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Study on Population Dynamics and Effects of Inbreeding on Performance Traits in Indian Murrah Buffalo

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ABSTRACT

Background: A population is continuously facing the changing environment and its directly influencing the production of animal so to adopt these changes population must be flexible and have sufficient variability to overcome the adverse affects of environment. The evaluation of animals in terms of production performance traits along with impact of inbreeding coefficient is essential to formulate breeding and selection strategies for higher genetic improvement.

Methods: Genealogy data of 6429 animals maintained at ICAR-NDRI, Karnal, India was analyzed by web-based POPREP application tool (http:// poprep.tzv.fal.de) and ENDOG V5.8 used to study the population structure and genetic diversity and regression model to study the effect of inbreeding on first lactation productive traits in Murrah buffaloes.

Result: The result indicated that 91.91% of the individuals had known pedigree. The maximum generation traced was 13 with mean, full and equivalent complete generation as 5.93, 1.67 and 3.25 respectively. The average generation interval was 8.28 years and longer for the sire-son pathway and 2.16% was average inbreeding in whole population. The average genetic diversity loss was 2.10% indicated that the population has been stable with sufficient diversity. The study also revealed non significant effect of inbreeding on all first lactation traits. The low inbreeding was firstly due to introduction of new genetic variant and culling of animals avoiding mating of related ones and secondly due to incompleteness of pedigree in earlier years. This can be used as a base line information of phenomic needs to be generated before applying genomics tools in particular herd to be used as reference population in future for genomic selection.

Key word: Genetic diversity, Inbreeding, Murrah, Population dynamic.

INTRODUCTION

Consistently observing of population structure and genetic diversity help the development of selection programme and support in development of the mating strategies to maintain the sustainable genetic improvement in next generations (Malhado *et al*., 2008). Murrah buffalo maintained at ICAR-NDRI, Karnal, India since more than 6 decades however, till date no investigation has been led to know its demography pattern, population dynamics variation since initiation of the herd dependent on descendant's statistics. These breed assumes a crucial part to support up the financial state of the nation by creating kind of revenue for pastoral people by giving work security particularly to the underneath neediness line ranchers and creating woman strengthening accordingly, any undertaking that would bring about manageable creation and lead to future hereditary increase would have expansive deduction on the vocations of the vital wards. As a result of inbreeding, there is an increment in recurrence of desirable/undesirable alleles in the population, consequently resulting into decrease in the economic important trait performance and mean phenotypic value of animals (Weigel, 2001). Notwithstanding, it is additionally to remember that inbreeding assuming not influencing the exhibition qualities, likewise checking is required with careful arranging so as not to pass the threshold level. The objectives of this study were to demonstrate the population structure, monitor the demographic pattern and genetic diversity and possessions of inbreeding on performance traits in the Murrah buffalo.

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MATERIALS AND METHODS

Population structure

The pedigree data consists of 65 years (1954-2018) of Murrah buffalo was collected from stock register maintained at record room of Animal Genetics and Breeding Division. A web-based POPREP application tool (http:// poprep. tzv.fal.de) was used to analyze the family size and to ENDOG V5.8 used to characterize the population structure

Family sizes was refers to the number of offspring of an individual that become breeding individuals in the next generation (Groeneveld *et al*. 2009) were calculated. In adding up, the number of offspring produced by sires and dams and the number of particular offspring (those used as breeding animals in future generation) per sire and dam also calculated.

Pedigree completeness index (PCI) was computed according to MacCleur *et al.* (1983) for each individual:

$$\mathrm{I}_d = \frac{4\, I_{dpat}\, I_{dmat}}{I_{dpat} + I_{dmat}}$$

$$I_{dk} = \left[\frac{1}{\mathrm{d}}\right] \sum_{i=1}^{d} a_i$$

Where,

k = maternal or paternal line; a_i = known ancestors proportion in i^{th} generation and d= generation considered for pedigree completeness.

Inbreeding coefficient (F_x) was calculated using the formula as modified by Gonzalez-Recio *et al*. (2007); Gutierrez *et al.* (2008) and Gutiérrez *et al.* (2009) as follow:

$$\Delta F_i = 1 - \sqrt[ti-1]{1 - F_i}$$

Where,

F_i is the inbreeding coefficient for the individual i and t_i is the equivalent complete generations for this individual.

