Genetic Evaluation of Murrah Buffaloes for Reproductive Disorders

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ABSTRACT

The present investigation was carried out on 459 Murrah buffaloes affected with some reproductive problem with 618 calving records(out of total 1336 Murrah buffaloes) sired by 118 sires over a period of 12 years from 2007 to 2018 at GADVASU, Ludhiana. The heritability estimates for dystocia, retention of placenta (ROP), anestrus, repeat breeding (RB), abortion and postpartum abnormal discharge (PPAD) were 0.04, 0.10, 0.05, 0.074, 0.085 and 0.121 respectively. The overall means for breeding values for dystocia, ROP, abortion, anestrus, RB and PPAD were 0.4, 0.2, 0.4, 0.2, 0.078 and 11.8%, respectively. Rank correlation of abortion with ROP was very high (0.99±0.02) and with anestrus, dystocia, RB and PPAD were also high i.e. 0.98±0.03, 0.98±0.03, 0.97±0.03, 0.95±0.04 respectively. Heritability estimates of reproductive problems have indicated appreciable values, signifying that incorporation of these traits in selection program will enhance the rate of improvement.

Keywords: Murrah Buffalo, Threshold traits, reproductive disorders, Heritability, Breeding value

India is predominantly an agricultural country with 70% of the population depend upon agriculture and rearing of livestock. The vastness of an Indian dairying may also be attributed to the fact that India possesses the largest bovine population of 299.6 million which comprises of 190.9 million cattle and 108.7 million buffaloes (DADHF, 2012). The total livestock population has decreased by about 3.33% but livestock population has increased in Punjab by 9.57% (DADHF, 2012). The share of Gross Value Added of livestock sector to the Agriculture Sector (Crops, Forestry, Livestock and Fishing) has increased from 21.8% in 2011-12 to 25.8% in 2015-16 and livestock sector contributes 4.5% of total GVA (DADHF, 2017).

Buffaloes are known as Indian milking machine. The superiority of buffalo over local cow with regard to milk production is widely accepted in India. Indians have preference for buffalo over cattle because of their distinctive qualiyies such as better feed conversion efficiency, more resistance to diseases and higher milk fat percentage and it is for this reason that the population of buffaloes is increasing day by day (Singh, 2015). However, there appears to be an international resistance by the dairy exporting countries to create a worldwide prebiased attitude against the products manufactured from buffalo milk. Therefore it is high time for India to stalwartly rebut this false notion against buffalo milk and highlight its positive attributes at the international forum. Inspite of buffaloes significant role as a milk producer, it did not find its desired place in scientific literature, especially w.r.t. health and survivability information coupled with specific reference to the role of inheritance. The accredited advantages of the buffalo are fully appreciated only by the persons who keep buffaloes for their livelihood.

Buffaloes contribute about fifty percent of the total milk production of our country though contributing to only

one-third of the total bovine population (DADHF, 2012). India is fortunate enough to have the world's best breeds of buffaloes. Special attention has to be made to Murrah breed of buffaloes,which is one of the best breed of buffaloes and can be considered as black diamond or Holstein-Friesian of the buffalo world (Singh, 2015) and it contributes 44.39% of total buffalo population (DADHF, 2017). Avoidably of superior germplasm of Murrah buffaloes in India gives us an opportunity to help other buffalo breeding countries in breed improvement programmes by shipping frozen semen to their destination. Therefore, all the countries of the world look forward to India for improvement of their native poor quality buffalo breeds. Hence, there is a dire need that we should exploit our high quality Murrah buffaloes for further improvement of their performance. Inspite of its unique ability to make ends meet under harsh condition, the buffaloes have been neglected by breeders and research scientists. Buffaloes are reputed as an efficient converter of low grade, fibrous feeds into high value milk, containing 7 percent fat, which is almost twice as that of cow milk (Taraphder, 2002). To make dairying a successful and profitable business, buffaloes should not only be the high producer but also be healthy, disease free and regular breeder. A low incidence of disease, mortality, and regular breeding may help to increase the selection differential thereby genetic improvement.

