Single-step evaluation for milking cow survival in Poland

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Interbull 2024

Goal

Develop and implement single step evaluation of milking cow survival for Polish Holstein-Friesian population using BLUPF90 software

Many possible phenotypes were tested. Here focus on 5 that made it to final validation round.

Survival – current model

- Current GE – Survival Kit
  - Longevity defined as days from first calving to removal date or last recorded herd test
  - Statistically superior model
  - Single step implementation problematic
  - Decided to move to BLUPF90 family of programs

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Option 1

1. Length of productive life (time in days from first calving to culling)
   - $h^2 = 0.12$

   Pros:
   - Simple single trait model
   - The closest phenotype to current evaluation
   - Good heritability

   Cons:
   - Phenotype only available after cow's death

Option 2

2. MT-ML-AM (9 trait model)
   - Survival to a given DIM during lactation. First three lactations are split into periods of time representing culling for different reasons
   - Time periods decided based on DIM at culling typical for main culling reasons (1-74, 75-249, 250-next calving)
   - Dry period included in the last period
   - h^2 = 0.006-0.029

Option 3

3. Survival from one parity to the next, parities 1-2, 2-3, 3-4, 4-5 as binary phenotype (4 trait model)
   - h^2 = 0.034-0.046
   - Higher h^2 than 9 trait model, less traits, more parities

Option 4

4. Survival to a given DIM during lactation. All lactations are split into periods of time representing culling for different reasons (like in 9 trait model)
   - Repeated records
   - 3 trait model with dry period included in the last period
   - h^2 = 0.012-0.026

Option 5

5. Survival from one calving to the next in parities 1 to 10
   - Repeated records
   - Single trait model
   - $h^2 = 0.04$

Options

1. Length of productive life in months (cont.). 1 trait (**prodlife_ebv**)

Binary:

2. Survival to a given DIM during lactation. First three lactations are split into three periods. 3 parities, 9 traits. (**surv9_ebv**)
3. Survival from one parity to the next. 4 parities, 4 traits. (**surv15_ebv**)
4. Option 2 as repeated records. 10 parities, 3 traits. (**prep_ebv**)
5. Option 3 as repeated records. 10 parities, 1 trait. (**rep_ebv**)

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Correlations with current EBVs (PBLUP)

	All bulls		Available bulls		Cows
evaluation type	Domestic	MACE	Domestic	MACE	Domestic
number of animals	19,568	36,099	621	777	2,490,297
average reliability	0.60	0.45	0.45	0.50	0.30
prodlife_ebv	0.46	0.34	-0.15	-0.14	0.54
surv9_ebv	0.58	0.47	0.34	0.44	0.59
surv15_ebv	0.58	0.48	0.32	0.42	0.59
prep_ebv	0.72	0.60	0.43	0.52	0.77
rep_ebv	0.73	0.64	0.49	0.57	0.78

