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CONTENTS

Effect of non-genetic factors and genetic parameter estimation of reproductive traits in Malpura sheep

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ABSTRACT

Malpura sheep is a heavy and well adapted breed of the semi-arid region of India. A total of 609 Malpura sheep, over a period of 10 years (1994 to 2003) at ICAR-CSWRI Avikanagar were studied. The least squares mean value of AFS, AFSS, WFS, WFSS and AFL for the Malpura ewes was obtained as 598.14 ± 8.43 days, 664.81 ± 13.42 days , 26.18 ± 0.19 kg, 27.08 ± 0.21 kg and 816.54 ± 13.45 days, respectively. Highly significant effect of year was observed on all these reproduction traits, whereas, lambing season of ewes was not significantly affecting all these traits. The heritability of reproductive traits viz., AFS, AFSS, AFL, WFS, WFSS and WFL were estimated as 0.15 ± 0.09, 0.19 ± 0.10, 0.18 ± 0.09, 0.34 ± 0.10, 0.20 ± 0.10and 0.16 ± 0.10 respectively. The heritability estimates were significant and with moderate values, which will be helpful in selective breeding of the animals for these traits.

Keywords: Malpura sheep, heritability, reproductive traits
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Abbreviation: AFS: Age at first service, AFSS: Age at first successful service, WFS: weight at first service, WFSS: weight at first successful service, AFL: Age at first lambing and WFL: weight at first lambing

INTRODUCTION

Sheep has played a noteworthy role in shaping and maintaining the socio-economic and cultural status of the rural folk. Rural human population constitutes 72.22 % out of which majority are dependent directly or indirectly on the agriculture and livestock related occupation. Malpura sheep is one of the well adapted and heavy breed of sheep in semi-arid (Tonk District) of Rajasthan,India. The information on reproductive traits in Malpura sheep is scanty and information with regards to components of these traits and their statistical and genetic analysis are also less. Therefore, there is a need to generate more information on these traits.

MATERIALS AND METHODS

Data and management of sheep

Data for the present study were collected from the livestock data registers such as inventory, reproduction registers maintained at the AG&B Division, CSWRI, Avikanagar (Rajasthan). A total of 609 Malpura sheep spread over a period of 10 years from 1994 to 2003 comprised the material for this study. The information on these animals were used to study reproductive trait

Statistical analysis of data

The data of reproductive traits, were analysed by taking year of birth, lambing season, WFS as fixed effect. Only two seasons (Jan-Jun and Jul-Dec) were taken because more in these seasons. Frequency distribution across year and across Weight at First Service group was tested using chi squares statistics. Least square means were estimated by SPSS14. The genetic parameters were analysed by using which Animal model using WOMBAT (Mayer, 2006).

A single-trait linear mixed animal models (in matrix notation) was fitted for NID traits as follows:

$y = X\beta + Z_a a + Z_m m + \varepsilon$; with $Cov(a_m, m_o) = A\sigma_{am}$

Where, y is the vector of records; β, a, m and ε are vectors of fixed, direct additive genetic, maternal genetic and residual effects, respectively; with association matrices X and Z_a and Z_m. Assumptions in the model were $V(a) = A\sigma_a^2$, $V(m) = A\sigma_m^2$; and $V(e) = I\sigma_e^2$; where I is an identity matrix, A is the numerator relationship matrix between animals and σ_a^2, σ_m^2 and σ_e^2 are additive direct, maternal direct and residual variances, respectively. Direct heritability was estimated using single trait analysis.

RESULTS AND DISCUSSION

Results reveal the performance of the lambs born to 609 ewes over the period of 10 years (1996 to 2003). In total 2341 lambs were born to 609 ewes, out of which 1165 were female lambs born (sex ratio 50.23%).

Age at first service (AFS) and Age at first successful service (AFSS) in Malpura ewes

The least squares mean value of AFS for the Malpura ewes was obtained as 598.14 ± 8.43 days (Table 1). The statistical analysis showed the effect of year was significant which supports the findings of Kumar et al., 2001 in Chokla and Avivastra sheep, Dass et al., 2000 in Muzaffarnagri sheep and Qureshi et al., 2010 but contradict with Dey and Poonia, 2005Dey and Poonia, 2005 reported that year had non-significant effect on AFS (662.20±52.98 to 888.73±88.73days) in Nali sheep. The analysis revealed (Table 1-2) that the effect of season on AFS is non-significant. This supports the study of Dass et al., 2000 in Muzaffarnagri sheep but contradict with findings of Kumar et al., 2001 in Chokla and Avivastra sheep, Qureshi et al., 2010 and Dey and Poonia, 2005 in Nali sheep, where effect of season was significant They showed that the effect of season on AFS was significant. The effect of weight at first service groups on AFS is significant. Highest number of observations were recorded in WFS group ≥29 kg and lowest in ≤23 kg. The least squares mean value of AFSS for the Malpura ewes was 664.8±13.42 (Table 1).

Weight at first service (WFS) and weight at first

Table 1. LSM±SE for Age at First Service (AFS), Age at First Successful Service (AFSS), Weight at First Service (WFS), Weight at First Successful Service (WFSS) and Age at First Lambing (AFL) traits in Malpura ewes

Effect	AFS (Days)	AFSS (Days)	WFS (Kg)	WFSS (Kg)	AFL (Days)
Overall	598.14 ± 8.43 (609)	664.81 ± 13.42 (597)	26.18 ± 0.19 (609)	27.08 ± 0.21 (597)	816.54 ± 13.45 (597)
Year	**	** **	**	**	
1994	^{de}666.58 ± 14.45 (82)	^{ab}680.29 ± 22.76 (81)	^{a}24.38 ± 0.31 (82)	^{a}25.02 ± 0.36 (81)	^{ab}832.12 ± 22.79 (81)
1995	^{a}504.91 ± 15.99 (66)	^{a}617.11 ± 25.68 (61)	^{b}26.29 ± 0.36 (66)	^{bc}27.35 ± 0.41 (61)	^{a}763.32 ± 25.72 (61)
1996	^{cd}609.08 ± 14.39 (70)	^{ab}673.88 ± 22.71 (68)	^{b}26.42 ± 0.32 (70)	^{bc}26.97 ± 0.36 (68)	^{ab}826.26 ± 25.72 (68)
1997	^{e}687.87 ± 29.47 (16)	^{b}732.45 ± 45.94 (16)	^{a}24.19 ± 0.66 (16)	^{a}24.69 ± 0.74 (16)	^{b}885.36 ± 46.02 (16)
1998	^{de}661.79 ± 18.47 (49)	^{b}751.36 ± 28.88 (49)	^{a}24.52 ± 0.41 (49)	^{a}25.73 ± 0.46 (49)	^{b}901.79 ± 28.93 (49)
1999	^{bc}576.57 ± 15.57 (66)	^{a}626.99 ± 24.59 (65)	^{b}26.11 ± 0.34 (66)	^{b}26.88 ± 0.39 (65)	^{a}779.18 ± 26.64 (65)
2000	^{bc}584.28 ± 17.23 (58)	^{a}637.02 ± 27.01 (58)	^{c}27.64 ± 0.39 (58)	^{c}28.42 ± 0.44 (58)	^{a}791.23 ± 27.06 (58)
2001	^{bc}572.17 ± 17.03 (64)	^{a}645.33 ± 26.69 (64)	^{b}25.99 ± 0.37 (64)	^{b}26.99 ± 0.42 (64)	^{a}798.12 ± 26.73 (64)
2002	^{bc}557.68 ± 26.77 (66)	^{a}638.44 ± 26.87 (64)	^{d}30.05 ± 0.36 (66)	^{d}30.94 ± 0.41 (64)	^{a}790.14 ± 26.91 (64)
2003	^{b}560.50 ± 15.41 (72)	^{a}645.26 ± 24.24 (71)	^{b}26.21 ± 0.35 (72)	^{bc}27.81 ± 0.39 (71)	^{a}797.86 ± 24.28 (71)
Wt. at	**	NS	-	-	NS
First Service(Kg)					
≤ 23	565.34 ± 14.23 (97)	666.08 ± 22.45 (96)	-	-	818.34 ± 22.49 (96)
23-26	588.97 ± 10.16 (227)	653.48 ± 16.14 (224)	-	-	805.79 ± 16.17 (224)
26-29	616.05 ± 10.85 (181)	665.91 ± 17.27 (173)	-	-	816.81 ± 17.30 (173)
≥ 29	622.21 ± 14.74 (104)	673.78 ± 23.11 (104)	-	-	825.20 ± 23.15 (104)
Lambing	NS	NS	NS	NS	NS
Season					
Jan.-June	599.91 ± 5.67 (543)	655.51 ± 8.86 (535)	26.16 ± 0.12 (543)	27.76 ± 0.14 (535)	806.74 ± 8.87 (535)
July-Dec.	596.37 ± 15.41 (66)	674.12 ± 24.66 (62)	26.19 ± 0.34 (66)	27.40 ± 0.39 (62)	826.34 ± 24.70 (62)

Number in the parentheses are total number of animals for the observations.
NS = Non- Significant, ** (P≤ 0.01) at level of significance.

Table 2. ANOVA for Age at First Service (AFS), Age at First Successful Service (AFSS), Weight at First Service (WFS), Weight at First Successful Service (WFSS) and Age at First Lambing (AFL) traits in Malpura ewes (M.S. Value).

Source of variation	D.F.	AFS	AFSS	WFS	WFSS	AFL
Year	9	149454.97**	81303.09**	174.07**	177.90**	82666.77**
Season	1	644.98	16870.63	0.08	20.38	18699.37
WFS_ Class	3	62277.10**	9783.36	-	-	879.19
Error	595	13108.76	31762.69	6.76	8.47	31868.89

** (P≤0.01) at level of significance

Table 3. Variance components and genetic parameters for different reproductive traits from univariate analysis in Malpura ewes.

Z	AFS	AFSS	AFL	WFS	WFSS	WFL
σ^2_a	2034.71±1198.74	6168.34±3304.79	6059.64±3293.09	2.17±0.73	1.68±0.89	1.64±1.06
σ^2_e	10212±1145.20	25903±2960.29	26110.90±2980.71	3.84±0.54	6.12±0.74	8.00±0.90
σ^2_p	12937.40±784.39	32073.60±1967.97	32182±1973.12	6.38±0.40	8.24±0.51	10.25±0.62
h^2	0.15±0.09	0.19±0.10	0.18±0.09	0.34±0.10	0.20±0.10	0.16±0.10
e^2	0.78±0.08	0.80±0.09	0.81±0.09	0.60±0.09	0.74±0.09	0.78±0.08
m^2	0.05±0.06	0.00±0.06	0.00±0.06	0.05±0.06	0.05±0.06	0.05±0.06

σ^2_a, σ^2_e and σ^2_p are additive direct, maternal genetic, residual variance and phenotypic variance, respectively;
h^2 obtained from WOMBAT (Meyer, 2006)

successful service (WFSS) in Malpura ewes

The least squares mean value of WFS for the Malpura ewes was obtained as 26.18±0.19 kg (Table 1). The statistical analysis showed the effect of year on WFS to be significant which supports the findings of Kumar et al., 2001 in Chokla and Avivastra sheep and Qureshi et al., 2010 but in contradiction with Dey and Poonia, 2005. They reported that year had non-significant effect on WFS (24.92 ±0.22kg) in Nali sheep (Table 2). In present study the effect of season on WFS is non-significant which supports the study of Dass et al., 2000 in Muzaffarnagri sheep but contradict with findings of Kumar et al., 2001 in Chokla and Avivastra sheep and Qureshi et al., 2010 and Dey and Poonia, 2005 in Nali sheep. They showed that effect of season on WFS was significant. The least squares mean value of WFSS for the Malpura ewes was 27.08±0.21kg (Table 1). This showed that the weight of ewes at first successful service was obtained around 27 kg. The statistical analysis showed that the year had significant effect on WFSS but season had non-significant effect.

