

Usage of Predictors for Fertility in the Genetic Evaluation, Application in the Netherlands

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1. Introduction

The last decade genetic evaluation of fertility traits has become common in most countries within the Interbull community. This was initiated by the fact that farmers were faced with lower pregnancy rates from first inseminations and also longer calving intervals. AI-organisations were recognising this too. The decrease in fertility is in fact the result of a long and severe selection for milkproduction traits in the dairy breeds, especially the Holstein-Friesian breed, and caused by a strong genetic correlation between production and fertility.

To be able to select also for fertility traits, traits were defined and evaluated. But one feature fertility traits have in common is the low heritability. This low heritability limits also the reliability of fertility breeding values for the bulls having only first crop daughters in their proof. As the reliabilities of fertility proofs stay on a much lower level, the impression of the users of these proofs, farmers and AI-organisations is, that it is hard to make real progress by selecting bulls on these proofs, although still the genetic variation is considerable. So to make breeding values for fertility more valuable for the users one should work one maximising the reliability, given the data available. One way is to make use of predictors. Body condition score (BCS) is known to be an informative trait for fertility. But also milkproduction traits could be used.

Another issue is how well the genetic trend of fertility traits can be estimated with a single trait analysis, while selection in population is heavily on production traits.

This paper will show the effect of the usage of BCS and milkproduction traits as predictor traits on the reliability of the Dutch fertility index. Further, the effect of using the trait milkproduction, as trait under selection, on the

genetic trends of fertility traits is shown. At the same time the effect of changing from a sire model to an animal model, where the animal model is assumed describe the data better, is presented. This will be demonstrated by experiences with the implementation of a new genetic evaluation system for the Netherlands and comparing results with the previous system.

2. Method and Materials

In 1995 the Netherlands introduced a genetic evaluation for non-return within 56 days (NR56) and interval calving-1st insemination (CFI). This evaluation was based on a single trait sire model, using first lactation data. Heritabilities for NR56 and CFI were 0.02 and 0.06, while genetic standard deviations were 6.55 % and 6.1 days, respectively. Breeding values were combined in a fertility index with the breeding goal to increase NR56 and to shorten calving interval (CI) (De Jong, 1995).

The new situation is a multivariate animal model evaluation for the fertility traits NR56, CFI and CI, using BCS and milkproduction traits as predictors.

The effect of using predictors on the reliability of the fertility index for a young test bull with 100 first crop daughters and a sire having 1000 daughters with observations, is determined by selection index calculation, using parameters of table 1. The fertility index combines two breeding goal traits, NR56 and CI, with economic value of 0.255 and 0.70 Euro respectively per percent or day.

Second analysis is focused on the effect of using milkproduction traits as correlated trait on the genetic trend for fertility traits. At the same time the effect of changing from sire model to an animal model is shown. Actually five evaluations were carried out:

st : sire model, old parameters, single trait;
 amparst : animal model, old parameters, single trait;
 am0 : animal model, new parameters single trait;
 amzp : animal model, new parameters multiple trait, not using production traits/predictors;
 amp : animal model, new parameters, multiple trait, using production traits and BCS.

Old parameters are parameters as used in the sire model; new parameters are parameters as used in animal model and presented in table 1.

For the analysis calving dates and 305-day milkproduction records were available from 1978 and onwards. Insemination data were available from 1988 and onwards and BCS since 1998. NR56, CFI and CI were defined for the first lactation cows. BCS was scored in the herd conformation classification program in which the first lactation cows are scored. The lactation records were precorrected for age at calving to the standard age of 24 months. BCS were on scale of 1-9 and were precorrected for stage of lactation and age at moment of scoring.

In total 4,795,305 first lactating animals had a known NR56 and CFI, 4.031.330 animals had CI and 8,553,103 animals had milkproduction records. 881,377 cows had a BCS available.

The genetic evaluation was carried out with the sire model as described in De Jong (1995).

The genetic evaluation with animal model was carried out with the following model:

$$Y_{ijklm} = HY_i + M_j + H_k + R_l + A_m + e_{ijklm}$$

where:

Y_{ijklm} = observation on cow m;
 HY_i = Herd-year season cow m was inseminated. A season is a one-year period;
 M_j = period of calving, defined for every 10 days (each year with 36 levels);
 H_k = heterosis effect k for cow m;
 R_l = recombination effect for cow m;
 A_m = additive genetic effect of cow m;
 e_{ijklm} = error term.

For the additive genetic effect pedigree of the cow was taken into account and was traced back as far as possible. For unknown ancestors genetic groups were defined based on breed, year of birth, country of origin and selection path.

Parameters used (new parameters) are presented in table 1.