Effective population size was calculated by two methods first based on individual inbreeding rate (N_eF_i) (Gutiérrez *et al.,* 2008) using following formula:

$$N_eF_i = \frac{1}{2\,\Delta F}$$

and second based on the effective population size (N_eC_i) from increase in coancestry (ΔC_{ij}) for all pairs of individuals i and j was estimated according to Cervantes *et al*. (2011) as follow:

$$\Delta C_{ij} = \sqrt[(ti-tj)/2]{1 - C_{ij}}$$

Where

C_{ij} was the coancestry coefficient between the individuals ij and t_it_j are their equivalent complete generations.

Generation interval (GI) was calculated by four different pathways; sire-son (SS), sire-daughter (SD), dam-son (DS) and dam-daughter (DD).

The probability of gene origin parameter

The genetic history of population in terms of probability of gene origin was assessed by calculating the number of founder, effective number of founders (f_e), number of ancestors, effective number of ancestors (f_a) and founder genome equivalent (f_{ge}) to evaluate the consequences of selection in the population studied.

Animals with unknown parent considered as a founder. The number of evenly contributing founders that would be likely to generate the equivalent genetic diversity as in the population is f_e computed by Lacy (1989) as follows:

$$f_e = \frac{1}{\sum_{k=1}^{f} q_k^2}$$

Where

q_k is the expected comparative genetic contribution of founder k, considered by the average association of the founder to animal in the population and f is the entirety number of founders.

Founder genome equivalents (f_{ge}) was calculated the formula Caballero and Toro (2000) as follow:

$$f_{ge} = \frac{1}{2\, f_g}$$

Where

f_g is the average coancestry of the individuals included in the reference population.

Loss of diversity in the population accounting due to genetic drift and imbalanced founder involvement using the formula Lacy, 1995 as follow:

$$GD = 1 - \frac{1}{2\, f_{ge}}$$

Effect of inbreeding on first lactation production traits

The first lactation production data of 49 years (1970-2018) and 24 years for milk composition traits (1986-2018) of Murrah buffaloes was used. The following traits were studied first lactation 305 days milk yield (FLMY), first lactation 305 days fat yield (FLFY), first lactation 305 days solid not fat yield (FLSNFY), first lactation total milk yield (FLTMY), first lactation length (FLL) and first lactation dry period (FDP). The data were classified into five inbreeding groups including non inbred are presented in Table 1.

The following regression model was used to study the effect of inbreeding on first lactation productive traits as follows:

$$Y_{ij} = a + bX_i + e_{ij}$$

Where

Y_{ij} is production trait of j^{th} animal with intercept as 'a' and regression coefficient as 'b' having i^{th} inbreeding coefficient value as 'x$_i$' and random error as e_{ij} (NID 0, σ^2).

RESULTS AND DISCUSSION

Breeding animals

Fig 1 shows the yearly number of males and females used for breeding. The number of females increased progressively until 1974 and utmost of 95 dams were recorded however, a declining trend was observed afterwards. An average of 389 bulls and 2147 females was used for mating per year from 1959 to 2016. In our herd the number of Murrah buffalo

Table 1: Classification of inbreeding group.

Inbreeding group (%)	Code Given
0	1
>0 - <1.25	2
>1.25 - <5	3
>5 - <10	4
>10	5

bulls and cows used for breeding according to the FAO (FAO, 2000) above the critical level.

Family sizes

Fig 2 and 3 indicating the number of progeny per dam and sire respectively of the Murrah buffalo. The average number of progeny per dam was three with a series of 1 to 10 calves per cow. There was a wide difference in the number of progeny per sire indicating to the utilization of superior sire in the herd (Fig 3). In our herd family sizes are indicative of population structure and reflect breeding plan due to selection of the genetically superior sire utilized more indicates uneven contribution of breedable sire to subsequent generations.