Age at first lambing (AFL) in Malpura ewes

The least square mean value of AFL for the Malpura ewes was obtained as 816.541±3.45 days (Table 1). Upto 1998 there was increase in AFL and then suddenly dropped and remain almost stagnant. This may be due to proper management in the farm in successive years. The statistical analysis showed the effect of year on AFL to be significant which were similar to findings of Dass et al., 2000 in Muzaffarnagri sheep and Qureshi et al., 2010 but was in contradiction with Dey and Poonia, 2005 study. They reported that year had Non-significant effect on AFS, AFL (925.08±13.02 days) in Nali sheep. The effect of season on AFL was non-significant that contradicts with findings of Qureshi et al., 2010 and Dey and Poonia, 2005 in Nali sheep. They showed that effect of season on AFL is significant. The effect of weight at first service groups on AFL is non-significant. Highest number of observations were recorded in WFS group ≥29 kg and lowest in 23-26 kg WFS group.

Genetic analysis

The analysis of variance and its components for reproductive life are presented in Table 3. The heritability estimates of AFS, AFSS, AFL, WFS, WFSS, WFL were observed to be 0.157±0.091 days, 0.192±0.10 days, 0.188±0.099 days, 0.34±0.107 kg, 0.205±0.105 kg and 0.160±0.102 kg, respectively (Table 3). The h2 for the best model obtained from WOMBAT (Meyer, 2006) was 0.34±0.107 for WFS.

CONCLUSION

The significant to highly significant effect of non-genetic factors (Year, Lambing season and WFS) play important role in reproductive performance of animal so higher emphasis on management practices, nutrition, health cover will help in improving the reproductive performance of animal. The low to moderate heritability observed in most of the traits under study indicated that improvement in management practices can further enhance the better expressibility of these reproduction traits.

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Abnormal acrocentric Y chromosome in crossbreed cattle bulls

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ABSTRACT

Reproductive efficiency is the most crucial issue faced by the dairy industries in India and abroad. A variety of factors affect the reproductive performance of farm animals. Chromosomal abnormalities cause a drop in reproductive performance or even complete infertility in the carrier animals. Present investigation was undertaken to detect chromosomal abnormality, if any, in 206 breeding bulls of exotic (*Bos taurus*, 2n=60), indigenous (*Bos indicus*, 2n=60) cattle breeds and crossbreeds maintained at Central Institute for Research on Cattle, Meerut and Animal Breeding Centre, Salon, Uttar Pradesh. Chromosomal preparations were made using standard blood lymphocyte culture from animals under study. At least 30 metaphase spreads were screened per animal to detect the chromosomal aberrations and prepare the karyotype. Giemsa staining of chromosome revealed that 98.06% cattle bulls possessed normal chromosome. However, 1.94% bulls showed abnormal Y chromosome complements in crossbreed bulls. Extensive use of breeding bulls in breeding programme through artificial insemination (AI) made it mandatory to screen for chromosomal anomalies before inclusion in breeding programme. It will not only check the quick spread of chromosomal abnormalities in animal population rather it will save the time and amount spent on rearing the abnormal animals. Various types of chromosomal anomalies have been reported in India but the frequency of chromosomal abnormalities is much less as compared to reported worldwide.

Keywords: Chromosomal abnormality, crossbred cattle, cytogenetic screening sterility, Y chromosome
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INTRODUCTION

Domestic cattle of *Bos taurus*, *Bos indicus* and their crosses possess a normal diploid number of 60 chromosomes, which comprises 29 pairs of autosomes and a pair of sex chromosomes (XX in females and XY in males). Structurally, all the 29 pairs of autosomes and the X chromosome are acrocentric and sub-metacentric, respectively, in both *Bos taurus* and *Bos indicus* cattle. The only difference is in the Y chromosome, which is sub-metacentric in *Bos taurus* but acrocentric in *Bos indicus* breeds (Yadav 1981, Prakash 1982).

Alteration in chromosome number and structure are the best known genetic based variations, which have direct effects on fertility and reproductive outcome in cattle (Maria and King, 2004). Chromosome abnormalities have been reported to be associated with reproductive performances in cattle (Patel and Khoda 1998) viz., infertility of carriers, degenerations of reproductive organs, poor semen quality (Ducos et al 2008).Chromosomal aberrations can affect a large population in two ways i) it can be transmitted to a large population through Artificial Insemination (AI) and ii) it can cause repeat breeding problems in females because of embryonic losses and poor semen quality in breeding bulls (Krumrych 2009).Reduced fertility and infertility are major concerns in the dairy animals in India which could be due to poor breeding, feeding and management. However, it could also be due to chromosomal aberrations. Chromosomal aberrations might be transmitted or generated spontaneously during mitotic or meiotic cell divisions. Therefore, complete eradication of chromosomal aberrations from the dairy animal population may not be possible. In view of this the regular chromosomal screening, especially of breeding bulls at the early age, ought to be done. This

Table 1. Details of bulls of different cattle breeds and crossbreeds screened for chromosomal abnormalities

Name of the organization	Cattle Breed					
	Holstein – Friesian	Jersey	Hariana	Sahiwal	Holstein – Friesian X Sahiwal	Jersey X Sahiwal
Central Institute for Research on cattle (CIRC), Meerut	-	-	-	-	176	-
Animal breeding Centre, Salon, Raibarelley, U.P.	13	07	02	02	03	03
TOTAL	13	07	02	02	179	03

practice will not only reduce the occurrence of chromosomal abnormalities in the dairy animal populations rather it will save the time and amount spent on rearing of abnormal animals. In most of the developed countries there is restriction on the import/export of semen/live breeding males without a certification of normal karyotype. On similar lines cytogenetic evaluation of all breeding males has been made essential under the National Programme for Cattle and Buffalo breeding (NPCBB) by Government of India to keep our farm animal species free of any chromosomal abnormalities.Cytogenetics in domestic animals was started in the early sixties and various abnormalities have been reported in Indian cattle (Prakash et al., 1995; Murlidharan et al., 2011) and in buffaloes (Balakrishnan and Yadav 1984; Yadav et al., 1990; Patel et al., 2006; Chauhan et al., 2009; Prakash and Singh, 2009).

MATERIALS AND METHODS

This work was conducted at Department of Zoology, Kurukshetra University, Kurukstetra and molecular cytogenetic laboratory of National Bureau of Animal Genetic Resources, Karnal to investigate the chromosomal abnormalities in breeding bulls of different breeds and crossbreeds of cattle.A total of 206 blood samples were collected in sterile heparinized vacutainer tubes from phenotypically normal 13 Holstein–Friesian(HF), 7 Jersey, 2 Sahiwal, 2 Hariana, 179 Frieswal (i.e.Holstein Friesian x Sahiwal) crossbred and 3 Jersey crossbreed cattle bulls maintained by various organizations (Table 1).The 72-hour lymphocyte culture was performed from whole blood in standard medium (RPMI 1640-Sigma, St. Louis, USA) supplemented with 15% of fetal calf serum,penicillin and streptomycin (100 IU/ml and 0.1 mg/ml of culture medium, respectively), and pokeweed mitogen (2.5 µg/L of culture medium, SIGMA, St. Louis, USA). To arrest the somatic cells at metaphase stage, colchicine (Sigma, India) 2 µg/mL was added for one hour before harvest. The cells were harvested by centrifugation at 1000 rpm for 20 minutes followed by hypotonic treatment with 0.075 M KCl for 20 minutes at 37°C and fixed thrice in Carnoy's fixative (3:1 ratio of methanol and glacial acetic acid). Finally, cell suspension was dropped on slides and air dried. Slides were stained with 2% Giemsa stain and DPX mounted. At least 30 Metaphase spreads for each animal were analyzed under bright field microscopy and karyotyping was done by using automatic karyotyping software(Genus).

RESULTS AND DISCUSSION

In Cattle there are two well-known species: Bos taurus (humpless, taurus) and Bos indicus (humped, Zebu). Both possess a normal somatic chromosome number of 60 (2n = 60) comprising of 29 pairs of autosomes and one pair of sex chromosome. All the autosomes are acrocentric in decreasing order of size and X-chromosome is a large Sub metacentric while Y-chromosome is small sub-metacentric in Bos taurus and smallest acrocentric in Bos indicus(figure1).

***Figure 1**. Normal karyotype of a zebu (2n=60; left) and taurus (2n=60; right) male cattle showing difference in the morphology of Y-chromosome.*

Table 2. Details of bulls showing chromosomal abnormalities

Sr. No.	Station	Species/ breed	Abnormality found	No. of bulls with abnormality
1	CIRC Merrut	Cattle (HF X Sah) Frieswal	Abnormal -Y chromosome (acrocentric)	03
2	Animal Breeding Centre Salon, Raibarelley (U.P.)	Cattle (JY X SAH)	Abnormal -Y chromosome (acrocentric)	01

While screening the chromosomes of 206 males in this study, three crossbred Frieswal (HF X Sahiwal) bulls belonging to Central Institute for Research on Cattle, Merrut, U.P. and one Jersey X Sahiwal crossbred bull from Animal Breeding Centre, Salon, U.P. were found to have acrocentric Y- chromosome instead of the anticipated sub-metacentric. The results of the study are presented in table 2 from which it is evident that out of 206 breeding bulls of cattle screened, only 4 bulls with anomalous karyotypes were detected. All the 4 bulls were crossbred but having acrocentric Y-chromosome. Representative metaphase spreads form two bulls are shown in Fig. 2. Crossbreeding in India always involved crossing of indigenous zebu females with exotic Bos taurus males. The crossbreds so generated are then inter-crossed to generate further filial crossbred generations. Same breeding programme is followed by the two organisations. Thus the source of Y chromosome in all crossbred males is invariably of taurine origin which is sub-metacentric in morphology. All the crossbred males investigated in this study were expected to possess a taurine type sub-metacentric Y chromosome. Thus, the presence of zebu type acrocentric Y chromosome in the four bulls was considered abnormal.

The abnormal Y-chromosome detected in the four bulls could also be due to wrong pedigree or undetected false mating. But the two organizations strictly follow AI and bulls are never kept in the vicinity of females, the possibilities were ruled out. While screening the literature, it was discovered that similar abnormality in HF crossbred bulls was detected by Yadav et al (1984). Analysing the comparative structure of Y chromosome in Bos taurus and B. indicus by FISH using region-specific, microdissected, and locus-specific DNA probes, Goldammer et al (1997) indicated that the Y chromosomes of B. indicus (BIN Y) and B. taurus (BTA Y) differ by a pericentric inversion. Similarly, using comparative FISH-mapping among Y chromosomes of cattle (Bos taurus, 2n = 60, BTA, submetacentric Y chromosome), zebu (Bos indicus, 2n = 60, BIN, acrocentric Y chromosome), river buffalo (Bubalus bubalis, 2n = 50, BBU, acrocentric Y chromosome), sheep (Ovis aries, 2n = 54, OAR, small metacentric Y chromosome) and goat (Capra hircus, 2n = 60, CHI, Y-chromosome as in sheep), Di Meo et al. (2005) concluded that BTA-Y and BIN-Y differed as a result of a centromere transposition or pericentric inversion since they retained the same gene order along their distal chromosome regions and had chromosome arms of different size. It was therefore, assumed that the existence of acrocentric Y chromosome in the four crossbred bulls in this study was due to pericentric inversion in the sub-metacentric Y chromosome leading to an acrocentric Y chromosome(Fig.3A). Similarly, an acrocentric chromosome can evolve into a sub-metacentric chromosome through pericentric inversion (Fig. 3B).

