Indian Journal of Animal Sciences **86** (6): 682–685, June 2016/Article

Heritability estimates of first lactation 300-day milk yield under single versus multi-trait animal models in Phule Triveni cattle

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Received: 26 August 2015; Accepted: 5 October 2015

ABSTRACT

First lactation records of 493 Phule Triveni cows sired by 55 bulls on production traits, viz. first lactation 300-day or less milk yield (FL300DMY), first lactation length (FLL), first dry period (FDP) and reproduction traits like age at first calving (AFC), first calving interval (FCI) and first service period (FSP) were used to compare the heritability estimates of FL300DMY under single-trait animal model (ST-AM) versus multi-trait animal models (MT-AM) in Phule Triveni cattle. Under two-trait models, the heritability estimate was found to be highest in FL300DMY-AFC combination as 0.34 ± 0.14. Under three-trait models, the heritability estimate was highest (0.33 ± 0.14) in FL300DMY- AFC- FDP combination. Under four-trait models, the highest estimate of heritability (0.53 ± 0.12) was in FL300DMY-FLL-AFC-FCI combination. Comparison of heritability estimates of FL300DMY from different models revealed that the estimates were varying from single to multiple traits in different combinations. The lowest residual variance (190566) and highest heritability (0.53 ± 0.12) of four-trait combination FL300DMY-FLL-AFC-FCI indicated that this four-trait combination should be used for selection of Phule Triveni cows.

Key words: Heritability estimates, Phule Triveni cattle, Single and multi-trait animal model, WOMBAT software

Selection objectives for dairy cattle in India have historically emphasized only on milk production and have not given due weightage to female fertility traits, which are considered as the second major reason for involuntary culling (Nehra 2011). An intense single-trait selection for milk production resulted in a considerable rise in milk production with a concomitant decline in fertility across the world (Pryce *et al*. 2004, Divya 2012). Female fertility has been neglected in the past in most dairy cattle genetic improvement programmes, mainly because of low heritability (Kadarmideen *et al*. 2003). Hence, the direct selection for fertility may not be efficient. Therefore, a multi-trait selection approach has to be used by combining milk production and reproduction traits. In India, very few studies (Divya 2012, Singh 2013) have been attempted using multi-trait models investigating the association among the reproduction and production traits. The aim of the present investigation was to compare the variation in heritability estimate by single versus multi-trait evaluation of Phule Triveni cows (having inheritance of 50% HF + 25% Jersey + 25% Gir developed at Research-Cum Development Project, Mahatma Phule Krishi Vidyapeeth, Rahuri) based on heritability of FL300DMY from single and multi-trait animal model analysis using WOMBAT software (Meyer 2007).

MATERIALS AND METHODS

The first lactation records on 493 Phule Triveni cows sired by 55 bulls maintained at Research-cum Development Project on Cattle, Mahatma Phule Krishi Vidyapeeth, Rahuri were collected over a period of 37 years from 1976 to 2012. The information on production traits, viz. FL300DMY, FLL, FDP and reproduction traits like AFC, FCI and FSP were collected for the present study.

The data were classified into different subclasses based on season and period of birth/calving and different age groups based on age at first calving for FL300DMY and reproduction traits. The year was classified into 3 seasons, viz. winter - October to February, summer- March to May, and rainy- June to September, period of calving into 7 groups, viz. <1980, 1981–1983, 1984–1988, 1989–1993, 1994–1998, 1999–2004, >2005, periods of birth into 7 groups viz. <1980, 1981–1983, 1984–1988, 1989–1993, 1994–1998, 1999–2004, >2005 and age at first calving was classified into 5 groups, viz. <803 days, 804–901 days, 902–1011 days, 1012–1147 days and >1148 days.

Variance–covariance components were estimated from single and multi-trait animal model analysis by REML method using WOMBAT software (Meyer 2007). Under multi-trait models, the two-trait, three-trait and four-trait

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models combining FL300DMY with first lactation production/reproduction traits were considered. As a part of data arranging, duplicate IDs were checked using Pedigree Viewer software.