Table 1. Parameters for the genetic evaluation with heritability on diagonal, the genetic correlations below the diagonal, error correlations above the diagonal. Genetic standard deviations are in the last row.

trait	NR56	CFI	CI	milk	fat	prot	BCS
NR56	.015	-.01	-.32	-.05	-.04	-.06	-.07
CFI	.20	.083	.46	.13	.10	.12	-.14
CI	-.28	.87	.058	.19	.16	.18	-.11
milk	-.33	.43	.57	.55	.73	.93	-.24
fat	-.34	.44	.56	.56	.44	.81	-.15
protein	-.40	.47	.61	.90	.70	.50	-.17
BCS	-.13	-.53	-.45	-.50	-.39	-.50	.43
genet	5.9	8.5	14.9	710	24.8	20.5	.93
stdev	%	day	day	kg	kg	kg	pt

NR56= non return within 56 days after insemination, CFI= interval calving to first service, CI= calving interval, milk, fat and protein= 305 day production for milk, fat and protein, BCS= body condition score.

3. Results

3.1 Effect on reliability

The effect of using different information sources on the reliability of the fertility index is shown in table 2.

The results are based on a bull getting 100 daughters in the first lactation. CI will become available for about 80 daughters and BCS on 64 daughters.

When using data of only one fertility trait, like NR56, CFI or CI, the reliability is highest with CI, giving a reliability of 0.58. When using milkproduction in the index as sole information source, the reliability of the fertility index reaches the level of 0.33, while using all three production traits results in a reliability of 0.44. When then adding BCS as fourth non-fertility source the reliability increases only one percent to .45.

An index based on only data for NR56 and CFI reaches in the given standard situation a reliability of 0.56. Adding CI as information source increases the reliability to 0.72. So adding CI in the genetic evaluation adds for sure extra information about the breeding goal, which is logic as CI is part of the breeding goal. Adding BCS as information source increases the reliability to 0.73. The advantage of BCS is that it is available early in the lactation and much earlier than CI. An index based on information for NR56, CFI and BCS results in a reliability of 0.57. When using milkproduction as predictor in the fertility index the reliability is 0.76. It appears that BCS is less important as predictor than milkproduction. By using all production traits as predictor, the reliability increases to 0.79. When then BCS is added the reliability does not increase anymore.

So a bull having 100 daughters in milk, of which also insemination data is available can reach a reliability of 0.79 for his fertility index.

Table 2. Reliability for several indexes using different information sources where the breeding goal is NR56 and CI.

Number of daughters							Ferti lity index
100	100	80	64	100	100	100	Relia bility
Traits in index							
NR56	CFI	CI	BCS	Milk	Fat	Prot	
X							.07
	X						.43
		X					.58
			X				.14
				X			.33
					X	X	.44
			X	X	X	X	.45
X	X						.56
X	X	X					.72
X	X	X	X				.73
X	X	X		X			.76
X	X	X		X	X	X	.79
X	X	X	X	X	X	X	.79
X	X		X				.57

3.2 Effect genetic trends

The genetic trends for the five evaluations were determined on a group of Holstein-Friesian bull having 50 or more daughters with observations for NR56 and CFI. The results for NR56 and CFI are presented in figure 1 and 2, respectively.

For both traits, NR56 and CFI, the genetic trend was larger in the animal model runs, compared with the sire model run.

The average genetic trend for NR56 in the sire model for the period 1982-1998 was -0.28%, while the trend was -.40% for animal model using also milkproduction as correlated trait (table 3). The largest increase in genetic trend was due to the change from sire model to animal model. Adding milkproduction as a correlated trait showed an increase in genetic trend of 10 percent, from -.36 (amzp) to -.40 (amp). The genetic trend for single trait animal model (am0) and animal model using the old parameters (amparst) were very similar.

The genetic trend for CFI showed the largest change, from 0.23 to 0.55 days when changing from sire model (st) to animal model (amparst). By adding milkproduction traits to the evaluation the genetic trend increased with about 20 percent from 0.55 days (amzp) to 0.65 (amp). The genetic trend for CFI seemed to be underestimated with the sire model compared with the genetic trend from the animal model evaluations. And by not taking milkproduction into account as correlated trait the trend of CFI is also underestimated.

The genetic trend of CI is presented for four testruns in table 3 and figure 3. It appeared that using milkproduction traits as correlated trait in the evaluation, the trend for CI increased.

The average trend per year expressed in genetic standard deviation for the three fertility traits NR56, CFI and CI were 7%, 8% and 10%, respectively. For all three fertility traits an undesirable genetic trend was found: decrease in NR56, and increase in CFI and CI.