Figure 2. *Representative metaphase spreads of crossbred bulls (HF X SAH, left) and (J X SAH) having acrocentric Y chromosome.*

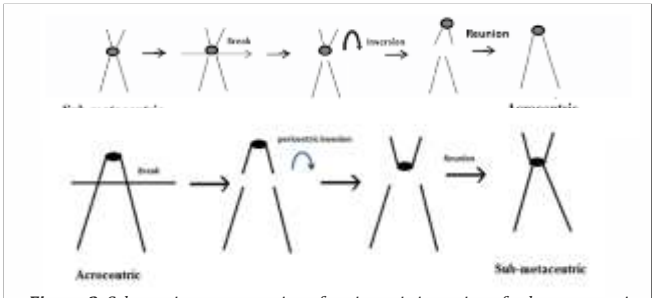

Figure 3. *Schematic representation of pericentric inversion of sub-metacentric chromosome leading to acrocentric chromosome (A) and evolution of sub-metacentric/metacentric chromosome from acrocentric through pericentric inversion (B)*

Thus, in the present study three Frieswal bull (i.e.Holstein Friesian X Sahiwal) and one crossbred (Jersey X Sahiwal) bulls, otherwise physically normal were found to have abnormal acrocentric Y-chromosome. These findings are perplexing because at these institutes crossbreeding has been carried out using males of only exotic breeds with zebu females and subsequent mating amongst the crossbreds. Hence all F1 hybrids must possess only sub-metacentric Y. Similar presence of acrocentric Y chromosome in HF X Tharparkar (Karan fries) cattle bulls was reported by Balakrishnan and Yadav (1987) and they hypothesized the instability of Y chromosome in crossbred bulls. Therefore, a hypothesis of pericentric inversion has been set up for such acrocentric Y chromosome in cattle crossbred bulls which is consistent with the interpretations of Yadav et al 1984, Di Meo et al 2005.

Breeding centers/stations from where samples were collected have been informed regarding the results of cytogenetic evaluation and accordingly the bulls may be culled or retained for AI programme in the view of above results. Extensive experience of chromosomal abnormalities during last six decades has explicitly demonstrated that most of the chromosomal anomalies have a negative impact on the phenotype /production or reproductive efficiency of the carrier animals. It is thus advisable to submit the reproductively inefficient animals to cytogenetic evaluation. More specifically the breeding bulls, which are a source of faster spread of any chromosomal anomaly due to their extensive use in AI, need to be essentially evaluated before putting them into any breeding programme. Cytogenetics can be very handy and cost effective in eliminating this risk and prevent spread of genetic disorders.

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Population trends and distribution of equines in India

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ABSTRACT

Donkeys, mules and horses are important animal genetic resources of India, used mainly for transportation in difficult areas. Present status of these species was evaluated in terms of their population trend and distribution. It is estimated that by 2027, the population of donkeys, mules and horses may decline to mere 1.36, 1.93 and 4.78 lakhs, respectively. Only eleven states in India have more than 5000 donkeys, whereas, only nine states have more than 5000 mules. Further, the populations of these species are now restricted to a few regions only. Fifty-two percent of the population of horses of the Karnataka state is now confined to the two districts of Belgaum and Bijapur. These results suggest that these species require immediate attention for their conservation and propagation.

Keywords: Equine, population trend
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INTRODUCTION

Domestic equine species namely horses, donkeys and mules are reared in India since time immemorial. They are mainly employed for transportation and form an important genetic resource of India. Due to their lower cost and easier maintenance, donkeys are mainly reared by marginalized and poorer sections of the society. A donkey, although much smaller in size with less feed and fodder requirements, is able to generate 0.35 HP per hour, about half the power compared to that of bullock (Prasad et al. 1990; Varshney and Gupta 1994). Horses, which are marginally lighter than bollocks in weight, are able to generate about 1 HP per hour compared to that of 0.75 HP per hour of bullocks. Mules which are only about 70 percent in weight to that of bullocks can generate equivalent power to that of bullocks (Ramaswamy and Narsimhan 1984; Prasad et al. 1990). However, with the improvement of road network and increased mechanization, the population of horses and donkeys has shown a sharp decline during last fifty or sixty years. Only the population of mules has shown an increasing trend. This paper attempts to describe the present status of equines in India in terms of their population trend and distribution.

MATERIALS AND METHODS

Secondary data from livestock census and other literature were obtained (Livestock Census 2012, Varshney and Gupta, 1994; Behl et al. 2008; Behl et al. 2010) and state wise population densities were calculated for these species. The district wise and state wise census data for these species were grouped for population intervals to obtain the number of districts or states with specified minimum population. The regression equation for the population trend was developed (Gupta, 2011) using census data for these species from 1987 onwards and the population for the years 2017, 2022 and 2027 were predicted by modified method Singh et al. (1991) as that of

$$P_t=P_{t-1}+\{P_{t-1}(e^b-1)\}$$

Where,

P_t=Population estimated in the year t

P_{t-1}= Population in the previous point in the time series data

b= Slope in the regression equation Y=a+bX [where, Y and X are dependent (population) and independent (year in time series) variables and a=Y, when X=0]

RESULTS AND DISCUSSION

Donkeys

The donkey (Equus asinus asinus) is a sure-footed, docile and hard working animal that is mainly used for transportation. Because of its lower price and low cost of maintenance it has been traditionally associated with comparatively weaker sections of the society. Despite its usefulness, the donkey has remained a neglected species, underfed and often overlooked. With the improvement of road network and increased mechanization, their population has decreased drastically to 3.19 lakhs (Livestock Census 2012) showing a decline of 69.8 percent compared to their population in 1956 (Fig. 1). It has shown a drastic decline of 27.17 percent from the last census in 2007. Taking into consideration the trend since 1987, their population is estimated to fall to mere 1.8 lakhs in 2022 and 1.36 lakhs in 2027 (Table 1).

Rajasthan has the maximum population (81468) of donkeys possessing about 25.56 percent of the total donkey population of India followed by Uttar Pradesh with 17.77 percent, Gujarat with 12.18 percent and Maharashtra with 9.14 percent (Table 2). In terms of population density, among large states, Rajasthan has the highest density at 0.238 donkeys per sq. km followed by Uttar Pradesh (0.235), Bihar (0.227), Himachal Pradesh (0.132) and Maharashtra (0.095). Delhi with 1087 donkeys has the highest overall population density of 0.732 donkeys per sq. km (Table 2).

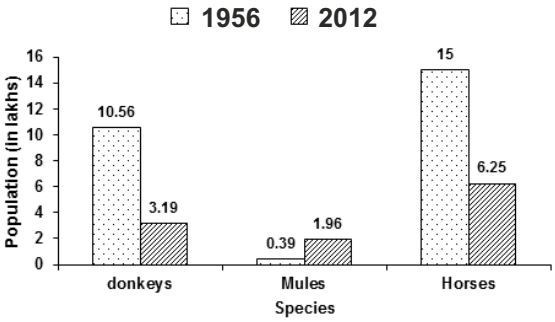

Figure 1: *A comparison of the population of donkeys, mules and horses in India based on Livestock census of 1956 and 2012.*

Only eleven states in India have more than 5000 donkeys (Table 5). Within these states, the donkey population is concentrated in some clusters only. For example, 91.96 percent of the donkey population of Andhra Pradesh in now confined to the districts of Kurnool and Ananthapur. Similarly 64.24 percent of the donkey population of Himachal Pradesh is confined to districts of Kinnour and Lahaul-Spiti. In Uttar Pradesh, donkey population is mainly confined

Table 1. Population trend of equines in India

Census Year	Donkeys		Mules		Horses	
	Total donkey population (in lakhs)	Percent change from previous census	Total mule population (in lakhs)	Percent change from previous census	Total horse population (in lakhs)	Percent change from previous census
1956	10.56	-	0.39	-	15.0	-
1961	10.96	3.65	0.53	35.9	13.0	-13.33
1966	10.54	-3.83	0.75	41.51	11.48	-11.69
1972	9.94	-5.69	0.75	0.0	8.65	-24.65
1977	9.78	-1.61	0.89	18.67	9.15	5.78
1982	10.24	4.70	1.31	47.19	9.0	-1.64
1987	9.60	-6.25	1.7	29.77	7.97	-11.44
1992	9.7	1.04	1.97	15.88	8.17	2.51
1997	8.82	-9.07	2.21	12.18	8.27	1.22
2003	6.5	-26.30	1.76	-20.36	7.51	-9.19
2007	4.38	-32.62	1.37	-22.16	6.12	-18.51
2012	3.19	-27.17	1.96	43.07	6.25	2.12
2017 (estimated)	2.4	-24.8	1.95	-0.47	5.72	-8.53
2022 (estimated)	1.8	-24.8	1.94	-0.47	5.23	-8.53
2027 (estimated)	1.36	-24.8	1.93	-0.47	4.78	-8.53

(Source: Livestock Census, 2012)

Table 2: Total population and population density of donkeys in the states of India as per 2012 livestock census

S. N.	State*	Total donkey population	Percent of total population of India	Density per square km
1.	Rajasthan	81468	25.56	0.238
2.	Uttar Pradesh	56643	17.77	0.235
3.	Gujarat	38834	12.18	0.198
4.	Maharashtra	29135	9.14	0.095
5.	Bihar	21377	6.71	0.227
6.	Jammu and Kashmir	17425	5.41	0.078
7.	Karnataka	16312	5.12	0.085
8.	Madhya Pradesh	14916	4.68	0.048
9.	Andhra Pradesh	10517	3.30	0.065
10.	Tamilnadu	9183	2.89	0.071
11.	Himachal Pradesh	7349	2.31	0.132
12.	Punjab	2909	0.91	0.058
13.	Telangana	2909	0.91	0.026
14.	Haryana	2903	0.91	0.066
15.	Uttarakhand	1509	0.47	0.028
16.	Delhi	1087	0.34	0.732
17.	Assam	1049	0.33	0.013
18.	Chhattisgarh	680	0.21	0.052
19.	West Bengal	609	0.19	0.007
20.	Odisha	523	0.16	0.003
21.	Meghalaya	522	0.15	0.023
22.	Kerala	504	0.16	0.013
23.	Jharkhand	381	0.12	0.005
24.	Manipur	126	0.04	0.006
25.	Arunachal Pradesh	39	0.01	0.0005
26.	Nagaland	39	0.01	0.002
	Total	318787		0.097

**States of Goa, Mizoram, Sikkim and Tripura do not have any donkey population. (Source: Livestock Census, 2012)*

Table 3: Total population and population density of mules in the states of India as per 2012 livestock census

S. N.	State*	Total mule population	Percent of total population of India	Density per square km
1.	Uttar Pradesh	42660	21.72	0.177
2.	Jammu and Kashmir	36508	18.59	0.164
3.	Uttarakhand	26897	13.7	0.503
4.	Bihar	25064	12.76	0.266
5.	Himachal Pradesh	23315	11.87	0.419
6.	Haryana	9009	4.59	0.204
7.	Madhya Pradesh	6989	3.56	0.023
8.	Odisha	5663	2.884	0.036
9.	Punjab	5164	2.63	0.103
10.	Jharkhand	3890	1.98	0.049
11.	Rajasthan	3375	1.72	0.01
12.	Maharashtra	2005	1.02	0.0065
13.	Chhattisgarh	1617	0.824	0.012
14.	Nagaland	1117	0.569	0.067
15.	Karnataka	762	0.388	0.004
16.	Telangana	539	0.27	0.005
17.	Manipur	336	0.171	0.015
18.	Arunachal Pradesh	334	0.17	0.004
19.	Kerala	233	0.119	0.006
20.	Andhra Pradesh	204	0.104	0.001
21.	Gujarat	159	0.0008	0.081
22.	Delhi	136	0.069	0.092
23.	Meghalaya	178	0.091	0.008
24.	West Bengal	113	0.057	0.001
25.	Assam	92	0.047	0.001
26.	Tamilnadu	2	0.001	-
	Total	196378		0.0597

**The mule population of Goa, Mizoram, Sikkim, Tamilnadu and Tripura is <10. (Source: Livestock Census, 2012)*

Table 4: Total population and population density of horses in the states of India as per 2012 census*

