

Genetic parameters, phenotypic and genetic correlations for female fertility traits derived from on-farm service records in South African Holstein cattle

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Introduction

- Poor fertility is among the primary reasons for involuntary culling in dairy herds.
- Heritabilities for fertility traits are low, indicating strong influence by environmental factors, which largely discouraged efforts for their genetic improvement through selection.
- The pleiotropic effect of common alleles for fertility and production traits resulted in the long-term deterioration in reproductive performance of high-yielding dairy cows.
- In SA, age at first calving (AFC) and inter-calving period (ICP) are used as indicator traits to improve fertility, but these traits are greatly influenced by management decisions.
- AI service data present additional selection criteria with minimum bias.
- Service data are not recorded routinely into the national database but are kept on farm for management purposes.

Aim

The aim of this study was to derive additional fertility traits from service data and estimate their genetic parameters for their possible inclusion in the South African Holstein cattle breeding programmes.

Materials and Methods

AI performance data

- AI Service data were collected from 18 SA Holstein herds (n=64 464).
- Pedigree data included animals born between 1992 and 2013
- Eight AI Service-based fertility traits were defined:

Heifer traits

- ✓ Age at first service (AFS)
- ✓ Number of services per conception (SPCh)

Cow traits

- ✓ Number of services per conception (SPC)
- ✓ Calving to first service (CFS)
- ✓ Days open (DO)
- ✓ Pregnant < 100 days (PD100d)
- ✓ Pregnant < 200 days (PD200d)
- ✓ First service < 80 days (FS80d)

Statistical Analysis

- Editing and descriptive statistics were performed in R-CRAN.
- Model effects for genetic evaluations were tested using the lme4 package (Bates et al., 2015) in R
- Models: $y_{i,j,k} = \mu + a_i + b_j + c_k + e_{i,j,k}$
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 $y_{i,j,k} = \mu + a_i + b_j + c_k + e_{i,j,k}$
- Multivariate analyses were carried out to estimate genetic variances and heritabilities using THRIGIBBS1F90 and POSTGIBBSF90 of Blup90 family of programs (Misztal et al., 2018).

Results and Discussion

Table 1: Descriptive statistics of fertility traits in South African Holsteins

	CFS	DO	SPC	FS80d	PD100d	PD200d	AFS	SPCh
No. of obs	24 909	24 909	24 909	24 909	24 909	24 909	10 019	10 019
Mean	89.6	137	2.18	1.45	1.38	1.82	96.8	1.54
SD	36.6	71.9	1.57	0.90	0.48	0.38	3.51	0.98
Min	21	21	1	1	1	1	10	1
Max	290	435	10	2	2	2	30	6

Table 2: Heritability estimates (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) with standard errors of service-based heifer and cow fertility traits

	AFS	SPCh	FS80d	PD100d	PD200d	SPC	CFS	DO
AFS	0.02 ± 0.04	0.73 ± 0.00	0.27 ± 0.00	0.62 ± 0.01	0.04 ± 0.01	0.84 ± 0.00	0.36 ± 0.03	0.62 ± 0.00
SPCh	-0.06 ± 0.01	0.02 ± 0.00	-0.48 ± 0.01	0.30 ± 0.00	0.36 ± 0.00	0.05 ± 0.01	0.73 ± 0.00	0.48 ± 0.00
FS80d	0.01 ± 0.01	0.01 ± 0.01	0.07 ± 0.02	0.39 ± 0.01	0.47 ± 0.01	-0.46 ± 0.00	-0.89 ± 0.00	-0.20 ± 0.00
PD100d	-0.02 ± 0.01	-0.01 ± 0.01	0.37 ± 0.01	0.13 ± 0.00	-0.47 ± 0.00	-0.54 ± 0.01	-0.27 ± 0.00	-0.76 ± 0.00
PD200d	-0.01 ± 0.01	0.01 ± 0.01	0.12 ± 0.01	0.36 ± 0.01	0.24 ± 0.00	-0.57 ± 0.01	-0.63 ± 0.01	-0.85 ± 0.00
SPC	-0.13 ± 0.02	0.01 ± 0.01	0.19 ± 0.00	-0.48 ± 0.01	-0.58 ± 0.01	0.04 ± 0.00	0.90 ± 0.01	0.19 ± 0.01
CFS	0.12 ± 0.01	0.03 ± 0.01	-0.71 ± 0.00	-0.42 ± 0.01	-0.25 ± 0.01	-0.15 ± 0.00	0.06 ± 0.00	0.70 ± 0.00
DO	-0.03 ± 0.02	0.01 ± 0.00	-0.29 ± 0.00	-0.07 ± 0.00	-0.80 ± 0.00	0.71 ± 0.00	0.42 ± 0.01	0.05 ± 0.01

- Trait averages were higher than most reported values (Abe et al., 2009; Potgieter et al., 2011) for the same breed, except SPC. Mean SPC was lower in heifers (1.52) and higher in cows (2.18), possibly because heifers haven't started lactating.
- The heritability estimates of the traits were low as expected, although they have considerable exploitable genetic basis for improvement of reproductive performance through selection.
- Genetic correlations between heifer and cow fertility traits were favorable indicating that selection for improved heifer traits is coupled with correlated response later in an animal's life.
- Phenotypic correlations between heifer and cow fertility traits were generally close to zero.



Conclusions and Recommendations

- The heifer traits could be useful in fertility indices as they are available early in an animal's life.
- The desirable improvement of heifer fertility performance could lead to a favorable reproductive performance for cows due to their positive genetic association.
- The exploitable genetic basis of the traits highlights the potential of these traits for use in selection programmes, in addition to AFC and ICP.

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