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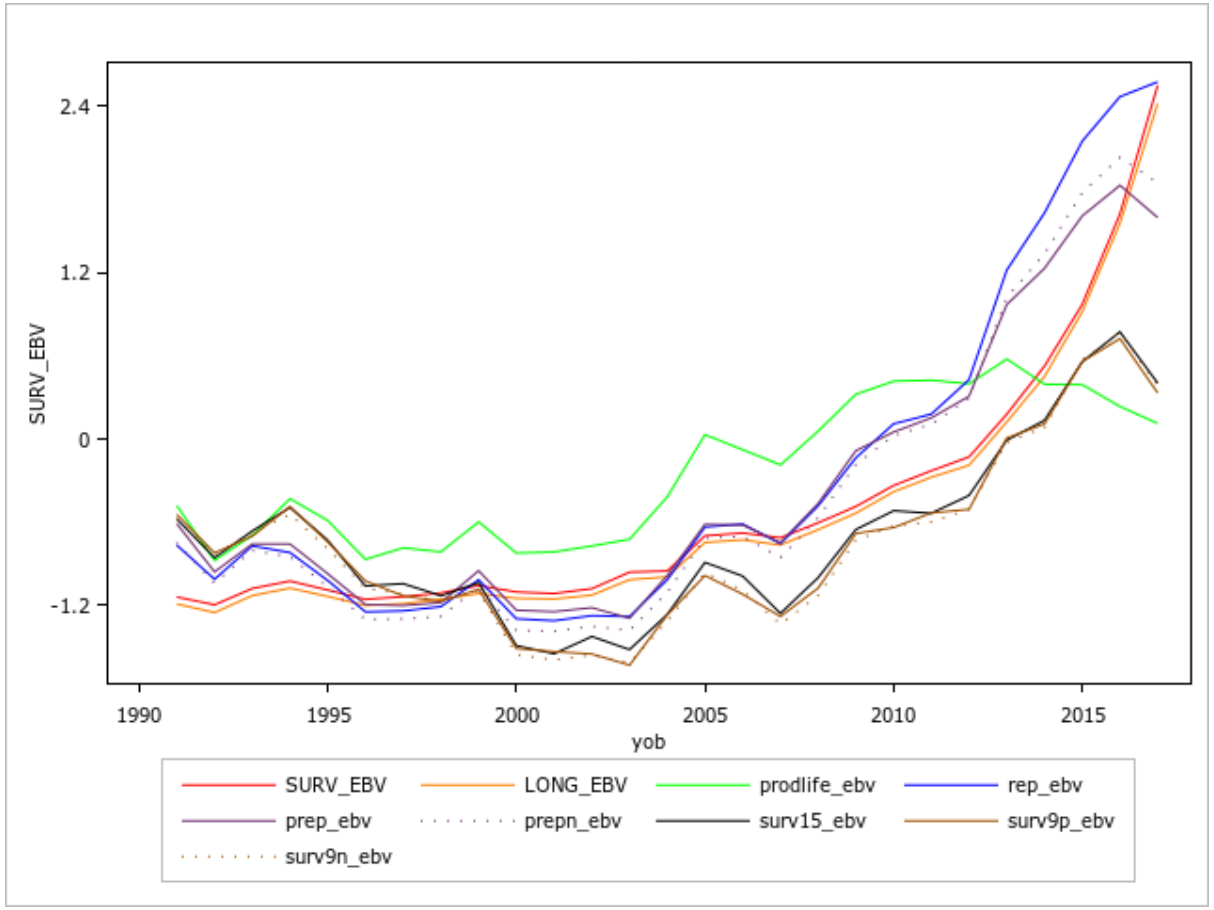
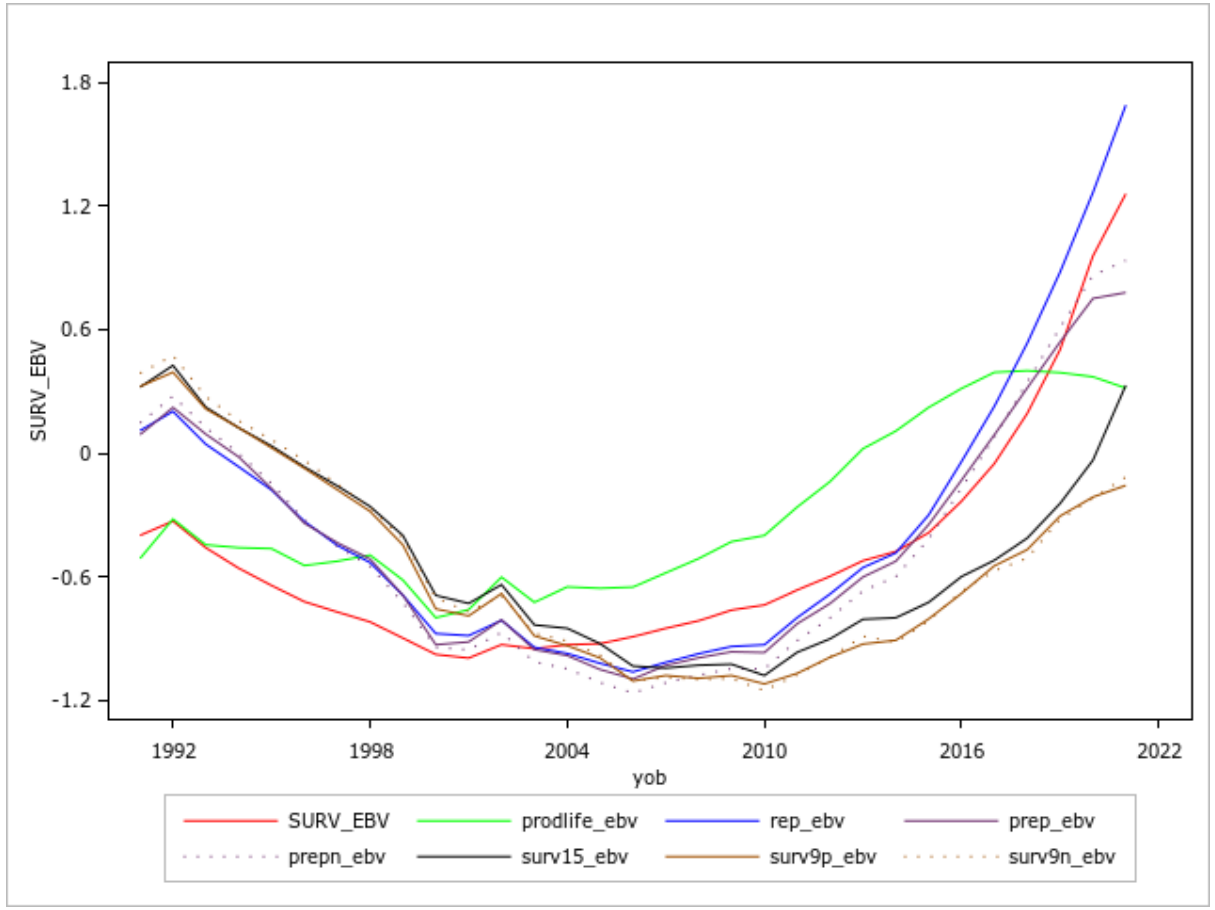
Genetic trends (SD of 1)
(bulls ←, cows →)