S. N.	State	Total horse population	Percent of total population of India	Density per square km
1.	Uttar Pradesh	151848	24.306	0.630
2.	Jammu and Kashmir	144493	23.129	0.650
3.	Bihar	48845	7.818	0.519
4.	Rajasthan	37776	6.047	0.110
5.	Maharashtra	37287	5.968	0.121
6.	Haryana	36655	5.867	0.829
7.	Punjab	32860	5.26	0.652
8.	Madhya Pradesh	18803	3.01	0.061
9.	Gujarat	18264	2.923	0.093
10.	Uttarakhand	16358	2.618	0.306
11.	Himachal Pradesh	15081	2.414	0.271
12.	Assam	14153	2.265	0.180
13.	Karnataka	12976	2.077	0.068
14.	Jharkhand	5706	0.913	0.072
15.	Tamilnadu	5303	0.849	0.041
16.	West Bengal	4408	0.706	0.05
17.	Arunachal Pradesh	4027	0.645	0.048
18.	Odisha	3397	0.544	0.022
19.	Telangana	3288	0.526	0.029
20.	Chhattisgarh	2963	0.474	0.022
21.	Delhi	2694	0.431	1.815
22.	Meghalaya	2314	0.37	0.103
23.	Andhra Pradesh	1898	0.304	0.012
24.	Manipur	1101	0.176	0.049
25.	Nagaland	473	0.076	0.029
26.	Kerala	218	0.035	0.006
	Total	624732		0.19

**The horse population of Goa and Tripura is <30. (Source: Livestock Census, 2012)*

Table 5: States of India with more than 5000 donkeys and districts with more than 3000 donkeys*

State	Population	Clusters of districts with sizable donkey population (Total population in the Cluster)	Districts in the state with about 3000 donkeys or more (population)
Rajasthan	81468	Barmer, Jaisalmer, Jodhpur, Pali, Bikaner, Churu, Hanumangarh, Ganganagar, Jalor, Jhunjhunoo, Nagaur, Sikar, Sirohi (60609)	Barmer (17495), Bikaner (8712),Jaisalmer (5846), Churu (5063),Ganganagar (4609), Jodhpur (4176), Hanumangarh (3370), Jalor (3334)
Uttar Pradesh	56643	Cluster I: Agra, Mathura, Aligarh, Bulandshahr, Etah, Farrukhabad, Firozabad, GoutamBudh Nagar, Mahamaya Nagar (20338) Cluster II: Azamgarh, Ballia, Deoria, Ghazipur, Mau, Chandauli (14653)	Agra (6991), Ballia (4884), Ghazipur (3973), Mathura (3159)
Gujarat	38834	Ahmedabad, Banaskantha, Mehsana, Kheda, Panchmahal, Vadodara, Katchchh, Sabarkantha, Dahod, Anand, Patan (31669)	Kheda (6682), Anand (4982), Vadodara (3300), Katchchh (3276), Sabarkantha (3159),
Maharashtra	29135	Ahmednagar, Pune, Bid, Latur, Nanded, Satara, Jalgaon, Sangali, Sholapur, Buldana (20548)	Nanded (6624)
Bihar	21377	Bhojpur, Buxor, Kaimur, Rohtas (10089)	Kaimur (3443), Buxar (3088),
Jammu & Kashmir	17245	Kargil, Leh (10940)	Kargil (5273), Leh (5072)
Karnataka	16312	Chitradurga, Tumkur (9286)	Tumkur (5072), Chitradurga ((4212)
Madhya Pradesh	14916	Nil	Nil
Andhra Pradesh	10517	Kurnool, Anathapur (9666)	Anathpur (6312), Kurnool (3354)
Tamilnadu	9183	Vellore, Krishnagiri (2691)	Nil
Himachal Pradesh	7349	Kinnaur, Lahaul&Spiti (4721)	Kinnaur (2918)

**Source: Livestock Census, 2012*

Table 6: States of India with more than 5000 mules and districts with more than 2000 mules*

S. N.	State	Population	Clusters of districts with sizable mule population (Total population in the Cluster)	Districts in the state with about 2000 mules or more (population)
1.	Uttar Pradesh	42660	Cluster I – Aligarh, Bulandshehr, Mathura, Agra, MahamayaNagar (8794) Cluster II – Ballia, Ghazipur, Varanasi, Mirzapur (4887)	AmbedkarNagar (2756), Mahamaya Nagar (2433), Aligarh (2085)
2.	J & K	36508	Kathua, Rajouri, Reasi, Udhampur, Doda, Kishtwar, Jammu (30007)	Doda (6649),Reasi (6377), Rajouri (5843), Kishtwar (5046), Kathua (2606), Udhampur (2072)
3.	Uttarakhand	26897	Cluster I – Almora, Bageshwar, Nainital, Pithoragarh (7726) Cluster II – Chamoli, Dehradun, Garhwal, Rudraprayag, TehriGarhwal, Uttarkashi (18261)	TehriGarhwal (5885),Pithoragarh (2750), Rudraprayag (2606), Bageshwar (1959)
4.	Bihar	25064	Cluster I – Supaul, Araria, Kishanganj (6596) Cluster II – Gaya, Aurangabad (2078) Cluster III – Motihari, Saran, Siwan (11834)	Saran (8218),Kishanganj (3082),Araria (2531), Motihari (2006)
5.	HP	23315	Chamba, Kangra, Mandi (14600)	Chamba (5418), Mandi (5114), Kangra (4068), Shimla (2786)
6.	Haryana	9009	Nil	Nil
7.	Madhya Pradesh	6989	Nil	Dhar (2050)
8.	Odisha	5663	Sundargarh, Kendujhargarh, Mayurbhanj (4310)	Nil
9.	Punjab	5164	Nil	Nil

**Source: Livestock Census, 2012*

to two regions. Region comprising nine districts of South-Western Uttar Pradesh (Table 5) holds about 35.91 percent of donkey population of Uttar Pradesh. Similarly, region comprising six districts of Eastern Uttar Pradesh (Table 5) bordering Bihar holds about 25.87 percent of the donkey population of the state. In Rajasthan, which has the maximum population of donkeys in India, 74.4 percent of the population is confined to the Western half of the state.

The Barmer district of Rajasthan with 17495 donkeys was the district with maximum donkey population in India having 21.47 percent of donkey population of Rajasthan and 5.49 percent of donkey population of India. Adjoining district of Bikaner with 8712 donkeys has second highest population of donkeys followed by Agra district of Uttar Pradesh (6991), Kheda district of Gujarat (6682) and Nanded district of Maharashtra (6624).

Only, twenty-seven districts in India have more than 3000 donkeys (Table 5). Rajasthan has eight districts with more than 3000 donkeys followed by Uttar Pradesh with six districts having more than 3000 donkeys.

Mules

Mules with the sure-footedness of donkeys and body conformity of horses are important transportation animals. Their population in 2012 was 1.96 lakhs showing an increase of 402.56 percent from their population in 1956 (Fig. 1). It has shown an increase of 43 percent from the last census in 2007. Taking into consideration their population trend from 1987 onwards, their population is estimated to remain at present levels (Table 1).

Uttar Pradesh with 42660 mules has the largest population of mules, which is 21.72 percent of the total mule population of the country followed by Jammu and Kashmir with 18.59%, Uttarakhand with 13.7% and Bihar with 12.76 percent (Table 3). In terms of population density, Uttarakhand, with 0.503 mules per square km, has the highest density of mules followed by Himachal Pradesh, Bihar and Haryana having 0.419, 0.266 and 0.204 mules per square km, respectively.

Only nine states in India have more than 5000 mules (table 6). Like donkeys most of the mule population is confined to specific regions or cluster of districts. For example, Jammu subdivision of the State of Jammu and Kashmir has 15.28 percent of the total mule population of the country (Table 6). Garhwal region of the Uttarakhand state (cluster II in

Table 7: States of India with more than 5000 horses and districts with more than 3000 horses*

S. N.	State	Population	Clusters of districts with sizable horse population (Total population in the Cluster)	Districts in the state with about 3000 horses or more (population)
1.	Uttar Pradesh	151848	Cluster I – Agra, Aligarh, Bulandshehr, Etah, Farrukhabad, Firozabad, GautamBudh Nagar, Mathura, Mahamaya Nagar, Kanshi Ram Nagar (24106) Cluster II – Rae Bareli, Amethi, Partapgarh, Allahabad, Kaushambhi, Banda (16481) Cluster III – Saharanpur, Shamli, Meerut, Muzaffarnagar, Baghpat, Ghaziabad, Hapur (20298) Cluster IV – Bijnour, JyotibaPhule Nagar, Bareilly, Badaun, Moradabad, Pilibhit, Rampur, Sambhal, Shahjahanpur Cluster V – Unnao, Kanpur Nagar, Sitapur, Hardoi, Lucknow, Barabanki, Bahraich, Shrawasti (17617)	Bareilley (9622), Badaun (9584), Bijnour (6006), Rae Bareli (5234), Aligarh (5185), Muzaffarnagar (5142), Sambhal (5010), Pilibhit (4958), Moradabad (4823), Shahjahanpur (4760), Saharanpur (4432), Agra (4406), Rampur (4308), Hardoi (4240), Bulandshahr (3850), Fatehpur (3834), Bahraich (3286), Pratapgarh (3268), Meerut (3051),
2.	J & K	144493	Cluster I – Anantnag, Badgam, Bandipora, Baramula, Ganderbal, Kulgam, Kupwara, Pulwama, Shupiyan Cluster II – Kargil, Leh (7719) Cluster III – Doda, Kishatwar, Udhampur, Ramban, Reasi, Punch, Rajouri, Jammu, Kathua, Samba(82102)	Rajouri (16066), Anantnag (13974), Reasi (12359), Jammu (10149), Kathua (10127), Punch (8805), Baramula (7639), Badgam (7433), Udhampur (6364), Ganderbal (6133), Kupwara (6024), Doda (5968), Leh (5066), Kishatwar (4987), Bandipore (4858), Samba (4161), Shupiyan (3598), Ramban (3116)
3.	Bihar	48845	Cluster I – Araria, Kishenganj, Katihar, Khagria, Madhepura, Madhubani, Purnea, Saharasa, Begusarai, Supual (24085) Cluster II – Aurangabad, Bhojpur, Buxar, Rohtas, Saran (7002) Cluster III – Munger, Nalanda, Patna, Bhagalpur, akhisarai (7405) Cluster IV – Motihari, PashchimChamparan (5057)	Araria (5035), Begusarai (4021), Kishanganj (3300), Khagaria (3284), Saharsa (2701), Pashchim Champaran (2593), Saran (2155)
4.	Rajasthan	37776	Nil	Bikaner (3047)
5.	Maharashtra	37287	Ahmednagar, Aurangabad, Dhule, Jalgaon, Mumbai, Thane, Nashik, Pune, Satara, Solapur, Sangli, Kolhapur (30752)	Nashik (5957), Pune (5413), Dhule (4055), Ahmadnagar (3789)
6.	Haryana	36655	Ambala, Yamuna Nagar, Kurukshetra, Karnal, Kaithal, Jind, Panipat, Sonipat (24904)	Ambala (11539), Karnal (2961)
7.	Punjab	32860	Cluster I – Amritsar, Tarantarn, Gurdaspur, Hoshiarpur, Jalandhar (13259) Cluster II – Firozepur, Patiala, Sangrur, Barnala, Muktsar, Moga, Ludhiana, Bathinda, Mansa, Faridkot (17212)	Gurdaspur (4834), Ludhiana (3116),Amritsar (3060)
8.	MP	18803	Mandsaur, Ratlam, Ujjain, Dhar, Indore (5088)	Nil
9.	Gujarat	18264	Ahmedabad, Mehsana, Katchchh, Bnaskantha, Amreli, Bhavnagar, Junagarh, Rajkot, Surender Nagar (12304)	Nil
10.	Uttarakhand	16358	Nil	Nil
11.	HP	15081	Chamba, Kangra, Mandi, Kullu (9798)	Kangra (3781)
12.	Assam	14153	Nil	Nil
13.	Karnataka	12976	Belgaum, Bijapur (6749)	Belgaum (4898)

**Source: Livestock Census, 2012*

Uttarakhand) has about 18000 mules which is 9.3 percent of the total mule population of the country. Similarly, the districts of Chamba, Kangra and Mandi have 7.43 percent of the total mule population of the country.

