

al. (2015).

Table 1. Residual correlations (below diagonal), genetic correlations (above diagonal) and heritabilities (diagonal) for PM21 in parities 1-3, CSD in parities 0-3 and GL (A=direct animal effect, M=maternal effect)

	CSD_0	CSD_1	CSD_2	CSD_3	PM21_1	PM21_2	PM21_3	GL_A	GL_M
CSD_0	0.02	0.66	0.39	0.40	0.07	0.22	0.04	0.57	0.08
CSD_1	0.12	0.02	0.30	0.34	-0.25	-0.03	-0.06	0.56	0.09
CSD_2	0.00	0.34	0.01	0.70	-0.49	-0.58	-0.42	0.45	0.09
CSD_3	0.03	0.06	0.16	0.02	-0.50	-0.47	-0.58	0.38	0.09
PM21_1	-0.12	-0.17	-0.05	-0.01	0.03	0.54	0.52	-0.15	-0.07
PM21_2	-0.04	-0.08	-0.16	-0.07	0.10	0.06	0.77	-0.21	-0.06
PM21_3	-0.03	-0.06	-0.11	-0.27	0.07	0.14	0.05	-0.22	-0.07
GL	0.01	-0.02	0.07	0.07	0.08	0.04	-0.02	0.68	-0.26

Recommendations. Based on data from a number of research projects, the following recommendations for changes in the national genetic evaluation model of fertility traits are made: 1) replace the binary CR42 with its continuous version CSD; 2) include heifer CSD in the model; 3) include the information on reproductive interventions in fertility phenotypes; 4) drop milk production traits from the model; 5) retain BCS in the model; 6) add GL as a new predictor trait to the model; 7) consider the inclusion of a direct GL EBV in the BW index to account for the advantage of shorter GL sires to the cows they are mated, over and above the improvements in the fertility of their daughters from shorter GL.

Future work. Variance components for the recommended model are currently being estimated. The next steps include the implementation of a new model for genetic evaluation to be run using the full national fertility data set. New results will be compared with the current genetic evaluation outcomes, prior to releasing new fertility breeding values to industry for consultation.

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