

Youngstock survival single step

Trine Andersen & Ulrik Sander Nielsen, April 2025

Introduction

Test runs

uSS is single step setup with official genotypes (uSS =full, uSS_r =reduc)

tSS is single step setup but where genotypes are manipulated (tSS =full, tSS_r =reduc)

EBV is single step setup but without any genotypes, thus a traditional model (ebv =full, ebv_r =reduc)

The model, the parameters, the dataset and the pedigree are the same for all runs. The data cut for reduc is the same for all runs. Only AI bulls born in 2009 or later included, because earlier investigations have shown, that including genotypes from calves have the effect of that the trends were severe overestimated.

```
RANDOM      RHY1
MODEL SCALE
BV1: HP1 = heterosis(bwxhf holxrdc) FHY1      - YS parity -  RHY1 G(nav_id) ! WEIGHT = wHP1
BV2: HP2 = heterosis(bwxhf holxrdc)      - FHY2 YS parity T2 RHY1 G(nav_id) ! WEIGHT = wHP2
BV3: BP1 = heterosis(bwxhf holxrdc) FHY1      - YS parity -  RHY1 G(nav_id) ! WEIGHT = wBP1
BV4: BP2 = heterosis(bwxhf holxrdc)      - FHY2 YS parity T2 RHY1 G(nav_id) ! WEIGHT = wBP2
BV5: combined YSSindex = HP1*3.582 + HP2*4.285 + BP1*1.781 + BP4*2.791;
```

Manipulation of genotypes are done based on the analysis of the allele frequencies, thus for SNPs changing more than 30 percent point in allele frequency from 2009 birth year class to 2024 birth year class, we have decided to manipulate the genotype file where the SNP is fixed to 0. That means that all animals are having the same homozygote for these SNPs. For uSS and tSS only genotypes from bulls born after 2008 are included thus 5428 genotypes, (different from "normal" single step setup where we included all genotypes animals born after 2008). The reason is, that only calves, that have survived has been genotyped and earlier runs with all genotypes has shown severe overestimation of genetic trend, when all genotypes has been included.

The breeding values are postprocessed/standardized, where base animals have same mean and std as in the traditional official youngstock survival breeding values. Base animals are here defined as females and males having a record for HP1, HP2, BP1 or BP2. All base animals are born 9-11 years ago, and without genotype, and have a Nordic country code in id_nor, in total 1010474 base animals.

Below you find tables for genetic trend and correlations for

- Nordic AI bulls with minimum of 50 offspring.
- Nordic AI bulls born >=2019 without any offspring

Legarra Reverter was done as linear regression: full = reduc, for Nordic AI bulls with minimum of 50 offspring in full run, no offspring in reduced run, and where the sire of the bull has minimum 50 offspring in reduced run.

Standardisation

Mean and std for base animals table 1

trait	Variable	N	Mean	Std
1	ebv1	1010474	96.57	6.92
1	ebv_r1	1010474	96.57	6.92
1	uss1	1010474	96.57	6.92
1	uss_r1	1010474	96.57	6.92
1	tss1	1010474	96.57	6.92
1	tss_r1	1010474	96.57	6.92
2	ebv2	1010474	97.77	5.87
2	ebv_r2	1010474	97.77	5.87
2	uss2	1010474	97.77	5.87
2	uss_r2	1010474	97.77	5.87
2	tss2	1010474	97.77	5.87
2	tss_r2	1010474	97.77	5.87
3	ebv3	1010474	96.54	6.90
3	ebv_r3	1010474	96.54	6.90
3	uss3	1010474	96.54	6.90
3	uss_r3	1010474	96.54	6.90
3	tss3	1010474	96.54	6.90
3	tss_r3	1010474	96.54	6.90
4	ebv4	1010474	98.00	5.75
4	ebv_r4	1010474	98.00	5.75
4	uss4	1010474	98.00	5.75
4	uss_r4	1010474	98.00	5.75
4	tss4	1010474	98.00	5.75
4	tss_r4	1010474	98.00	5.75
5	ebv5	1010474	97.07	6.02
5	ebv_r5	1010474	97.07	6.02
5	uss5	1010474	97.07	6.02
5	uss_r5	1010474	97.07	6.02
5	tss5	1010474	97.07	6.02
5	tss_r5	1010474	97.07	6.02

