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Estimation of breeding values of first lactation 305-day milk yield from single and multi-trait animal models in Karan Fries cattle

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ABSTRACT

First lactation data on 528 cows sired by 98 sires maintained at National Dairy Research Institute, Karnal over a period of 26 years (1986–2011) were used to estimate heritability and breeding value of the first lactation 305-day or less milk yield and 4 fertility traits like age at first calving (AFC), first service period (FSP), first calving interval (FCI) and cow pregnancy rate (CPR) using single and multi-trait models with the help of WOMBAT software. The heritability of FL305DMY was 0.235 using single trait animal models, 0.223, 0.213, 0.196 and 0.147 from 2 trait analysis with FCI, FSP, AFC and CPR respectively. In 3 trait analysis (FL305DMY-FCI- AFC) heritability FL305DMY was 0.199. There were marginal deviations in heritability estimates of fertility traits also, from single trait to multiple trait estimation combining milk production. The Spearman's rank correlations between rankings based on estimated breeding values (EBVs) of FL305DMY from single trait (only FL305DMY) animal model with 2 traits (FL305DMY-AFC, FL305DMY-FCI and FL305DMY-FSP) and 3 traits (FL305DMY-AFC-FCI) animal models were 0.86, 0.92, 0.94 and 0.82 respectively. It was inferred that if the Karan Fries cows are culled exclusively on the basis of EBVs estimated from single trait analysis, the culling decision will be erroneous. Further, the study on lowest ranking 100 cows (20% of data) which are generally culled from the herd revealed that 59 - 65% of the cows which were poor only in FL305DMY would be culled irrespective of their superiority in reproductive traits.

Key words: Multiple-trait animal model, WOMBAT software, EBVs, Karan Fries

Selection objectives for dairy cattle in India have historically emphasized only on milk production and has not given due weightage for female fertility traits, which are considered as the second major reason for involuntary culling (Nehra 2011). An intense single-trait selection for milk production has resulted in a considerable rise in milk production with a concomitant decline in fertility across the world (Lucy 2001, Pryce *et al*. 2004). 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. Hence, a multi-trait selection has to be done by combining milk production and fertility traits. In India, very few studies have been attempted using multi-trait models (Jain and Sadana 2000) investigating the association among the fertility traits and production traits. The aim of the present investigation was to evaluate the variation in ranking of Karan Fries cows based on EBVs of FL305DMY from single and multi-trait analysis using WOMBAT software (Meyer 2007).

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MATERIALS AND METHODS

The first lactation records of 1,016 Karan Fries cows maintained at NDRI, Karnal were collected which were spread over a period of 26 years from 1986 to 2011. The date of first calving was recorded for all these animals, first lactation 305 day milk yield were recorded for 936 animals and date of second calving for 645 animals. As the study involved comparison of single trait estimates to that of multi-trait estimates, the data from same set of animals were used for both single and multi-trait analysis. So after normalising and avoiding bisexuality, where both male and female animals having same animal number, the first lactation records of 528 Karan-Fries cows sired by 98 sires on FL305DMY (first lactation 305-day or less milk yield) and fertility traits like AFC (age at first calving), FCI (first calving interval), FSP (first service period) and CPR (cow pregnancy rate) were collected / generated. The minimum length of lactation period for selection of records for analysis was 100 days. The mean lactation period was 347.24 days. The minimum number of progeny per sire considered for the study and average number of progeny per sire were 1 and 5.4 respectively. The cow pregnancy rate (CPR) was estimated using the formula given by Van Raden *et al*. (2004) as under:

CPR = 21/ (days open - voluntary waiting period + 11)

To estimate CPR, the voluntary waiting period was standardized as 51 days using class interval method based on highest total milk yield / first calving interval and total milk yield / first lactation length in the 51 to 56 class. As the voluntary waiting period was standardized as 51 days, for the single and multi-trait analysis of CPR the data from those animals whose calving to first service period was above 51 days were taken. Hence, the data set used for CPR analysis was different from the rest. Out of 528 animals 440 animals had calving to first service period above 51 days. So observations from these animals were taken for analysis of CPR.