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Validation method

- Validation runs performed with phenotypes from last 4 full seasons removed (2018-2022)
- Full pedigree used in both
- Conventional (PBLUP) and single-step (SSBLUP) runs for all options

Focal groups for LR validation

- Young Sires - bulls with 0 daughters in truncated and min 25 in full run (679; 64% genotyped)
- Proven Sires - bulls with 5-25 daughters in truncated and min 2x in full run (196 ; 54% genotyped)
- Cows – cows with phenotypes removed in truncated runs (21,977 ; 5% genotyped)

LR Validation Results

	PBLUP			SSBLUP		
surv9_ebv (9 trait model)						
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc
Young Sires	-0.012	1.011	0.606	0.163	0.819	0.814
Proven Sires	0.025	0.920	0.757	0.094	0.893	0.865
Cows	0.029	0.953	0.782	0.095	0.907	0.846
surv15_ebv (4 trait model)						
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc
Young Sires	0.061	0.892	0.570	0.181	0.783	0.806
Proven Sires	0.041	0.867	0.740	0.087	0.849	0.858
Cows	0.038	0.909	0.759	0.087	0.887	0.834
prep_ebv (3 trait repeatability model)						
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc
Young Sires	-0.161	1.113	0.658	0.187	0.831	0.820
Proven Sires	0.149	1.028	0.738	0.285	0.905	0.838
Cows	0.132	1.023	0.768	0.262	0.930	0.843
rep_ebv (single trait repeatability model)						
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc
Young Sires	0.271	1.017	0.631	0.004	0.852	0.818
Proven Sires	0.554	0.933	0.727	0.105	0.860	0.829
Cows	0.535	0.930	0.751	0.078	0.896	0.831
prodlife_ebv (single trait model)						
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc
Young Sires	0.263	0.397	0.468	0.518	0.449	0.828
Proven Sires	0.056	0.671	0.789	0.218	0.594	0.847
Cows	0.069	0.719	0.768	0.233	0.643	0.820

