

Efficiency of Random Regression model over conventional univariate animal model for estimation of breeding values for first lactation 305-day milk yields in Mehsana buffaloes

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ABSTRACT: Analysis was done on 71,536 test-day milk yield records (TD) of 7,378 Mehsana buffaloes. A Random Regression model (M-1) was used for estimating sire breeding values (EBV) for first lactation 305-day milk yields (305-DMY) using Legendre polynomials of order three with year-season of calving and herd-year-month of record as fixed effects, age at first calving and days in milk as co-variables; animal and permanent environmental effects as random. For model M-2, 305-DMY were predicted on TD and their EBVs were calculated. M-1 yielded daily heritability ranging from 0.11 (day 305) to 0.27 (day 117). Maximum genetic variability was realized at around 3.5 to 4 months. Reliability of EBVs for 305-DMY from M-1 were on an average 42.30% higher compared to M-2. Rank correlation of EBVs was 76.81%. Hence, it is proposed to use the Random Regression model for genetic evaluations of the Mehsana buffalo.

Keywords: Buffalo; Breeding value; Model

Introduction

The buffalo is a highly resilient bovine species with better efficiency in conversion of feed into milk solids. It is well adapted to smallholder production systems. The Mehsana buffalo is a cross between Murrah and Surti breeds. Systematic genetic improvement of Mehsana breed started in 1987 under the Dairy Herd Improvement Actions (DIPA) program of NDDB implemented by Mehsana District Cooperative Milk Producers' Union. The Mehsana buffaloes are well reputed for regularity in breeding and efficient milk production with average first lactation milk yield of 1972 ± 33 kg (Pundir et al. (2000)). At present in Mehsana buffalo, breeding values for first lactation 305-day milk yield (305-DMY) are estimated by projecting 305-DMY from monthly test day records using test interval method (Trivedi (1998)). An alternative to the current method may be the use of Random Regression model, which is more appropriate for analysis of longitudinal data. It account for the test day effect on the test day records as well as for the persistency of lactation. The objective of this study was to compare the reliability of sire estimated breeding values (EBVs) obtained using a Random Regression model with the conventional model wherein EBVs were calculated based on predicted 305-DMY.

Materials and Methods

Data. Data consisted of 71,536 first lactation test day milk yield records (TD) collected during the period 1988 to 2012 from 7378 Mehsana buffaloes of the Mehsana district in the state of Gujarat. These buffaloes

were sired by 185 sires. Pedigree consisted of 10,975 animals. Average herd size ranged between 2 and 5 animals per farmers and a "village" effect was used in the model. All buffaloes were milk recorded monthly following the ICAR reference method (ICAR (2012)) and total yield was calculated by the Test Interval Method (Sargent (1968)).

On the basis of date of calving of the recorded daughter, the season was classified into two categories, namely favorable season (November through May) and unfavorable season (June through October). Effect of herd-year-month of record was considered to correct for environmental variations on TD and all the breeding transactions in the herd were meticulously recorded. Number of levels for days in milk (DIM), year-season of calving and herd-year-month of record was 301, 50 and 7190, respectively.

Random Regression Model (M-1). The Random Regression model included year-season of calving and herd-year-month of records as fixed effects, age at first calving (AFC) and DIM as co-variables and animal as well as permanent environmental effects as random effects in the analysis. Legendre polynomials of order three were fitted for random effects with DIM as a random regression control variable. EBVs for 305-DMY were calculated using the following model.

$$y = Xb + Za + Wc + e$$

y = vector of observations (TD)

b = vector of systematic effects (herd-year-month of records and year-season of calving as fixed effects while, AFC and DIM as linear and quadratic covariables)

a = vector of additive genetic random regression coefficients

c = vector of permanent environmental random regression coefficients

e = residual effects

X, Z and W are corresponding incidence matrices for b, a and c, respectively.

Model using estimated 305-DMY (M-2). Lactation milk yields were estimated using the test interval method were standardized to 305-DMY and EBVs were estimated for 305-DMY using a lactation animal model.

$$\text{Model: } y = Xb + Za + e$$

y = vector of observations (305-DMY)

b = vector of systematic effects (herd-year-month of records and year-season of calving as fixed effect while, AFC as linear and quadratic covariables)
a = vector of additive genetic effects
e = vector of residual effects

X and Z are corresponding incidence matrices for b and a, respectively.