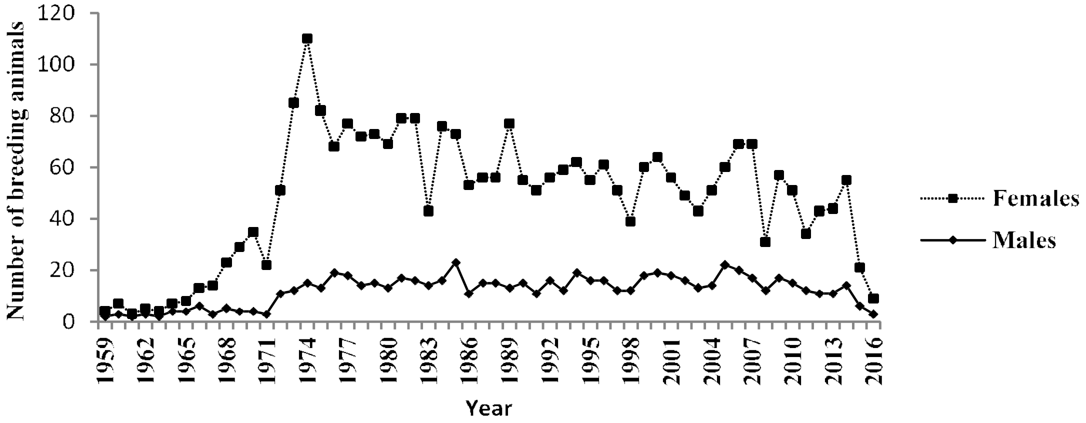

Fig 1: Number of males and females used for breeding annually Murrah buffalo.

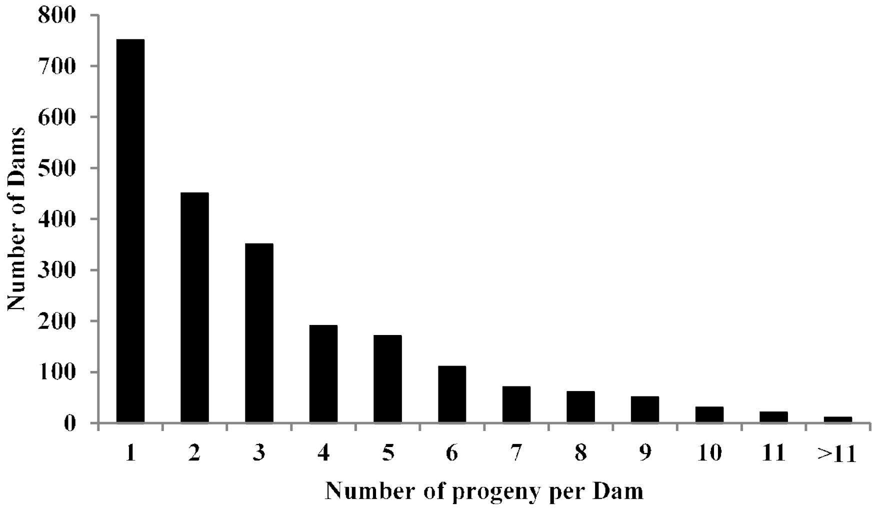

Fig 2: Number of progeny per dam of the registered the Murrah buffalo.

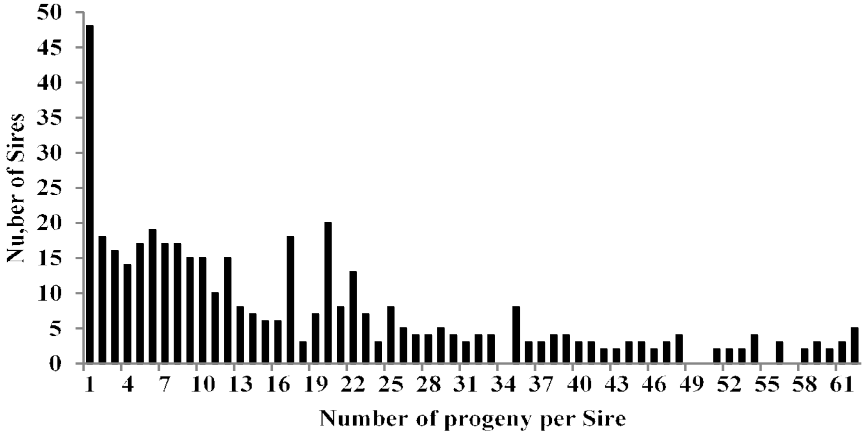

Fig 3: Number of progeny per sire of the registered the Murrah buffalo.