Losses due to diseases i.e. losses due to mortality, reduced production, cost of treatment and reduced consumers preference have a remarkable impact on the dairy industry. Culling of buffaloes because of reproductive problems accounts for a great loss of milk production as well as offspring (Taraphder, 2002). Reproductive disorders and lower fertility condenses the income to dairy farmer by decreasing milk yield and reproduction. Further high veterinary expenses in addition to reduction in longevity of buffaloes also create burden.

Among the reproductive disorders, repeat breeding (RB), anestrus, retention of fetal membranes, and abortion are the most important livestock maladies affecting a variety of livestock species including cattle and buffaloes. The reproductive disorders affect the dairy industry with profound economic loss and trade impact in India (Khan *et al.*, 2011). Whenever possible, the diseases of livestock should be avoided by use of prophylactic measures like immunization, sanitation, management and removal of stresses. Those diseases which are not responsive to preventive measures and are inherited could be controlled through the development of genetically resistant animals. Studies on disease resistance have been mainly conducted in the field of plant breeding and consequently genetically resistant varieties to various plant pathogens have been evolved (Taraphder, 2002). The information on the incidence and inheritance of diseases and mortality in dairy cattle of advanced countries is well documented, but such estimates are scanty for Indian breeds of cattle and especially buffaloes.

Majority of the animals would respond to genetic selection for resistance to disease because the genetic merit of the population for a certain trait can be changed through selection and breeding programme. Such process requires the estimation of genetic variability present for a trait. There is an evidence that the life span is determined by heredity and there also exists genetic variability for resistance to diseases (Hut, 1958). It provides a means for improving the response to selection which can be utilized for disease resistance and longer life span.

The information on the incidence and inheritance of reproductive disorders in buffaloes are scanty and probably no information is available. Meager reports are available regarding the economic aspects (expenditure or cost involved in treatment) as well as the estimates of breeding value for reproductive disorders and construction of selection indices incorporating the important reproductive disorders.

Therefore, there is a dire need to find out the role of inheritance of reproductive disorders in genetic improvement programme of Murrah buffaloes. Keeping in view the above aspects, the present study was envisaged to investigate the inheritance of reproductive disorders in the Murrah buffalo herd maintained at dairy farm, Guru Angad Dev Veterinary and Animal Sciences (GADVASU), Ludhiana.

MATERIALS AND METHODS

Location

The present study was carried out on Murrah buffalo herd maintained at the dairy farm of the Directorate of Livestock Farms (DLF), GADVASU, Ludhiana.

Source of data

The data pertaining to the reproductive problems of Murrah buffaloes were collected from the records and history sheets maintained at DLF, GADVASU, Ludhiana.

Management and feeding of herd

The animals were kept in loose housing system with one third shaded area at the dairy farm. Ad-libitum feeding and free access to water was practiced. The animals were housed separately on the basis of their age and production levels.

The weaning of calves was done immediately after birth and then they were fed on colostrum for first five days and then whole milk from sixth day to sixteen weeks of age.

All the female animals were bred through artificial insemination. Animals in advance stage of pregnancy were segregated to calving pens at least six weeks before the expected date of calving. Body weights were recorded by weighing the animals monthly in the morning before feeding and newly born were weighed before colostrums feeding.

The maintenance and growth ration were fed to the animals in the morning hours once a day and feeding total mixed ration (TMR) was practiced post 2012. While production ration was given to the milking buffaloes at the time of milking. Concentrate ration (CP= 18% and TDN= 70%) were formulated using cereals, cakes, brans, mineral mixture, salt and additives depending upon season and physiological status (age, production, stage of pregnancy etc.) of animal.

