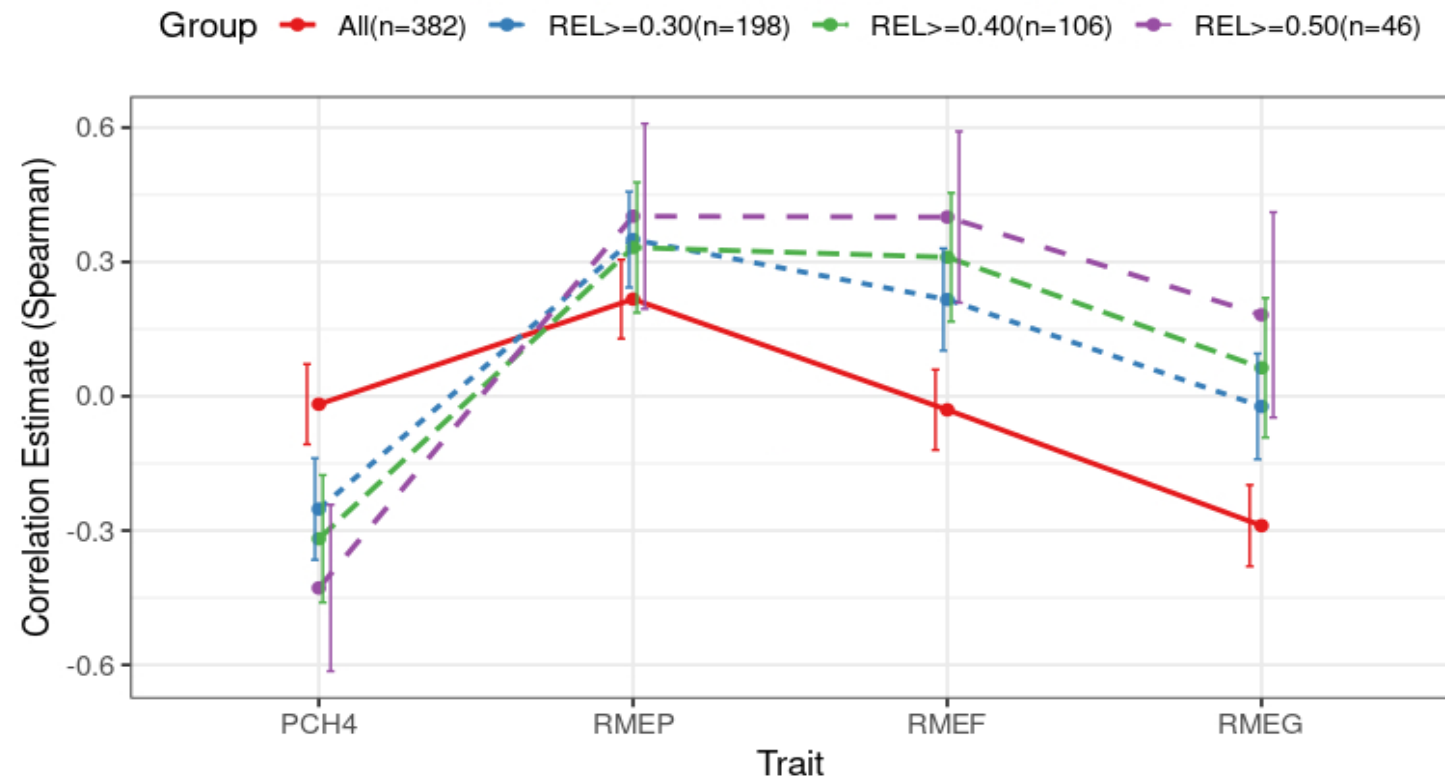
NLD	USA	CAN	DEU	ITA	FRA	BEL	DNK	GBR	CHE	HUN
105	103	57	46	23	21	10	8	6	2	1



Approximated genetic correlation (Spearman correlation, Blanchard et al.,1983)



	PCH4	RMEP	RMEF	RMEG	PCH4_SE	RMEP_SE	RMEF_SE	RMEG_SE
All	-0.02	0.22	-0.03	-0.29	0.09	0.09	0.09	0.09
REL>=0.30	-0.25	0.35	0.21	-0.02	0.11	0.11	0.11	0.12
REL>=0.40	-0.30	0.32	0.31	0.07	0.14	0.15	0.14	0.16
REL>=0.50	-0.41	0.40	0.40	0.17	0.19	0.21	0.19	0.23