The following animal model was used:

$$Y= Xb +Zu + e$$

For three traits, the model can be expressed as:

$$\begin{pmatrix} Y_1 \\ Y_2 \\ Y3 \end{pmatrix} = \begin{pmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \\ b3 \end{pmatrix} + \begin{pmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{pmatrix} \begin{pmatrix} u_1 \\ u_2 \\ u3 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \\ e3 \end{pmatrix}$$

where,Y, vector of observations for traits under study; b,vector of observations of unknown fixed effects of period and season; m, a vector of observations of unknown random effects (animals); X and Z, incidence matrices pertaining for fixed and random animal effect respectively.

The following are the assumptions of the model:

E (Y) = Xb, Var (s) = G, Var (h) = R and Cov (s, e') = 0 so that,

$$V (y) = ZGZ' + R$$

In 2, 3 and 4 trait model analysis, the FL300DMY was combined with FLL, FDP, AFC, FCI and FSP traits. The multi-trait model of two-trait combinations had 5 models of different trait combinations with FL300DMY, three-trait combinations had 6 models of different traits combination with FL300DMY and four-trait combinations had 4 models of different trait combinations with FL300DMY for estimation of heritability.

RESULTS AND DISCUSSION

Factors affecting first lactation traits: The various single and multi-trait models incorporated seasons, periods, age at first calving as fixed effects and sires as random effect. Sire had significant (P< 0.05) effect on FL300DMY and AFC and nonsignificant effect on remaining (FLL, FDP, FCI and FSP) traits. The effect of season of calving was found to be significant (P< 0.05) on FL300DMY and non-significant on rest of the first lactation traits. The effect of period of calving was highly significant (P< 0.01) on all the first lactation traits except FSP which had significant (P< 0.05) effect. The effect of age groups was significant (P< 0.05) on FLL and nonsignificant on remaining traits.

Heritability estimates of FL300DMY using single-trait animal model: The heritability estimate of FL300DMY was 0.29 ± 0.07 using single-trait animal model (Table 1). Divya (2012) and Singh (2013) reported somewhat lower estimates of heritability for 305 day milk yield as 0.23 ± 0.11 and 0.24 ± 0.09, respectively by ST-AM in Karan Fries cattle.

Heritability estimates of FL300DMY by multi-trait animal models

Two-trait animal models: The heritability estimates of FL300DMY by 2 traits animal models were 0.34 ± 0.14 for FL300DMY-AFC combination, 0.29 ± 0.13 for FL300DMY-FLL combination, 0.29 ± 0.14 for FL300DMY-FDP combination, 0.28 ± 0.12 for FL300DMY-FSP combination and 0.30 ± 0.13 for FL300DMY- FCI combinations (Table 1). The heritability estimates revealed that the best of the two-trait combination was FL300DMY-AFC with highest heritability (0.34 ± 0.14) and lowest residual error variance (251335). This may be ascribed to fairly sufficient additive genetic variation present in both these traits. Heritability estimate for 305DMY-AFC combination was 0.20 as reported by Atil and Khattab (2005). Divya (2012) reported heritability estimate of FL305DMY as 0.287 ± 0.107 for FL305DMY-FCI combination, 0.228 ± 0.103 for FL305DMY-FSP combination and 0.187 ± 0.100 for FL305DMY- AFC combination in Karan Fries cattle.

In other 2-trait combinations, the heritability of FL300DMY did not show significant improvement. The heritability estimates of FL300DMY from 2 traits animal models were moderate in magnitude and produced changed (lower or higher) heritability estimates compared to heritability estimate obtained from ST-AM. The specific combinations of traits under two trait animal models could be taken for genetic evaluation of animals, depending upon breeding objective and selection criteria of genetic improvement programme.