Information of Murrah buffaloes

General information e.g. animal number, dam number, sire number, date of successful service, total number of artificial insemination done, date of calving (upto 6th calving), types of calving in each lactation (upto 6th calving) and parity number (upto 6th parity) was collected for the identification and classification of Murrah buffaloes.

Information regarding reproductive disorders

The information pertaining to reproductive disorders since January 2007 to December 2018, recorded on the Murrah buffaloes of the herd maintained at GADVASU was compiled. The various reproductive disorders to be incorporated in the current study were divided into two main categories i.e. periparturient complications which included dystocia, still birth (SB),premature birth and retention of placenta (ROP) and successively other reproductive problems such as anestrus, repeat breeding (RB), prolapse, postpartum abnormal discharge (PPAD) and abortion.

Data structure

The data on reproductive disorders were collected from the records maintained at dairy farm GADVASU, Ludhiana. Data comprised of records on calving, reproductive performance and reproductive disorders. The study included 618 calving records of 459 Murrah buffaloes (affected with any of the reproductive disorders mentioned above), from total of 1336 Murrah buffaloes.

The records of Murrah buffalo with known pedigree were used for analysis of reproductive disorders. Animals with improper records were not included in the study.

Classification of non-genetic factors

Non-genetic factors viz. Parity, Period and Season of calving were classified into subclasses to assess the effect of non-genetic factors on different reproductive traits.

Parity

Parities were taken into consideration upto recent lactation recorded in the available reproduction sheets of the herd. The data were classified for different parities upto sixth parity and each parity was coded starting from code "1" to code "6" upto sixth parity.

Period of calving

The data on reproductive disorders from a span of 12 years were classified into 4 periods with each period covering 3 years of duration (Table 1).

Season of calving

The months of an year were grouped into 4 seasons on the basis of prevailing climatic conditions of Punjab.

December to February, had been classified as Winter season, followed by March to May as Summer season. The Rainy season had be regarded as from months June to August whereas the following months from September to November were classified as Autumn season.

STATISTICAL ANALYSIS

For statistical analysis of the data, Statistical analysis system software programme (SAS, 2011) version 9.3 was used. The means, standard deviations, standard error were estimated by using standard statistical procedures.

Estimation of heritability

Robertson and Lerner (1949) estimated the heritability as the ratio of selection response to selection differential which is regression of genotype on phenotype. The genotypic values for viability of the members in terms of the probabilities of survival of the corresponding genotype under the given array of environmental conditions are taken as P1, P2.......Pn with mean p and the variance σ^2_P. The expectation for the gain is σ^2_P/P. The phenotypic selection differential is 1-p which is the difference between the phenotype of survivors (taken as unity) and the mean phenotype of the population. Therefore heritability is taken as:

$$h^2 = \frac{\text{Genetic gain}}{\text{Selection differential}} = \frac{\sigma^2_A}{\overline{P}\left(1-\overline{P}\right)}$$

Where,

σ^2_P is the genetic variance and estimated as:

$$\sigma^2_A = \frac{\left[\Sigma \frac{a_i^2}{n_i} - \frac{\left(\Sigma a_i\right)^2}{\Sigma n_i}\right] - \left(N-1\right)\overline{p}\left(1-\overline{p}\right)}{rn_0}$$

$$\sum_{i=1}^{N} \frac{a_i^2}{n_i} - \frac{\left(\Sigma a_i\right)^2}{\Sigma n_i} = \text{Sum of squares between classes}$$

With N-1 Degree of freedom

The expected value of this sum of squares is

$$\left(N-1\right)\left(\overline{P}\right)\left(1-\overline{P}\right) + rn_0\sigma\frac{2}{p}$$

Where,

r = difference in genetic relationship between and within classes or the genetic relationship between the members of a sire family.

r = ½ for full sibs and ¼ for half sibs

$$n_0 = \Sigma n_i - \frac{\Sigma n_i^2}{\Sigma n_i} - \left(N-1\right) = \left(K-1\right)\left(S-1\right)$$