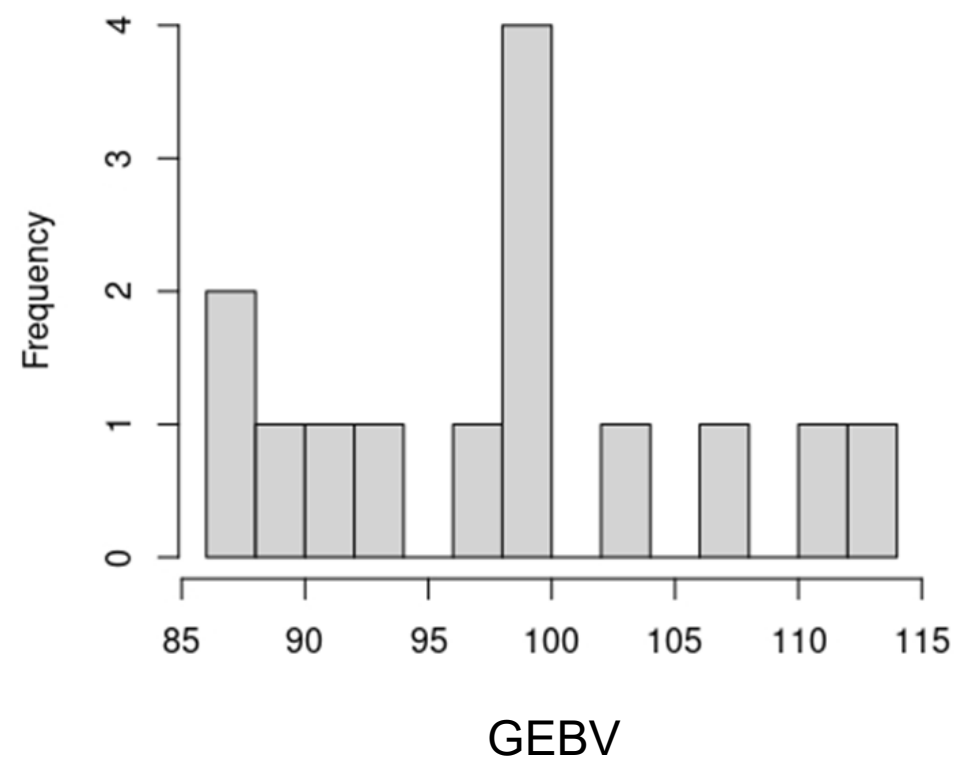
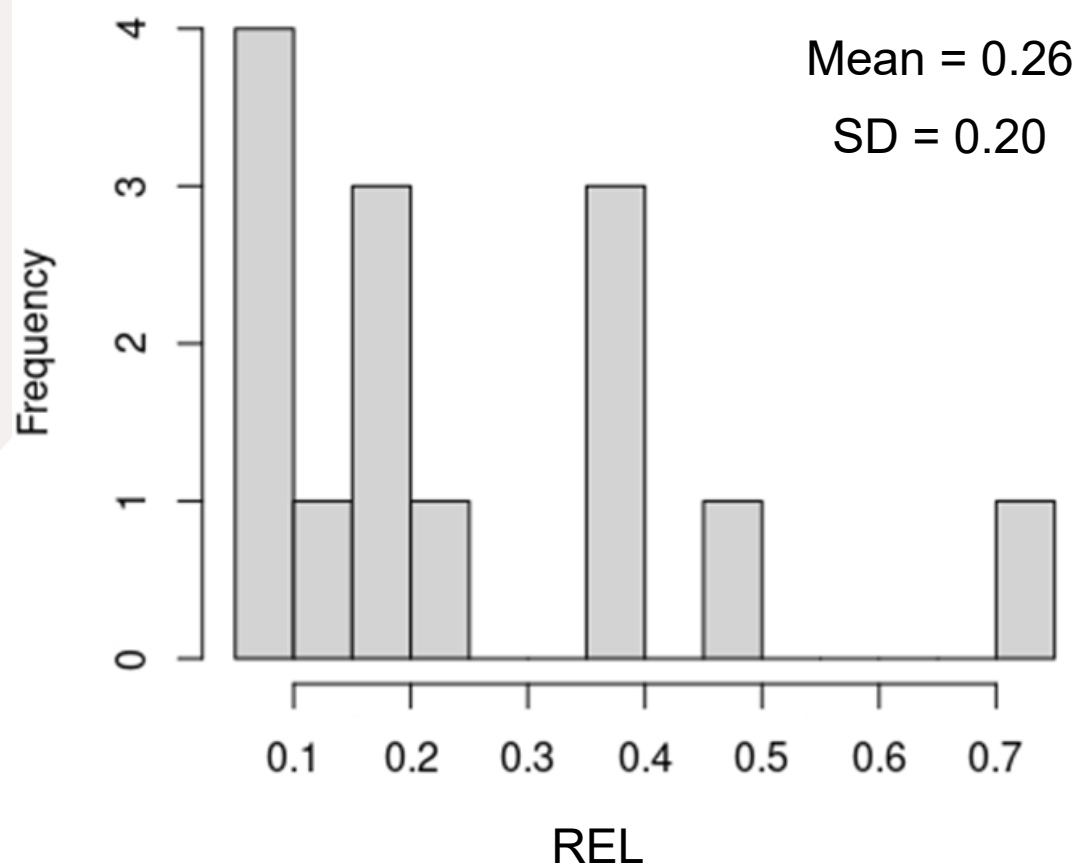


