STØTTET AF
Mælkeafgiftsfonden

Project on adapting "Golden Standard" to NAV evaluation of calving traits

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NAV project on adapting "Golden Standards" to NAV evaluation of calving traits

Items to be harmonized

- IDs on all calves in the registration system: That include especially ID on stillborn calves and in some countries on male calves. If calf ID is not known at least sire and dam of the calf must be identified.
- Calving ease recorded at 100% of calvings.
    - In DNK, it is voluntary for the farmer to register calving ease. In DNK calving ease is recorded at close to 90% of the calvings.
    - In FIN registration of calving ease started in 2004 and percent recorded have been steadily increasing and is now around 70%.
    - In SWE the percent calvings with recorded calving ease score is close to 100%. However, a 2-point scale have been used up to 2012-2015.
    - In Norwegian data Calving Ease is scored on a 3-point scale (Actual for HOL and Jersey data – also calf size is scored on a 3-point scale).
    - Below is some statistics on recorded calving ease scores (figure 1).

- Maternal and direct heterosis. It is an important effect to include in the model. However, it has turned out that it is very difficult to separate maternal and direct heterosis in populations where there is heavy import of foreign breeds over time – or if systematic crossings systems are used. Also, if there is very large difference in frequencies (e.g. dairy x beef). The current evaluation model include direct and maternal heterosis for RDC and JER, but not for HOL.

For this project 3 items are in focus:

- Include permanent environmental effect of dam for 2nd and later calvings in the model. Currently, this effect is not included in the evaluation model
- Use of Snell scores as input: The recommendation in the "Golden Standard" note was: "In case of a linear model, an approximation to a normal distribution – using Snell scores – should be used".
- Analysis of the effect of including inbreeding in the A-matrix when breeding values are estimated – and of adding a regression of inbreeding as an effect in the model.

Estimation of genetic parameters

The changes in model would require reestimation of genetic parameters. I anticipate that:

- Change of input to Snell score would not change genetic parameters very much (heritability and correlations would not change very much – but of cause the size of genetic and environmental variance change due to change of scale
- We need to estimate genetic parameters for permanent effect at later calvings

The genetic parameters were estimated by the MCEM-method described by Lidauer et al. (2015) in "TECHNICAL REFERENCE GUIDE FOR MiX99 SOLVER". In order to reduce computing time, the input data was reduced by deleting data on calves born before 2005 and data from small herds. Additionally, data was deleted herdwise until manageable input datasets was obtained. The data was balanced such that each country contribute according to the total distribution of data on countries.

The following models have been analysed. All models include fixed effects, random herd x year effect, direct and maternal genetic effects and random cow effect for traits with more calvings (SB2 and CE2).

Series of 2-trait models are analysed in order to obtain all the needed correlations between traits. The combinations analysed up to now are:

- SB1-CE1
- SB2-CE2
- SB1-SB2
- CE1-CE2
- SB1-CE2
- CE1-SB2

Estimates of heritabilities and genetic correlations

The results of the estimates of heritabilities are show in table 1-3. The estimates of SB1, SB2, CE1 and CE2 is obtained both in single trait analyses and in 2-trait analyses. The results shown in table 1-3 is averages of all the estimates. The results are all compared to the current values. The variances and covariances will change due to the rescaling of input data to Snell score. Therefor it is most relevant to compare heritabilities and correlations.

The procedure was:

- All correlations between -0.05 and +0.05 was assumed to be equal zero, because standard error of the estimates indicated the correlations of that size was not significantly different from zero. Therefor all correlations between direct and maternal traits were zero. Also, many of the correlations between CS1 and CS2 and the other traits were low in these analyses
- After these adjustments, the eigenvalues the variance-covariance matrices were calculated. If the eigenvalues turned out to be negative some manual adjustments were made

The general results were nearly the same in all breeds:

- Most heritabilities are quite similar to those currently used.

- Many of genetic correlations are quite close to those used in the current model. The exceptions were correlation for CS1 and CS2 the were generally much lower than used in the current evaluation model.