The data were classified into different subclasses based on season and period of birth, season and period of calving and different age groups based on age at first calving for FL305DMY and different fertility traits. The year was classified into 4 seasons (1. Winter - December to March, 2. Summer-April to June, 3. Rainy- July to September, 4. Autumn- October to November), periods of calving into 7 groups (1. 1989 to 1991, 2. 1992 to 1994, 3. 1995 to 1997, 4. 1998 to 2000, 5. 2001 to 2003, 6. 2004 to 2006, 7. 2007 to 2011), periods of birth into 7 groups (1. 1986 to 1988, 2. 1989 to 1991, 3. 1992 to1994, 4. 1995 to 1997, 5. 1998 to 2000, 6. 2001 to 2003, 7. 2004 to 2011) and age at first calving was classified using Sturges' rule into 6 groups (1. $\leq$ 823, 2. 824 to 921, 3. 922 to 1019, 4. 1020 to 1117, 5. 1118 to 1215, 6. $\geq$1216).

To estimate the effect of genetic and non-genetic factors on fertility and FL305DMY, mixed model analysis of data was employed using least-squares maximum likelihood programme (Harvey 1990). The sire was considered as random effect, period and season of calving and age groups were considered as fixed effects in case of FL305DMY and fertility traits other than AFC. In AFC, the fixed effects were period and season of birth. DMRT as modified by Kramer (1957) was used for testing differences among least squares means (using the inverse coefficient matrix).

Variance–covariance components were estimated from single and multi-trait animal model analysis by REML method using WOMBAT software (Meyer 2007). WOMBAT is the improvised version of DFREML, which has been withdrawn from distribution by the end of 2005. Under multi-trait models, the 2 trait and 3 trait models combining FL305DMY with fertility traits were considered. As a part of data arranging duplicate IDs and bisexuality were checked using Pedigree Viewer software.

Three different models and 2 data sets were used for estimating the heritability of FL305DMY. The first 2 models compared the heritability of FL305DMY with and without age group and in the third model AFC was taken as covariable. All the fertility traits considered were also analyzed using single trait animal models. In the first set of data 528 observations and in second set 440 observations were used.

In 2 trait analysis, FL305DMY was combined with the fertility traits like AFC, FCI, FSP and CPR individually. The two fertility traits - AFC and FCI were also analyzed together using 2 trait animal models for estimating heritability. Two combinations of traits were analyzed using 3 trait animal model as follows, FL305DMY with FCI and AFC and FL305DMY with FSP and AFC for estimating heritability and breeding value.

The breeding values of cows were estimated by adding the mean value from the output file Sum Model of WOMBAT to the solutions obtained from the output file SumEstimates. The cows were ranked based on EBVs for FL305DMY and the Spearman's Rank correlations were estimated to ascertain degree of similarity between the rankings based on multivariate and univariate analysis. The EBVs of lowest ranking 100 cows (around 20% of total number of cows), which are generally culled from the herd were studied in detail in relation to single vis-à-vis multi-trait models.

RESULTS AND DISCUSSION

Least-squares means of first lactation 305- day or less milk yield and various fertility traits: The least-squares means for FL305DMY, AFC, FCI, FSP and CPR were 3226±61kg, 1015±10 days, 419±6 days, 137±6 days and 0.38±0.03 respectively. The averages of FL305DMY and FCI were in agreement with Rashia (2010). Singh and Tomar (1991) reported similar estimate of FSP in Karan Fries cows.

Effect of genetic and non genetic factors on FL305DMY and fertility traits: The sire had highly significant ($P\leq0.01$) effect on FL305DMY and AFC but nonsignificant effect on other traits (Table 1). Season and age group had nonsignificant effect on all the traits. This was in agreement with Nehra (2011). Period had significant effect ($P\leq0.05$) on FSP and AFC and highly significant effect ($P\leq0.01$) on FCI and nonsignificant effect on FL305DMY. Kokate (2009) however, reported significant effect of period of calving on FL305DMY in Karan Fries cattle.

