

Experiences with single step 305day model for protein for Danish HOL

USN June 2021

Single step has been investigated on type types with general good results. These results have not been in line with the results for production based on the current test day model used by NAV. Denmark has used a 305 day repeatability animal model until the introduction of the common Nordic test day model. The 305 day model has been used for calculation EBVs for crossbred animals.

Data input file for this Animal model has been used the test runs with SS, but all other cows than HOL cows have been deleted. 305 days records since 1982 are included. Effect of the heterosis was not included.

Model:

```
S_PRT = MAN_GR LG14 KLV_A_M K_ALDER PE3(nav_id) (G)NAV_ID ! weigh=W_P
```

Parameters:

```
1 1 1 0.272727
2 1 1 0.545454
3 1 1 1.000000
```

The pedigree was been traced for three generations. The method is used in the current two step procedure and is also used for type traits. Different runs with different input data or genomic pedigree has been compared. All runs have been standardized to a common base, which has been defined as cows born in 2005 and records in the official test day model and in the test runs.

The results from the runs:

p_indeks: Test day results from current test day model. No genomic information included.

p_ebv: Indeks for protein from the model, where no genomic information is included. Correlations between these indexes and official p-indexes for females are app. 0.9 within year and estimated genetic trends for females are similar. In a 10 year period from 2005-2016 the trend is 16 units and the difference only 0.3 units. Correlations between Viking AI bulls within year are app. 0.97 for bulls with a least 50 Danish daughters with production.

GEBVredprot: Official two step method.

p_ss: Single step results based on all phenotypes and genotypes. Data input is the same as for run (p_ebv)

p_ss_dam: Phenotypic data deleted for dams of all genomic tested male. It means that all data for bull dams and dams of candidate bulls have been deleted. Pedigree is unchanged.

p_ss_dam10: Phenotypic data deleted for bull dams, which have a tested son born before 2010. Pedigree is unchanged.

p_ebv_dam: As p_ss_dam for traditional model.

p_ss_damg: Phenotypic data is the same as in run p_ss, but genomic information is deleted for all for dams of all genomic tested males

p_ss_15: h2 set to 0.15

p_ss_nobull: Genomic information not included for genomic bulls born in DNK, FIN or Sweden but not selected as AI VG bull

“red-runs”: Phenotypic data deleted for progeny after tested bulls, which are born after 2012.

With genomic prediction it is crucial, that the genetic level for coming AI bulls is correctly estimated. Viking Genetics bulls born in 2020 have been selected to investigate. If the genetic level is correct estimated, the mean GEBV from the reduced run (p_ss_red) should be at the same level as in the full run (p_ss). But the mean GEBV in the reduced and full run are 130.0 and 123.4. This means that the GEBVs are inflated, and the GEBV for young animals will decrease more over time than can be explained by genetic progress. None of the alternative runs could solve the problem.

Table 1. Statistics for selected Viking Genetics AI bulls born in 2020. Protein index.

The MEANS Procedure

Variable	N	Mean	Std Dev	Minimum	Maximum
p_indeks	0
GEBVredprot	66	116.4989651	7.8069351	102.4047258	133.7838858
p_ss	66	123.4285787	9.2658547	104.5713975	144.0882576
p_ss_dam	66	120.4845663	9.6096656	101.6076838	140.5618976
p_ss_dam10	66	122.8680070	9.2110115	104.1336284	143.2605775
p_ss_nobull	66	122.4429559	9.3939242	101.4870051	143.5947584
p_ss_damg	66	120.2268451	9.6020574	101.6579509	140.2640112
p_ss_red	66	129.9630460	8.3543795	109.6447321	148.8975324
p_ss_red_dam	66	125.9155745	8.5179634	106.8155957	144.5627306
p_ss_red_dam10	66	129.3383728	8.2678854	109.5508286	149.3887756
p_ss_red_nobull	66	128.2330231	8.4257241	109.8436119	146.0744667
p_ss_red_damg	66	125.5890058	8.4774899	106.2740738	144.3920145
p_ebv	66	108.0671983	5.8275187	90.7777958	121.4124776
p_ebv_dam	66	105.8525096	5.8567338	90.5785191	117.5729501
p_ss_15	66	130.9355024	11.0318341	110.9069403	154.6565922
p_ss_red_15	66	137.3555999	10.1483023	111.2479535	160.6377890
p_ebv_15	66	112.1225671	6.4664655	94.1451016	126.9401294