Table 1. Estimates of HOL heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	**0.040** *0.049*	**0.709** *0.720*	**-0.523** *-0.550*	**0.617** *0.621*	**0.532** *0.550*	**-0.513** **-0.530**	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE1		**0.117** *0.101*	**-0.546** *-0.750*	**0.584** *0.600*	**0.608** *0.630*	**-0.534** *-0.700*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCS1	-	-	**0.223** *0.247*	**-0.419** *-0.530*	**-0.464** *-0.770*	**0.600** *0.790*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dSB2			-	**0.011** *0.012*	**0.631** *0.649*	**-0.485** *-0.530*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE2			-		**0.077** *0.061*	**-0.518** *-0.750*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** **0.0**	**0.000** *0.0*	**0.000** *0.0*
dCS2	-	-	-	-	-	**0.205** *0.222*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
mSB1			-			-	**0.036** *0.043*	**0.591** *0.600*	**0.000** *-0.020*	**0.599** *0.604*	**0.329** *0.340*	**0.000** ***0.0***
mCE1			-			-		**0.090** *0.078*	**0.000** *-0.450*	**0.623** *0.643*	**0.716** *0.740*	**0.000** *-0.260*
mCS1	-	-	-	-	-	-	-	-	**0.059** *0.062*	**0.000** *-0.430*	**0.000** *-0.430*	**0.600** *0.700*
mSB2			-			-			-	**0.011** *0.012*	**0.582** *0.604*	**0.000** *-0.391*
mCE2			-			-			-		**0.047** *0.038*	**0.000** *-0.390*
mCS2	-	-	-	-	-	-	-	-	-	-	-	**0.057** *0.060*

Table 2. Estimates of RDC heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	**0.058** *0.042*	**0.700** *0.750*	**-0.550** *-0.360*	**0.728** *0.649*	**0.485** *0.480*	**-0.540** *-0.380*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE1		**0.077** *0.074*	**-0.591** *-0.770*	**0.435** *0.440*	**0.500** *0.780*	**-0.451** *-0750*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCS1	-	-	**0.247** *0.284*	**-0.406** *-0.400*	**-0.576** *-0.900*	**0.500** *0.800*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dSB2			-	**0.082** *0.012*	**0.600** *0.650*	**-0.514** *-0.390*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE2			-		**0.035** *0.024*	**-0.564** *-0.760*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** **0.0**	**0.000** *0.0*	**0.000** *0.0*
dCS2	-	-	-	-	-	**0.234** *0.261*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
mSB1			-			-	**0.038** *0.025*	**0.601** *0.700*	**0.000** *-0.140*	**0.650** *0.598*	**0.337** *0.341*	**0.000** *0.050*
mCE1			-			-		**0.065** *0.051*	**0.000** **-0.520**	**0.630** *0.639*	**0.600** *0.740*	**0.000** *-0.260*
mCS1	-	-	-	-	-	-	-	-	**0.060** *0.065*	**0.000** *-0.430*	**0.000** *-0.430*	**0.500** *0.700*
mSB2			-			-			-	**0.0.52** *0.012*	**0.500** *0.701*	**0.000** *-0.580*
mCE2			-			-			-		**0.035** *0.024*	**0.000** *-0.540*
mCS2	-	-	-	-	-	-	-	-	-	-	-	**0.058** *0.070*

Table 3. Estimates of JER heritabilities and genetic correlations. Heritabilities on diagonal, genetic correlations above diagonal. Upper number is the new estimates. Lower number is the values used in the current evaluation

	dSB1	dCE1	dCS1	dSB2	dCE2	dCS2	mSB1	mCE1	mCS1	mSB2	mCE2	mCS2
dSB1	**0.035** *0.036*	**0.441** *0.440*	**0.000** *0.130*	**0.786** *0.789*	**0.335** *0.340*	**0.000** *0.140*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE1		**0.022** *0.012*	**0.000** *-0.670*	**0.389** *0.389*	**0.800** *0.811*	**0.000** *-0.680*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCS1	-	-	**0.150** *0.134*	**0.000** *0.130*	**0.000** *-0.620*	**0.600** *0.910*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dSB2			-	**0.017** *0.012*	**0.443** *0.449*	**0.000** *0.040*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
dCE2			-		**0.026** *0.012*	**0.000** *-0.650*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** **0.0**	**0.000** *0.0*	**0.000** *0.0*
dCS2	-	-	-	-	-	**0.154** *0.134*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*	**0.000** *0.0*
mSB1			-			-	**0.024** *0.024*	**0.479** *0.589*	**0.000** *0.100*	**0.479** *0.480*	**0.162** *0.169*	**0.000** *-0.070*
mCE1			-			-		**0.043** *0.024*	**0.000** *-0.340*	**0.238** *0.239*	**0.512** *0.529*	**0.000** *-0.320*
mCS1	-	-	-	-	-	-	-	-	**0.040** *0.041*	**0.000** *-0.020*	**0.000** *-0.330*	**0.500** *0.890*
mSB2			-			-			-	**0.017** *0.012*	**0.481** *0.490*	**0.000** *0.040*
mCE2			-			-			-		**0.026** *0.012*	**0.000** *-0.291*
mCS2	-	-	-	-	-	-	-	-	-	-	-	**0.040** *0.041*

Table 4 show the estimates of the direct and maternal genetic variances. They are not comparable to the values currently used, because the scales are changed

Table 4. Direct and maternal genetic variances.

