The only way to judge the efficiency of any breeding programme is to estimate the genetic improvement per year. Reliable estimates of annual genetic gain allow comparison of expected and realised improvement and assessment of progress in a particular trait. Accordingly, the present study was undertaken to estimate the genetic progress in 300 day/less first lactation milk yield.

The breeding records of 784 Murrah buffaloes from Military Dairy Farm Jabalpur, between 1941 and 1977 were used for estimation of phenotypic and genetic progress in milk yield. A definite policy of culling and selection was followed. Bulls were selected on the basis of their dam’s production records. Male calf was retained in the herd when his dam's milk yield for 300 days was more than 2700 kg. For female calf to be retained, the dam’s milk yield must not be less than 2400 kg and each of these female calves was given a chance to complete her first lactation. The remaining calves were disposed off. Natural service was practised in this herd.

The phenotypic trend was computed based on the data adjusted by least squares procedure as described by Nurnaide and Legates (1967). The genetic trends were estimated using four regression methods as:

\[ \Delta G_1 = 2b_{p,T} - b_{p,T/S}, \]
\[ \Delta G_2 = -2b(p-P) \frac{T}{S}, \]
\[ \Delta G_3 = -2b(p-P_H) \frac{T}{S} \text{ and} \]
\[ \Delta G_4 = 2b(\Delta G + \Delta E) - b(\Delta G/2 + \Delta E) \]

Where,
\[ b_{p,T} \] is the linear regression of population performance \( p \) on time \( T \),
\[ b_{p,T/S} \] is the pooled within sire regression of sire progeny performance on time. The weights were used to pool the individual regression within sire. Each weight was the inverse of the variance of the regression within a sire,
\[ b(p-P)T/S \] the within sire regression of records of sire progeny on time, each record being expressed as deviation from the herd average,
\[ b(p-P_H)T/S \] the within sire regression of records of sire progeny on time, each record being expressed as deviation from the herdmate average,
\[ b(\Delta G + \Delta E) \] the weighted regression of year constants on years, indicating the phenotypic change, and

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\[ b(\Delta \frac{0}{2} + \Delta E) \] is the weighted regression coefficient which expressed one half of the genetic trend plus the environmental trend.

\[ \Delta G \] was based on data adjusted for month and age at first calving by the least squares procedure. The second and third method tend to eliminate any effect of year to year fluctuations and are more dependable than the first method. The genetic change by direct selection was estimated using the four paths from parent to offspring (dam to son, dam to daughter, sire to son and sire to daughter).

The estimates of phenotypic, genetic and environmental trends for milk yield are given in Table 1.

### TABLE 1

Phenotypic, genetic and environmental trends.

<table>
<thead>
<tr>
<th>Number of sires</th>
<th>37</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of daughters</td>
<td>686</td>
</tr>
<tr>
<td>Phenotypic trend</td>
<td>$-5.59 \pm 3.43$</td>
</tr>
</tbody>
</table>

**Genetic trend**

<table>
<thead>
<tr>
<th>Method</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>$-28.63 \pm 12.05^*$</td>
</tr>
<tr>
<td>2</td>
<td>$2.27 \pm 11.95$</td>
</tr>
<tr>
<td>3</td>
<td>$5.91 \pm 12.69$</td>
</tr>
<tr>
<td>4</td>
<td>$11.76 \pm 10.64$</td>
</tr>
<tr>
<td>Environmental trend</td>
<td>$-17.56 \pm 11.18$</td>
</tr>
</tbody>
</table>

* Significant at 5% level

The phenotypic trend was negative. The estimate of genetic trend by third method was larger than that by second method. This was due to the exclusion of paternal half-sibs from contemporary average, which would increase sire to sire variation depending on the number of contemporaries and paternal half-sibs. The genetic trend by least square method was $11.76 \text{ kg}$ which was equal to 0.73% of the herd average of 1611.26 kg. The negative environmental trend was probably because of limited fodder resources compared to the size of the herd.

