INTRODUCTION

Procedure for multiple trait genetic evaluation of livestock requires accurate estimates of genetic and environmental parameters. Best linear unbiased prediction is the current method of choice for genetic evaluation of continuously distributed traits and assumes that (co)variances are known with out error, although in reality this is seldom, if ever, the case. When population (co)variances are not known, the generally accepted current strategy is to estimate necessary (co)variances using REML and use these estimates for BLUP of breeding values. In such a situation, one must also decide whether to estimate (co)variances separately, and often with limited accuracy, for each population or to use pooled values estimated from many populations.

In selection programmes applied to buffalo’s production, reproduction and growth traits can be considered. However, the larger the number of traits, the smaller genetic gain obtained in each trait. The decision about which traits should be considered depends not only on the economics involved, but also on genetic parameters of the traits and the "Practical" importance of the trait. The definition is taken by the geneticist and the breeder, always considering market reasons.

Use of Different Animal Models in Prediction of Genetic Parameters of First Lactation and Herd Life Traits of Murrah Buffaloes

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In order to compare different animal models, the methodology of mixed models under animal models was used to predict (Co) variance components of 8 traits related to production, reproduction and life traits of 1312 Murrah buffaloes descendent from 122 Sires and 341 dams raised at four military dairy farm viz. Ambala, Agra, Lucknow and Bareilly. The phenotypic mean (LSD) of body weight at first calving, age at first calving, first lactation milk yield, herd life milk yield, first lactation period, first dry period, first calving interval and first service period were 497.86 ± 57.95 kg, 1267.04 ± 232.94 days, 1761.57 ± 506.91 kg, 5630.00 ± 1383.88 kg, 306.76 ± 65.39 days, 177.08 ± 96.19 days, 481.86 ± 126.21 days and 179.54 ± 125.61 days respectively.

Additive variance (direct) component estimated for all the traits from univariate, model 2 and model 8 were not similar. Univariate RMEL analysis had higher values of additive variance for WFC, AFC, FLMY, HLMY, FLP, FDP, FCI and FSP than the estimate of model 2 and model 8. However, model 2 had lower values of additive variances only for WFC than univariate and model 8, but higher values for all other traits than univariate and model 8. Model 8 and univariate REML had similar values of environmental variances for all the traits but values estimated by model 2 were much lower than the other two models. The phenotypic variances estimated by model 2 and 8 univariate animal model were agreed for all the traits under study. The heritability estimates obtained under model 2 and univariate REML were found almost similar for all the traits while the heritability estimated under model 8 was low. The values for coefficient of variation estimated under different models were found to be almost similar. Genetic correlations among different traits ranged from very low to very high under model 2. Phenotypic and environmental correlations also showed same trend.

Keywords: REML, BLUP, Lifetime production, murrah buffaloes, heritability, animal models
Studies on genetic parameters of several traits of buffaloes have been made by some authors. However, the studies of parameters estimated for populations are not very many using different models, including animal models.

Genetic parameters are ratios of variances and covariance's, so these estimates are needed for the complete genetic knowledge of populations. The estimation of variance and covariance components evolved from Henderson's method I and III (Henderson, 1953) though maximum likelihood, iterative maximum likelihood (Cunningham and Henderson 1968), MINQUE, restricted maximum likelihood. REML (Patterson and Thompson 1971), best linear unbiased predictors- BLUP (Henderson 1949), using methodology of mixed models is becoming the preferred method of estimation for animal breeders. REML co (variance) component estimation is also becoming the most commonly used algorithm in such estimations.

The objectives of this study were to compare different animal models used to estimate genetic parameters of productive and reproductive traits of Murrah buffaloes, using single trait analysis with models methodology. The aim was to have a better knowledge of genetic of these traits to choose the best model for each one of the traits which can be used as selection criteria.

MATERIALS AND METHODS

The data spread over the period of 25 years from 1957 to 1981 for the present study. Data were obtained from the history sheets of 1312 Murrah buffaloes maintained at four military dairy farms of northern India viz. Ambala, Agra, Lucknow and Bareilly.

