

SS calving trait evaluation March 2024, Ulrik Sander Nielsen

The current official evaluation is a multi-trait evaluation with direct and maternal effect. 6 traits are evaluated: stillbirth, calving ease and calf size in first lactation and stillbirth, calving ease and calf size in and later lactation. Traits in the table 1 are in the same order with direct effect first and maternal effect later.

The traditional evaluation was redone in MIX99, with the only change, that the pedigree was changed, so it also included genotyped animals, and the pedigree were built in the same manner as done for other traits, which now are calculated with SS. Correlations were above 0.99.

Three extra runs per breed were performed:

1. A traditional evaluation were phenotypic data for progeny of genotyped bulls born after 2016 were deleted. Same pedigree kept (red EBV).
2. A Single Step evaluation with all phenotypic data. Same traditional pedigree (GEBV).
3. A Single Step evaluation were phenotypic data for progeny of genotyped bulls born after 2016 were deleted (red GEBV).

All indexes were standardized and transformed to relative indexes.

Three forms of regressions were made for genotyped bulls with min. 50 daughters in the full data for bulls born after 2016:

1. EBV on red EBV. It is the same as Legara/Reverter on traditional model on pedigree indexes (model 1).
2. Full EBV on red GEBV. The test shows if genomic information adds extra information, compared to pedigree index. IF r^2 for this model (model 2) is bigger for model 1, then genomic information adds information compared pedigree information. The model avoid autocorrelation between full and reduced dataset on the genomic part.
3. GEBV on red GEBV. It is the same as Legara/Reverter regression. (Model3)

Results are shown in table 1. The results are disappointing. Regressions are far below 1 and R^2 are not as high as expected.

Table 1. Results of different regressions. See text

		EBV on red EBV		EBV on red GEBV		GEBV on red GEBV		GEBV on red GEBV VG bulls		
		B1	R2	B1	R2	B1	R2	B1	R2	
HOL										
Bv1		0,07	0,02	0,17	0,08	0,18	0,10			
Bv2		0,07	0,02	0,27	0,14	0,30	0,18			
Bv3		0,22	0,06	0,52	0,32	0,58	0,40			
Bv4		0,03	0,00	0,06	0,02	0,06	0,03			
Bv5		0,03	0,00	0,16	0,08	0,18	0,10			
Bv6		0,18	0,04	0,59	0,39	0,61	0,42			
Bv7		0,49	0,26	0,51	0,36	0,65	0,51			
Bv8		0,41	0,22	0,40	0,27	0,51	0,43			
Bv9		0,57	0,16	0,49	0,21	0,69	0,38			
Bv10		0,32	0,14	0,26	0,12	0,38	0,24			
Bv11		0,24	0,09	0,16	0,06	0,35	0,26			
Bv12		0,67	0,23	0,46	0,20	0,75	0,45			
N		208								
RDC										
Bv1		0,07	0,06	0,08	0,06	0,08	0,07			
Bv2		0,29	0,14	0,30	0,16	0,30	0,16			
Bv3		0,32	0,14	0,34	0,15	0,35	0,15			
Bv4		0,05	0,03	0,05	0,03	0,05	0,03			
Bv5		0,19	0,09	0,20	0,10	0,20	0,10			
Bv6		0,20	0,07	0,22	0,07	0,22	0,08			
Bv7		0,44	0,25	0,45	0,23	0,45	0,22			
Bv8		0,72	0,31	0,72	0,31	0,73	0,31			
Bv9		0,62	0,20	0,63	0,20	0,63	0,20			
Bv10		0,34	0,20	0,33	0,18	0,33	0,18			
Bv11		0,46	0,20	0,46	0,19	0,46	0,20			
Bv12		0,60	0,19	0,61	0,19	0,61	0,19			
N		130								
Bv1		-0,22	0,04	-0,13	0,01	-0,14	0,01			
Bv2		0,40	0,09	0,36	0,09	0,44	0,14			
Bv3		0,72	0,26	0,72	0,43	0,82	0,54			
Bv4		-0,17	0,03	-0,17	0,02	-0,14	0,01			
Bv5		0,17	0,01	0,26	0,03	0,36	0,07			
Bv6		0,85	0,29	0,72	0,44	0,80	0,52			
Bv7		0,32	0,05	0,57	0,15	0,69	0,20			
Bv8		0,41	0,13	0,44	0,24	0,60	0,37			
Bv9		0,67	0,14	0,53	0,16	0,67	0,25			
Bv10		0,71	0,15	0,63	0,15	0,78	0,27			
Bv11		0,48	0,12	0,37	0,11	0,72	0,35			
Bv12		0,72	0,16	0,62	0,26	0,81	0,41			
N		67								

Results look very strange especially for RDC. Without changing data and pedigree, the SS models and traditional models were redone with just direct effects. Models were run for RDC and with full and reduced data. Models with both direct and maternal trait are model1, and models with only direct effect are called model2.

Correlations between the models are calculated for calf survival in 1st lactation are shown in table 2, but results for the other traits are similar. Correlations are calculated for VG bulls born from 2013 to 2022. Correlations indicate that models with direct and maternal give nearly the same results with models with only direct effect. It indicates that the model with direct and maternal effect works as expected. The results also indicate that the SS prediction for candidates is with low accuracy. Correlations between full and reduced model are very low for birth year 2017 and 2018, where data is included in the full model. Correlations between models with full and reduced data are also low for birth year 2021 and 2022, where bulls in both full and reduced dataset are candidates. It indicates that the genomic information from animals born after 2016 has a big influence on the estimate of the genomic part.

	Correlations				
	model1- model2 SS full data	model1- model2 SS reduced data	model1- model1 SS full/reduced data	model2- model2 full/reduced data	
2013	0,95	0,96	0,97	0,98	
2014	0,96	0,97	0,99	0,99	
2015	0,95	0,99	0,70	0,69	
2016	0,97	0,99	0,95	0,92	
2017	0,91	0,99	0,25	0,24	
2018	0,97	0,99	0,12	0,11	
2019	0,99	0,99	0,46	0,46	
2020	0,99	0,99	0,24	0,23	
2021	0,99	0,99	0,47	0,47	
2022	0,99	0,99	0,33	0,35	

The current traditional model includes data from early 80ties. It is a lot of data with no interest. The SS models run for a very long time, HOL for 7 days. For future testing I suggest that data will be cut off at year 2000.