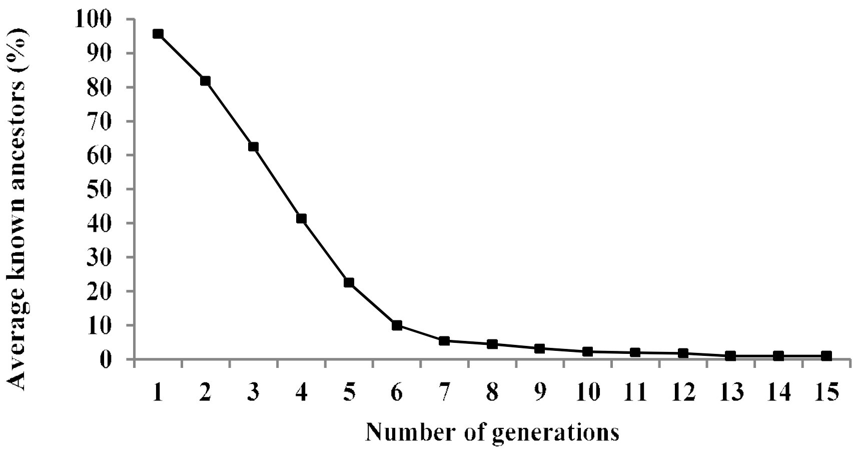

Fig 4: Average known ancestors (%) per generations in Murrah buffalo.

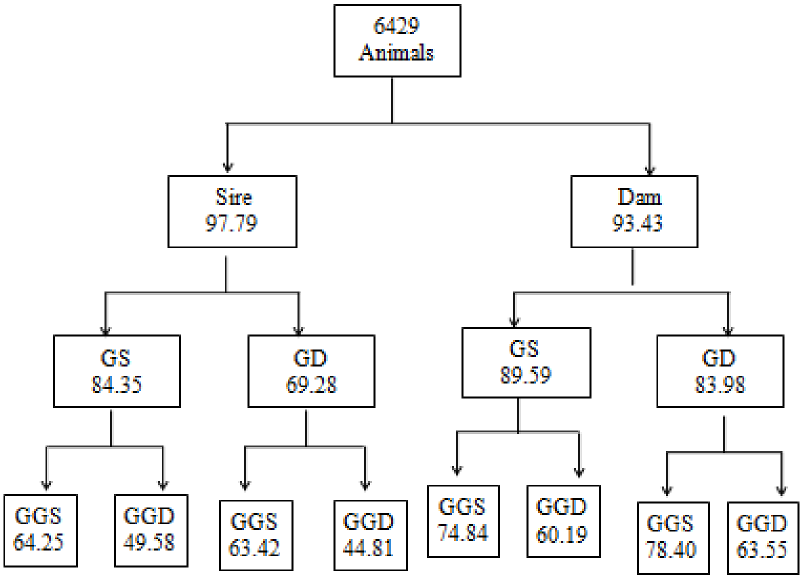

Fig 5: Overview of Pedigree Complete Index (%) in Murrah buffalo.

Table 2: Description of pedigree since inception in Murrah buffalo.

Parameter	Murrah
Data	1954-2018
Number of animals	6429
Male Female	29333496
Individuals had known parent (%)	91.91
Pedigree completeness index (%)	
1st Generation	95.60
2nd Generation	81.80
3rd Generation	62.38
4th Generation	41.33
5th Generation	23.02
Mean maximum generations	5.93
Mean complete generations	1.67
Mean equivalent generations	3.25

Pedigree completeness index

The average known ancestors (%) per generation increased over year (Fig 4) up to sixth generations more than 7% ancestors were known but after the eighth generations extremely less individuals had identified ancestors, creating the complexity in recognizing the pedigrees further than. The maximum generations traced was 13 and mean maximum, complete and equivalent generations were 5.93, 1.67 and 3.25 (Table 2) respectively.

