



Comparison of heritability estimates of first lactation fertility traits in Mehsana buffaloes

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ABSTRACT

First lactation records of 3068 Mehsana buffaloes sired by 118 sires, under field progeny testing programme distributed in different 149 villages of 14 *talukas* maintained at Dudhsagar Research and Development Association, Dudhsagar Dairy, Mehsana over a period of 24 years (1989–2012) were used to estimate least squares means and heritability of fertility traits like, first service period (FSP), first calving interval (FCI) and daughter pregnancy rate (DPR). The least squares means of these traits were found to be 189.05±3.34 days, 472.97±2.87 days and 31.08±0.59%, respectively. Non genetic factors such as age at first calving and period of calving were found to have highly significant effect on all the traits, whereas, cluster found to be non-significant for FSP and significant for FCI and DPR. Heritability were estimated for FSP, FCI and DPR as 0.02±0.02, 0.004±0.015 and 0.095±0.031; 0.04±0.03, 0.026±0.024 and 0.089±0.032; and 0.01±0.02, 0.032±0.026 and 0.095±0.034 by LSML, BLUP-SM and BLUP-AM, respectively. BLUP-AM was found to be the best model for heritability estimation based on error variance and BLUP-AM gave highly significant and more accurate results than BLUP-SM and LSML in Mehsana buffaloes.

Keywords: BLUP, Field progeny testing, Fertility traits, Heritability, Mehsana buffaloes

India is a leading milk producer (since 1998) in the world having production to the tune of 187.75 million tonnes, with per capita availability of 394 g/day in 2018–19, which has increased by 6.5% over the previous year (BAHS 2019). Out of total milk produced in the country, about 49% is contributed by buffaloes, of which 35% of total milk is by well-defined 17 breeds (BAHS 2019). Gujarat model for milk production is emulated not only in India but in various parts of the world. The state is rich in indigenous buffalo germplasm with four buffalo breeds including Banni, Jaffrabadi, Mehsana and Surti. Among these, Mehsana is one of the important breeds with 3.6 million population (ranked 3rd in the country). These animals have natural habitat within areas of North Gujarat, which has great influence on dairy sector in Gujarat (DAHD&F 2013). These buffaloes are also known to be persistent milker and regular breeder.

In recent past, livestock sector has improved a lot but the pace of improvement is not as needed. It is expected that in near future with increase in population, the demand of animal products will increase simultaneously. To achieve ceiling milk production, there should be optimum balance

between productivity and fertility. Female fertility is an important feature in animal breeding. Indiscriminate breeding with sole objective of increasing milk production has severely compromised the reproducibility of dairy animals. Lower female fertility performance reduces the percentage of animals in their peak production period, restricts the rate of genetic gain for production traits, increases insemination costs which lead to increased involuntary culling and reduces the overall milk yield per animal. Continuous selection and breeding of animals for production traits lead to decrease in fertility because production traits are mostly negatively correlated with fertility traits. Considering all this, attention on improvement of reproductive traits along with production trait is highly desirable.

Reproductive traits have lower heritability compared to production traits. Greater environmental influences over the components of reproductive efficiency, fertility, pregnancy rate and success of insemination may be the reason behind this. So, it is important to find out the optimum method of heritability estimation of various fertility traits in order to plan proper breeding strategies for overall herd improvement. Breeding programs depend on the identification of various useful traits of high heritability and ease to measure for breeding improvement (Sonja *et al.* 2017). Heritability estimates were computed using either paternal half sib correlation method after

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adjustment of data for significant non-genetic effects by mixed model methodology taking sire as a random effect in the model (Harvey 1990). Very limited studies (Ambhore *et al.* 2016) are available on the comparison of various methods for estimation of heritability, so that suitability of estimation methodology under different set of scenario can be ascertained. In due of such studies in Mehsana buffaloes, an attempt was made to compare the magnitude and accuracy of heritability estimates of first lactation fertility traits, viz. first service period (FSP), first calving interval (FCI) and daughter pregnancy rate (DPR) using paternal half sib correlation method, BLUP sire and animal models using WOMBAT software, advocated by Meyer (2007) in Mehsana buffaloes.

MATERIALS AND METHODS

The lactation record of 8,222 Mehsana buffaloes maintained under field progeny testing programme, spread over a period of 24 years (1989 to 2012), comprising information of 3458 animals records on various fertility performances was utilised for estimation of fertility traits like, first service period (FSP), first calving interval (FCI) and daughter pregnancy rate (DPR). The obtained fertility traits data on 3458 buffalo were subjected to standardisation (Normalization, removal of outliers, etc.) and finally records pertaining to 3068 buffaloes sired by 118 sires, distributed in 149 different villages of 14 *talukas* were considered.