Statistical analysis. Heritability of TD and EBVs from M-1 were estimated using AIREML methodology by WOMBAT software package (Meyer (2007)). Reliability of EBV was estimated using standard formula as: Reliability = 1 - (Predicted error variance) / (Additive genetic variance) (Mrode and Thompson (2005)). Spearman's rank correlations were estimated for EBVs obtained from the two models used in this study. Criterion for comparison was reliabilities of EBVs with validation of results using rank correlations.

Results and discussion

Estimation of heritability. Heritability estimates are determined by multiple factors like statistical models used and methods adopted for interpolation of 305-DMY.

The TD ranged from 0.10 to 19.60 kg with a standard deviation of 2.08 kg. The average TD was 6.29 kg. Figure 1 plots daily heritability values. M-1 yielded daily heritability ranging from 0.11 (day 305) to 0.27 (day 117). These estimates are comparable with reports of Breda et al. (2010) and Chakraborty et al. (2010), who reported low to medium estimates heritability for TD in Murrah buffaloes. However, these estimates are higher than heritability estimates reported for Italian buffaloes (Rosati and Vleck (2002)). The lowest value was observed at day 305 (0.11), whereas the highest heritability was obtained at day 117 (0.27). Heritability at day 5 was 0.12, which increased to 0.13 at day 10, and reached a peak at day 117 (0.27). Similar observation was reported by Jamrozik and Schaeffer (1997) and Silvestre et al. (2005) in dairy cattle. This peak in heritability reduced gradually and reached 0.14 by day 270. During the latter part of lactation, the heritability reduced from 0.12 (day 294) to 0.11 (day 305). The maximum genetic variability was observed at 3.5 to 4 months of lactation. On the contrary, Geetha et al. (2006) reported higher estimate of heritability (0.58) in the beginning of lactation (5 days) in Murrah buffaloes.

There was no major selection in this breed before inception of the DIPA programme and hence considerable variability is expected. Low to moderate heritability estimates in this study confirm the expectations indicating that there exists considerable scope for selection in Mehsana buffalo for milk yield.

Breeding value estimation. EBVs obtained from M-1 ranged from -422.59 to 456.61 kg, whereas those from M-2 ranged from -340.43 to 260.04 kg. Reliability of EBVs from M-1 ranged from 0.08 to 0.88 with an average of 0.70 whereas those for M-2 ranged from 0.03

to 0.69 with an average of 0.42. The gains in reliability of EBVs from M-1 over those from M-2 ranged from 20.86% to 70.71% with an average gain of 42.30%. Two curves of daily EBVs of sire with the highest EBV (S1) and sire with the lowest EBV (S2) obtained from M-1 are presented in Figure 2. The rank correlation of EBVs between two models was 76.80%. Table 1 compares EBV and their reliability obtained from the two models.

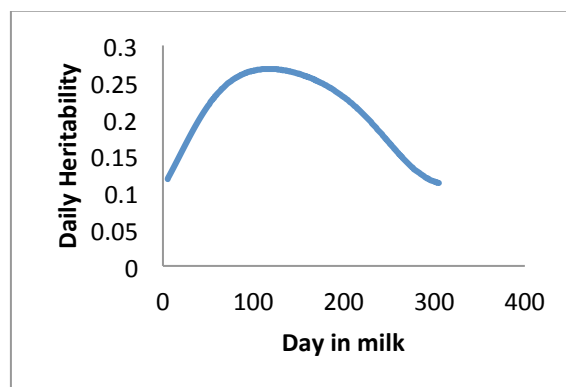


Figure 1. Curve for daily heritability estimates

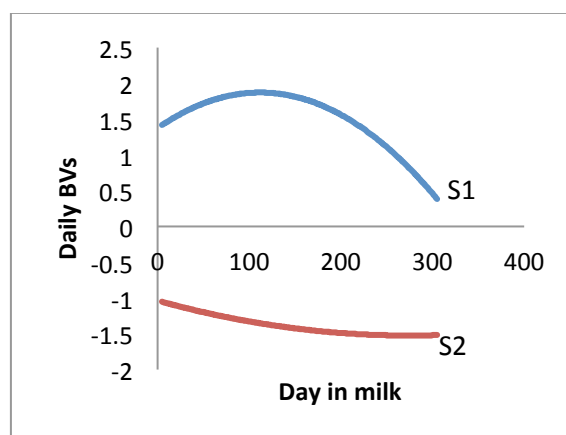


Figure 2. Curves of daily EBVs

Conclusion

Daily heritability ranged from 0.11 (day 305) to 0.27 (day 117). Use of M-1 provided more reliable estimates of EBVs for 305-DMY as compared to M-2 in Mehsana buffaloes and thus recommended in estimating EBVs for 305-DMY in ongoing programme.

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