	Direct			**Maternal**		
Trait	**HOL**	**RDC**	**JER**	**HOL**	**RDC**	**JER**
SB1	**0.0108**	**0.0091**	**0.0074**	**0.0097**	**0.0058**	**0.0050**
SB2	**0.0016**	**0.0086**	**0.0017**	**0.0017**	**0.0053**	**0.0017**
CE1	**0.0538**	**0.0326**	**0.0042**	**0.0270**	**0.0270**	**0.0083**
CE2	**0.0252**	**0.0110**	**0.0026**	**0.0150**	**0.0108**	**0.0026**
CS1	**0.1365**	**0.1583**	**0.0937**	**0.0298**	**0.0306**	**0.0221**
CS2	**0.1197**	**0.1477**	**0.0957**	**0.0282**	**0.0297**	**0.0226**

Estimates of the non-genetic random variables

The estimates of the HxY variances (within 5-year periods) are shown in table 5. The current values are shown as well, because the new results are substantially different from the new estimates. Currently, it is assumed that HxY variance is 18-20% of the residual variance. The new estimates are 1-2% of the residual variance for SB and 2-6% for CE.

Also the residual variances are shown in table 5.

Table 5. HxY variances and residual variances – new and current

Trait	**Residual variance**		**H x Y variance**		**H x Y pct of residual**	
	Current	**New**	Current	**New**	Current	**New**
	HOL					
SB1	0.2170	**0.2573**	0.0420	**0.0012**	19.4%	**0.5%**
CE1	0.5183	**0.4077**	0.1095	**0.0482**	21.1%	**11.8%**
CS1	0.4697	**0.4764**	0.1155	**0.0306**	24.6%	**6.4%**
SB2	0.1411	**0.1530**	0.0255	**0.0005**	18.1%	**0.3%**
CE2	0.4312	**0.3035**	0.0840	**0.0011**	19.5%	**0.4%**
CS2	0.4725	**0.4616**	0.1125	**0.0277**	23.8%	**6.0%**
	RDC					
SB1	0.1483	**0.1590**	0.0300	**0.0014**	18.9%	**0.9%**
CE1	0.3897	**0.5175**	0.1035	**0.0213**	20.0%	**5.5%**
CS1	0.4829	**0.4640**	0.1200	**0.0173**	25.9%	**3.6%**
SB2	0.0959	**0.1411**	0.0255	**0.0009**	18.1%	**0.9%**
CE2	0.3021	**0.4455**	0.0825	**0.0093**	18.5%	**3.1%**
CS2	0.4829	**0.4701**	0.1185	**0.0143**	25.2%	**3.0%**
	JER					
SB1	0.2000	**0.2111**	0.0375	**0.0013**	18.8%	**0.6%**
CE1	0.3444	**0.1850**	0.0630	**0.0034**	18.3%	**1.8%**
CS1	0.5396	**0.5312**	0.1140	**0.0586**	21.1%	**11.0%**
SB2	0.1494	**0.1055**	0.0270	**0.0006**	18.1%	**0.5%**
CE2	0.2241	**0.0958**	0.0405	**0.0011**	18.1%	**1.1%**
CS2	0.5254	**0.5425**	0.1110	**0.0287**	21.1%	**5.3%**

The estimates of variance of the permanent cow effect is shown in table 6. This effect is not included in the current model, but the new estimates show that they is nearly of the same size at the maternal effect (table 5). Therefor it is important to include this effect in the model.