Where,

$$K = \frac{1}{S-1}\left[\Sigma n_i - \frac{\Sigma n_i^2}{\Sigma n_i}\right]$$

S = No. of sires

$\overline{P}(1-\overline{P})$ = total variance which is the normal expression for the variance of a binomial population

The heritability equals,

$$h^2 = \frac{\sigma^2_A}{\overline{p}\left(1-\overline{p}\right)} = \left[\frac{\Sigma \frac{a_i^2}{n_i} - \frac{\left(\Sigma a_i\right)^2}{\Sigma n_i}}{\overline{p}\left(1-\overline{p}\right)} - \left(N-1\right)\right]/$$

$$rn_0 = \frac{\chi^2 - \left(N-1\right)}{rn_0}$$

a_1 and n_1 = number of surviving and total progeny of ith sire

N = Number of sires

n = number of progeny per sire.

The heterogeneity χ can be estimated from SX2 contingency table for the data on survival according to sire groups giving the number of survivors and non-survivors for each of S sires.

The analysis of variance can be applied to determine the genetic variance of binominal data. The phenotypic value can be denoted by the model as:

$$X_{tj} = U + S_i + e_{tj}$$

Where,

X_{tj} is the phenotypic value of the progeny of ith sire which is a random variable and takes the value 1if jth progeny survive and takes the value zero if it dies.

u is the general mean representing overall survival and is taken as fixed effect

S_i is the effect of ith sire and treated as a random effect with mean zero and variance as σ^2_s

e_{tj} is the random error component for survival of jth progeny of ith sire. It is a binomial variate with parameter p which means that e_{tj} takes value 1 with probability p and takes value with probability $(1-p)$.

Then,

$$E(e_{tj}) = 1xp + ox\ (1{-}p) = p$$

$$V(e_{tj}) = E(e_{tj} - p)\ 2$$

$$= p{-}p^2 = p(1{-}p)$$

The s_1's are independent. The e_{tj}'s are also independent amongst themselves.

The sire-wise data on progeny for survivability takes the form as given in Table 1

Table 1: Sire-progeny Groups

Sire No.	No. of Progenies	
	Affected (n)	Non- affected(a)
1	n1	a1
2	n2	..
..	..	..
S	Ns	As
Total	Σn_i	Σn_i

With as estimate of the phenotypic value of the overall survival ($\overline{P}$) as :

$$\overline{p} = \frac{\sum\limits_{i=j}^{s} a_i}{\Sigma n_i}$$

The phenotypic variance can be divided by ANOVA into observational components attributable to differences between the progeny of different sires (σ^2_s) and to the same sire (between dams within sire component, (σ^2_s). The sum of the two is an estimate of the phenotypic variance of the observational components as $(\sigma^2_s) + (\sigma^2_e)$.

The standard error of h^2 is (σ/r)

$$s_t = \frac{1+\big[(n-1)t\big](1-t)\sqrt{2}}{\sqrt{n(n-1)(n-2)}}$$

Where t is the phenotypic correlation between the members of the sire family and equal rh^2.

Estimation of expected breeding value

The sires were evaluated by following sire index method on the basis of first lactation performance of daughters for reproductive disorder traits.

The sire index value will be computed as,

$$I = A + \frac{2nh^2}{\big[4+(n-1)h^2\big]}(S_i)$$

Where,

   I = Sire index

   A = Population mean

   n = Number of daughters of the sire.

   h^2 = Heritability of trait

   S_i = Sire constant for ith sire

The percent superiority of the sire indices over the herd average will be calculated for each sire using the following formula:

Percent superiority over herd average = $\dfrac{I - A}{A} \times 100$

Where,

   I = Sire index value

   A = Herd average

The sires were ranked by sire indexing procedure for reproductive disorder traits. The correlations between the ranking of sires based on various traits will be calculated

by Pearson and Spearman's rank correlation coefficient (Steel and Torrie, 1960).