Saran district in Bihar, with 8218 mules which is 32.79 percent of the total mule population of the state and 4.18 percent of the total mule population of the country, has the largest population of the mules in India (Table 6).Doda district of Jammu and Kashmir is ranked second with 6649 mules which forms 3.39 percent of the total mule population of the country.

Horses

Besides transportation, horses are also used for

riding. Unlike donkeys, horses are generally looked after well by their owners. Horses, with their population at 6.25 lakhs (census2012), though, have registered a marginal increase of 2.12 percent during 2007 to 2012, but their overall population declined by 58.33 percent during 1956-2012 (Fig. 1). Based on the trend of their population from 1987 onwards, the population of horses is estimated to decrease to 5.23 lakhs in 2022 and 4.78 lakhs in 2027 (Table 1).

Uttar Pradesh with 151848 horses has maximum population of horses, having about 24.31 percent of total horse population of India followed by Jammu and Kashmir with 23.13 percent, Bihar with 7.82 percent and Rajasthan with 6.05 percent horse population of the country (Table 4). In terms of population density, among large States, Haryana with 0.829 horse per square km has the highest density of horses followed by Punjab (0.652), Jammu and Kashmir (0.65) and Uttar Pradesh (0.63). Delhi with 2694 horses has the highest overall density of 1.82 horses per square km among the small States.

Only thirteen states in India have more than 10000 horses (Table 7). Although, unlike donkeys and mules, horse population is more spread out, still some clusters of districts or regions hold majority of the population. For example, 52 percent of the population of horses of the Karnataka state is confined to the two districts of Belgaum and Bijapur. Similarly, 49.31 percent of the horse population of Bihar is localized in North Eastern region of Bihar (Table 7).

Rajouri district of Jammu and Kashmir with 2.57 percent of the total horse population of the country has the largest horse population (16066) followed by Anatnag (13974) of the same State (Table 7). Only 24 districts in the country have more than 5000 horses which includes 12 districts of Jammu and Kashmir followed by seven of Uttar Pradesh.

CONCLUSION

The above analysis has clearly shown that the population of donkeys and horses has shown a sharp decline compared to their population status in 1950s. Although, the population of mules has shown an increasing trend, their total population is only 1.96 lakhs. Further, these three equine species are localized to certain regions only, showing great regional imbalances. These facts suggest that special interventions are required for the conservation and propagation of these important animal genetic resources of our country.

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Transferrin polymorphism and its correlation with lactation length and dry period in Tarai buffalo and Sahiwal cattle

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ABSTRACT

In the present study a total of 50 Tarai buffalo and 30 Sahiwal cattle were typed for transferrin. Two transferrin phenotypes were found viz. T_f^{BC} and T_f^{CC} in Tarai buffalo with gene frequency of T_f^{B} and T_f^{C} as 0.14 and 0.86, respectively. Whereas, five transferrin phenotypes were observed in Sahiwal cattle *viz*. T_f^{AA}, T_f^{AE}, T_f^{DE}, T_f^{EE} and T_f^{DD} with a gene frequency of T_f^{E} (0.6161), T_f^{D} (0.2283) and T_f^{A} (0.1551), respectively. The higher lactation length was observed in T_f^{CC} (297.95 days) as compared to 281.25 days in T_f^{BC} group of transferrin phenotypes in Tarai buffalo. The dry period of 137.87 and 132.90 days were reported in T_f^{BC} and T_f^{CC} groups, respectively in Tarai buffalo. The lactation length for different transferrin types viz. T_f^{AA}, T_f^{AE}, T_f^{DE}, T_f^{EE} and T_f^{DD} were reported to be 274.00, 292 ± 13.20, 251.00 ± 32.58, 272.66 ± 30.58 and 244.25 ± 25.30 days, respectively where as dry period for these transferrin types were reported as 256.00, 184.25 ± 25.80, 202.22 ± 41.72, 266.41 ± 42.54 and 322.50 ± 70.02 days, respectively in Sahiwal cattle. The production traits *viz*. lactation length and dry period were found to be non-significant with different transferrin types in Tarai buffalo and Sahiwal cattle.

Key Words: Transferrin, Polymorphism Gene frequency, Polyacrylamide, Lactation length
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INTRODUCTION

The early evaluation of animal that is selection practice followed long back can be made possible if economic traits are associated with any character expressed during early stage of life. Thus, a gene marker associated with economic character could be ideally utilized for evaluating the breeding worth of dairy cattle at an early age. In recent years, attention has been directed to study the genetic variation of serum protein owing to their vital role in the metabolic process.

Transferrin is an iron binding protein. The transferrin also participates in the regulation and control of iron absorption and protect against iron intoxication (Putnam 1965). Polymorphic variants of transferrin were separated by vertical slab electrophoresis in polyacrylamide gel (Ballewar et al., 1997). Polymorphism studies on transferrin exhibits different variants in Holstein cows (Dragomir, L. and Vidovic, V.; 2013). There is a growing convention among researchers that a better understanding of the biochemical differences and their genetic basis may help in conventional selection procedure as an important supplement. The polymorphism of serum transferrin was first of all described independently by (Ashton 1957) and (Hickman & Smithies 1957) in British breed of cattle. It has not been studies in Tarai breed of buffalo, therefore this study was undertaken to study the transferrin polymorphism in Tarai breed and compare it with the Sahiwal cattle.

MATERIALS AND METHODS

Blood sample was taken out from 30 females of Tarai breed of buffalo from different villages of U.S. Nagar maintained under scheme "Animal Genetic Resources Biodiversity: Characterization and Conservation of Tarai Buffalo" (NATP scheme) and 30 Sahiwal cattle maintained at Instructional Dairy Farm G.B. Pant University of Agriculture and Technology, Pantnagar. Serum was taken out aseptically and freezed at- 20oC until used for further analysis.

The polymorphic variants of transferrin were separated by vertical gel electrophoresis in polyacrylamide gel (PAGE) using a discontinuous buffer system according to method suggested by Gahane et al. (1977) with modification. One microgram of standard transferrin viz. holo transferrin of bovine an iron saturated, >95% powder, cell culture and endotoxin tested was loaded in one well in each gel along with other test-sample.

RESULTS AND DISCUSSION

Mean lactation length, standard error (SE) and coefficient of variation (C.V.) for different transferrin groups were presented in table 1. Only TfBC and TfCC transferrin groups could be isolated in Tarai breed of buffalo where as TfAA, TfAE, TfDE, TfEE and TfDD were observed in Sahiwal cows. As per the transferrin group, animals were classified for lactation length and dry period. The result of high lactation length in Tarai buffalo was observed in TfCC as compared to TfBC group (297.95 days and 281.25 days), respectively. The result also revealed that the mean dry period was higher in those animals grouped in transferrin type TfBC as compared to transferring TfCC group 137.87 days and 132.90 days, respectively.

When comperison was made with Sahiwal cattle it was observed that mean lactation length was higher in TfAE (292.00 days) and lowest was in TfDD (244.25 days) type of cows. It was also observed that

Table 1: Lactation Length and Dry Period in different transferrin groups of Tarai buffalo and Sahiwal cattle

Type of transferrin groups	No. of animals	Mean ± SE (days)	CV (%)
Lactation length in different Transferrin groups of Tarai Buffalo			
BC	8	281.25 ± 9.71	9.77
CC	22	297.95 ± 6.71	10.57
Overall	30	289.60 ± 8.21	10.17
Dry Period in different Transferrin groups of Tarai Buffalo			
Type of transferrin groups	No. of animals	Mean ± SE (days)	CV (%)
BC	8	137.87 ± 2.40	5.06
CC	22	132.90 ± 3.03	10.71
Overall	30	135.58 ± 2.71	7.88
Lactation length in different Transferrin groups of Sahiwal cattle			
Type of transferrin groups	No. of animals	Mean ± SE (days)	CV (%)
DD	4	244.25 ± 25.30	20.71
EE	12	272.66 ± 30.38	38.60
AE	4	292.00 ± 13.20	9.04
DE	9	251.00 ± 32.58	38.95
AA	1	274.00	-
Overall	30	266.78 ± 25.36	26.82
Dry Period in different Transferrin groups of Sahiwal cattle			
Type of transferrin groups	No. of animals	Mean ± SE (days)	CV (%)
DD	4	322.50 ± 70.02	43.42
EE	12	266.41 ± 42.54	56.59
AE	4	184.25 ± 25.87	28.01
DE	9	202.22 ± 41.72	61.89
AA	1	256.00	-
Overall	30	246.27 ± 45.02	47.47

**The mule population of Goa, Mizoram, Sikkim, Tamilnadu and Tripura is <10. (Source: Livestock Census, 2012)*

Table 2. ANOVA of Lactation Length and Dry Period in Tarai buffalo and Sahiwal cattle

Source	d. f.	Mean sum of square	
		Lactation Length	Dry Period
Tarai buffalo			
Between groups	1	1637	144.68
Error	28	932.87	164.16
Sahiwal cattle			
Between groups	3	2264.75	24632.38
Error	25	4085.34	16261.13

mean dry period was higher in TfDD cows (322.50 days), while lowest dry period was reported in TfAE (184.25 days)

In Tarai buffaloes around 70% animal characterized in TfCC group and showed higher lactation length as compared to those of TfBC groups of animals. Only around 30% of animals were of TfBC groups. The mean dry period was higher in the animals of TfBC groups. When compared with Sahiwal cattle TfAE groups animal showed highest lactation length and lowest was reported in TfDD groups of animals and highest dry period was exhibited by TfDD groups of animals and lowest in TfAE groups of animals.

Analysis of variance was carried out for ascertaining the effect of different transferrin types on lactation length (L.L.) and dry period (D.P.) in Tarai buffalo and Sahiwal cattle. The perusal of the table 2 revealed that lactation length and dry period have non-significant correlation with different transferrin types in both Tarai buffalo and Sahiwal cattle. These finding was totally different as reported by Ballewar et al. (1997) who reported significant difference in different transferrin groups and lactation length and dry period; breed being different.

CONCLUSION

Serum transferrin polymorphism was studied by polyacrylamide gel electrophoresis method. The electrophoresis studies revealed 5 phenotype of transferrin in Sahiwal cattle viz. TfAA , TfDD , TfEE , TfAE and TfDE in the present study and two phenotypes in Tarai buffalo viz. TfBC and TfCC . All homozygotes in Sahiwal cattle had three bands whereas heterozygotes had bands ranging from 4 to 6. In Tarai breed the homozygotes transferrin produces three bands whereas heterozygotes transferrin presents four bands. The analysis of variance for lactation length and dry period revealed that these traits were statistically non-significant in different transferrin types for both Tarai buffalo and Sahiwal cattle. It can thus be concluded that comprehensive studies involving large sample size be undertaken to have the clear relationship of these traits with different transferrin groups in Tarai buffalo and Sahiwal cattle.