The animals with known pedigree and complete records on all target traits viz. weight at first calving, age at first calving, first lactation milk yield, herd life milk yield (first three lactations milk yield), first lactation period, first dry period, first calving interval and first service period were considered for the present study. The sires with less than 4 progenies had been deleted from the analysis.

STATISTICAL METHODOLOGY

For the estimation of parameters and (co) variance components, least-squares analysis (LSA) and derivative free restricted maximum likelihood (DFREML) methods were employed.

Data were subjected to LSMLMW and MIXMDL package of Harvey (1990) under different models. Two models were considered to examine the effect of genetic and non-genetic factors on various first lactation traits and herd life milk yield.

Model 2

The model 2 considered was from LSMLMW and MIXMDL package of Harvey (1990) which consists one set of cross classified non-interacting random effect. All eight traits were analyzed simultaneously, the model is as follows.

\[ y_{ijklm} = u_c + s_i + F_j + p_k + s_l + e_{ijklm} \]

Where,
- \( y_{ijklm} \) is observation on 1st progeny of ith sire of jth farm lth season in kth year.
- \( u_c \) is the over all mean.
- \( s_i \) is the random effect of ith sire (i = 1, 2, ..., 122)
- \( F_j \) is the fixed effect of the jth farm (j =1,2, ..., 4)
- \( p_k \) is the fixed effect of kth period of birth (k = 1, 2, ..., 5)
- \( s_l \) is the fixed effect of lth season of birth
- \( e_{ijklm} \) is the random error which is normally and independently distributed with mean 0 and variance \( \sigma^2_e \).

The analysis was computed with the mixed model least squares program which utilizes the method 3 of Henderson (1953).

Model 8

The model 8 considered was from LSMLMW and MIXMDL package of Harvey (1990), non-interacting random effect. The same model was fitted on all the traits and the traits were analyzed separately. The general formulation of the mixed model fitted is as follows.

\[ y_{ijklm} = u_c + s_i + F_j + p_k + s_l + e_{ijklm} \]

Where, all the abbreviations are same as described in first model. The formulation of model in matrix notation is as follows.

\[ Y = l u_c + xb + za + e \]

Where
- \( l \) is the column vector of the means.
- \( u_c \) is an over all mean.
- \( b \) is the column vector of fixed effects.
- \( a \) is a column vector of random effect.
- \( z \) is an incidence matrix of 0’s and 1’s.
x is an incidence matrix of 0's, 1's & -1's and
x-x values for the discrete effects, and
e is a column vector of the random errors.
This model is same as first model, except the
random effect may be correlated.

UNIVARIATE
In univariate analysis, all the traits under study
were analyzed separately. The same model was
fitted on all traits. The general formulation of
the mixed model fitted is as follows.

\[ y_{ijklm} = \mu + A_i + F_j + p_k + s_l + e_{ijklm} \]

Where,
\( A_i \) is random effect of ith animal and all the
other abbreviations are same as described in
earlier models. The formulation of general single
trait animal model is matrix notation is as
follows:

\[ y = xf + z a + e \]

Where,
\( y \) is a vector of Nx1 records,
\( f \) is a vector of fixed environmental effects of
sex and year, and co variable was taken here,
\( a \) is vector of breeding values for additive direct
genetic effects fitted which is random
\( s \) is a N*N F design matrix for fixed effects with
column ranks N*F*,
\( z \) is a N* NR design matrix for random animal
effects, where z=1, and e is a vector of N random
residual errors.