BV1 is HP1 heifer early survival

Sires with minimum 50 offspring, 1 table 2															
Obs	BYR	_TYPE_	_FREQ_	ebv1	ebv_r1	uss1	uss_r1	tss1	tss_r1	sebv1	sebv_r1	suss1	suss_r1	stss1	stss_r1
1	2009	1	223	97.3	97.4	97.0	97.3	97.1	97.3	10.4	10.3	10.3	10.2	10.2	10.1
2	2010	1	193	95.0	95.2	94.9	95.2	94.9	95.2	11.1	11.1	11.4	11.4	11.2	11.2
3	2011	1	154	97.1	97.5	96.9	97.3	96.8	97.3	11.4	11.2	11.1	11.0	11.0	10.8
4	2012	1	171	100.1	100.4	100.2	100.3	100.1	100.3	11.1	11.1	11.6	11.5	11.4	11.3
5	2013	1	151	98.9	98.6	99.7	99.0	99.5	99.0	10.9	10.6	11.2	11.0	11.1	10.9
6	2014	1	114	101.8	101.0	102.4	101.3	102.2	101.1	12.5	12.2	12.6	12.3	12.5	12.2
7	2015	1	83	100.1	99.2	100.6	99.2	100.4	99.0	10.5	10.0	10.6	10.0	10.5	9.9
8	2016	1	66	103.5	101.5	104.0	102.6	103.8	102.3	10.1	7.6	10.2	8.4	10.1	8.2
9	2017	1	66	100.2	98.8	100.9	100.1	100.7	99.8	10.1	7.9	9.6	8.0	9.5	7.9
10	2018	1	78	102.8	100.8	104.4	102.9	104.1	102.5	10.6	6.5	10.2	7.8	10.1	7.6
11	2019	1	56	106.6	100.3	108.2	103.2	107.8	102.8	9.6	4.8	9.5	5.3	9.3	5.2
12	2020	1	58	106.6	102.1	107.7	104.0	107.4	103.6	9.8	4.7	9.5	7.2	9.4	7.0
13	2021	1	40	106.6	101.7	108.1	104.1	107.8	103.7	10.3	3.5	10.7	6.0	10.7	5.8
Sires with minimum 50 offspring, 1 table 3															
Obs	_TYPE_	_NAME_		ebv1	ebv_r1	uss1	uss_r1		tss1		tss_r1				
1	MEAN			99.69	98.83	100.06	99.33		99.95		99.21				
2	STD			11.32		10.16		11.55		10.56		11.38		10.40	
3	N			1454.00		1454.00		1454.00		1454.00		1454.00		1454.00	
4	CORR	ebv1		1.00		0.88		0.97		0.87		0.97		0.87	
5	CORR	ebv_r1		0.88		1.00		0.86		0.95		0.86		0.96	
6	CORR	uss1		0.97		0.86		1.00		0.90		1.00		0.90	
7	CORR	uss_r1		0.87		0.95		0.90		1.00		0.91		1.00	
8	CORR	tss1		0.97		0.86		1.00		0.91		1.00		0.90	
9	CORR	tss_r1		0.87		0.96		0.90		1.00		0.90		1.00	
sires without any offspring, 1 table 4															
Obs	BYR	_TYPE_	_FREQ_	ebv1	ebv_r1	uss1	uss_r1	tss1	tss_r1	sebv1	sebv_r1	suss1	suss_r1	stss1	stss_r1
1	2019	1	8	102.5	102.5	103.9	101.9	103.5	101.5	4.8	3.7	6.1	5.1	6.0	4.8
2	2020	1	8	105.1	99.1	106.5	102.4	106.3	101.9	5.7	3.9	6.9	8.5	6.8	8.1
4	2022	1	19	104.3	101.2	106.7	103.7	106.3	103.3	6.3	2.3	7.2	6.5	7.2	6.3
5	2023	1	42	104.6	99.9	107.0	103.1	106.7	102.8	6.9	2.9	7.8	5.9	7.7	5.7
6	2024	1	23	105.9	100.3	107.0	104.0	106.6	103.3	7.9	2.5	7.1	4.9	7.0	4.7
sires without any offspring, 1 table															
Obs	_TYPE_	_NAME_		ebv1	ebv_r1	uss1	uss_r1		tss1		tss_r1				
1	MEAN			104.686	100.412	106.696	103.284		106.333		102.824				
2	STD			6.709		3.016		7.235		5.999		7.192		5.732	
3	N			102.000		102.000		102.000		102.000		102.000		102.000	
4	CORR	ebv1		1.000		0.147		0.729		0.020		0.741		0.025	
5	CORR	ebv_r1		0.147		1.000		0.160		0.468		0.151		0.469	
6	CORR	uss1		0.729		0.160		1.000		0.492		0.998		0.503	
7	CORR	uss_r1		0.020		0.468		0.492		1.000		0.479		0.996	
8	CORR	tss1		0.741		0.151		0.998		0.479		1.000		0.492	
9	CORR	tss_r1		0.025		0.469		0.503		0.996		0.492		1.000	

Dif_r	N	Corr_full_reduc
0	26074	0.81
10	7197	0.81
15	4697	0.81
20	3100	0.81
25	2023	0.81
30	1275	0.81
35	709	0.81
40	432	0.81
45	216	0.78
50	139	0.81
55	95	0.82
60	83	0.88
65	62	0.89
70	48	0.80
75	47	0.88
80	33	0.93
85	40	0.85
90	60	0.92
95	5	0.76
100	7	0.95

DGV

Base on the SNP solution DGVs were calculated for all four runs.

dgv_full_all: Full run and all SNPs used to calculate DGVs

dgv_full_del: Full run and only SNPs with dif_r less than 30 are used.

dgv_red_all: Reduced run and all SNPs used to calculate DGVs

dgv_red_del: Reduced run and only SNPs with dir_r less than 30 are used.