RESULTS AND DISCUSSION

Heritability

Heritability of a trait gives an idea of the amount of additive genetic variance present in a particular trait. The amount of genetic variance determines the breeding and selection procedure for future genetic improvement. Heritability was estimated for six parities collectively. Binary and continuous estimates of heritability for various reproductive disorders has been presented in Table 2.

Table 2: Heritability estimate for reproductive disorders

Traits	Heritability (Continous)	Standard Error
Dystocia	0.04	0.020
ROP	0.10	0.003
Anestrus	0.05	0.001
RB	0.074	0.010
PPAD	0.121	0.020
Abortion	0.085	0.010

The heritability estimates for dystocia, retention of placenta, anestrus, repeat breeding and abortion were found to be highly appreciable i.e. 0.04, 0.10, 0.05, 0.074 and 0.85 respectively. So while the heritability estimates for postpartum abnormal discharge has been 0.121 i.e. with 12% additive gene action. The estimates obtained for reproductive disorders were lower than reports of Tomar (1984) and Taraphder (2002) in Murrah buffaloes. Low heritability estimates were found in case of dystocia (0.05), abortion (0.11), still-birth (0.07) premature birth (0.06) and retained placenta 0.15 while medium value of heritability was observed for prolapse and metritis (0.25 and 0.23) by Taraphder (2002) in Murrah buffaloes. Higher heritability has been reported for various reproductive disorders in Karan swiss cows by Balasundaram (2008).

Therefore very low heritabilities indicate that the above reproductive disorders occurring in a small population of an organized farm are mainly governed by non- genetic factors. It means the incidence of above reproductive disorders can be reduced through better management.

Breeding values of sires for reproductive disorders

Breeding values of sires were estimated for reproductive disorder traits. The results have been shown in Table 3. The rank correlations among various reproductive disorders traits have been given in Table 4.

Table 3: Distribution of sires in different classes of breeding values for reproductive disorders

Reproductive problem	Breeding Value Average (%)	Sires below herd average Number	Sires below herd average %
Dystocia	0.4	10	8
Retention of placenta	0.2	97	82
Abortion	0.4	79	67
Anestrus	0.2	48	40
Repeat breeding	7.8	68	58
Postpartum abnormal discharge	11.8	68	58

Table 4: Rank correlation estimates for reproductive disorders

	Abortion	Anestrus	Dystocia	Retention of Placenta	Repeat Breeding	Postpartum Abnormal Discharge
Abortion	1	0.98 ± 0.03	0.98 ± 0.03	0.99 ± 0.02	0.97 ± 0.03	0.95 ± 0.04
Anoestrus		1	0.99 ± 0.02	0.97 ± 0.03	0.98 ± 0.02	0.97 ± 0.03
Dystocia			1	0.96 ± 0.03	0.98 ± 0.02	0.95 ± 0.04
Retention of Placenta				1	0.96 ± 0.03	0.94 ± 0.04
Repeat Breeding					1	0.96 ± 0.03
Postpartum Abnormal Discharge						1

Breeding values of sires for reproductive traits

The overall mean for breeding value for dystocia was 0.4% (Table 3). The research findings showed that 8 % sires used in the herdfrom 2007 to 2018 had breeding values lower than the overall average of the herd. The results suggested that there is enough scope for improvement of dystocia. This suggested that selection of superior sires should be practiced to further reduce incidence of dystocia. Sharma (2010) reported that 71.43% primiparous and 81.06% pluriparous cows have breeding value below the herd average.

