

Report on analyses of RDC maternal single traits

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Single trait evaluation of RDC (maternal) calving traits were made for

- Current parameters and data
- New parameters and snell score data

Table 1. Correlations for single trait models (142 sires with at least 100 daughters and 300 progenies) – this table was also show at the meeting 1.7.2022

	Current with		Curr single	New with	
	Curr single	New single	New single	Curr single	New single
dSB1	0.94	0.93	0.99	0.97	0.97
dCE1	0.99	0.99	1.00	0.99	1.00
dSB2	0.93	0.92	0.99	0.97	0.98
dCE2	0.95	0.95	0.99	0.98	0.99
mSB1	0.93	0.93	0.99	0.98	0.99
mCE1	0.99	0.98	0.99	0.99	0.99
mSB2	0.69	0.70	0.99	0.94	0.94
mCE2	0.90	0.89	0.98	0.94	0.96

Table 1a. Correlations for single trait models (113 sires with at least 1000 daughters and 300 progenies) – proposal at the meeting 1.7.2022

	Current with		Curr single	New with	
	Curr single	New single	New single	Curr single	New single
dSB1	0.95	0.94	0.99	0.97	0.97
dCE1	0.99	0.99	1.00	0.99	1.00
dSB2	0.94	0.94	0.99	0.98	0.98
dCE2	0.96	0.96	0.99	0.98	0.99
mSB1	0.94	0.94	0.99	0.98	0.99
mCE1	0.99	0.99	1.00	0.99	0.99
mSB2	0.72	0.73	0.99	0.96	0.96
mCE2	0.93	0.92	0.98	0.95	0.97

Table 1b. Correlations for "single" trait models. "Single" trait means models where SB1 and SB2, CE1 and CE2 and CS1 and CS2 are included with their internal correlations – proposal at the meeting 1.7.2022

	Current with		Curr "single"	New with	
	Curr "single"	New "single"	New "single"	Curr "single"	New "single"
dSB1	0.95	0.95	0.99	0.97	0.97
dCE1	1.00	0.99	1.00	0.99	1.00
dSB2	0.96	0.95	0.99	0.97	0.98
dCE2	0.98	0.96	0.99	0.98	0.99

mSB1	0.94	0.94	0.99	0.98	0.99
mCE1	1.00	0.99	0.99	0.99	0.99
mSB2	0.77	0.77	0.99	0.94	0.94
mCE2	0.99	0.96	0.97	0.94	0.96

The results were compared to current and new “full” model by using Trines correlation program

- NAV AI sires born 2010-15
- As a standard, at least 300 progenies and 100 daughters per sire was required - based on data in the current evaluation. The average reliabilities for the direct traits are 90-96 and for the maternal traits 85-90.
- An additional test was made with at least 300 progenies and 1000 daughters (results in table 1a).
 - The expectation is that the correlations between a model with the complete parameter set and the single trait model will be close to 1.0 for sires with high reliability.
 - In the “standard” test with 300 progenies and 100 daughters 142 sires were included. When the number of daughters were increased to 1000 daughters the number of sires included was 113. So, most of the sires in the standard analyses have a very high reliability.
 - Increasing the number daughters (increasing maternal reliability) lead to slightly increased correlations (table 1 compared to table 1a).
- It has been proposed to analyse an alternative approach to single trait (by Freddy Fikse):
 - SB1 and SB2 was included with their internal correlations
 - CE1 and CE2 was included with their internal correlations
 - CS1 and CS2 was included with their internal correlations
 - But no correlations between SB, CE and CS were included
 - The results are shown in table 1 b.

The initial results are shown table 1. As reliability of the sires included in the model is high, a high correlation between single trait evaluation and evaluation by the full model is expected.

- An important result is the very high correlations between current and new single trait evaluation. That indicate that the current and the new model give the same results for the very reliable sires included in this test. The differences we observe with the “full” model are probably due to the parameters used (variances and covariances/correlations)
- For mSB2, the correlation to the current full model was around 0.7, and the correlation to the new full model was somewhat higher, 0.94.
- The correlations to the current model were also lower than expected for dSB1 and dSB2 – and for mSB1 and mCE2

All those results indicate that the problem with the RDC results is mainly due to problems with parameters used in the current evaluation. And especially with correlations between SB, CE and CS.

