

# Singlestep

**Youngstock survival, Birth and Calving**

9. September 2025

Andreas Bøgh Poulsen, Trine Andersen and Ulrik Sander Nielsen



STØTTET AF

**Mælke**afgiftsfonden

# Genotype selection

- Normally we have all genotypes included in singlestep
- For those traits, we have more alive than dead calves that are genotyped
- Thus, we have used a subset of genotypes (HOL below)

<b>Trait</b>	<b>Genotyped males</b>	<b>Genotyped foreign bulls</b>	<b>Genotyped females</b>	<b>"Monthly" genotypes</b>
Youngstock survival	5608 Status 1 & 2	None	None	696243
Birth	5608 Status 1 & 2	7435 non-nordic	None	688808
Calving	5608 Status 1 & 2	7435 non-nordic	307733 Cows with a calf in data	381075

# Legarra Reverter Youngstock survival

		HOL			RDC			JER			HOL	RDC	JER
		b1	rsquare	n	b1	rsquare	n	b1	rsquare	n	ltb test	ltb test	ltb test
SS	HP1	0.78	0.39	153	0.92	0.27	143	0.93	0.46	58	Fail	hiSE	Pass
	HP2	0.75	0.34	151	0.83	0.22	143	1.17	0.33	58	Pass	hiSE	Pass
	BP1	0.82	0.41	154	0.86	0.26	143	0.79	0.42	45	Fail	hiSE	Pass
	BP2	0.82	0.39	154	1.00	0.33	143	1.21	0.29	44	Pass	Pass	Pass
EBV	HP1	0.74	0.28	153	0.70	0.15	143	0.87	0.37	58			
	HP2	0.64	0.18	151	0.59	0.10	143	1.08	0.24	58			
	BP1	0.80	0.31	154	0.70	0.15	143	0.75	0.33	45			
	BP2	0.71	0.23	154	0.80	0.19	143	0.94	0.15	44			

Legarra Reverter b1 value are not close to 1 either for SS or EBV  
 Interbull test fails for most traits

# Legarra Reverter Birth

		HOL			RDC			JER			HOL	RDC	JER
		b1	rsquare	n	b1	rsquare	n	b1	rsquare	n	ltb test	ltb test	ltb test
SS	nysb1	0.72	0.55	141	0.87	0.32	111	0.97	0.35	52	Fail	Pass	hiSE
	nyce1	0.50	0.43	140	0.87	0.44	111	0.71	0.29	52	Fail	Pass	hiSE
	nycs1	0.61	0.36	126	1.00	0.40	46	0.65	0.30	51	Fail	Pass	Fail
	nysb2	0.56	0.27	141	0.88	0.36	116	0.89	0.21	58	Fail	Pass	hiSE
	nyce2	0.44	0.28	141	0.83	0.39	115	0.85	0.24	58	Fail	Pass	hiSE
	nycs2	0.84	0.56	134	1.00	0.39	66	0.74	0.38	58	Fail	Pass	Fail
EBV	nysb1	0.71	0.35	141	0.88	0.22	111	0.90	0.26	52			
	nyce1	0.49	0.17	140	0.78	0.27	111	0.63	0.22	52			
	nycs1	0.47	0.15	126	0.78	0.24	46	0.56	0.19	51			
	nysb2	0.49	0.12	141	0.87	0.21	116	0.62	0.10	58			
	nyce2	0.45	0.13	141	0.76	0.26	115	0.90	0.22	58			
	nycs2	0.78	0.30	134	0.91	0.29	66	0.73	0.32	58			

Legarra Reverter b1 value are not close to 1 either for SS or EBV  
 Interbull test fails for most traits

# Legarra Reverter Calving

		HOL			RDC			JER			HOL	RDC	JER
		b1	rsquare	n	b1	rsquare	n	b1	rsquare	n	ltb test	ltb test	ltb test
SS	nysb1	0.74	0.66	312	0.75	0.34	285	0.76	0.23	119			
	nyce1	0.55	0.58	311	0.79	0.46	279	0.60	0.23	117			
	nycs1	0.77	0.48	290	0.84	0.36	103	0.61	0.25	116			
	nysb2	0.49	0.29	266	0.81	0.37	226	0.64	0.26	96			
	nyce2	0.36	0.26	262	0.71	0.39	216	0.61	0.17	91			
	nycs2	0.75	0.47	248	0.93	0.40	79	0.96	0.47	90			
EBV	nysb1	0.77	0.36	312	0.95	0.23	285	0.55	0.08	119			
	nyce1	0.58	0.34	311	0.76	0.20	279	0.49	0.09	117			
	nycs1	0.74	0.21	290	0.94	0.29	103	0.44	0.08	116			
	nysb2	0.49	0.13	266	0.80	0.17	226	0.59	0.10	96			
	nyce2	0.33	0.08	262	0.74	0.18	216	0.28	0.02	91			
	nycs2	0.73	0.19	248	0.73	0.21	79	0.61	0.11	90			

Legarra Reverter b1 value are not close to 1 either for SS or EBV  
 Interbull test not ready yet

# Full reduc table for birth

- The std for full is decreasing by birth year and dropping more than for reduc
- We see the same for official EBV
- Could bias correction post processing be necessary?

Genetic trend for calving ease first parity for singlestep full and reduc for Nordic HOL AI bulls with minimum of 30 offspring in full dataset  
Std of official EBV run is also added

BYR	trait	N	mean		std		corr	
			SSfull	SSreduc	SSfull	SSreduc		
2010	ce1	194	97	97	7.7	7.7	7.6	1.00
2011	ce1	154	98	98	7.0	7.1	7.2	1.00
2012	ce1	170	98	98	7.7	7.8	7.8	1.00
2013	ce1	151	101	101	6.6	6.7	6.8	1.00
2014	ce1	113	100	100	6.8	6.9	7.0	1.00
2015	ce1	82	101	101	4.7	4.7	4.8	0.99
2016	ce1	65	100	101	5.7	5.7	5.7	0.99
2017	ce1	65	100	101	5.4	5.7	5.6	0.99
2018	ce1	78	100	101	4.8	6.4	4.7	0.66
2019	ce1	56	101	102	4.7	5.6	4.6	0.65
2020	ce1	53	102	103	4.0	7.0	3.5	0.75
2021	ce1	43	100	101	4.6	6.4	4.2	0.70
2022	ce1	41	101	103	3.2	5.9	3.0	0.62

# Youngstock survival problem

- We see that the std of raw solutions are higher for candidates than for breeding values from the singlestep big run
- The correlation between candidate monthly breeding values and pedigree based breeding values are very low

# Youngstock survival problem

- For a group of bulls in the genomic reference group:

Variable	N	Mean	Std Dev
bv1	1583	0.01080	0.00696
ebv1	1583	0.01084	0.00513
dgv1	1583	0.05377	0.03617

- bv = genomic breeding value from MiX99
- ebv = non-genomic breeding value
- dgv = direct genomic value

# Youngstock survival problem

- For a group of candidate bulls:

	<b>ebv1</b>	<b>bv1</b>	<b>cbv1</b>	<b>dgv1</b>
<b>ebv1</b>	1	0.98	0.18	0.60
<b>bv1</b>	0.98	1	0.18	0.63
<b>cbv1</b>	0.18	0.18	1	0.84
<b>dgv1</b>	0.60	0.63	0.84	1

# Youngstock survival problem

- Attempted solutions:
  - Expand reference population by including 10000 cows (2000 with dead calves, 8000 with alive calves)
  - Single trait variation
  - Remove problematic genomic markers
- The problem is persistent