LR Validation Results

	PBLUP			SSBLUP			SSBLUP-PBLUP		
surv9_ebv (9 trait model)							abs(diff)	diff-1	diff
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc	higher bias	further from 1	higher acc
Young Sires	-0.012	1.011	0.606	0.163	0.819	0.814	0.15	-0.17	0.21
Proven Sires	0.025	0.920	0.757	0.094	0.893	0.865	0.07	-0.03	0.11
Cows	0.029	0.953	0.782	0.095	0.907	0.846	0.07	-0.05	0.06
surv15_ebv (4 trait model)							abs(diff)	diff-1	diff
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc	higher bias	further from 1	higher acc
Young Sires	0.061	0.892	0.570	0.181	0.783	0.806	0.12	-0.11	0.24
Proven Sires	0.041	0.867	0.740	0.087	0.849	0.858	0.05	-0.02	0.12
Cows	0.038	0.909	0.759	0.087	0.887	0.834	0.05	-0.02	0.08
prep_ebv (3 trait repeatability model)							abs(diff)	diff-1	diff
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc	higher bias	further from 1	higher acc
Young Sires	-0.161	1.113	0.658	0.187	0.831	0.820	0.03	-0.06	0.16
Proven Sires	0.149	1.028	0.738	0.285	0.905	0.838	0.14	-0.07	0.10
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Proven Sires	0.554	0.933	0.727	0.105	0.860	0.829	-0.45	-0.07	0.10
Cows	0.535	0.930	0.751	0.078	0.896	0.831	-0.46	-0.03	0.08
prodlife_ebv (single trait model)							abs(diff)	diff-1	diff
focal_group	bias	slope	ratio_acc	bias	slope	ratio_acc	higher bias	further from 1	higher acc
Young Sires	0.263	0.397	0.468	0.518	0.449	0.828	0.26	0.05	0.36
Proven Sires	0.056	0.671	0.789	0.218	0.594	0.847	0.16	-0.08	0.06
Cows	0.069	0.719	0.768	0.233	0.643	0.820	0.16	-0.08	0.05

LR Validation Results

PBLUP	1	2	3
bias	surv9	surv15	prep
slope	prep	surv9	rep
ratio_acc	surv9	prep	surv15/rep

SSBLUP	1	2	3
bias	rep	surv15	surv9
slope	prep	surv9	rep
ratio_acc	surv9	prep	surv15

