

SS claw evaluation, preliminary results. 2022, USN

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The current official claw evaluation is multi trait evaluation with 7 claw traits evaluated in 3 lactations. Traits and frequencies in first lactation for the last year are shown in table 1.

The evaluation is done in DMU, and the evaluation was changed to MIX99. 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 for SS-type. The only change was caused by other phenotypic data than for type traits. EBV's from DMU and MIX99 were compared. 21 indexes were calculated in all evaluations (7 traits and 3 lactations). Bulls with min. 50 progenies in first lactation were compared. Results are shown in table 2. Standard deviations of raw solutions for traits in first lactation are shown. SD for the first 4 traits are bigger than for last 3 three traits especially for JER. Correlations between result were above 0,99 for most traits.

Three runs per breed were performed:

1. A traditional evaluation were phenotypic data for progeny of genotyped bulls born after 2014 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 2014 were deleted (red GEBV).

All indexes were standardized and transformed to relative indexes. Combined indexes for the 7 traits were made, but not the overall claw index. Only indexes from first lactation were used in the analyses to ensure, that reduced indexes include information from phenotypes.

Three forms of regressions were made for genotyped bulls with min. 50 daughters in the full data for bulls born after 2014:

1. EBV on red EBV. It is the same as Legara/Reverter on traditional model on pedigree indexes (model 1).
2. Full GEBV on red EBV. The test shows if genomic information add 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 tables 3-5. Results from model 1, where traditional EBV's from full and reduced model, show b_1 below 1 and r^2 in the expected range. When reduced EBV's are substituted by reduced GEBV's in model 2 r^2 increase. This is a clear indication, that genomic information add value to the pedigree information about the true EBV for the animal. The genomic test will add additional information and this the reason, why r^2 for model 3 are even higher. This value may be an overprediction, because the same genomic information is included in GEBV and reduced GEBV.

Table 1. Klovlidelser i 1. laktation hos RDC-, Holstein- og Jerseykøer
Claw diseases in 1 st lactation in red breeds, Holstein and Jersey , 2021-2022

Forekomst i % / Occurrence in %	RDC			Holstein			JER
	DNK	SWE	FIN	DNK	SWE	FIN	DNK
Dermatitis (Digital + spaltebet.) / <i>Dermatitis</i>	20,9	10,3	2,3	26,6	13,0	4,1	15,2
Balleforrådnelse / <i>Heel horn erosion</i>	2,9	5,8	4,6	6,0	3,4	4,6	2,2
Såleblødning / <i>Sole heamorrhage</i>	14,5	13,7	6,9	19,9	14,9	8,0	9,6
Sålesår / <i>Sole ulcer</i>	2,8	2,4	1,8	2,3	1,9	2,2	4,6
Proptrækker klov / <i>Cork screw claws</i>	4,3	2,3	3,7	5,1	1,5	2,2	5,0
Nydannelse + digital vorte / <i>Skin proliferation</i>	3,4	1,8	1,1	2,9	1,9	1,3	1,0
Hul væg + dobbelt sål / <i>White line separation + Double sole</i>	6,9	1,5	4,0	7,3	1,8	6,2	5,2

Table 2. Correlations between indexes in first lactation calculated in DMU and Mix99. SD for raw indexes for bulls with more than 50 progenies with data.

Trait	HOL		RDC		JER	
	SD	Correlation	SD	Correlation	SD	Correlation
dde1	0.07982	0.999	0.05561	0,998	0.08240	0,988
hhe1	0.05583	0,997	0.07174	0,995	0.02556	0,979
sh1	0.06091	0,996	0.08624	0,993	0.05125	0,976
su1	0.04666	0,996	0.03405	0,991	0.03761	0,979
clc1	0.00767	0,994	0.01702	0,992	0.00564	0,970
skp1	0.02681	0,999	0.01953	0,997	0.00739	0,979
wls1	0.01191	0,996	0.00961	0,987	0.00463	0,982

Table 3. Results of different regressions for HOL. See text.

	EBV on red EBV		GEBV on red EBV		GEBV on red GEBV		GEBV on red GEBV VG bulls		
	B1	R2	B1	R2	B1	R2	B1	R2	Bias
dde1	0,78	0,22	0,80	0,49	0,95	0,65	0,96	0,64	-0,9
hhe1	0,72	0,27	0,71	0,44	0,87	0,64	0,84	0,57	0,4
sh1	0,67	0,17	0,72	0,44	0,92	0,63	0,92	0,63	0,7
su1	0,68	0,15	0,73	0,38	0,88	0,53	0,86	0,52	0,9
clc1	0,77	0,26	0,69	0,42	0,91	0,63	0,91	0,60	2,3
skp1	0,75	0,25	0,74	0,47	0,87	0,61	0,87	0,59	-0,4
wls1	0,97	0,22	0,82	0,41	1,05	0,63	1,05	0,63	-1,1
N	310		310		310		236		

Table 4. Results of different regressions for RDC. See text

	EBV on red EBV		GEBV on red EBV		GEBV on red GEBV	
N	B1	R2	B1	R2	B1	R2
dde1	0,96	0,40	0,96	0,53	1,04	0,64
hhe1	1,02	0,35	0,91	0,46	1,04	0,63
sh1	0,95	0,32	0,89	0,50	1,02	0,62
su1	0,99	0,31	0,94	0,49	1,06	0,61
clc1	0,83	0,35	0,87	0,45	0,98	0,58
skp1	0,88	0,34	0,92	0,50	1,02	0,60
wls1	1,16	0,50	1,02	0,61	1,14	0,73
N	169		169		169	

Table 4. Results of different regressions for JER. See text

	EBV on red EBV		GEBV on red EBV		GEBV on red GEBV	
	B1	R2	B1	R2	B1	R2
dde1	1,21	0,35	0,94	0,53	1,02	0,62
hhe1	0,99	0,34	0,87	0,52	1,04	0,66
sh1	0,92	0,37	1,04	0,49	1,09	0,54
su1	0,97	0,39	0,94	0,47	1,03	0,58
clc1	1,51	0,52	1,19	0,48	1,36	0,62
skp1	1,02	0,30	0,92	0,45	1,02	0,55
wls1	1,14	0,50	1,06	0,51	1,17	0,60
N	78		78		78	