The overall means for breeding values for retention of placenta and abortion were 0.2 and 0.4%, respectively (Table 3). Overall results indicated that 82 and 67 percent sires used in the herd had breeding values less than the herd average which was in desirable direction for these traits. The overall means for breeding values based on anestrus, RB and PPAD were 0.2, 7.8 and 11.8%, respectively. About 40, 58 and 58% sires had breeding values lower than the overall average of the herd for incidence of anestrus, RB and PPAD. About 48 sires had breeding values lower than 0.2%, whereas another 70 had breeding values higher than 0.2% for anestrus. About 40, 58 and 58% sires had the breeding values lower than 0.2, 7.8 and 11.8 while 60, 42 and 42 sires had the breeding values higher than 0.2, 7.8 and 11.8% for RB and PPAD. Sharma (2010) reported that 57.90 and 56.58% of sires have breeding values lower than herd averages for stillbirth and abortion in pluriparous cows; for anestrus about 66.66 and 50% sires showed low breeding value than the herd average in primiparous and pluriparous cows.

Rank correlation

The present study had also carried out to examine if one reproductive problem had any association with other reproductive problem. Genetic correlation among reproductive disorders were high and significant. Rank correlation among different reproductive disorders have been given in Table 4.

Rank correlation of abortion with other reproductive disorders was significantly high. Rank correlation of abortion with ROP was very high (0.99±0.02) and with anestrus, dystocia, RB and PPAD were also high i.e. 0.98±0.03, 0.98±0.03, 0.97±0.03, 0.95±0.04 respectively. It means ranking of sires for those reproductive disorders

were not different from those of abortion. In other words, sires evaluated for abortion on the basis of their progeny performance would give similar rankings as if sires had been assessed for more incidence of anestrus, dystocia, RB and PPAD condition in their daughters. Positive, moderate and significant correlation of abnormal calving (dystocia, abortion, PB and SB) with prolapse, ROP and metritis (0.532, 0.423 and 0.373 respectively) was reported by Taraphder (2002) in Murrah buffaloes.

From rank correlation analysis it was analysed that correlation of anestrus with RB, ROP and PPAD were significantly high i.e. 0.98±0.02, 0.97±0.03 and 0.97±0.03 respectively. But rank correlation between anstrus and dystocia was very high (0.99±0.02). However, for anestrus the rank correlations was significant and high magnitude thereby indicating that ranking of sires for anestrus was dependent of ranking of sires for other reproductive disorders like RB, ROP and PPAD. Taraphder (2002) found that in Murrah buffalo rank correlation of anestrus with abnormal calving, uterovaginal and udder problems were low and non-significant.

Rank correlation was significant for dystocia with ROP, RB and PPAD. Correlation between dystocia, ROP, RB and PPAD were 0.96±0.03, 0.98±0.02 and 0.95±0.04 respectively. This indicated that the selection of sire for reduced incidence of dystocia will make improvement for ROP, RB and PPAD also. Taraphder (2002) reported that rank correlation of abnormal calving (dystocia, abortion, premature birth and stillbirth) with retention of placenta was positive, moderate (0.423) and significant in Murrah buffaloes.

Significant effect of retention of placenta with RB and PPAD for rank correlation has been found. Rank correlation between ROP with RB and PPAD were 0.96±0.03 and 0.94±0.04 respectively. It means the improvement in these traits can bring improvement in ROP. The results indicated that the sires ranking lower were those which also had higher incidence of these reproductive disorders in their progeny. Low (0.270) and non-significant correlation of anestrus with retention of placenta was reported by Taraphder (2002) in Murrah buffaloes.

Rank correlation between RB and PPAD was significant and of high magnitude (0.96±0.03). This indicated that progeny of sires had more chances of repeat breeding also had more chances of postpartum abnormal discharge.

If there is any association between two disorders (rank correlation for two reproductive problems is high) then it means, the sire containing the gene for first reproductive disorder, also contain the gene for other correlated problem. Due to which in daughters of that sire if one reproductive problem is high then the chances of other correlated problem will be high.

CONCLUSION

Heritability estimates of reproductive problems have indicated appreciable values, signifying that incorporation of these traits in selection program will enhance the rate of improvement.

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