Adjustment of current parameters

It was decided to analyse the effect of adjusted parameters (correlations) in the current model.

- Adjustment 1(Adj1): Adjustment of mSB-mCE correlations (mSB1-mCE1, mSB2-mCE2, mSB2-mCE1) towards correlations in the new parameters
- Adjustment 2(Adj2): All CS correlations are set to 0 as in the new parameter data
- Adjustment 3(Adj2): Adj1 and Adj2 combined

The results are shown in table 2. Of course the results for the direct traits remain unchanged because the parameters for the direct traits are left unchanged. Both the adjustment 1, 2 and 3 “improve” the correlations for mSB2. However, the results are not satisfying.

Table 2. Effect of adjustments of current maternal RDC parameters

	Curr. single	Current with		Adj1: Current with		Adj2: Current with		Adj3: Current with	
	New single	Curr. single	New single	Curr. single	New single	Curr. single	New single	Curr. single	New single
dSB1	0.99	0.94	0.93	0.94	0.94	0.94	0.93	0.94	0.94
dCE1	1.00	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
dSB2	0.99	0.93	0.92	0.93	0.93	0.93	0.93	0.93	0.93
dCE2	0.99	0.95	0.95	0.95	0.95	0.95	0.95	0.95	0.95
mSB1	0.99	0.93	0.93	0.96	0.96	0.94	0.94	0.97	0.97
mCE1	0.99	0.99	0.98	0.99	0.99	0.99	0.98	0.99	0.99
mSB2	0.99	0.69	0.70	0.72	0.73	0.78	0.78	0.87	0.87
mCE2	0.98	0.90	0.89	0.90	0.89	0.91	0.89	0.94	0.93

Adjustment of the new parameters

For the new parameter three set of adjustment was tested (table 3).

- Adj 1: In the first adjustment, the main purpose was to test lower correlation between mSB1 and mSB2 because both HOL and JER parameters showed lower correlations for mSB1-mSB2 than for mCE1-mCE2. In order to obtain more harmonic parameters also the correlation for mSB1-mCE2 and mSB2-mCE2 were reduced slightly.
- Adj 2: In second adjustment the correlations between mSB1-mSB2, mCE1-mCE2 and mCS1-CS2 was equal to the HOL-correlations
- Adj 3: In the third adjustment the correlations SB1-CE2 and SB2-CE1 was reduces as in Adj1
- Adj 4: Finally, the result for a previous testrun (Feb. 2022) with complete HOL parameters are show (now correlated to single trait results – previously only correlation to the current model were reported)

The results are shown in table 3. The best results are obtained by adjustment 1.

Table 3. Effect of adjustments of new maternal RDC parameters

	Curr. single	New with		Adj1: New with		Adj2: New with		Adj3: New with		Adj4 (All HOL): New with	
	New single	Curr. single	New single	Curr. single	New single	Curr. single	New single	Curr. single	New single	Curr. single	New single
dSB1	0.99	0.97	0.97	0.97	0.97	0.97	0.97	0.97	0.97	0.87	0.87
dCE1	1.00	0.99	1.00	0.99	1.00	0.99	1.00	0.99	1.00	0.99	0.99
dSB2	0.99	0.97	0.98	0.97	0.98	0.97	0.98	0.97	0.98	0.91	0.90
dCE2	0.99	0.98	0.99	0.98	0.99	0.98	0.99	0.98	0.99	0.97	0.99
mSB1	0.99	0.98	0.99	0.98	0.99	0.98	0.99	0.98	0.99	0.97	0.98
mCE1	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.98	0.99
mSB2	0.99	0.94	0.94	0.97	0.97	0.95	0.95	0.94	0.95	0.90	0.89
mCE2	0.98	0.94	0.96	0.95	0.96	0.93	0.94	0.95	0.96	0.93	0.95

Conclusions

The main reason for the low correlation between the current model and the new model for mSB2 in RDC is the very high (too high) correlations used in the current evaluation.

The correlations observed for the single trait models indicate that the parameters of the new model are most correct – may be with some adjustments