First service period was calculated as the time interval between date of next successful service and date of first calving. Similarly, interval between second and first calving was noted as first calving interval. Daughter pregnancy rate (DPR) is another fertility trait which gives a comprehensive idea about the fertility status of a farm. DPR further measures how quickly animals become pregnant again after calving and can be defined as the percentage of non-pregnant animal become pregnant during each 21-days period. It was estimated as follows:

$$DPR = 21 / (\text{First Service Period} - \text{Voluntary Waiting Period} + 11)$$

where, the constant factor 11, centralize the measures of possible conception within each 21 days time period. Voluntary waiting period in Mehsana buffaloes was standardized as 63 days (Sathwara *et al.* 2020).

Before estimation of heritability, these three fertility traits were adjusted for significant non-genetic factors. The data were classified into three different clusters (based on geographical location of the place where animal was reared), six periods (P_1 : 1989–1992, P_2 : 1993–1996, P_3 : 1997–2000, P_4 : 2001–2004, P_5 : 2005–2008 and P_6 : 2009–2012) and three age at first calving groups (A_1 : $< \bar{X} - 1$ SD = <1105 days, A_2 : $\bar{X} \pm 1$ SD = 1106 – 1666 days and A_3 : $> \bar{X} + 1$ SD = >1666 days). The clusters were classified, into cluster 1 (C_1) as Northern part (>23.30°N), cluster 2 (C_2) as middle part (23.15°N to 23.30°N) and cluster 3 (C_3) as southern part (<23.15°N).

Following classification, least squares analysis of variance for unequal sub-class numbers was used to analyse

the data on these fertility traits using the statistical model as suggested by Harvey 1990. The difference of means between any two sub-classes of cluster, period and age at first calving groups was tested for significance using Duncan's Multiple Range Test (DMRT) as modified by Kramer (1957).

Heritability was first estimated by the method which utilises the paternal half sib correlation as suggested by Becker (1975):

$$Y_{ij} = \mu + S_i + e_{ij}$$

where, Y_{ij} , observation of the j^{th} progeny of i^{th} sire; μ , population mean of that particular trait; S_i , effect of the i^{th} sire and e_{ij} , random error assumed to be normally and independently distributed with zero mean and constant variance NID (0, $\sigma^2 e$).

Further, variance-covariance components were also estimated by REML method using WOMBAT software (Meyer 2007). Both Best Linear unbiased prediction- Sire model (BLUP-SM) and Best Linear unbiased prediction- Animal model (BLUP-AM) were used for estimation of heritability. Pedigree data were checked for any duplicity of the genealogy using Pedigree Viewer software. The three methods of heritability estimates were compared based on the error variance, the method having minimum error variance was identified as the best method. Relative efficiency were estimated for other methods as under:

$$RE (\%) = \frac{\text{Error variance of method 1}}{\text{Error variance of method 2}} \times 100$$

RESULTS AND DISCUSSION

In general, service period of 60 days is highly desirable in dairy animals. Though, it is highly affected by management and environmental factors, gonadal hormones which are having direct effect on estrus regulation have important role in service period regulation. The mean of FSP in the present investigation was estimated to be 189.05 ± 3.34 days which had coefficient of variation of 68.3% (Table 1). The present estimate is in accordance with the estimates obtained by Bhatt (2019), Prajapati (2017) and Sathwara (2018) in Mehsana buffalo and Jakhar *et al.* (2016) in Murrah buffaloes.

Partitioning of variance further revealed non-significant effect of cluster in which animals were reared on the first service period. Upward estimation trend for service period from cluster 1 to cluster 3 (Table 1) affirms the variation in management practices in various villages clustered together. However, these differences were not significant and this was in agreement with Parmar *et al.* (2017) in Mehsana buffaloes. The period in which animal was calved, significantly ($P \leq 0.01$) influence the first service period. Galsar *et al.* (2016^a) and Parmar *et al.* (2017) in Mehsana also indicated the similar effect of period of calving. Variation in the precipitation pattern in the arid and semi-arid region (progeny testing area) during different periods may be the reason for such effect. Effect of age at first

Table 1. Least squares means $\pm$ SE and factors affecting various first lactation fertility traits