Table 6. Permanent cow variances – new and current

Trait	Residual variance		Permanent cow variance		Pct of residual	
	Current	**New**	Current	**New**	Current	**New**
	HOL					
SB2	0.1411	0.1530	0	**0.0026**	0.0%	**1.7%**
CE2	0.4312	0.3035	0	**0.0116**	0.0%	**3.8%**
CS2	0.4725	0.4616	0		0.0%	
	RDC					
SB2	0.1411	0.0959	0	**0.0023**	0.0%	**2.3%**
CE2	0.4455	0.3021	0	**0.0101**	0.0%	**3.4%**
CS2	0.4701	0.4829	0		0.0%	
	JER					
SB2	0.1494	0.1055	0	**0.0017**	0.0%	**1.6%**
CE2	0.2241	0.0958	0	**0.0021**	0.0%	**2.2%**
CS2	0.5254	0.5425	0		0.0%	

Conclusion on non-genetic random effects

- The herd x year variance (within 5-year periods) was much smaller compared to total variance than assumed in the current evaluation. Actually, it was quite close to zero.
- The permanent cow variance was of the same size as the maternal variance. Therefore, it is important to include this effect in the model. It is not included in the current evaluation model.

Including inbreeding in the A-matrix and effect of inbreeding depression in the model

A final objective of this project was to analyse the effect of including inbreeding in the A-matrix and the effect of inbreeding depression.

Coefficients of inbreeding was calculated by the RelaX2-program (RelaX2 Program for pedigree analysis by Ismo Standen). In figure 1 is showed the development in HOL inbreeding coefficients. The current level of inbreeding is just below 6%. As expected, the coefficient of inbreeding is slightly higher for calves than for cows. That indicate a slight increase in inbreeding.

Table 7 show the correlation between inbreeding of calf and cow. During the last 20 years this correlation have between between 0.35 and 0.40 for HOL. The relatively low correlation indicate that there should not be problems with estimation of effect of calf and of cow inbreeding. Across year the correlation was higher, because some of the trend in coefficient of inbreeding is included in the correlation.

Figure 1. HOL inbreeding coefficients

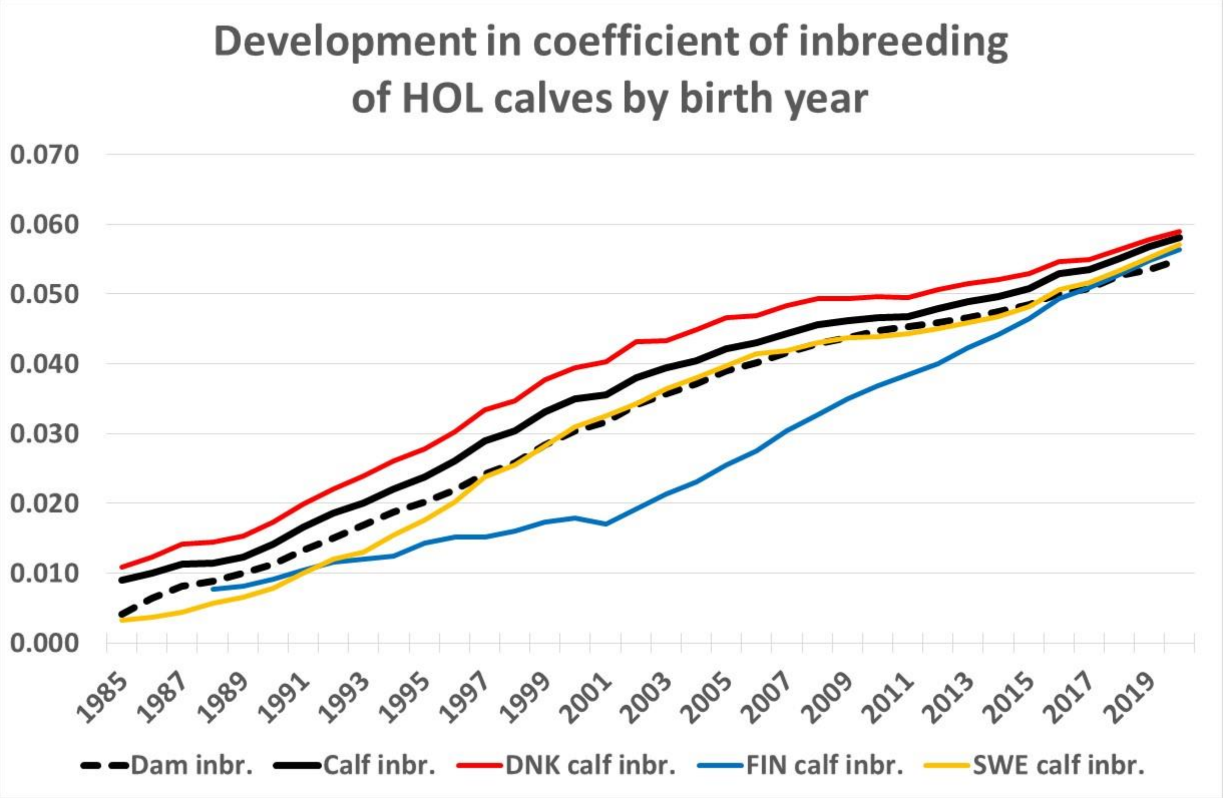

Table 7. Correlations between coefficients of inbreeding of dam and calf.