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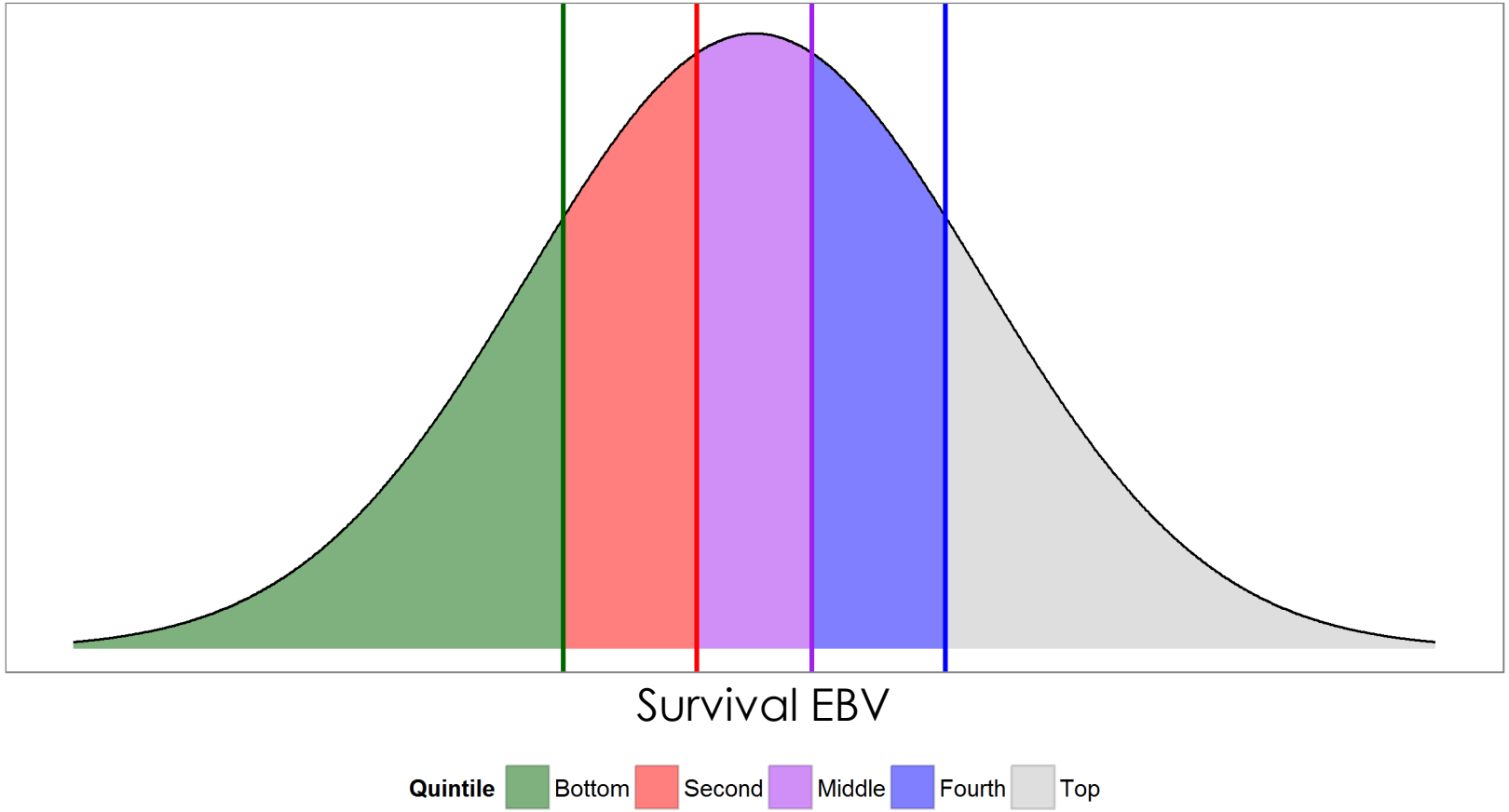
Validation method



Validation phenotype = Quintile + CG + Age + error

→ LSM(Q5) – LSM(Q1)