Table 3. Genetic trend for AI-tested Holstein-Friesian bulls with at least 50 daughters with NR56 and CFI observations in the genetic evaluation and born in period 1982-1998. Expressed in breeding values.

run	NR56 (%)	CFI (day)	CI (day)
st	-.28	.23	--
amparst	-.33	.55	1.31
am0	-.34	.54	1.31
amzp	-.36	.55	1.26
amp	-.40	.65	1.45

4. Conclusions

- To increase the reliability for fertility index milkproduction traits are valuable and cause a larger increase in reliability than BCS. BCS only adds extra information when it is scored early in lactation.
- The average reliability of fertility index for young bulls is about 80 percent, based on 100 daughters in lactation.
- Adding milkproduction trait as correlated trait in the genetic evaluation for fertility has

an effect on the estimated genetic trend of fertility traits of 10 to 20 percent.

- Using an animal model instead of a sire model had larger impact on the estimated genetic trend of fertility traits than adding milkproduction traits as predictor traits.

5. Implementation

The animal model using milkproduction traits and BCS as correlated traits was introduced for the genetic evaluation in the Netherlands in February 2005.

6. References

De Jong, G. 1995. Sire breeding values for daughters' fertility in The Netherlands. *Interbull Bulletin 11*, Proceedings of the open session of the Interbull annual meeting Prague, Czech Republic, September 7-8, 1995.

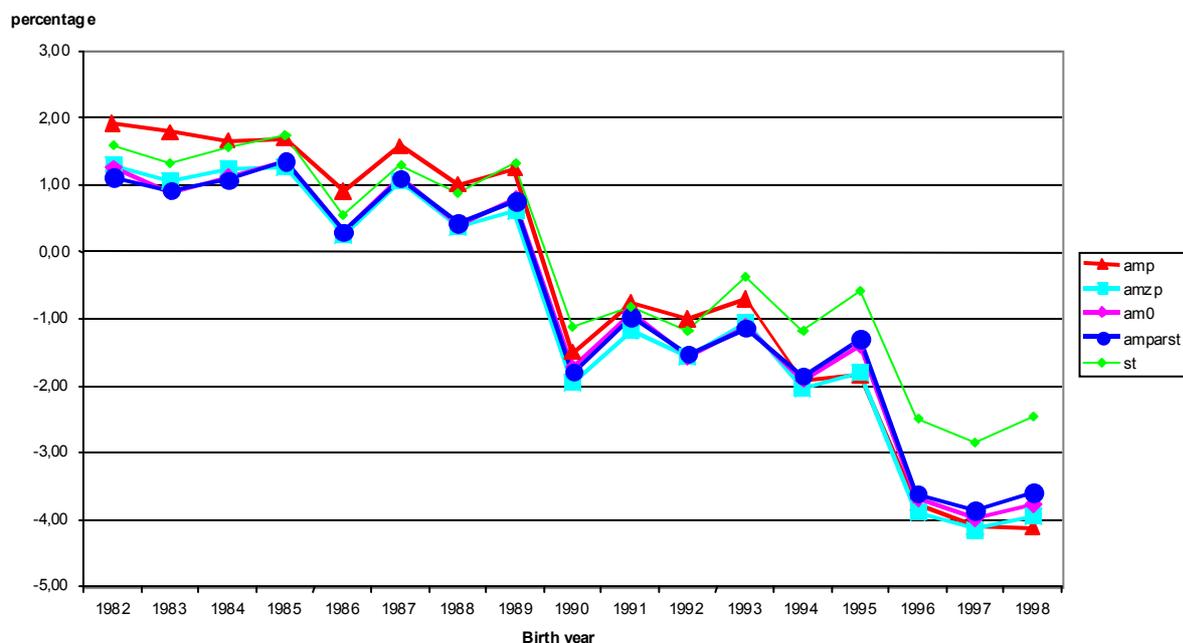


Figure 1. Genetic trend for nr56 based on AI-tested Holstein Friesian bull having at least 50 daughters, estimated in evaluations as st (sire model, single trait, old parameters), amparst (animal model, single trait, old parameters), am0 (animal model, single trait, new parameters) amzp (animal model, multiple trait, new parameters and not using milkproduction traits and BCS observations) and amp (animal model, multiple trait, new parameters and using milkproduction traits and BCS observations).