RESULTS AND DISCUSSION
Least Squares Means and standard deviations
for each trait and characteristics of data
structure summarized in Table 1. Estimates of
(co) variance components and genetic parameters
for first lactation production traits and herd life
time yield have been presented in Table-2. Additive variance (direct) component estimated
for all the traits from univariate REML, model 2
and model 8 were not similar. Univariate REML
analysis had higher values of additive variance
for WFC, AFC, FLMY, HLMY, FLP, FDP, FCI and FSP than estimates of model 8 while model 2
had lower values of additive variances only for
WFC than univariate and model 8 but values
estimated for AFC, FLMY, HLMY, FLP, FDP, FCI
and FSP had higher \( \sigma^2_a \) than the estimated by
univariate and model 8 analysis. Model 8 and
univariate REML had similar values of
environmental variances for WFC, AFC, FLMY,
HLMY, FLP, FDP, FCI and FSP but values
estimated by model 2 analyses were much lower
than univariate REML and model 8 analyses for
all the traits. Phenotypic variances estimated
by model 2 and 8 and univariate animal model
were agreed for all the traits under study.
The \( h^2 \) estimates for weight at first calving (WFC)
were 0.032 ± 0.058, 0.012 and 0.095 respectively
under mode 2 and 8 and univariate REML
analyses. The lower \( h^2 \) estimates with relatively
small C.V. suggest that weight at first calving
alone would not be appropriate for evaluation of
animals.
The \( h^2 \) estimated for age at first calving by model
2, model 8 and univariate animal were 0.571 ±
0.102, 0.110 and 0.325 respectively. The
heritability estimated under model 8 was lower
than estimated by model 2 and univariate animal
model. There was positive correlation between
C.V. and heritability estimates in univariate
animal model and model 8. However, AFC had
negative correlation between C.V. and \( h^2 \)
estimated by model 2.
The \( h^2 \) estimates for first lactation milk yield
by model 2 (0.282) and univariate REML (0.238)
were almost similar. Model 2 and univariate
REML had higher \( h^2 \) estimates than model 8
analysis (0.070). The positive correlation between
C.V. and \( h^2 \) estimates were observed under all
methods for first lactation milk yield.
The \( h^2 \) estimates for herd life milk yield under
model 2 and unvariate REML methods were
almost similar but \( h^2 \) estimated by model 8 was
lower than the values estimated by model 8 and
univariate REML analysis. There was positive
correlation between C.V. and \( h^2 \) estimates in
model 2, model 8 and univariate REML.
The heritability estimated for first lactation milk
yield by model 2, model 8 and univariate REML
were 0.245 ± 0.077, 0.060 and 0.186 respectively.
The \( h^2 \) estimated by model 8 was lower than
the values estimated by model 2 and univariate
REML. There was positive correlation between
C.V. and \( h^2 \) estimates by all the methods. The
heritability estimates for first dry period ranged
from 0.031 (model 8) to 0.174 ± 0.078 (model 2).
The heritability estimated by model 8 and
univariate REML had lower estimates of \( h^2 \) than
Table 1: Data Structure, mean and standard deviation estimated by model 2

<table>
<thead>
<tr>
<th>Characteristics of data</th>
<th>No. of observation</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of animals</td>
<td>1213</td>
</tr>
<tr>
<td>No. of base animals</td>
<td>485</td>
</tr>
<tr>
<td>No. of animals with unknown sire</td>
<td>34</td>
</tr>
<tr>
<td>No. of animals with unknown dam</td>
<td>23</td>
</tr>
<tr>
<td>No. of sire with progeny records</td>
<td>122</td>
</tr>
<tr>
<td>No. of dams with progeny records</td>
<td>341</td>
</tr>
<tr>
<td>Weight at first calving</td>
<td>497.86 ± 57.95</td>
</tr>
<tr>
<td>Age at first calving</td>
<td>1276.04 ± 232.94</td>
</tr>
<tr>
<td>First lactation milk yield</td>
<td>1761.57 ± 506.91</td>
</tr>
<tr>
<td>Herd life milk yield</td>
<td>5630.00 ± 1383.88</td>
</tr>
<tr>
<td>First lactation period</td>
<td>306.76 ± 65.39</td>
</tr>
<tr>
<td>First dry period</td>
<td>177.08 ± 96.19</td>
</tr>
<tr>
<td>First calving interval</td>
<td>481.86 ± 126.21</td>
</tr>
<tr>
<td>First service period</td>
<td>179.54 ± 125.61</td>
</tr>
</tbody>
</table>

Table 2: Estimates of (co) variance components and genetic parameters for production and reproduction traits