Three-trait animal models: The heritability estimates of FL300DMY, FL300DMY-FLL-AFC combination, FL300DMY-FLL-FDP combination, FL300DMY-FLL-FSP combination, FL300DMY-AFC-FSP combination, for FL300DMY-AFC-FDP combination and FL300DMY-FSP-FDP combination, FL3 00DMY-AFC-FDP combination under three-trait animal models are given in Table 1. The heritability estimates of FL300DMY under three-trait animal models had relatively higher magnitude compared

Table 1. Heritability estimates of first lactation 300-day milk yield by single and multi- trait animal model

Model	Residual variance	Heritability
Single-trait model		
FL300DMY	267473	0.29 ± 0.07
Two-trait models		
FL300DMY-AFC	251335	0.34 ± 0.14
FL300DMY-FLL	267822	0.29 ± 0.13
FL300DMY-FDP	265487	0.29 ± 0.14
FL300DMY-FCI	264919	0.30 ± 0.13
FL300DMY-FSP	267437	0.28 ± 0.12
Three-trait models		
FL300DMY-FLL- AFC	259623	0.32 ± 0.14
FL300DMY-FLL-FDP	260441	0.31 ± 0.14
FL300DMY-FLL- FSP	263186	0.30 ± 0.14
FL300DMY-AFC- FSP	263348	0.30 ± 0.14
FL300DMY-AFC-FDP	254305	0.33 ± 0.14
FL300DMY- FSP-FDP	263186	0.30 ± 0.14
Four-trait models		
FL300DMY-FLL-AFC-FSP	206835	0.51 ± 0.13
FL300DMY-FLL-AFC-FCI	190566	0.53 ± 0.12
FL300DMY-AFC-FSP-FDP	198192	0.45 ± 0.14
FL300DMY-AFC-FCI-FDP	196544	0.46 ± 0.15

to ST-AM. The estimate of heritability of FL300DMY was close to the estimate reported by Zulkadir *et al.* (2009) as 0.33 for MY-LL-Fat% combination in Brown Swiss cow. Relatively lower heritability estimates for FL305DMY in three-trait model were reported by Divya (2012) in Karan Fries cattle as 0.19 ± 0.10 for FL305DMY-FCI-AFC combination and 0.23 ± 0.02 for FL305DMY-AFC-FSP combination.

Four-trait animal models: The heritability estimates of FL300DMY for FL300DMY-FLL-AFC-FSP, FL300DMY-FLL-AFC-FCI combination, FL300DMY-AFC-FSP-FDP combination and FL300DMY-AFC-FCI-FDP combination under four trait animal models are given in Table 1. The heritability estimates of FL300DMY from 4-trait animal model, viz. *FL300DMY-FLL-AFC -FCI* and *FL300DMY-FLL-AFC-FSP* were close to each other and were higher than the heritability estimates from other four-trait animal models. Both of these combinations of traits under 4-trait animal models could be taken for genetic evaluation of animals, depending upon breeding objective of genetic improvement programme. Singh (2013) observed heritability estimates under four trait animal model using fat yield (FY) and SNF yield (SNFY) in the model as 0.23 ± 0.02 for FL305MY-FY-AFC-FSP combination and 0.24 ± 0.02 for FL305MY- SNFY-AFC-FSP combination in Karan Fries cattle.

Heritability estimates of FL300DMY from different models revealed that the estimates varied from single to multiple traits in different combinations. This could be due to positive or negative genetic correlations among the traits used in different multi-trait models as espoused by Lin and Lee (1986). The lowest residual variance (190566) and

Table 2. Genetic and phenotypic correlations of FL300DMY with production and reproduction traits for various multi-traits models