The low estimate of PCI in the earlier generation was due to the fact that in the beginning of herd establishment complete pedigree information was not available for many animal, Any individuals with either of its parent unknown was taken as founder. In Murrah it was lower (93.43%) in dam pathway compared to sire pathway (97.79%) when considering recent generation (Fig 5) might be due to purchase of more female animals as compared to male ones in earlier generation. The pattern of pedigree completeness is similar to earlier reported by Muasya *et al.* (2011) in Sahiwal; Muasya *et al*. (2013) in HF breed and lower estimates was reported by Santana Jr *et al*. (2011) in berzilian Murrah; Ferraz *et al.* (2015) in Jaffarabadi buffaloes and Malhado *et al*. (2012) in Murrah buffaloes in comparison to present findings.

Inbreeding coefficient (F_x) and Average relatedness coefficient (AR)

The average F_x for the whole analyzed pedigree and inbred population was 2.16% and 3.36% and AR was 4.41% (Table 3) indicated that mating among closely related individuals was avoided. A total of 187 (2.91%) matings between half sibs and 21(0.33%) pairings between parent-offspring were identified throughout the study period. Out of 6429 individuals, 4417 were inbred (Table 4) with inbreeding range from 0.1 to 32.23% and only 5.55% had more than 10 per cent inbreeding. The observed F_x is in accordance with the earlier reports of Santana Jr *et al.* (2011) in Berzalian buffalo (2.14%), however, lower values of F_x have been reported by Marcondes *et al*. (2010) (0.50%) in water buffalo.

Table 3: Percentage of inbred within different inbreeding levels.

Inbreeding	Value
Average inbreeding (%)	2.16
Inbred individual (%)	68.70
Non inbred individual (%)	31.30
Maximum inbreeding coefficient (%)	32.22
Increase of inbreeding per generation	
Mean Maximum Generations	0.30
Mean Complete Generations	1.09
Mean Equivalent Generations	0.56
Mean Average Relatedness	4.41

Table 4: Inbred levels showing number of animals and inter and intra classes.

Inbreeding level	N	Inter class (%)	Intra inbred classes (%)
0	2012	31.31	-
0>F≤1.0	1084	16.86	24.54
1.0>F≤2.0	1119	17.41	25.34
2.0>F≤3.0	607	9.44	13.75
3.0>F≤4.0	605	9.41	13.70
4.0>F≤5.0	257	4.00	5.82
5.0>F≤10.0	499	7.76	11.30
F>10.0	245	3.81	5.55

N = the total number of individuals.

The observed trend indicates that, the F_x and AR consistently increased upto 1992 and then slowly start decreasing continuously upto recent years (Fig 6). From 1965 to 1988, the average F_x was 2.17%, which start rising to 2.77% from 1989 to 1998 and then showing decreasing trend 2.66% to 1.42% from 2008 to 2018. Inbreeding in the present study was however, not very high for significant number of animals, Scientific planning and execution of mating plan make it possible to avoid mating of animals within same sire line might have helped to keep the inbreeding levels under control.

Additive genetic relationships (AGR)

Fig 7 shows the relationship between inbreeding and AGR per year of birth of animals. The whole population AGR was 0.3% and the rate of change of the AGR (Δf) between 1954 and 2018 was 0.01% per year resulting in a Δf per generation was 0.2%. The two parameters showed a continuous decrease over time, but AGR remained higher than the inbreeding coefficient before the year 1963, indicating between herd mating to utilised more potential animal to increase the production as opposite to observed in Kenya Sahiwal cattle (Kamiti *et al*., 2016). After 1968, AGR decreased and remained constant and almost similar than inbreeding coefficient that led to minimal use of related individuals within the breed and maintained the diversity in herd.