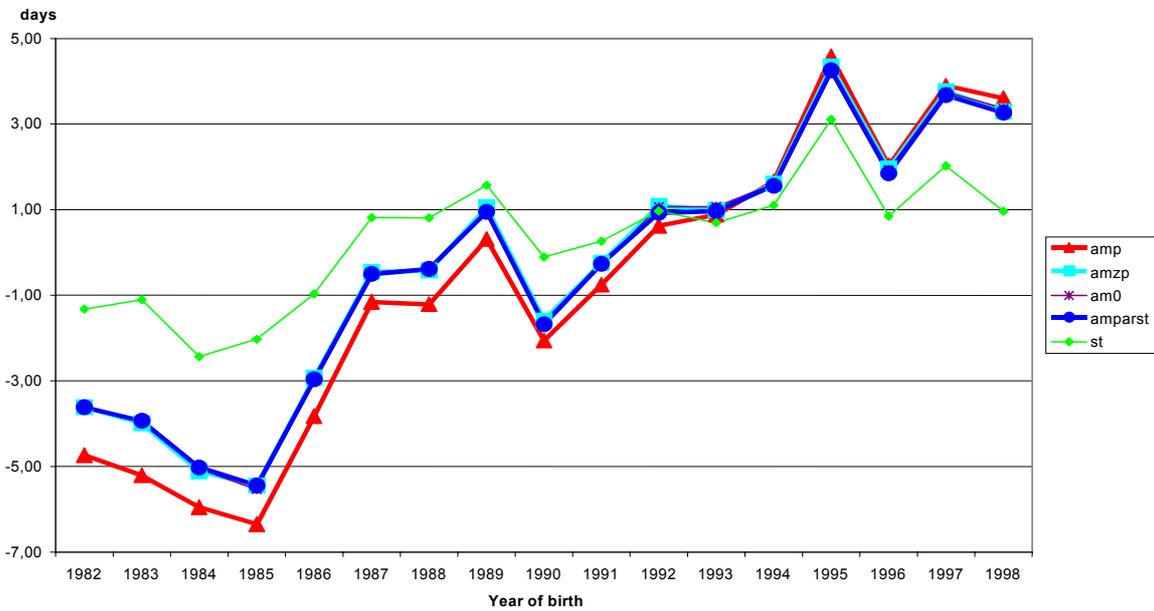


Figure 2. Genetic trend for CFI (in days) based on AI-tested Holstein Friesian bull having at least 50 daughters, estimated in evaluations as st (sire model, single trait, old parameters), amparst (animal model, single trait, old parameters), am0 (animal model, single trait, new parameters) amzp (animal model, multiple trait, new parameters and not using milkproduction traits and BCS observations) and amp (animal model, multiple trait, new parameters and using milkproduction traits and BCS observations).

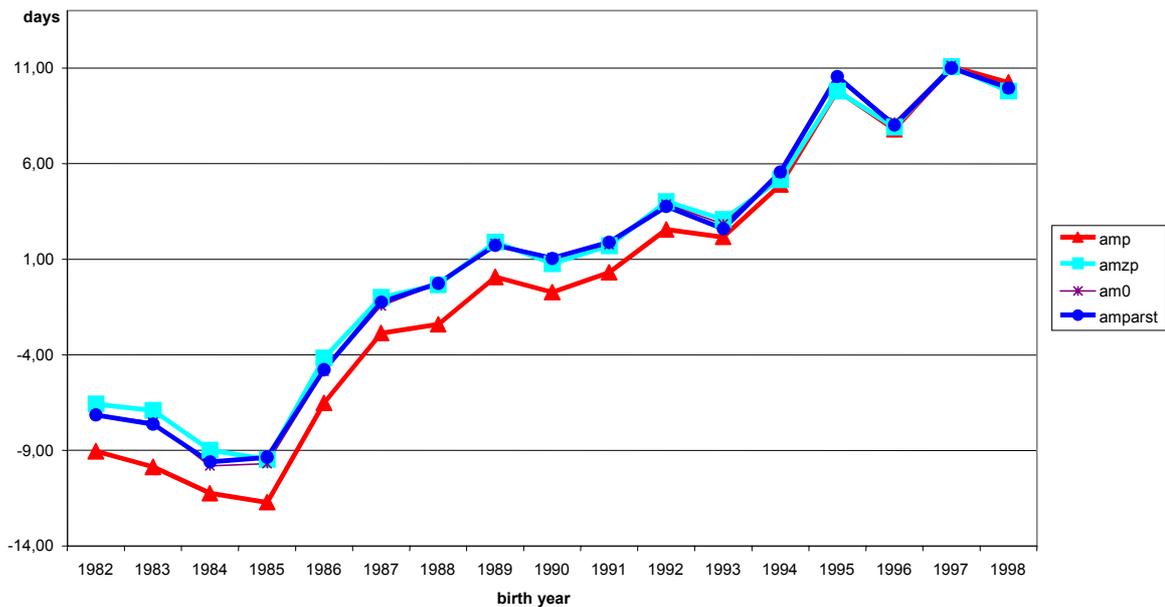


Figure 3. Genetic trend for CI based on AI-tested Holstein Friesian bull having at least 50 daughters, amparst (animal model, single trait, old parameters), am0 (animal model, single trait, new parameters) amzp (animal model, multiple trait, new parameters and not using milkproduction traits and BCS observations) and amp (animal model, multiple trait, new parameters and using milkproduction traits and BCS observations).