Raw means of bulls used for standardization clearly show that SD is bigger, when all SNPs are used.

DGV's are standardized, so VG bulls (status 1) born I 2010 have nearly same mean and SD. Genetic trends are biggest when all SNPs are used, and it is biggest in the full run.

The SAS System						15:09 Thu
The MEANS Procedure						
Variable	N	Mean	Std Dev	Minimum	Maximum	
dgv_full_all	193	-0.0086365	0.0448447	-0.1987984	0.0727971	
dgv_full_del	193	0.000919224	0.0409719	-0.1715642	0.0753948	
dgv_red_all	193	0.0012187	0.0449071	-0.1921987	0.0900564	
dgv_red_del	193	0.0061828	0.0411066	-0.1684924	0.0842230	

The SAS System										15:09 Thursday, April 24, 202		
Obs	year	_TYPE_	_FREQ_	sdgv_full_all	sdgv_full_del	sdgv_red_all	sdgv_red_del	ssdgv_full_all	ssdgv_full_del	ssdgv_red_all	ssdgv_red_del	

1	2010	0	249	99.670	99.666	99.672	99.667	9.8052	9.8372	9.7904	9.8176
2	2011	0	192	102.250	101.832	102.177	101.914	9.0986	9.0855	8.8191	8.7647
3	2012	0	212	104.854	104.303	104.302	103.962	9.7257	9.8895	9.6055	9.7259
4	2013	0	173	104.383	103.812	103.501	103.137	9.8427	9.8085	9.5859	9.5551
5	2014	0	134	107.344	106.262	105.624	104.902	10.7505	10.6417	10.4409	10.4092
6	2015	0	104	104.391	103.416	102.595	101.861	9.9670	9.8713	9.4060	9.2885
7	2016	0	86	107.378	106.318	105.543	104.697	9.3092	9.3208	8.3117	8.2309
8	2017	0	82	106.760	105.320	104.889	103.826	8.1384	8.1966	7.3389	7.4287
9	2018	0	109	109.019	107.628	106.514	105.481	8.6564	8.8117	7.5200	7.5231
10	2019	0	84	110.695	109.066	107.021	105.762	8.2424	8.3228	5.7477	5.7333
11	2020	0	88	111.062	109.533	107.519	106.284	8.7828	8.8215	7.2462	7.3104
12	2021	0	61	112.200	110.616	108.339	107.082	10.3076	10.5089	6.8288	6.7851
13	2022	0	72	109.659	107.715	107.054	105.686	9.2668	9.4536	7.7999	7.8153
14	2023	0	51	111.499	109.849	107.657	106.438	8.1280	8.2352	6.6333	6.5622
15	2024	0	25	111.107	108.922	108.113	106.435	5.7743	5.9798	5.5195	5.5516

Legara Reverter tests were done both when all SNPs were used and when only SNPs with dir_r less than 30 were used. Results are similar. Correlation for bulls used in the test was 0.995.

Conclusion of the investigations of changes in SNP frequency on DGVs:

- Bigger SD
- Steeper genetic tend
- Little effect on Legara Reverter test
- High correlation of DGVs in the two runs

Analysis of Variance					
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	6397.82188	6397.82188	168.64	<.0001
Error	157	5956.12260	37.93709		
Corrected Total	158	12354			
Root MSE		6.15931	R-Square	0.5179	
Dependent Mean		107.81126	Adj R-Sq	0.5148	
Coeff Var		5.71305			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	t Value	Pr > t
Intercept	1	21.44740	6.66832	3.22	0.0016
sdgv_red_all	1	0.81729	0.06294	12.99	<.0001
The SAS System					
15:09 T					

Analysis of Variance					
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	6397.22001	6397.22001	165.24	<.0001
Error	157	6078.27539	38.71513		
Corrected Total	158	12475			
Root MSE		6.22215	R-Square	0.5128	
Dependent Mean		106.54123	Adj R-Sq	0.5097	
Coeff Var		5.84013			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	t Value	Pr > t
Intercept	1	20.53312	6.70906	3.06	0.0026
sdgv_red_del	1	0.82148	0.06391	12.85	<.0001
The SAS System					
15:09 T					