↓ Higher value = better prediction

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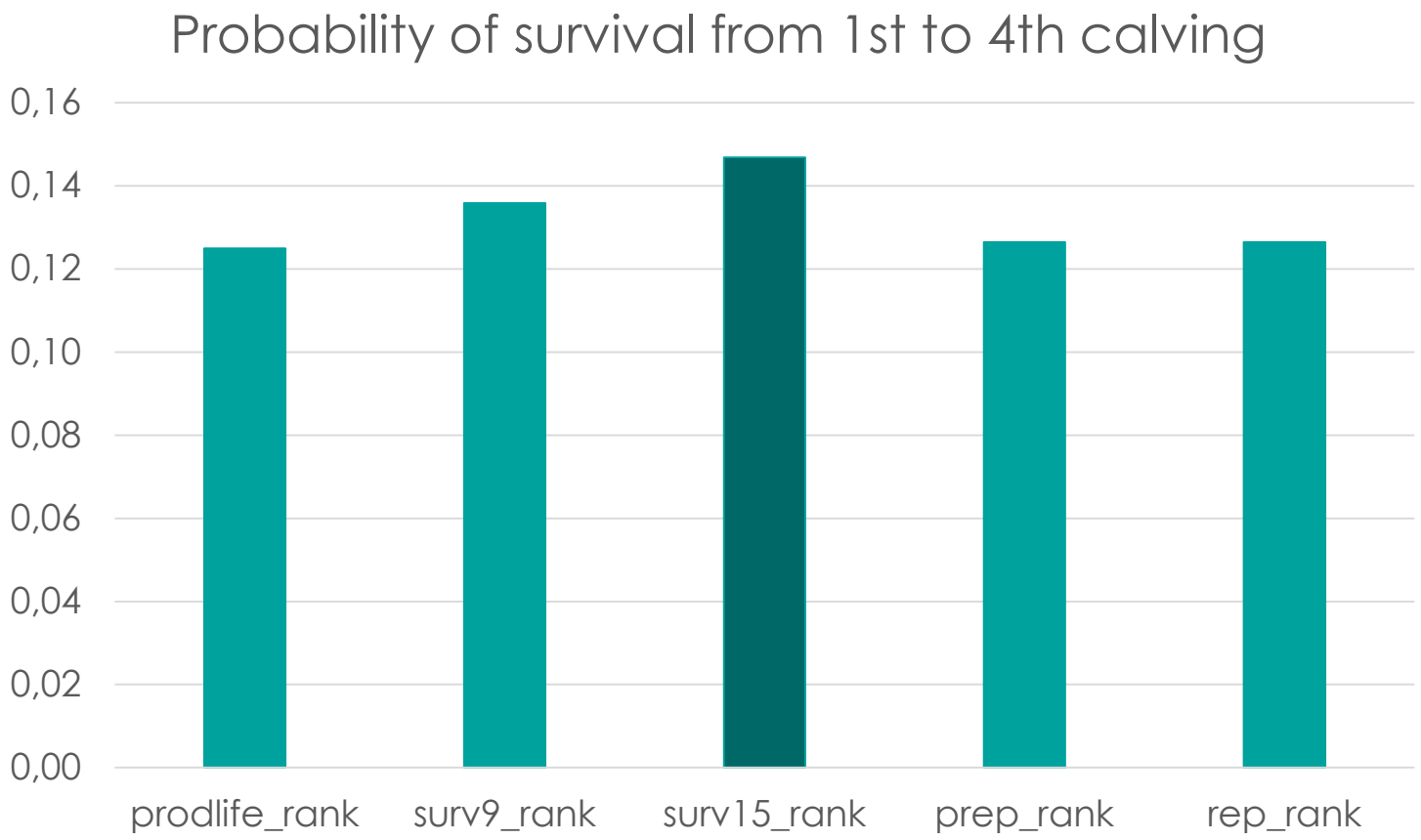
Validation results



Validation results

Ranking of EBVs:

1. surv15
2. surv9
3. prep
4. rep
5. prodlife

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MS and Trend Test III Results

		Trend test III				MS test	
Trait	Model	pass	stat	biol	N	bulls	cows
prodlife_ebv	PBLUP	PASS	PASS	PASS	195	-13.4	-12.3
surv9_ebv	PBLUP	PASS	PASS	FAIL	142	-5.9	1
surv15_ebv	PBLUP	PASS	PASS	FAIL	168	-4.6	1.2
prep_ebv	PBLUP	FAIL	FAIL	FAIL	215	-5.3	-1.2
rep_ebv	PBLUP	PASS	PASS	FAIL	213	0	2

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- Based on LR valid
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- Based on "quintile" valid
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- *Results look good!*
- *Differences are small!*

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Recommendations

My list:

1. 3 trait repeatability
2. 4 trait
3. 9 trait
4. Single trait repeatability

Recommendations

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3. 9 trait
4. Single trait repeatability

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Next steps

- Choose model
- Test/parallel runs
- Interbull test run in September
- MACE integration into SSPBUP
- Implementation in December

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