Heritability estimates: The heritability estimates of FL305DMY from single-trait and multi-trait animal models using WOMBAT are presented in the Table 2.

Single-trait model: The heritability estimate of FL305DMY with age group as fixed effect in the model was 0.235±0.109 using single-trait animal model, which was 12.44 % higher than the model where age group was not considered (Table 2). The heritability estimate, however, witnessed a decline to the tune of 16.91% when AFC was taken as a co-variable in the model. The error variances in the above 3 models were 392824, 402492 and 407377 respectively. This clearly suggested that AFC should not be taken as a co-variable but as age-groups in the model. The heritability using animal model was similar to that estimated (0.280±0.021) by Kadarmideen *et al*. (2003) in cattle breeds in UK.

Two-trait animal model: The heritability of milk yield

Table 1. Least squares means and standard errors of FL305DMY and fertility traits

	FL305DMY LSM±SE	FCI LSM±SE	FSP LSM±SE	CPR LSM±SE	AFC LSM±SE
Overall	3226±61(528)	419±6(528)	137± 6(528)	0.38±0.03(440)	1015±10 (528)
Season	NS	NS	NS	NS	NS
1	3237±76(224)	416±7(224)	135±7(224)	0.35±0.04(185)	1022±13(200)
2	3227±79(139)	417±7(139)	137±7(139)	0.41±0.04(120)	996±16(120)
3	3164±93(93)	427±9(93)	145±9(93)	0.34±0.06(76)	998±15(127)
4	3276±104(72)	414 ±10(72)	131 ±10(72)	0.43±0.06(59)	1043±18(81)
Period	NS	**	*	NS	NS
1	3273±304(22)	391±30 ^{a}(22)	110 ±30^{a}(22)	0.33±0.20(17)	983±55(22)
2	3315±171(99)	419±17^{b}(99)	135 ±17^{b}(99)	0.47±0.11(70)	1049±31(103)
3	3300±149(101)	389 ±15^{a}(101)	112±15^{a}(101)	0.53±0.09(83)	993±27(87)
4	2977±156(62)	448±15^{c}(62)	166±15^{d}(62)	0.28±0.09(55)	1009±30(70)
5	3159±156(56)	424 ±15 ^{b}(56)	141 ±15^{bc}(56)	0.39±0.09(46)	1048±32(53)
6	3415±164(88)	430±16^{b}(88)	150±16 ^{c}(88)	0.31±0.09(81)	1046±31(75)
7	3145±252(100)	428 ±25^{b}(100)	147 ±25^{c}(100)	0.37±0.15(88)	975±48(118)
Age gp	NS	NS	NS	NS	-
1	3058 ±140(39)	430±14(39)	146±14(39)	0.30±0.09(31)	-
2	3153±95(108)	428±9(108)	144±9(108)	0.35±0.06(85)	-
3	3227± 84(154)	419±8(154)	138±8(154)	0.35±0.05(129)	-
4	3226±94(104)	414±9(104)	134±9(104)	0.47±0.06(90)	-
5	3340±103(78)	415±10(78)	134±10(78)	0.42±0.06(66)	-
6	3354±122(45)	406±12(45)	127±12(45)	0.41±0.07(39)	-

Within parentheses are number of observations. Least-squares means with different superscripts differ significantly from each other; *Significant at P≤0.05; **significant at P≤0.01.