Trait	FSP (days)	FCI (days)	DPR (%)
M	189.05 $\pm$ 3.34 (68.3, 3068)	472.97 $\pm$ 2.87 (22.7, 2870)	31.08 $\pm$ 0.59 (64.9, 2751)
Cluster	NS	*	*
1	179.35 $\pm$ 6.31 (69.8, 482)	465.69 $\pm$ 5.38 ^b (21.9, 459)	33.71 $\pm$ 1.12 ^a (62.4, 426)
2	193.30 $\pm$ 3.77 (69.9, 1711)	471.59 $\pm$ 3.27 ^b (23.0, 1586)	30.73 $\pm$ 0.67 ^{ab} (65.2, 1524)
3	194.52 $\pm$ 4.75 (63.7, 875)	481.63 $\pm$ 4.08 ^a (22.4, 825)	28.86 $\pm$ 0.83 ^a (65.3, 801)
Period	**	**	**
1	215.43 $\pm$ 7.32 ^a (64.6, 348)	489.86 $\pm$ 6.39 ^{ab} (22.6, 314)	26.54 $\pm$ 1.26 ^{bc} (65.8, 328)
2	215.21 $\pm$ 5.95 ^a (62.8, 558)	490.88 $\pm$ 5.18 ^a (22.8, 504)	24.90 $\pm$ 1.04 ^c (64.4, 516)
3	188.99 $\pm$ 5.31 ^b (65.9, 695)	476.73 $\pm$ 4.55 ^b (22.9, 656)	30.90 $\pm$ 0.93 ^b (64.9, 632)
4	169.88 $\pm$ 4.51 ^c (70.5, 1100)	459.47 $\pm$ 3.88 ^c (22.2, 1047)	35.97 $\pm$ 0.80 ^a (63.6, 969)
5	155.76 $\pm$ 7.02 ^c (72.7, 367)	448.20 $\pm$ 5.98 ^c (21.9, 349)	37.66 $\pm$ 1.27 ^a (62.6, 306)
6	—	—	—
AFC	**	**	**
1	167.72 $\pm$ 5.36 ^b (72, 621)	457.94 $\pm$ 4.58 ^b (22, 587)	36.22 $\pm$ 0.95 ^a (61.8, 550)
2	197.02 $\pm$ 3.28 ^a (66.9, 2062)	482.47 $\pm$ 2.82 ^a (22.8, 1933)	28.72 $\pm$ 0.58 ^b (65.7, 1848)
3	202.43 $\pm$ 6.86 ^a (68.1, 385)	478.50 $\pm$ 5.97 ^a (22.8, 350)	28.47 $\pm$ 1.20 ^b (64.8, 353)

Figures within parenthesis are the coefficient of variation and number of observations, **, $P \leq 0.01$; *, $P \leq 0.05$; NS, non-significant. Superscripts may be read column wise for each effect of mean comparison. Similar superscript shows that the means do not differ significantly.

calving group (from which buffalo belonged) was found to be highly significant ($P \leq 0.01$) on first service period and it was higher for those group of animals which were having higher AFC. Parmar *et al.* (2017) in Mehsana buffaloes reported similar effect.

Genetic parameters estimate of a trait is of prime importance before adopting proper breeding strategy for animal improvement. Fertility traits in general have low heritability estimates. In present study, heritability of FSP was estimated as, 0.02 ± 0.02 , 0.004 ± 0.015 and 0.095 ± 0.031 by LSML, BLUP-SM and BLUP-AM, respectively. It was in equivalence with those reported by Sathwara (2018) and Bhatt (2019) in Mehsana buffaloes, and Gupta *et al.* (2015) in Murrah buffaloes. All these methods were compared for their relative efficiency based on the variances accounted for unexplained factors (error variance) and standard error associated with the heritability estimates (Table 2) and lowest error variance was estimated by BLUP-AM followed by BLUP-SM and LSML (Table 3). The heritability estimate obtained by BLUP-SM was quite low. Similar low estimate of heritability was also

Table 2. Heritability estimates of various first lactation fertility traits under different models

Trait	Heritability $\pm$ S.E.		
	LSML	Sire model	Animal model
FSP	0.024 ± 0.025^{NS}	0.004 ± 0.015^{NS}	$0.095 \pm 0.031^{**}$
FCI	0.040 ± 0.028^{NS}	0.026 ± 0.024^{NS}	$0.089 \pm 0.032^{**}$
DPR	0.013 ± 0.024^{NS}	0.032 ± 0.026^{NS}	$0.095 \pm 0.034^{**}$

**, indicated highly significant ($P < 0.01$); ^{NS}, indicated non-significant ($P > 0.05$).

reported by Ambhore *et al.* (2016) in Phule Triveni cattle. Heritability estimated by BLUP-AM was found to be highly significant ($P < 0.01$), whereas, estimates by LSML and BLUP-SM were non-significant ($P > 0.05$) for first service period.