Country B



- Only 14 bulls in common to our 1,020 bulls

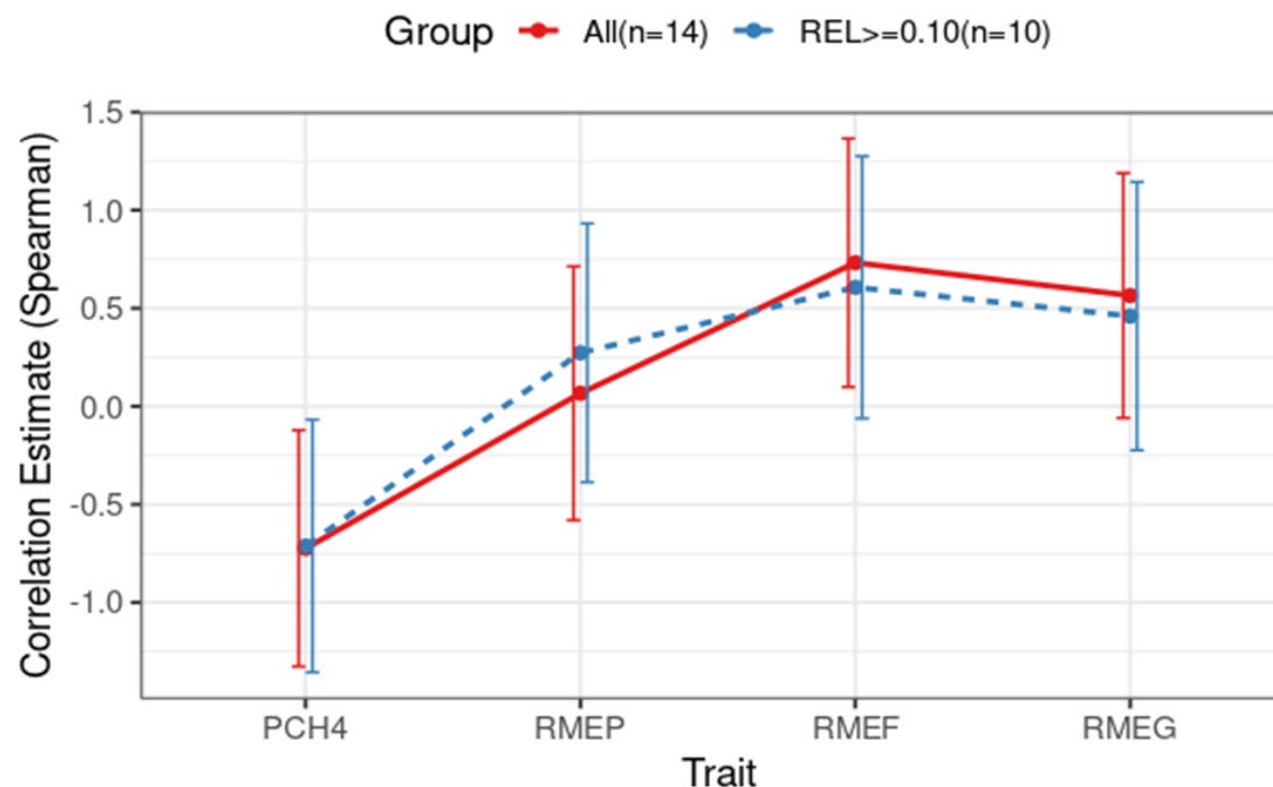
USA	NLD	CAN	FRA
8	4	1	1



Approximated genetic correlation (Spearman correlation, Blanchard et al., 1983)



	PCH4	RMEP	RMEF	RMEG	PCH4_SE	RMEP_SE	RMEF_SE	RMEG_SE
All	-0.72	0.07	0.73	0.56	0.60	0.65	0.63	0.62
REL>=0.10	-0.71	0.27	0.61	0.46	0.64	0.66	0.67	0.68



GEV → SNP effects → DGV



- ▶ Launch in July 2025 → GEV for group of bulls
- ▶ Estimation of SNP effects → Estimation of DGV
 - ▶ Allowing others to get access to our predictions ← contact us if interested
- ▶ In progress → fine tuning → next evaluation end of 2025 – beginning 2026
 - ▶ Based on routine run of end of 2025

Conclusions



- ▶ We have high confidence in our system
- ▶ Comparing it to other → GEBV in same direction
- ▶ But **more collaboration needed**, examples:
 - ▶ MIR equation
 - ▶ CH₄ – MACE
 - ▶ SNP effects....

Thank you for your attention!



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