Table 2. Heritability estimate of FL305DMY from single and multiple-trait combinations using WOMBAT software

Model	Trait combination (N=528)	Heritability ±S.E.
Single-trait animal model	FL305DMYwith age group as fixed effect	0.235±0.109
	FL305DMYwithout age group as fixed effect	0.209±0.108
	FL305DMY with AFC as co-variable	0.201±0.100
	FL305DMY (N = 440)	0.109±0.130
Two-trait animal model	FL305DMY- FCI	0.223±0.102
	FL305DMY- FSP	0.213±0.102
	FL305DMY- FTSS	0.237±0.104
	FL305DMY- CTFS	0.236±0.105
	FL305DMY- AFC	0.196±0.100
	FL305DMY- CPR (N=440)	0.147±0.114
Three-trait animal model	FL305DMY-FCI- AFC	0.199±0.098

N, Number of observations.

in combination with fertility traits like AFC, FCI, FSP, ranged from 0.196 to 0.223 (Table 2). Comparison of estimates obtained by single-trait (FL305DMY) versus 2-trait combinations with fertility traits showed decline in heritability of milk yield. The decline in heritabilities of FL305DMY with addition of one more trait in analysis were 16.60, 2.20 and 1.20% with AFC, FSP and FCI respectively in decreasing order of heritability.

Three-trait animal model: The heritability estimate from three-trait (FL305DMY-FCI-AFC) combination was similar to that of 2-trait combination of FL305DMY-AFC and smaller than that of single trait estimate of FL305DMY. In this single trait (FL305DMY alone) analysis age group was not taken in the model for a fare comparison with FL305DMY-AFC 2 trait model. Addition of FCI in the 2-trait model - FL305DMY-AFC did not improve the heritability estimate. The heritability estimates from single-trait and multiple-trait animal models using REML (WOMBAT) method revealed that the heritability varied with different trait combinations.

Single-trait estimation of sire variance in each trait ignores correlated information from the other trait, and the sire component of covariance is based on these single-trait estimates (Lin and Lee 1986). The heritability estimate of FL305DMY was higher in single-trait analysis compared to multi-trait analysis indicating the correlated effects of other traits. In a multi-trait estimation of sire variance, the heritability of FL305DMY was lower in combination with AFC. FL305DMY had a negative genetic correlation with fertility traits, AFC, FCI and FSP as –0.23±0.32, –0.24±0.33 and –0.17±0.33 and a positive phenotypic correlation as 0.04±0.04, 0.12±0.04 and 0.12±0.04. However, the estimates had higher SE. The magnitude in variation of heritability was not in accordance with the magnitude of genetic correlation. Lin and Lee (1986) reported that it is difficult to assess whether adding a positively or negatively correlated trait influence the heritability estimate differently.

Heritability estimates of fertility traits from single-trait and multiple-trait animal models using WOMBAT

Heritability estimate of AFC: The heritability of AFC was estimated using single-trait and multiple-trait animal models using WOMBAT. In 2-trait combinations, the AFC was combined with FL305DMY and with FCI. The heritability of AFC using single-trait animal model was 0.276± 0.105 which got declined to 0.258±0.103 using 2-trait model in combination with FL305DMY. But in combination with FCI heritability was improved to 0.282±0.104. From 3-trait model (FL305DMY-FCI-AFC) the heritability estimate of AFC was 0.260±0.102.

Heritability estimates of fertility traits other than AFC from single-trait and multiple-trait animal models using WOMBAT software: The heritability estimates of fertility traits other than AFC from single and multiple-trait combinations are presented in Table 3. The heritability estimates of fertility traits other than AFC were in general, smaller in magnitude with high SE under single and 2-trait animal models. This indicated that these traits could be improved by providing better management and proper environment and not through selection. Comparison of heritability from single-trait and 2-trait models revealed only marginal improvement in magnitude in fertility traits except FCI.

The FL305DMY and different fertility traits were analyzed by single and multi-trait animal models using WOMBAT software. When heritability estimates of FL305DMY from different models were compared it was found that the estimates were varying from single (only FL305DMY) to multiple traits and even from combination of one fertility trait to another fertility trait.