Traits included in model analysis	Genetic correlation	Phenotypic correlation
Correlation between FL300DMY and FLL		
Two-trait animal model (FL300DMY and FLL)	-0.20 ± 0.75	0.22 ± 0.04
Three-trait animal model (FL300DMY, FLL and AFC)	0.45 ± 0.79	0.10 ± 0.05
Three-trait animal model (FL300DMY, FLL and FDP)	0.09 ±0.47	0.22 ± 0.04
Three-trait animal model (FL300DMY, FLL and FSP)	-0.06 ± 0.50	0.22 ± 0.04
Four-trait animal model (FL300DMY, FLL, AFC and FSP)	-0.01 ± 0.43	0.22 ± 0.04
Four-trait animal model (FL300DMY, FLL, AFC and FCI)	-0.13 ± 0.54	0.22 ± 0.04
Correlation between FL300DMY and AFC		
Two-trait animal model (FL300DMY and AFC)	-0.21 ± 0.35	0.03 ± 0.05
Three-trait animal model (FL300DMY, FLL and AFC)	-0.19 ± 0.28	0.05 ± 0.05
Three-trait animal model (FL300DMY, AFC and FSP)	-0.17 ± 0.28	0.05 ± 0.05
Three-trait animal model (FL300DMY, AFC and FDP)	-0.20 ± 0.35	0.03 ± 0.05
Four-trait animal model (FL300DMY, FLL, AFC and FSP)	-0.11 ± 0.44	-0.07 ± 0.04
Four-trait animal model (FL300DMY, FLL, AFC and FCI)	-0.07 ± 0.49	-0.07 ± 0.05
Four-trait animal model (FL300DMY, AFC, FSP and FDP)	-0.42 ± 0.28	-0.02 ± 0.05
Four-trait animal model (FL300DMY, AFC, FCI and FDP)	-0.05 ± 0.65	-0.06 ± 0.04
Correlation between FL300DMY and FDP		
Two-trait animal model (FL300DMY and FDP)	-0.43 ± 0.21	-0.02 ± 0.04
Three-trait animal model (FL300DMY, FLL and FDP)	-0.58 ± 0.28	-0.02 ± 0.04
Three-trait animal model (FL300DMY, AFC and FDP)	-0.57 ± 0.29	-0.02 ± 0.04
Three-trait animal model (FL300DMY, FSP and FDP)	-0.006 ± 0.50	0.22 ± 0.04
Four-trait animal model (FL300DMY, AFC, FSP and FDP)	-0.47 ± 0.22	-0.09 ± 0.05
Four-trait animal model (FL300DMY, AFC, FCI and FDP)	-0.46 ± 0.22	-0.08 ± 0.04
Correlation between FL300DMY and FCI		
Two-trait animal model (FL300DMY and FCI)	-0.31 ± 0.19	0.18 ± 0.04
Four-trait animal model (FL300DMY, FLL, AFC and FCI)	-0.46 ± 0.30	0.10 ± 0.05
Correlation between FL300DMY and FSP		
Two-trait animal model (FL300DMY and FSP)	-0.35 ± 0.48	0.13 ± 0.04
Three-trait animal model (FL300DMY, FLL and FSP)	-0.25 ± 0.38	0.12 ± 0.04
Three-trait animal model (FL300DMY, AFC and FSP)	-0.35 ± 0.47	0.12 ± 0.04
Three-trait animal model (FL300DMY, FSP and FDP)	-0.25 ± 0.38	0.13 ± 0.05
Four-trait animal model (FL300DMY, FLL, AFC and FSP)	-0.39 ± 0.30	0.01 ± 0.04
Four-trait animal model (FL300DMY, AFC, FSP and FDP)	-0.41 ± 0.27	0.03 ± 0.05

highest heritability (0.53 ± 0.12) of 4-trait combinations FL300DMY-FLL-AFC-FCI indicated that this 4-trait combination should be used for selection of Phule Triveni cows.

Genetic and phenotypic correlations of FL300DMY with production and reproduction traits under multi-trait animal models

Genetic and phenotypic correlations between FL300DMY and FLL: The estimates of genetic correlation between FL300DMY and FLL from 2-trait animal model changed in magnitude and direction than the corresponding estimates from 3-trait models (Table 2). The genetic and phenotypic correlations between these 2 traits were obtained in the range of –0.01 ± 0.43 to 0.45 ± 0.79 and 0.10 ± 0.05 to 0.22 ± 0.04, respectively, from various animal models. The results were in agreement with the report of Lin and Lee (1986), Divya (2012) and Singh (2013).