<table>
<thead>
<tr>
<th>Model 2</th>
<th>WFC</th>
<th>AFC</th>
<th>FLMY</th>
<th>HLMY</th>
<th>FLP</th>
<th>FDP</th>
<th>FCI</th>
<th>FSP</th>
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</thead>
<tbody>
<tr>
<td>$\sigma^2_a$</td>
<td>104.16</td>
<td>28577.04</td>
<td>70199.28</td>
<td>334661.92</td>
<td>1012.44</td>
<td>1602.40</td>
<td>3900.92</td>
<td>2662.88</td>
</tr>
<tr>
<td>$\sigma^2_s$</td>
<td>26.04</td>
<td>7144.26</td>
<td>17549.82</td>
<td>83665.48</td>
<td>253.11</td>
<td>400.60</td>
<td>975.23</td>
<td>665.72</td>
</tr>
<tr>
<td>$\sigma^2_e$</td>
<td>3278.46</td>
<td>42895.95</td>
<td>231503.88</td>
<td>1750908.21</td>
<td>3877.64</td>
<td>8810.01</td>
<td>14722.35</td>
<td>14879.70</td>
</tr>
<tr>
<td>$\sigma^2_p$</td>
<td>3304.86</td>
<td>50040.21</td>
<td>249053.70</td>
<td>1834573.69</td>
<td>4130.75</td>
<td>9210.65</td>
<td>15697.58</td>
<td>15545.42</td>
</tr>
<tr>
<td>$h^2$ ± SE</td>
<td>0.032 ± 0.571 ± 0.282 ± 0.182 ± 0.245 ± 0.174 ± 0.248 ± 0.171 ± 0.058 0.102 0.080 0.072 0.077 0.078 0.078 0.071</td>
<td></td>
<td></td>
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<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Model 8</th>
<th>WFC</th>
<th>AFC</th>
<th>FLMY</th>
<th>HLMY</th>
<th>FLP</th>
<th>FDP</th>
<th>FCI</th>
<th>FSP</th>
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</thead>
<tbody>
<tr>
<td>$\sigma^2_a$</td>
<td>40.530</td>
<td>5609.790</td>
<td>17567.710</td>
<td>80527.120</td>
<td>249.480</td>
<td>287.430</td>
<td>834.300</td>
<td>554.280</td>
</tr>
<tr>
<td>$\sigma^2_s$</td>
<td>3263.620</td>
<td>45284.090</td>
<td>233315.150</td>
<td>1757906.570</td>
<td>3898.390</td>
<td>8930.820</td>
<td>14959.650</td>
<td>15015.100</td>
</tr>
<tr>
<td>$\sigma^2_e$</td>
<td>3320.750</td>
<td>50895.500</td>
<td>250884.060</td>
<td>1838470.570</td>
<td>4147.800</td>
<td>9218.730</td>
<td>15794.450</td>
<td>15570.180</td>
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<tr>
<td>$h^2$</td>
<td>0.012</td>
<td>0.0110</td>
<td>0.070</td>
<td>0.044</td>
<td>0.060</td>
<td>0.031</td>
<td>0.052</td>
<td>0.035</td>
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<tr>
<td>$\sigma^2_p$</td>
<td>10.130</td>
<td>1402.440</td>
<td>4391.920</td>
<td>20131.780</td>
<td>62.370</td>
<td>71.850</td>
<td>208.570</td>
<td>138.570</td>
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<table>
<thead>
<tr>
<th>Univariate REML</th>
<th>WFC</th>
<th>AFC</th>
<th>FLMY</th>
<th>HLMY</th>
<th>FLP</th>
<th>FDP</th>
<th>FCI</th>
<th>FSP</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2_a$ (div.)</td>
<td>313.820</td>
<td>16372.09</td>
<td>5868.98</td>
<td>359386.63</td>
<td>772.15</td>
<td>866.74</td>
<td>2973.04</td>
<td>1275.12</td>
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<tr>
<td>$\sigma^2_s$</td>
<td>2993.82</td>
<td>34049.46</td>
<td>191612.39</td>
<td>1481977.73</td>
<td>3666.97</td>
<td>8347.35</td>
<td>12813.17</td>
<td>14270.46</td>
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<tr>
<td>$\sigma^2_e$</td>
<td>3307.27</td>
<td>50421.55</td>
<td>250292.46</td>
<td>1841364.37</td>
<td>4139.13</td>
<td>9214.09</td>
<td>15786.21</td>
<td>15545.57</td>
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<tr>
<td>Log L</td>
<td>-5947.68</td>
<td>-7698.39</td>
<td>-8750.98</td>
<td>-10052.91</td>
<td>-6087.07</td>
<td>-6614.23</td>
<td>-6957.71</td>
<td>-6955.09</td>
</tr>
<tr>
<td>$h^2$</td>
<td>0.095</td>
<td>0.325</td>
<td>0.238</td>
<td>0.195</td>
<td>0.186</td>
<td>0.094</td>
<td>0.188</td>
<td>0.082</td>
</tr>
</tbody>
</table>