Breeding value estimates for first lactation 305 day milk yields from single and multi-trait animal models: The EBVs of FL305DMY ranged from 2,645 to 3,778 kg with age group in the model and 2,689 to 3,709 kg without age group in the model. In the 2-trait animal models combining FL305DMY with fertility traits, the EBVs ranged from 2,497 kg (FL305DMY-AFC combination) to 3,868 (FL305DMY-AFC combination), presented in Table 4. When 3 traits were combined (FL305DMY-AFC-FCI) the EBVs of FL305DMY varied between 2,511 and 3,905 kg. In the analysis with 440 records, the cows having highest and lowest EBVs were different from univariate analysis to bivariate analysis (FL305DMY with CPR). The estimates from 3 trait model, FL305DMY with AFC and FCI, were by and large closer to that of 2 trait combination of FL305DMY with AFC.

Table 3. Heritability estimates along with S.E. of fertility traits other than AFC from single and multiple-trait combinations

Trait	Single-trait animal Model	Two-trait animal model with FL305DMY
FCI	0.055±0.084	0.055±0.083
CTFS	0.016±0.078	0.030±0.080
FTSS	0.089±0.092	0.090±0.091
FSP	0.032± 0.082	0.039±0.081
CPR	0.048± 0.098	0.070±0.101

The Spearman's Rank correlations between single-trait (FL305DMY) and multi-trait models with different fertility traits were different from unity, indicating variation in ranking of animals based on EBVs from single-trait (FL305DMY) model and that of multi-trait models including fertility (Table 5). Similarly, Kadarmideen *et al.* (2003) and Sun *et al.* (2010) analyzed fertility traits using single- and multi-trait models, where production traits were included in the multi-trait analysis and estimated the Spearman's rank correlations. The Spearman's rank correlations ranged between 0.69 and 0.83 and 0.998 and 0.929 respectively.

The lowest rank correlation was obtained between rankings based on FL305DMY and rankings based on 3 trait combinations of FL305DMY with AFC and FCI followed by bivariate model with AFC. These rank correlations indicated that when AFC or both AFC and FCI were included in the model with FL305DMY, the rankings of cows varied significantly compared to other combinations. It was inferred from these rank correlations that if the Karan Fries cows are culled on the basis of EBVs of FL305DMY alone, the culling decision will be erroneous.

The lowest ranking 100 animals (20% of data) which are generally culled from the herd were identified based on EBVs of FL305DMY estimated from single and multi-trait models. The numbers of animals which are different in lowest 100 EBV groups of single trait analysis and multi-trait analysis are presented in the Table 5. This revealed that even though rank correlations were higher, more than 50% animals were different under both the single trait and multi-trait analysis. This demonstrated that more than 50% of the cows which were poor only in milk production would be culled irrespective of their superiority in reproductive traits.

The actual worth of an animal depends on many traits

Table 4. EBVs of FL305DMY

	Model	Avg.EBV	Max. EBV	Min.EBV
Two traits	FL305DMY-AFC	3232	3868(5533)	2497(5309)
	FL305DMY -FCI	3235	3822(5533)	2642(6837)
	FL305DMY -FSP	3236	3783(5533)	2651(6837)
Three traits	FL305DMY -AFC-FCI	3234	3905(5533)	2511(5309)
Single trait with N=440	FL305DMY	3301	3571(5533)	3085(6505)
Two traits with N=440	FL305DMY -CPR	3301	3776(6547)	2995(6635)

Table 5. Spearman's Rank correlations between single-trait FL305DMY and multi-trait models FL305DMY with different fertility traits

Model	Spearman's Rank correlation	Number of animals ranked differently in lowest ranking 100 animals
FL305DMY and FL305DMY -AFC	0.86	64
FL305DMY and FL305DMY -FCI	0.92	59
FL305DMY and FL305DMY -FSP	0.94	59
FL305DMY and FL305DMY -CPR	0.92	61
FL305DMY and FL305DMY -AFC-FCI	0.82	65

like production, reproduction and many other functional traits, so evaluation of animal based on estimates from only single-trait analysis will be erroneous. In Karan Fries herd at NDRI, the fertility traits are showing a undesirable trend as per Nehra (2011). Therefore, it is recommended that multi-trait models combining milk production and fertility traits be used for genetic improvement in overall performance of the animals.

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