Genetic and phenotypic correlations between FL300DMY and AFC: The genetic correlation between FL300DMY and AFC were negative in direction, low to moderate in magnitude and ranged from –0.05 ± 0.65 to –0.42 ± 0.28. The estimates of phenotypic correlations revealed that the correlations were positive in direction and smaller in magnitude for 2-trait or 3-trait models. For 4-trait models, the correlation was negative in direction. Phenotypic correlations among these traits ranged from –0.02 ± 0.05 to 0.05 ± 0.05 (Table 2).

Genetic and phenotypic correlations between FL300DMY and FDP: The estimates of genetic correlation between FL300DMY and FDP were negative in direction and ranged from –0.006 ± 0.50 to –0.58 ± 0.28 (Table 2). Phenotypic correlations among these traits were also negative except for FL300DMY-AFC-FDP combination and smaller in magnitude and ranged from –0.02 ± 0.04 to 0.09 ± 0.05.

Genetic and phenotypic correlations between FL300DMY and FCI: The estimates of genetic correlation between FL300DMY and FCI were negative in direction and range from –0.31 ± 0.19 to –0.46 ± 0.30. However, phenotypic correlation was positive among these traits (Table 2). The results were in agreement with the report of Lin and Lee (1986).

Genetic and phenotypic correlations between FL300DMY and FSP: The estimates of genetic correlation among these 2 traits were all negative in direction and moderate in magnitude ranging from –0.25 ± 0.38 to –0.41 ± 0.27 (Table 2). However, phenotypic correlations were positive in direction, ranging from 0.01 ± 0.04 to 0.13 ± 0.04.

Difference in genetic and phenotypic correlations estimates of 2-trait animal model from 3-trait and 4-trait animal models reflects joint contribution of other inter-correlated traits included in the multi-trait models. Multi-trait model analysis remove biasness from selection of any correlated traits included in model of analysis (Rothschild and Henderson 1979) which add further in reliability and accuracy of estimates obtained. The difference in sign between genetic and phenotypic correlation estimates from various animal models analysis exerts the need of traits to be included in multi-trait analysis and multi-trait animal model evaluation of animals.

ACKNOWLEDGEMENT

The authors wish to express their gratitude to the Director, ICAR-NDRI, Karnal for providing necessary facilities for conducting the investigation and Vice-Chancellor, MPKV, Rahuri for granting the permission to utilize research data on Phule-Triveni cattle for this study.

REFERENCES

Atil H and Khattab A S. 1999. Lifetime production and longetivity of Holstein Friesian cows in relation to their Sire transmitting abilities. *Pakistan Journal of Biological Sciences* **2** (1): 69–73.

Divya P. 2012. 'Single versus multi-trait models for genetic evaluation of fertility traits in Karan Fries cattle. ' M.V.Sc. Thesis, NDRI, Karnal.

Harvey W R. 1990. Guide for LSMLMW, PC–1version, mixed model least squares and maximum likelihood computer programme, *Mimeograph* Ohio State University, USA.

Lin C Y and Lee A J. 1986. Sequential estimation of genetic and phenotypic parameters in multi-trait mixed model analysis. *Journal of Dairy Science* **69**: 2696–703.

Meyer K. 2007. WOMBAT – A tool for mixed model analyses in quantitative genetics by REML. *Journal of Zhejiang University*. SCIENCE B **8**: 815–21.

Nehra M. 2011. 'Genetic analysis of performance trends in Karan Fries cattle.' M.V.Sc. Thesis, NDRI, Karnal.

Pryce J E, Royal M D, Garnsworthy P C and Mao I L. 2004. Fertility in the high yielding dairy cow. *Livestock Production Science* **86**: 125–35.

Rothschild M F and Henderson C R. 1979. Maximum likelihood estimates of parameters of first and second lactation milk records. *Journal of Dairy Science* **62**: 990–95.

Singh R. 2013.'*Genetic evaluation of Karan Fries sires using multiple trait models*.' Ph.D. Thesis. NDRI Deemed University, Karnal, India.

Zulkadir U, Aytekin I and Pala A. 2009. Estimation of genetic trends for productive and reproductive traits of Holstein cattle in Turkey. *Journal of Animal and Veterinary Advances* **8** (5): 857–62.