Effective population size (N_e)

In present study, the ratio between N_eC_i/N_eF_i was 0.88 (Table 5), which are similar to the ratio (0.96) observed by

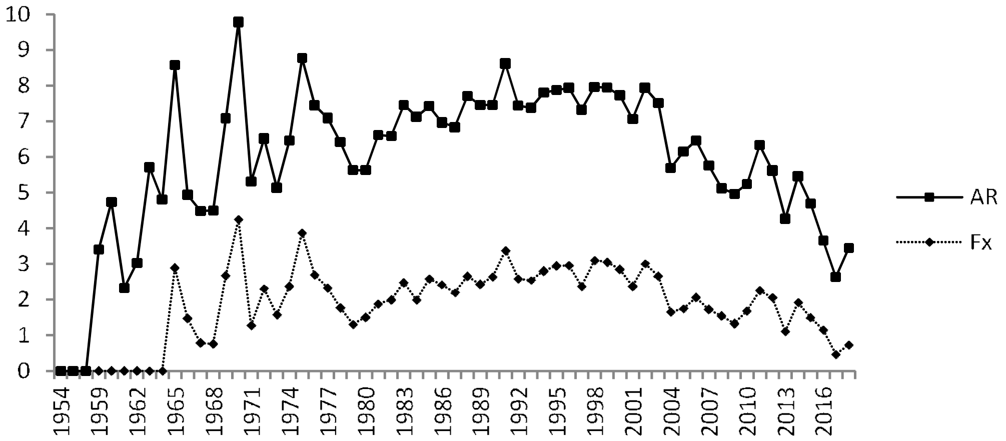

Fig 6: Inbreeding and average relatedness coefficient in Murrah buffalo.

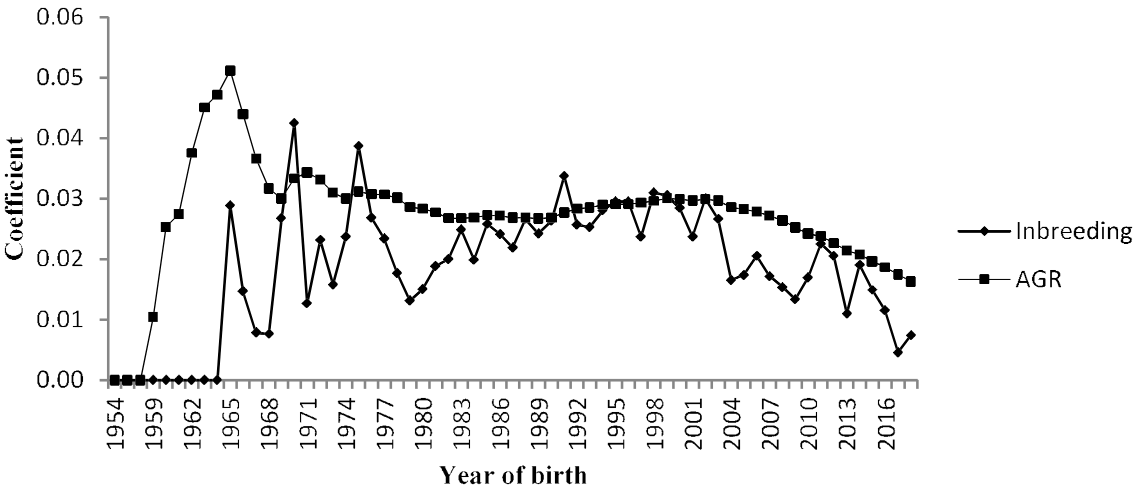

Fig 7: Average inbreeding coefficient and additive genetic relationship of the Murrah buffalo.

Santanta *et al.* (2016) in brazilian Zebu cattle.

In contrast to present study, Santana Jr *et al.* (2011) reported small N_e (40) in various herd of Murrah buffaloes then the present findings. Malhado *et al.* (2013) reported 10.40±3.69 in Jaffarabadi buffaloes, which are very low in comparison to present study. To maintain the genetic diversity and to avoid genetic drift in herd minimum 500 animals required (Frankham, 1995). It is important to note that although the current estimated N_e reported within the limits and higher in as recommended by FAO (2007), however estimates of N_e are not constant and do change with time according to change in inbreeding level of the population.

Generation interval (GI)

The sire-progeny average GI (Table 6) was longer than the dam-progeny. The longest average GI was observed might be due to longer age of first calving in Murrah. The shortest GI were observed for dam-offspring pathways due to replacement of older ones with young female buffaloes. GI reported by Ferraz *et al.* (2015) was 10.17±5.43 years in Jaffarabadi buffalo from Brazil that was very higher.