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Study on herd life traits of culled and disposed Kankrej cattle at organized farms

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ABSTRACT

An analysis was performed to study the herd life traits of culled and disposed Kankrej cattle at organized farms of Gujarat State. Data were collected from different disposal and production registers for the period from January 2003 to December 2013 and these were analyzed by using General Linear Model (GLM) procedure in the SPSS statistical software (version 20.0). The least squares analysis of disposed Kankrej cows at organized farms was performed to study on various life time traits like Age at First Calving, Number of Lactations Completed, Total Lactation Days, Life time Milk Yield, Herd Life, Herd Productive Life, Herd Unproductive Life, Milk Yield Per Day of Productive Life and Milk Yield Per Day of Herd life. The overall least squares means for above mentioned life time traits in Kankrej cows were 1548.12 ± 11.26 days, 3.29 ± 0.10 number, 1012.58 ± 30.66 days, 6427.01 ± 229.67 kg, 3225.91 ± 49.70 days, 1745.20 ± 86.62 days, 1174.63 ± 23.56 days, 3.73 ± 0.06 kg and 1.74 ± 0.04 kg, respectively for Kankrej herd of organized farm.

Keywords: Kankrej, herd life traits, culling, disposal
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INTRODUCTION

Kankrej is one of the heaviest breeds of cattle in India. The breed has originated from Kankrej area of Banaskantha district of Gujarat state and is maintained by Bharwad and Rabari communities. The breeding tract of Kankrej cattle mainly lies in north Gujarat region and Kutch district comprising of Banaskantha, Sabarkantha, Mehsana, Ahmadabad and Patan district of Gujarat and Barmer, Jodhpur areas of Rajasthan. However, the Kankrej cattle is distributed throughout the state of Gujarat.

A long herd life of a cow substantially decreases the replacement costs per lactation and enables a cow to achieve her maximum capacity of performance when attaining full maturity. In addition, the potential for a long herd life resting on good health and fertility reduces treatment costs and the incidences of involuntary culling. Genetic contribution in the form of living progeny to the next generation from a cow is associated with herd life, calf production and their survival for better replacement. Longer herd life increases the total lifetime and milk production, which in turn leads to higher selection intensity. The present investigation was made to explore the herd life traits of culled and disposed Kankrej cattle.

MATERIALS AND METHODS

Data of each disposed cattle from LRS, Sardarkrushinagar, CBF, Thara and CBF, Bhuj farms were taken from the periods 2003 to 2013. Data like date of birth, date of first calving, lactating days of all lactations, total milk produced in all lactations, number of parity and date of auctioned or disposed were collected from different registers of the farm and on the basis of above data various attributes like Herd Life (HL), Herd Productive Life (HPL), Herd Unproductive Life (HUNPL), Life Time Milk Yield (LTMY), Total Number of Lactations Completed (LN), Milk Yield Per Day of Productive Life (MYPDPL), Age at First Calving (AFC) and Milk Yield Per Day of Herd Life (MYPDHL) were calculated.

The data used in this study comprised of different normal production records of the cows of different

herds. The records for first to maximum twelve lactations were considered for calculation of herd life performance traits. Records considered abnormal cowing to one or more of the following reasons were not considered for calculation of the herd life performance traits.

* Short lactation (Less than 200 days).

* Lactations following abortion or dystocia.

The herd life (HL) was considered as the period from date of birth to the date of disposal, whereas herd productive life (HPL) was considered as the date of first calving to the date of disposal. The explanations for other herd life traits are as under (Pundir and Raheja, 1997).

Herd Unproductive Life (HUNPL)

= Herd life (HL) - Total Lactation Days (TLD)

Life Time Milk Yield (LTMY)

= Amount of milk produced over herd life

Total number of lactations completed (LN) over herd life.

Milk yield per day of productive life (MYPDPL)

= LTMY/HPL

Milk yield per day of herd life (MYPDHL)

= LTMY/HL

Age at first calving (AFC)

= Date of first calving – Date of Birth

Method of Statistical analysis

The data obtained for various herd life traits were analyzed statistically and expressed as Mean ± S.E. Data were analysed by CRD (Completely Randomized Design) using General Linear Model (GLM) procedure in the SPSS statistical software, version 20.0 (2001). One way ANOVA between herd life traits and pattern for disposal and also between herd life traits and reason for disposal followed by the Duncan post hoc test was performed to determine significant differences among the patterns and among reasons for disposal using General Linear Model (GLM) procedure in the SPSS statistical software (version 20.0).

The statistical model and ANOVA (Analysis of Variance) table for the design is as under.

$$Y_{ij} = \mu + T_i + E_{ij}$$

Where,

Y_{ij} = Response due to ith treatment in jth experimental unit.

μ = General mean

T_i = Effect of pattern or reason of culling, where i= 1,2,3,4 for pattern / i= 1,2,3,4,5,6 for reason of culling

E_{ij} = Experimental error associated due to ith treatment in jth experimental unit.

RESULTS AND DISCUSSION

Age at First Calving

Age at first calving (AFC) in Kankrej cattle at LRS, Sardarkrushinagar was 1323.72 ± 13.89 days (3.63 years). It was 348 days lower than CBF, Thara and

Table 1. Comparison of Least squares means for various life time traits of Kankrej cattle between three farms

S. N.	Name of farm	No. of Observation	AFC (days)	Parity (n)	TLD (days)	LTMY (kg)	Herd Life (days)	HPL (days)	HUNPL (days)	MYPDPL (kg)	MYPD HL (kg)
1.	LRS,SKN	205	1323.72^{b} ± 13.89	3.64^{a} ± 0.19	1025.87^{ab} ± 55.29	7600.00^{a} ± 452.06	2982.46^{b} ± 90.58	1834.33^{a} ± 205.23	1959.84^{a} ± 42.63	4.66^{a} ± 0.11	2.18^{a} ± 0.08
2.	CBF, Thara	200	1671.75^{a} ± 21.19	2.85^{ab} ± 0.13	915.34^{b} ± 43.76	4957.79^{b} ± 288.78	3263.80^{a} ± 72.07	1592.06^{b} ± 73.08	676.72^{b} ± 36.49	2.91^{b} ± 0.07	1.34^{b} ± 0.06
3.	CBF, Bhuj	129	1713.07^{a} ± 24.66	3.40^{a} ± 0.18	1142.21^{a} ± 61.55	6840.836^{a} ± 432.67	3554.04^{a} ± 95.49	1840.97^{a} ± 96.35	698.77^{b} ± 41.46	3.52^{b} ± 0.10	1.68b ± 0.08
	OVERALL	534	1548.12 ± 11.26	3.29 ± 0.10	1012.58 ± 30.66	6427.01 ± 229.67	3225.91 ± 49.70	1745.20 ± 86.62	1174.63 ± 23.56	3.73 ± 0.06	1.74 ± 0.04

The means with different superscript within a column among farms differ significantly at P < 0.05.

389 days lower than CBF, Bhuj observed during study period which indicated better care and feeding of animals at LRS, Sardarkrushinagar (Table 1). Overall age at first calving of Kankrej cattle in North Gujarat region was 1548.12 ± 11.26 days which was lower than the reports of Bhadoria et al. (2002) and Khatri et al. (2004) and higher than the earlier studies for indigenous cattle reported by Rehman et al. (2008), Das et al. (2011), Dangar and Vataliya (2014) and Anonymous, 2014. In general, AFC in zebu cattle is much higher as compared to their exotic or crossbred counterparts which is largely attributed to inherent character and lack of selection for their traits from generation to generation.

Herd Life

The overall herd life (HL) of Kankrej cattle at farms was 3225.91±49.70 days which was lower than the reports of Pundir and Raheja (1997) for Hariana cattle (3673.00 ± 50.80 days) and Bhattacharya et al. (2000) for Tharparkar cattle. The overall herd life of Kankrej cattle was found to be 3225 ± 49.70 days (8.84 years) at organized farms of North Gujarat. The overall mean herd life of Kankrej cows at CBF, Bhuj was higher {3554.04 ± 95.49 days (9.74 years)} than CBF, Thara {3263.80 ± 72.07 days (8.94 years)} and lower at LRS, Sardarkrushinagar {2982.46 ± 90.58 days (8.17 years)}. Results of herd life for Kankrej cows at three farms under present study were higher (8.84 years) than the Hariana cattle (2.74, 4.67 and 3.25 years) as reported by earlier workers Kaushik et al. (1994) and Sahiwal cattle (8.19 years) as reported by Pundir and Raheja (1997).

Herd Productive Life

Herd productive life (HPL), a health trait that evaluates a cow's genetic ability to stay in the herd, takes into account various characteristics that make a cow more sustainable thus more profitable.

The overall herd productive life for Kankrej cows at the organized farms at North Gujarat was 1745.20 ± 86.62 days (4.78 years). The overall HPL of Kankrej cows at organized farm under present study was lower than Hariana cattle (2227.00 days) as reported by Pundir and Raheja (1997), Rathi cattle (1940.55 days) as reported by Singh et al. (1997) and Sahiwal cattle (1872.28 days) as reported by Singh et al. (2011).

The present findings regarding mean herd productive life (HPL) of Kankrej cattle observed was higher at CBF, Bhuj {1840.97 ± 96.35 days (5.40 years)} followed by at LRS, Sardarkrushinagar {1834.33 ± 205.23 days (5.02 years)} and lower at CBF, Thara{1592.06 ± 73.08 days (4.36 years)}. The results were higher than the reports of Patel (1971) for Kankrej cattle at Anand (3.45 years) and Chharodi (4.58 years), Chaudhary (1999) for Gir cattle (1641.99 ± 71.81 days) and Jakhar et al. (2010) for Hariana cattle (4.38 ± 0.20 years).

However, these findings of HPL (1745.20 days) of Kankrej cattle was higher than those obtained (1061.64 ± 47.65 days) by Burte (1995) for Kankrej cattle, Burte (1995) for Jersey X Kankrej crossbred (1431.33 ± 110.29 days) and Pundir and Raheja (1997) for Sahiwal cattle (1171.00 ± 101.40 days). HPL of Kankrej cattle at CBF, Bhuj (5.04 years) and LRS, Sardarkrushinagar (5.03 years) were comparable with the results (4.94 years) reported by Reddy and Nagarcenkar (1988) for Sahiwal cattle.

Total Lactation Days

The overall total lactation days (TDL) in Kankrej cow's disposal from organized farm were 1012.58 ± 30.66 days. Table 1 revealed that total lactation days of Kankrej cows was higher at CBF, Bhuj (1142.21 ± 61.55 days) followed by at LRS, Sardarkrushinagar (1025.87 ± 55.29 days) and CBF, Thara (915.34 ± 43.76 days). Present TLD of Kankrej cows at all three stations were higher than findings of Kaushik et al. (1994) for Hariana cattle of G. L. F., Hastinapur –Meerut (899.10 ± 76.57 days) and were lower than Kaushik et al. (1994) for Hariana cattle of Babugadh-Gaziabad (1373.39 ± 72.6 days).

Life Time Milk Yield

Looking to the economic aspect, milk yield is an important trait amongst all traits. The overall life time milk yield (LTMY) in Kankrej cows disposed from organized farm of North Gujarat was 6427.01 ± 229.67 kg. The present findings related to mean life

time milk yield (LTMY) of Kankrej cattle observed was higher at LRS, Sardarkrushinagar (7600.00 ± 452.06 kg) followed by CBF, Bhuj (6840.836 ± 432.67 kg) at and lower at CBF, Thara (4957.79 ± 288.78 kg). Though the TLD was lower (1025.89 days), the LTMY at LRS, Sardarkrushinagar was better (7600.00 kg) than the C.B.F., Bhuj indicated better daily milk production of Kankrej cows at LRS, Sardarkrushinagar. LTMY of Kankrej cows at LRS, Sardarkrushinagar and CBF, Bhuj were higher than those reported by Burte (1995) for Kankrej cattle (5862.69 ± 289.36 kg) and Singh et al. (1997) for Rathi cattle (5706.96 ± 580.13 kg).

LTMY of Kankrej cows at all three farms were higher than those reported by Kaushik et al. (1994) for Hariana cattle (2662.04 ± 306.92 and 4090.02 ± 291.03 kg, respectively) at Meerut and Babugadh farm, Pundir and Raheja (1997) for Sahiwal cattle and Hariana cattle (4707.00 ± 195.90 kg, and 4192.00 ± 123.70 kg, respectively). The present findings of LTMY of Kankrej cows were lower than the earlier studies for crossbred cow reported by Burte, (1995) and Singh et al. (1997).