The effect of two sources of bias i.e., non-random distribution of mates with respect to production level and the tendency of older females being mated to older males, on estimates of genetic trend was examined. The unbiased estimate of genetic trend was calculated as suggested by Harville and Henderson (1967). The intra-sire subclass regression of dam production deviation on sire age was $1.08 \pm 0.95 \text{ kg per month of sire age}$. The estimate was non-significant indicating that there was no tendency of high yielding cows to be mated to sires with advancing age. The within sire regression of dam's age on sire's age was also non-significant being $0.09 \pm 0.10$. This indicated that there was no significant increase in age of mates with the increase in age of sires. The estimate of genetic trend for milk yield using $2(b_1 - b_{11})$, regression method as suggested by Smith (1962) was 4.48 and the unbiased estimator of genetic trend after correction for these two sources was 4.36. Almost equal estimates indicated that these two sources of bias were not important enough to be considered for estimation of genetic trend in this data.
The genetic superiority through four paths from parent to offspring, sire to daughter, sire to son, dam to daughter and dam to son was estimated using the method suggested by Rendel and Robertson (1950). The heritability estimate of 0.24±0.12 from intra-sire regression of daughter production deviations on dam production deviations from herd average and repeatability estimate of 0.50±0.02 based on data adjusted by Sander's method were used.

The weighted average genetic superiority of sires of cows (weighted by the number of daughters in production) was 7.92 kg. It was equal to 0.49% of the herd average of 1611.26 kg. The generation interval from sire to daughter path was 87.77±1.04 months. The average genetic superiority of sires of bulls was 4.91 kg, which was very low and equal to 0.30% of the herd average. The generation interval from sire to son path was 87.14±6.06 months. The estimate was almost equal to that of sire to daughter path indicating little evidence of any delay in selecting young bulls while awaiting primary information on their paternal sisters' performance.

Genetic superiority of each dam was calculated as:

\[
\frac{nb^2}{14+(n-1)r} (\text{Dams' average} - \text{Herd average}), \text{where n was the number of lactations, } h^2 \text{ and } r \text{ were the estimates of heritability and repeatability respectively.}
\]

The herd average was composite of the production of all cows other than the dam herself in the year in which she had made her record. Only six lactations of the dam were used to calculate genetic superiority. All later lactation records were corrected to first lactation equivalent using Sander's conversion factors. The performance of the dam in different lactations and the number of lactations are needed for estimation of genetic superiority of dams of cows. Hence, the phenotypic superiority of cows in subsequent lactations was studied. The selection differentials over the lactations increased which was due to extensive culling in later lactations. Of the total buffaloes in first lactation, 85.08, 67.98, 56.51, 46.17 and 37.63% entered the second, third, fourth, fifth and sixth lactation respectively. It was apparent from these figures that more than 50% of the animals were culled by the time they reach the fifth lactation. The average milk yield based on unadjusted data in different lactations increased gradually upto fourth, indicating that lactational maturity in these animals was attained by fourth lactation. The average based on selected individuals showed an increase upto fifth lactation. The range of selection differential from 24.75 to 71.04 kg in first and fifth lactation would indicate that there had been a conscious practice of selecting females based on their individual performance at each lactation. In order to account for the effect of culling in terms of its contribution to genetic improvement, the number of daughters of the dam that entered the herd were taken as the weights to compute genetic superiority of dams of cows. Further, the number of lactations on which the dam's genetic superiority is based was also considered. The average genetic superiority of dams of cows was 80.45 kg which was equal to 4.99% of the herd average. The genetic gain through this path could be affected by factors like mastitis etc. which were not investigated in the present study. The expected genetic gain through dam to daughter path (80.45 kg) was higher than the estimates of
7.92 and 4.91 kg from sire to daughter and sire to son paths respectively. The higher genetic gain from dam to daughter path indicated that there was selection of dams of future heifers as a result of continuous culling of cows in successive lactations. The generation interval from dam to daughter path was 95.44±2.06 months.