Where,
$\sigma^2_a$ is additive genetic variance, $\sigma^2_s$ is sire component of variance, $\sigma^2_e$ is residual variance, $\sigma^2_p$ is phenotypic variance and Log L is the log of the likelihood function.

For first calving interval, the heritability estimated by model 2 $(0.248 \pm 0.078)$ was higher than the model 8 $(0.052)$ and univariate REML procedure $(0.188)$. There was positive correlation between C.V. and $h^2$ estimates in all the methods. FCI had lower C.V. with lower estimates of $h^2$ under all the methods.
Model 2 had higher heritability estimates among all three methods employed for first service period. The negative correlation between C.V. and $h^2$ for FCI were observed under all the methods. For FCI heritability estimates were very low under all the methods while C.V. were very high under all the methods. Since the positive trait correlation has a direct physical origin, it might be expected that their variances, or at least their heritabilities, would show positive correlation (Koots et al. 1994a).

The results in the present study showed that different estimates of heritability could be obtained for all the traits using different estimation procedures with same or different models. There may be model effect for difference in $h^2$ values obtained by different methods.

The genetic correlations of WFC with FLMY, HLMY, FLP, FDP, FCI and FSP were found positive with very low (0.101 FLP) to very high (0.766 HLMY) magnitude. The genetic correlation of WFC with AFC was found negative with higher magnitude (> 1.0).

The genetic correlations of AFC with FLP, FDP, FCI and FSP were found positive with moderate magnitude while with FLMY and HLMY were found negative with low magnitude. The genetic correlations of first lactation milk yield (FLMY) with HLMY, FLP, FDP, FCI and FSP were observed highly positive.

The genetic correlation of HLMY with FLP, FDP, FCI and FSP period were found highly positive. The genetic correlation of FDP with FCI and FSP were observed highly positive. The genetic correlation between FCI and FSP was observed highly positive.

The phenotypic correlations of WFC with all the traits were positive with lower magnitude except with AFC and FLP with were observed negative with lower magnitude.
The phenotypic correlations of AFC with FLMY, HLMY, FLP, FDP and FCI were found positive with low magnitude while negative genetic correlation was observed with FSP.

The phenotypic correlations of FLMY with all the traits were found positive with very low to high magnitude which is of general interest in selection for these traits. The genetic correlations of HLMY with FLP, FCI and FSP were found positive with very low to medium magnitude while negative genetic correlation was observed with FDP.

The phenotypic correlations of FLP with FDP, FCI and FSP were found highly positive. The phenotypic correlations of FDP with FCI and FSP were found highly positive. The phenotypic correlation between FCI and FSP was also observed highly positive. Hansen and Shrestha (1999) found none of the 3 mixed model methodologies (LS, ML and REML) were consistently superior to the other methods in all the sampling space with the exception of trivial examples.

Additive variance (direct) component estimated for all the traits from univariate REML, model 2 and model 8 were not similar. Univariate REML analysis had higher values of additive variance for all the traits under study.

REFERENCES


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