

SS calving trait evaluation

April 2024, USN

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). Results was shown in March.

Data from early 80 ties is included in the traditional runs. But with SS runs executing time increase much. At the blending meeting in March, it was decided to cut off calving data before 2000. The cut off has no effect the latest birth year classes. Because of the poor test results, it was decided to make data cut for the reduced run more stringent. In the reduced runs, calvings in 2020 or later were deleted. The extra runs per breed were:

- 4. A traditional evaluation where calvings in 2020 or later were deleted. Same pedigree kept (red EBV).
- 5. A Single Step evaluation with all phenotypic data. Same traditional pedigree (GEBV).
- 6. A Single Step evaluation where calvings in 2020 or later 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 and no data in the reduced data. The check was done for each trait, so the number of bulls was different from trait to trait.

- 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 r2 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. For RDC the SS results were the same as the traditional results. The reason has not been found. For HOL and JER b1 value is still far from 1 for some traits, but R2 looks better.

		EBV on red		EBV on red		GEBV on red		GEBV on red GEBV		
		ERA ERA		GEBV		GEBV		VG bulls		
		B1	R2	B1	R2	B1	R2	B1	R2	
HOL										
Bv1		0,78	0,33	0,79	0,44	0,73	0,45			
Bv2		0,60	0,25	0,57	0,38	0,54	0,45			
Bv3		0,45	0,11	0,60	0,38	0,64	0,50			
Bv4		0,44	0,09	0,45	0,15	0,56	0,26			
Bv5		0,45	0,17	0,49	0,36	0,51	0,41			
Bv6		0,72	0,26	0,70	0,53	0,73	0,57			
Bv7		0,69	0,20	0,62	0,38	0,82	0,57			
Bv8		0,50	0,12	0,45	0,27	0,60	0,45			
Bv9		0,76	0,19	0,59	0,27	0,71	0,40			
Bv10		0,52	0,13	0,49	0,19	0,62	0,32			
Bv11		0,32	0,09	0,26	0,10	0,39	0,26			
Bv12		0,74	0,26	0,59	0,32	0,71	0,46			
Ν	211-									
	308									
RDC										
Bv1										
Bv2										
Bv3										
Bv4										
Bv5										
Bv6										
Bv7										
Bv8										
Bv9										

Table 1. Results of different regressions. See text.

Bv10									
Bv11									
Bv12									
Ν									
Bv1		1,01	0,27	1,31	0,45	1,35	0,41		
Bv2		0,63	0,28	0,55	0,28	0,70	0,36		
Bv3		0,61	0,20	0,54	0,32	0,55	0,36		
Bv4		0,64	0,13	1,11	0,31	1,12	0,27		
Bv5		0,72	0,17	0,57	0,17	0,73	0,31		
Bv6		0,91	0,36	0,56	0,33	0,64	0,48		
Bv7		0,80	0,13	0,97	0,23	1,16	0,33		
Bv8		0,40	0,02	0,37	0,07	0,60	0,17		
Bv9		0,50	0,08	0,51	0,17	0,71	0,31		
Bv10		1,08	0,16	0,64	0,09	0,81	0,19		
Bv11		0,45	0,03	0,18	0,01	0,47	0,08		
Bv12		0,97	0,21	0,94	0,47	1,06	0,58		
Ν	75-83								