	Correlation between cow and calf inbreeding			**Pct cow-calf pairs where both coefficients > 0**		
Birth year	HOL	RDC	JER	HOL	RDC	JER
1985-89	0.0983			35.26%		
1990-94	0.1902			72.92%		
1995-99	0.2846			88.69%		
2000-04	0.3559			93.07%		
2005-09	0.3867			96.74%		
2010-14	0.3584			98.25%		
2015-	0.3920			98.82%		
Across years	0.5727					

The Mix99-program have a facility to include the coefficients of inbreeding in the A-matrix. This version was compared the a “standard” model. This “standard” model included the following effects:

- Age * country (age in month/parity), fixed effect
- Year * month * country, fixed effect
- Herd * 5-year period, fixed effect
- Regression on direct and maternal heterozygoty in RDC and JER, fixed effect
- Herd * Year (with 5-year period), random effect
- Permanent cow effect (only for later calvings), random effect
- Genetic effect of dam
- Genetic effect of calf
- Residual

Input was the 4 calving traits, all converted to Snell Score. The parameters used was the new estimates from table 1 -6.

The next step was to include the coefficients of inbreeding as fixed regression effects of the model. Three versions of the model were analysed:

- A model with fixed regression effect of inbreeding of the calf
- A model with fixed regression effect of inbreeding of the dam of calves
- A model with fixed regression effect of inbreeding of both calf and cow

In total 4 models are compared to the new “standard” model.

- For the model with inbreeding included in the A-matrix the correlations are differ. from 1.00000 on the fifth decimal. No correlations are lower than 0.9999 and no sire indexes change more than one unit.
- For the model that include effect of dam and/or calf inbreeding the difference is slightly larger. The correlations differ from 1.00000 on the fourth decimal – and no correlations are smaller than 0.9992. No sire index change by more than one unit – except 2 sires for

the birth index (and in these analyses the standardization has remained unchanged compared to the current routine, so the SD is somewhat larger than 10 units).

The conclusion is that:

- **Including inbreeding in the A-matrix do not change the results significantly**
- **Correction for inbreeding depression in calves and/or cows do not change the results significantly**

Estimates of effect of inbreeding

Table 8 show the estimates of inbreeding. The estimates are the effect of 100% inbreeding – and the current level is 6%. In the table the estimates are converted to index units (new standardization) and they are also shown for the average level of inbreeding of 6% (Note: A sire – daughter mating gives 25% inbreeding – note also that mating of full cousins give 6,25% inbreeding)

The estimates are nearly the same if both calf and cow inbreeding are included in the model or if they are included separately.

The effect of calf inbreeding for calving ease (CE1 and CE2) is positive. It is surprising and need to be analysed further

Table 8. Effect of 100% inbreeding

	Both calf and cow inbreeding In model			
Trait	**Effect of calf inbreeding**	**Effect of cow inbreeding**	**Effect of calf inbreeding (alone)**	**Effect of cow inbreeding (alone)**
	Estimates on Snell Score scale (solutions)			
SB1	-0.1219	-0.0685	-0.1198	-0.0689
CE1	0.1482	-0.3311	0.1543	-0.3322
SB2	-0.0912	-0.0574	-0.0906	-0.0579
CE2	0.0700	-0.2187	0.0773	-0.2228
	Index units – after standardization to SD = 10 (a new standardization)			
SB1	-17.1	-7.4	-16.8	-7.4
CE1	9.0	-23.5	9.3	-23.6
SB2	-34.6	-17.2	-34.3	-17.4
CE2	6.9	-17.7	7.6	-18.0
	Index units for 6% inbreeding (current level of inbreeding)			
SB1	-1.0	-0.4	-1.0	-0.4
CE1	0.5	-1.4	0.6	-1.4
SB2	-2.1	-1.0	-2.1	-1.0
CE2	0.4	-1.1	0.5	-1.1