The lower calving interval means production of more number of young ones during life span which is must for a buffalo to remain in the dairy herd as a profitable producer. The least squares mean for FCI in the present study was estimated as, 472.97 ± 2.87 days, which was in concert with those reported by Galsar *et al.* (2016a) and Patel *et al.* (2019) in Mehsana buffaloes and Yadav *et al.* (2007) and Jakhar *et al.* (2016) in Murrah buffaloes. The trait was significantly influenced ($P \leq 0.05$) by cluster in which animals were reared and trend was similar as explained for FSP. This finding was in harmony with the results of Prajapati (2017) in Mehsana buffaloes. However, Yadav *et al.* (2007) could not obtain significant association of cluster with FCI in Murrah buffaloes. Further, from the Table 1 it is evident that the period of calving and age at first calving group had highly significant ($P \leq 0.01$) effect on FCI, which were in harmony with Parmar *et al.* (2017) in same breed. This finding is also in analogy with those reported by Galsar *et al.* (2016a) in same breed of buffalo.

Estimation of variance and covariance components revealed the heritable variance as 0.04 ± 0.03 , 0.026 ± 0.024 and 0.089 ± 0.032 respectively, by LSML, BLUP-SM and BLUP-AM. The lower estimate of heritability for FCI in Mehsana buffaloes was in line with those reported by Galsar *et al.* (2016^b) and Parmar *et al.* (2017) in Mehsana buffaloes. Looking at the criteria that we have set for heritability comparison by various methods, BLUP-AM was identified as best model for heritability estimation in Mehsana buffaloes very similar to that of first service period. Similar to FSP, for FCI also heritability estimates through BLUP-

Table 3. Comparison of error variance for heritability estimates for fertility traits under different models

Trait	Method					
	BLUP-SM	RE	BLUP-AM	RE	LSML	RE
FSP	16,222.40	94.61	15,347.60	100	16,232.76	94.55
FCI	11,010.70	96.52	10,627.40	100	11,144.01	95.36
DPR	438.17	95.96	420.44	100	449.97	93.44

AM was only found to be highly significantly ($P < 0.01$) different from zero.

In general pregnancy rate measures, how many animals become pregnant from total animal served, but DPR gives a comprehensive idea about how quickly an animal becomes pregnant again after calving. The estimate of least squares mean measured in Mehsana buffaloes for daughter pregnancy rate in present study was $31.08 \pm 0.59\%$. The results were in close agreement with Sathwara *et al.* (2020) in Mehsana buffaloes and also in concert with those reported by Dash *et al.* (2015) in Murrah buffaloes. However, comparatively higher estimate of DPR has been reported in crossbred cattle (Divya *et al.* 2014). It is quintessential to know the factors which affect this comprehensive measure of fertility at field level. The analysis of variance reveals that there was significant effect ($P \leq 0.05$) of cluster on DPR and it was having decreasing trend from C_1 to C_3 . It also had highly significant ($P \leq 0.01$) influence of period of calving as well as the age at first calving group. It was observed that DPR was higher for those buffaloes which are classified under group having relatively lower AFC. Result obtained in present study is in concert with that reported by Sathwara *et al.* (2020). However, contrary to this, statistical non-significant effect of period of calving and age at first calving group was reported by Divya *et al.* (2014) in Karan-Fries cattle.

The Heritability estimates of daughter pregnancy rate was estimated to be 0.01 ± 0.02 , 0.032 ± 0.026 and 0.095 ± 0.034 by LSML, BLUP-SM and BLUP-AM, respectively, which was very low. Close agreement was observed with the estimates obtained by Sathwara (2018) in Mehsana buffaloes and Jamuna *et al.* (2015) in Murrah buffaloes. Lower heritability estimate is in line with the estimates obtained for other fertility traits and indicates that there was higher influence of environment on these traits. As observed in FSP and FCI, for daughter pregnancy rate also, only BLUP-AM estimates highly significant ($P < 0.01$) heritability.

The study concluded that BLUP-AM was the most efficient model for estimation of heritability for fertility traits in Mehsana buffaloes based on error variance in comparison of BLUP-SM and LSML method and give highly significant ($P < 0.01$) estimates of it. Relative efficiency estimated for all three methods shows that LSML have relative efficiency as 94.55, 95.36 and 93.44% for FSP, FCI and DPR whereas efficiency observed for BLUP-SM was 94.61, 96.52 and 95.96 in comparison of BLUP-AM (Table 3). The numerator relationship matrix developed in BLUP-AM takes consideration of all the relationships among all the animals.

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