In order to estimate the average genetic superiority of dams of bulls, the genetic superiority of each dam was weighted by the number of daughters her son sired. The number of daughters of the 13 sons in the herd were 320 with an average of 25 per son. The average genetic superiority of dams of bulls was 438.94 kg, which was equal to 27.24% of the herd average. The genetic contribution through this path was the highest. The average generation interval of dams of bulls was 131.8±12.33 months or approximately six lactations of dam. This generation interval was higher than that of sires of bulls (87.15±6.06 months). The longer generation interval from dam to son path indicated that selection of young bulls was primarily based on later records of the dam. It may be mentioned that hardly anything would be gained by increasing the number of dams' lactations beyond three for selecting the bulls in view of the moderate repeatability estimate of 0.50 for lactation milk yield.

The absolute values of genetic superiority through four paths; sire to daughter, sire to son, dam to daughter and dam to son were 7.92, 4.91, 80.45 and 438.94 kg which were equal to 1.49, 0.92, 15.12 and 82.47% of the total. The relative contributions from four paths in the present study are fairly in agreement with the theoretical values of 0, 0, 25 and 75% predicted by Rendel and Robertson (1950), under the assumptions that all the selection practised was in culling of cows and in selecting sires based on their dams' performance. The genetic contribution from dam to daughter path was much higher than sire to daughter path. In selection of bulls also, maximum emphasis on dam's performance was indicated by the highest genetic superiority through dam to son path (82.47%). Thus in selecting both cows and bulls, the emphasis was observed to be mostly on their dams' performance. This was expected in the absence of progeny testing. However, to maximise the rate of genetic gain, a combination of selection of outstanding bull mothers and progeny testing of bulls should be practised.

The annual genetic gain in 300 day first lactation milk yield was 15.88 kg, which was equal to 0.99% of the herd average of 1611.26 kg. The expected genetic gain was equal to the level (1%) theoretically predicted by Rendel and Robertson (1950). The expected genetic gain was higher than the realised genetic gain of 11.76 kg per year based on the data adjusted by least squares procedure. The realised genetic gain was based on first lactation records alone and hence it was not biased by lactation conversion factors. This was also free from the bias in the estimates of heritability and repeatability. As the first lactation records were adjusted for age at first calving, the realised genetic gain was also free from the influence of age at first calving. The expected genetic gain, however, would be influenced by the bias, if any, in the estimates of genetic parameters and lactation conversion factors. The lactation conversion factors might have little effect on the estimates of genetic superiority of selected parents since the records were corrected to the first lactation equivalent instead of mature equivalent. The heritability and repeatability estimates were computed from the data used.
for estimating the realised genetic gain. These estimates, therefore, must have been affected by the genetic and environmental trends and the limited size of data. This bias, therefore, in the estimates of heritability and repeatability might have affected the estimates of genetic gain. In spite of such limitations, the expected genetic gain of 15.88 kg per year indicated reasonably large genetic improvement in milk production in this herd.

**SUMMARY (1) (3)**

The genetic trends for first lactation milk yield in Murrah buffaloes were estimated using four methods: (i) \(2(b_P - b_H)T/S\), (ii) \(-2b(P-P_H)T/S\), (iii) \(-2b(P-P_H)T/S\) and (iv) least squares procedure. The estimate by third method was larger than the second method. The estimate of 11.76 kg by least squares procedure was equal to 0.73% of the herd average of 1611 kg. The bias due to two sources i.e. non-random distribution of mates with respect to production level and older females being mated to older males was not important. The estimates of genetic gain expected from direct selection through four paths sire to daughter, sire to son, dam to daughter and dam to son were 7.92, 4.91, 80.45 and 438.94 kg which were 1.49, 0.92, 15.12 and 82.47% of the total respectively. The annual expected genetic gain of 15.88 kg per year was higher than the realised gain of 11.76 kg.

**REFERENCES**