Total lactation number/parity

Overall lactation completed by Kankrej cows disposed from organized farms of north Gujarat was 3.29 ± 0.010. The mean lactation number / parity of Kankrej cows disposed observed during the period at LRS, Sardarkrushinagar, CBF, Bhuj and CBF, Thara was 3.64 ± 0.19, 2.85 ± 0.13 and 3.40 ± 0.18 nos., respectively. Present findings of parity of Kankrej cows disposed were more or less comparable with earlier reports for Hariana (3.87) and Gir (3.37) reported by Jakhar et al. (2010) and Chaudhary (1999), respectively. However, the present findings of parity of disposed Kankrej cows (4.68), Rathi cows (4.70) and Tharparkar cows (4.38) reported by Reddy and Nagarcenkar (1988), Singh et al. (1997), Bhattacharya et al. (2000), respectively. The present findings of parity were also lower than crossbred cows (4.85 and 5.04) reported by earlier workers (Burte, 1995 and Singh et al. 1997)

Milk yield per day of productive life and Milk yield per day of herd life

The overall Milk yield per day of productive life and Milk yield per day of herd life of Kankrej cows disposed from organized farms of North Gujarat were 3.73 ± 0.06 and 1.74 ± 0.04 kg, respectively. Milk yield per day of productive life and Milk yield per day of herd life of Kankrej cattle were highest (4.66 ± 0.11 and 2.18 ± 0.08 kg.) at LRS, Sardarkrushinagar followed at CBF, Bhuj (3.52 ± 0.10 and 1.68 ± 0.08 kg.) and CBF, Thara (2.91 ± 0.07 and 1.34 ± 0.06 kg.).

Overall findings for Milk yield per day of productive life (MYPDPL) of all three stations were lower (3.73 kg) than earlier reports for Hariana (6.02 kg), Gir (4.35 kg), reported by Yadav and Rathi (1992) and Chaudhary (1999), respectively. However, overall findings for Milk yield per day of productive life of all three stations were higher than the reports for Tharparkar cattle (1.71 ± 0.09 kg) reported by Bhattacharya et al. (2000). Overall findings for Milk yield per day of herd life of Kankrej cows was lower (1.74 ± 0.04 kg) than the reports for Gir cattle (1.97 ± 0.88 kg) by Chaudhary (1999).

CONCLUSION

Performance of Kankrej cattle of Livestock Research Station, S. D. Agricultural University, Sardarkrushinagar (Gujarat) was better than other two organized farms. Looking to the performance of Kankrej cattle it can be concluded that Kankrej cattle has genetic potential which by means of proper breeding strategies and management can be exploited further.

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Cytogenetic screening of cattle and buffalo breeding bulls

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ABSTRACT

Chromosomal abnormalities cause a drop in reproductive performance or even complete infertility/sterility in the carrier animals. Present investigation was undertaken to detect chromosomal abnormality, if any, in 155 breeding bulls of exotic (*Bos taurus*, 2n=60), indigenous (*Bos indicus*, 2n=60) cattle, their crossbreeds and Murrah buffalo (*Bubalus bubalis*, 2n = 50) maintained by various organizations. Mitotic chromosome spreads were prepared and analysed from cultured lymphocytes of 155 breeding bulls of different indicus, exotic and crossbred cattle (Holstein Friesian, Jersey, Red Sindhi and Sahiwal) and 41 Murrah buffalo bulls reserved for breeding and maintained at different stations of State Livestock Development Boards from the state of Haryana, Punjab, Uttrakhand, Jammu and Kashmir, Rajasthan and Assam. Giemsa staining of chromosomes revealed that 98.2% cattle bulls possessed normal chromosome complements. One Holstein-Friesian and one HF crossbred bulls were found to be sex chromosome chimeric (60, XX/60, XY). No chromosomal abnormality could be detected in any of the Murrah buffalo bulls studied. Such regular cytogenetic screening will not only reduce the occurrence of chromosomal abnormalities in dairy animal population but also will save the time and cost of rearing the abnormal animals.

Key Words: Chromosomal abnormality, infertility, sterility, sex chromosome chimeric, cytogenetic screening.
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INTRODUCTION

Reproductive efficiency is one of the corner-stone in enhancing productivity of dairy animals. Infertility and / or sub fertility are the most crucial issues being faced by the dairy industry. The infertility problem can occur at different levels and of course due to different factors like poor breeding, feeding management. However, chromosomal aberrations or abnormal karyotype could be one of the reasons for reproductive failure in dairy animals. Eliminating bulls with physical problems or reduced fertility from the breeding herd will improve overall reproductive efficiency of the herd (Jamir et al., 2015).

Chromosomal aberrations can affect a large population in two ways. It can be transmitted to a large population through artificial insemination (AI) and secondly it can cause repeat breeding problems in females because of embryonic loss and poor semen quality in breeding bulls (Krumrych 2009). Chromosomal abnormalities have been reported to be associated with reproductive performance in Indian cattle (Patel and Khoda 1998), which include infertility of carriers, degeneration of reproductive organs, poor semen quality (Ducos et al., 2008). Chimerism is very common in cattle (Peretti et al 2008) but also has been reported in buffalo (Balakrishnan et al. 1981; Iannunzzi et al. 2005; Kumar et al. 2009). When two or more populations (XX/XY) derived from heterosexual zygotes exist in the same individual, the condition is known as Chimerism (Patel and Patel, 2014). Chimerism usually affects fertility of females but males are not grossly affected. However, on the contrary many reports have been published on reduced fertility or infertility of chimeric bulls. Reduced fertility was

observed and many bulls were culled due to no semen ejaculation, low sperm count or a high incidence of abnormal spermatozoa (Dunn et al., 1979). Cytogenetic investigations in domestic animals were started in early sixties globally and various abnormalities have been reported in Indian cattle (Prakash et al., 1995; Patel and Patel, 2000; Yadav, 2000; Patel, 2002; Patel, 2003) and buffaloes (Chauhan et al., 2009; Prakash et al., 2009).

Due to wide spread use of AI, the risk of spreading genetic defects through bulls has increased manifold. There is therefore a pressing need for cytogenetic screening of bulls before using them for AI to keep the herd free from genetic defects. Even in India it is now mandatory to karyotype each and every cattle and buffalo bull before putting it into breeding programme under the recently formulated National Programme for Cattle and Buffalo Breeding (NPCBB) by DAHDF, Govt. of India. Any animal can be screened or karyotyped even at calf hood stage. Subsequently, the animal with chromosomal abnormality can be removed from breeding programme to avoid the transmission of chromosomal abnormality or genetic defects in progeny.

The present study was conducted to screen the breeding bulls of cattle and buffalo from different states of India for any karyotypic abnormality, so that bull can be culled at early stage before putting into breeding programme and such abnormality are not transmitted to the next generations through breeding.

MATERIALS AND METHODS

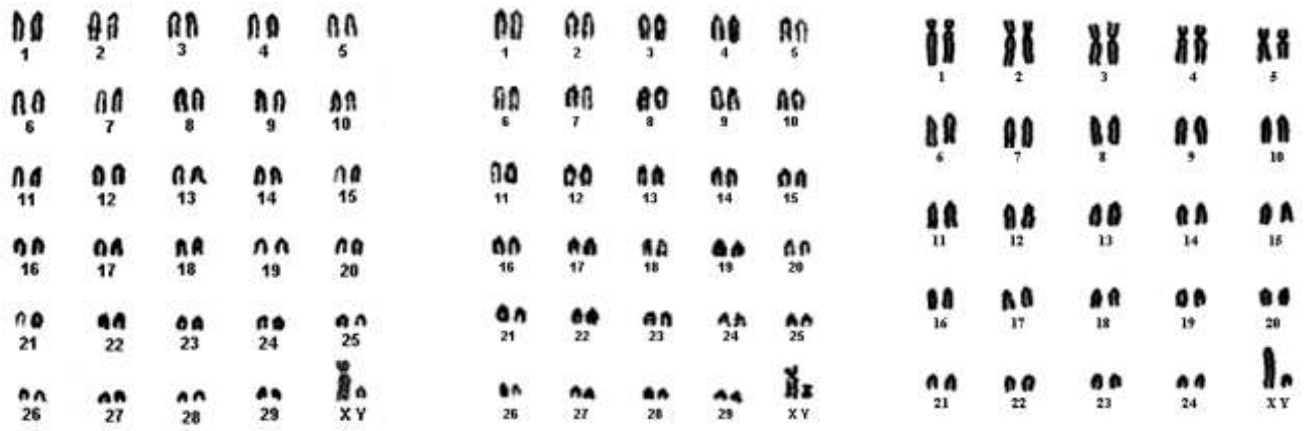
This work was conducted at the Department of Zoology, Kurukshetra University, Kurukshtra and molecular cytogenetic lab of ICAR-National Bureau of Animal Genetic Resources, Karnal to investigate the chromosomal abnormalities in breeding bulls of different breeds and crossbreds of cattle and buffalo.

A total of 155 blood samples were collected from in sterile heparinized vacutainer tubes from phenotypically normal 69 Holstein–Friesian (HF), 7 Jersey, 6 Red Sindhi, 6 Sahiwal, 20 HF crossbred, 6 Jersey crossbreed bulls and 41 Murrah buffalo bulls (Table 1) maintained at different stations of State livestock development boards from Haryana, Punjab, Uttrakhand, Jammu and Kashmir, Rajasthan & Assam.

Whole blood lymphocyte cultures were set-up for 72 hours at 37^0C for each bull in standard medium (RPMI 1640-Sigma, St. Louis, USA) supplemented with 15% fetal calf serum, Penicillin and streptomycin (100 IU/ml and 0.1 mg/ml of culture medium, respectively) and pokeweed mitogen (2.5 µg/mL of culture medium, SIGMA, St. Louis, USA). To arrest the somatic cells at metaphase stage, colchicine (Sigma, India) 2 µg/mL was added for one

Table 1 Details of bulls of cattle and buffalo breed wise screened for chromosomal abnormalities.

Name of the Station	Cattle Breed								Buffalo Breed
	HF	Jersey	Red Sindhi	Sahiwal	HF X Sahiwal	Jersey x Sahiwal	HFX Gir	Jersey X Red Sindhi	Murrah
1. Semen Bank, Hisar (Haryana)	05	-	-	-	02	-	-	-	20
2. Animal Breeding Centre, Salon(UP)	13	-	03	01	08	-	02	03	10
3. Semen Bank Nabha (Punjab)	13	-	-	-	05	-	-	-	02
4. Semen Bank, Roper (Punjab)	12	01	-	03	03	-	-	-	-
5. Deep Frozen Semen Production Centre, Rishikesh, (Uttrakhand)	08	01	03	02	-	02	-	-	09
6. Kashmir Livestock Development Board, Kashmir (Jammu and Kashmir)	05	-	-	-	-	-	-	-	-
7. Rajasthan Livestock Development Board, Jaipur (Rajasthan)	12	-	-	-	-	-	-	-	-
8. Frozen Semen Bank, Jagadhari (Haryana)	01	-	-	-	-	-	-	-	-
9. Assam Livestock Development Board, Guwahati(Assam)	00	05	-	-	-	01	-	-	-
TOTAL	69	07	06	06	18	03	02	03	41



A B C

Figure 1. Normal karyotype of zebu (A; 2n:60), taurus (B; 2n:60) and river buffalo (C; 2n:50) males

hour before harvest. The cells were harvested by centrifugation at 2000 rpm for 20 minutes, followed by hypotonic treatment with 0.075 M KCl for 20 minutes at 37°C to lyse the RBCs and lymphocytes were fixed in Carnoy's fixative (3:1 ratio of methanol and glacial acetic acid). Finally, cell suspension was dropped on slides and air dried to prepare chromosome spreads. Slides were stained with 2% Giemsa stain and DPX mounted. At least 30 metaphase spreads for each animal were analyzed under bright field microscopy under oil immersion (100X magnification) and karyotyping was done by using automatic karyotyping software (Genus).

