

RDC Correlations calculated with Trines program

ooo	Current data, current model, current parameters
ono	Current data, model without heterosis, current parameters
onn1	Current data, model without heterosis, new parameters (direct - without correction of new variances)
onn2	Current data, model without heterosis, new parameters (variances and covariances changed to fit old data - that will re-introduce old h2)
onn3	Current data, model without heterosis, new parameters (variances and covariances changed to fit old data - and genetic variances changed such that new h2 is used)
nnn1	New snell score data, model without heterosis - new parameters - new snell score data
nnn2	New snell score data, model without heterosis - new parameters - new snell score data Run by using the current inputdatasets with data replaced by snell score (deeper pedigree, slightly changed PHP-grouping)

Test of models

	ooo	ono	New parameters			nnn1	nnn2
			onn2	onn3	onn1		
dSB1	1.00	1.00	0.98	0.98	0.98	0.98	0.98
dCE1	1.00	1.00	1.00	1.00	1.00	0.99	0.99
dSB2	1.00	1.00	0.98	0.98	0.98	0.97	0.97
dCE2	1.00	1.00	0.98	0.98	0.98	0.97	0.97
mSB1	1.00	1.00	0.98	0.98	0.96	0.95	0.95
mCE1	1.00	1.00	0.99	0.99	0.99	0.99	0.99
mSB2	1.00	1.00	0.89	0.89	0.84	0.80	0.80
mCE2	1.00	1.00	0.98	0.98	0.97	0.96	0.96

Conclusion

It is the introduction of new parameters that have the largest effect on SB2 results

Other test runs

- With and without heterosis - effect on direct SB1 and SB2
- No Nordic heterosis - effect on direct SB1 and SB2
- Data >= 2000: No effect
- Single trait: Most effect on SB - direct and maternal