The probability of gene origin parameter

To estimates these parameter, a reference population was considered as those animals born from year 2011-2018 (8 years) equivalent to GI. In the present study it was observed that more than 50% of the population genetic variability was explained by 26 ancestors explaining the same variability in the herd. Marcondes *et al.* (2010) reported that only 20 ancestors (founders or non-founders) creating 69.10% out of the total genetic variation in Murrah population, that supported our present finding. The ratio of f_e/f was 0.18 (Table 7) that help to determine balance contribution of founder or the extent of pedigree completeness.

The f_e (58 and 60) and f_a (35 and 36) by Santana Jr *et al.* (2011) and Malhado *et al.* (2012) reported in Murrah buffaloes. The ratio of f_e/f in present study was higher than

Table 5: Effective population size (N_e) estimated by different method.

Parameter	Average
N_eC_i	90.79 ± 2.39
N_eF_i	102.78 ± 18.27
N_eC_i/N_eF_i ratio	0.88

N_e computed via individual increase in coancestry = N_eC_i and N_e computed via individual increase in inbreeding = N_eF_i

Table 6: Generation interval for four selection pathways Murrah buffaloes.

Path	Number of animals	Generation Interval
Sire to Bull	343	10.18 ± 0.34
Sire to Cow	2049	8.74 ±.013
Dam to Bull	232	7.79 ± 0.18
Dam to Cow	1880	6.44 ± .01
Total	4504	8.28 years

Table 7: Parameters characterizing the probability of gene origin in the.

Parameters	Value
Number of animals in the reference Population	969
Number of Founders(f)	376
Number of ancestors contributing to the reference population	363
Effective number of founders (f_e)	65
Effective number of ancestors (f_a)	59
Founder genome equivalent(f_{ge})	22.67
f_e/f	0.18
f_a / f_e	0.90
f_g / f_e	0.35
Number of ancestors explaining more than 50% genetic variability	26
Genetic diversity (%)	97.79

Table 8: Effects of inbreeding on first lactation production traits of Murrah.

Traits (days)	Number of observation	Mean ± S. E.	Regression
FLMY	974	1914.28±17.50	-3.57
FLFY	427	162.03±2.62	-1.45
FLSNFY	427	198.40±3.45	-2.47
FLTMY	974	2023.70±21.33	-2.69
FLL	974	318.09±2.16	0.12
DP	758	142.68±2.68	-0.47

those reported by Muasya *et al*. (2013) was 0.08 for HF and 0.04 by Hammami *et al*. (2007) in Luxembourg Holstein. In an ideal population the ratio f_a/f_e is equal to unity and any deviation from this indicated that population is undergoing bottle neck. However, in genetically improving herd it is common since selective breeding is practiced and utmost care have been given to maintain the optimum level of inbreeding and diversity. The results of GD are in agreement with the findings of Santana Jr *et al*. (2014), who reported 2.30% loss of genetic diversity in Brazilian Gir breed.

Effects of inbreeding on production traits in Murrah buffaloes

The effects of inbreeding on various production traits are given in Table 8 indicating non significant influence on all the traits, the regression analysis of the production traits indicated negative effects of inbreeding except FLL.

CONCLUSION

The current genetic variability is well maintained within the Murrah herds because of large number of animals contributing to the herd. The observed levels of inbreeding and the values of the AR are low within the recommended level and does not effecting the production traits and well defined pedigree structure of three breeds. To keep this diversity maintained in the herd we have to maintain the same breeding policy like introduction of new reproductive individuals with the lowest possible AR is strongly recommend and adoption of mating strategies that minimize generation interval by replacement of older ones with young female and the less intensive use of few bulls is highly desirable to maintain genetic variability in future generations. This action will reduce the probability of suffering deleterious effects related to inbreeding and increase future genetic variability in the herd. Based on the effective population sizes and its ratio (N_eC_i/N_eF_i) indicates that population is still highly structured and there is ample scope for artificial selection. Moreover, there was negligible founder effects and no evidence of population bottleneck. In spite of minimum number of animals creating genetic variation but does not emerge to have impaired the population's genetic structure.

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