RESULTS AND DISCUSSION

Domestic cattle of *Bos taurus* (humpless taurine), Bos indicus (humped, Zebu) and their crosses possess a normal diploid number of 60 chromosome (2n = 60), which comprises 29 pairs of autosomes and a pair of sex chromosomes (XX in females and XY in males). Structurally, all the 29 pairs of autosomes and the X chromosome are acrocentric and submetacentric, respectively, in both *Bos taurus* and *Bos indicus* cattle. The only difference is in the Y chromosome, which is submetacentric in Bos taurus but acrocentric in *Bos indicus* cattle (Lightner, 2008). A normal karyotype of male zebu and Taurus cattle is shown in Fig.1 A-B.

Normal Karyotypic profile of a Murrah buffalo (*Bubalus bubalis*) comprises 50 chromosomes composed of 24 pair of autosomes and a pair of sex chromosomes (CSKBB1994). First five pairs of autosomes are biarmed (metacentric or submetacentric) and the remaining 19 pair are acrocentric. The X chromosome is morphologically distinguishable because it is largest acrocentric chromosome, almost 25% larger than the largest autosome pair (Prakash et al., 2009). The Y chromosome is amongst the smaller acrocentric chromosome and not distinguishable from smaller acrocentric autosome pairs (Kumar and Yadav, 1991). A normal karyotype of male river (Murrah) buffalo (*Bubalus bubalis*) is shown in Fig.1 C.

The results of the study are presented in Table 2. Out of the 155 breeding bulls of cattle and buffalo screened, only 2 cases of anomalous karyotype were detected. Both were cattle bulls which were chimeric with respect to 60, XX/60,XY. First case was a crossbred i.e. Frieswal (HF x Sahiwal) belonging to Animal Breeding Centre, Salon (U.P) and the other was a pure HF bull maintained at Semen Bank, Nabha of Punjab Livestock Development Board.

Both the bulls showed the presence of male (60,XY) as well as female (60,XX) cells in the chromosome preparations obtained from blood leukocytes. One bull showed 17% female cells while the other had 28% female cells (60,XX). Presence of male and female cells in the two bulls is shown in Fig. 2. At present, Sex chromosome chimerism (XX/XY) may

Table 2. Details of bulls having chromosomal abnormalities

S.N.	Station	Species/ breed	Abnormality found	No. of bulls afflicted
1	Animal Breeding Centre Salon, Raibareilly (U.P.)	Cattle (HF X Sahiwal) Frieswal	XX/XY (Chimeric)	01
2	Semen Bank, Nabha (Punjab)	Cattle (H.F.)	XX/XY (Chimeric)	01

be diagnosed by karyotyping (as in the present study), blood typing, polymerase chain reaction (PCR) or fluorescence identification of Y-chromosome directed probes (FISH).

Chromosome chimerism occurs in cattle (60,XX/60,XY) as well as buffalo (50,XX/50,XY) heterosexual twins. The female co-twin of such twins is usually defined as a sterile female (Freemartin) calf that shows underdeveloped or misdeveloped genital tract as a result of early development of vascular anastomoses between fetuses of different gender. As consequence of placental anastomoses between the heterosexual twins, blood chimaerism occurs (60, XX/XY) and passage of male gonad determinants or hormones (such as Anti-Mullerian hormone and androgens) are responsible for disrupted differentiation of the female embryonic gonads and disturbed genital tract development (Padula, 2005; Schlafer and Miller, 2007). Compared to the dramatic changes observed in genital differentiation in the freemartin heifer, the male co-twin only displays minimal gross defects, though a decrease in male fertility has been reported (Dunn et al., 1979; Padula, 2005). The pedigree record of the two bulls in the present study could not be confirmed, but the findings suggest their births as co-twin to female partners.

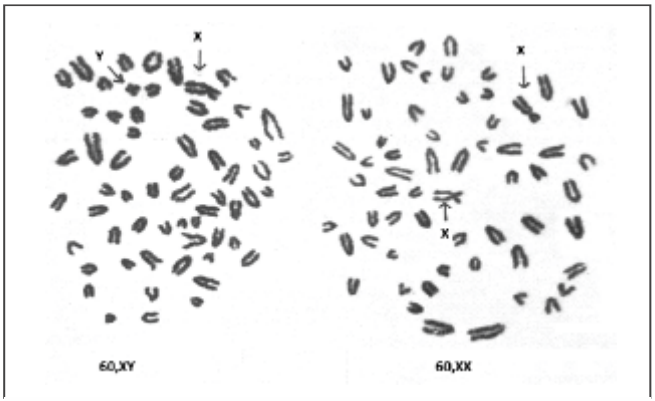


Figure 2. *Presence of male (60,XY) and female (60,XX) cells in two bulls*

As a rule, heterosexual twins have to be considered abnormal and should be identified as early as possible to cull them from the breeding stock. Twining seems to have some genetic background and varying incidence of twining among breeds has been reported (Table 3). Additionally, twinning incidence may vary with men-imposed artificial selection, either by culling or by intentionally using cows with higher twinning rates (Gregory et al., 1997), or even as a consequence of multiple non-sexed embryo transfer, where the deposition of two or more embryoes is currently performed (Padula, 2005). Multiple pregnancies are strongly affected by age and parity, but only slightly influenced by season. Multiple pregnancies in cattle also have some other drawbacks like the prolonged postpartum resumption of the ovarian cyclic activity, an increase in the number of abortion, the still birth and the premature births, and the predisposition to dystocia.

A male born as co-twin to a freemartin calf rarely exhibits gross morphological deformities (Kovacs et al.,1977, Schlafer and Miller, 2007). However, reports of associated male infertility and poor libido exists (Dunn et al., 1979). Still, the basis for infertility remains contentious. Some of the reports describe the presence of focal areas of testicular degeneration (Dunn et al., 1979) and of testicular hypoplasia (Meinecke et al., 2003) could lead to infertility. In addition, the presence of spermatogonial XX/XY chimerism (Redjuch et al., 2000) associated with chromosomal fragility, as demonstrated by Peretti et al. (2008), or to increased degenerative changes could also contribute to loss of fertility in males born co-twin to a female. XX germ cells do not survive in male gonads (Willier, 1921). In some situations, infertility has also been associated to changes in the quality of sperm (motility, concentration, morphology and viability) co-existing with of

Table 3. Reported incidence of twinning in different cattle breeds

S.N.	Breed	Twinning (%)	Reference
1	Holstein Friesian	3.40	Rutledge, 1975
2	Holstein Friesian	4.75	Cady and Van Vleck, 1978
3	Holstein Friesian	2.91	Silva del Rio et al., 2006
4	Jersey	1.30	Rutledge, 1975
5	Jersey	1.83	Cady and Van Vleck, 1978
6	Simmental	4.6	Weber, 1944
7	Guernsey	2.33	Cady and Van Vleck, 1978
8	Swedish Friesian	1.95	Johansson et al., 1974
9	Swedish Friesian	2.57	Gregory et al., 1990
10	Swedish Red and White	1.47	Johansson et al., 1974
11	Brown Swiss	8.90	Rutledge, 1975
12	Brown Swiss	4.08	Cady and Van Vleck, 1978
13	Hereford	0.40	Rutledge, 1975
14	German Fleckvieh	3.16	Silva del Rio et al., 2006
15	Angus	1.10	Rutledge, 1975
16	Santa Gertrudis	0.40	Rutledge, 1975
17	Brahman	0.20	Rutledge, 1975

From Esteves et al. (2012)

acrosome defects (Redjuch et al., 2000).

Cytogenetic screening should be used as diagnostic tool to improve the herd quality by selecting superior animals and culling the abnormality carrier from breeding programmes. Chromosomal abnormalities reduce the reproductive potential of farm animals through decreasing ability or complete failure to produce viable gametes and death of embryos. Moreover, there is a pressing need to establish a proper monitoring and regulatory system to ensure that the males (local or imported) selected for breeding are regularly screened against cytogenetic abnormalities. This would intensify benefits of the farming industry by reducing associated reproductive failure. In the present study one Frieswal bull and one Holstein–Friesian bull were found to be chimeric which were otherwise physically normal. Because of a number of reports indicating low fertility in chimeric bulls (Dunn et al., 1979), the concerned organizations were informed to exclude the afflicted bulls from the breeding programme in the view of the results of this investigation.

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Evaluation of reproduction performance of Gir cattle (*Bos indicus*) reared in Hot-Humid condition of Konkan region

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ABSTRACT

The study was conducted at Dr. B.S. Konkan Krishi Vidyapeeth Dapoli, Maharashtra to assess the reproductive efficiency of Gir cattle. A total of 226 Gir cows were selected and their information regarding reproductive parameters were collected from farm records (Bombay Gorakshak Mandali, Akurli Road, Kandivali (East) Mumbai, Maharashtra) for a period of 26 years (1981 to 2005). Data representing 226 Gir cows from 1090 total records of reproductive parameters for a period of 25 years (1981 to 2005) were analysed to determine Body weight (BW), age at puberty (AP), age at first calving (AFC), service period (SP), calving interval (CI), gestation period (GP), dry period (DP), weight at first calving, reproductive and breeding efficiency (%). The overall least squares means of age at puberty (979.08±12.77 days), age of first calving (1254.29±12.83 days), service period (107.93±0.64 days), calving interval (387.26±0.63 days), gestation period (279.86±0.20 days), dry period (87.74±0.95 days), weight at first calving (352.63±1.64 kg), with reproductive and breeding efficiency and persistency index, 40.70±0.11 per cent and 89.29±0.40 per cent, respectively. Therefore, it can be concluded that Gir cattle shows optimum reproductive performance under Konkan region of Maharashtra.

Key Words: Age of first calving, calving interval, dry period, Gir cattle, service period.
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INTRODUCTION

The reproductive performance of the breeding female is probably the single most important factor that is a prerequisite for sustainable dairy production system and influencing the productivity. The size of the calf crop is important for herd replacement and the production of milk depends on heavily on the cow reproductive activity (Kiwuwa et al., 1983).

Maharashtra second largest livestock population state in India. The livestock sector has been contributing considerable portion to the economy of the country and still promising to rally round the economic development of the country. The total cattle population of the state is estimated to be about 16.2 million. Out of this the indigenous cattle constitute about 13.1 million and the remaining 3.1 million are crossbred cattle (Anonymous, 2015).

Reproductive performance of cattle is influenced by feed, genetic, disease and management practices (Perera, 1999).Number of services per conception, days opens and calving interval are important reproductive traits which are crucial for determining the profitability of dairy production (Alemayehu et al., 2014). The aim of the present study was therefore, to investigate the reproductive performance of Gir cattle in Konkan region of Maharashtra, India.

MATERIALS AND METHODS

The data of 226 cows for the reproduction performance observations viz. body weight (BW), age at puberty (AP), age at first calving (AFC), service

period (SP), calving interval (CI), gestation period (GP), dry period (DP), persistency index, reproductive efficiency (%) and breeding efficiency (%) of Gir cattle maintained at Bombay Gorakshak Mandali, Akurli Road, Kandivali (East) Mumbai, Maharashtra in jurisdiction of the Dr. B. S. Konkan Krishi Vidyapeeth, Dapoli, Dist. Ratnagiri, Maharashtra State in India for the period of 25 years (1981 to 2005) were utilized for the study. Breeding efficiency was estimated by formula given by Tomar (1965), reproduction efficiency by Banerjee, (2004) and persistency index by Rao and Sundaresan (1982) as follows.

Breeding efficiency

= (Number of calving interval x (365) + 1020)/(Age of cow) x 100

Reproduction efficiency

=12 x (Number of calves born)/(Age of cow (month) – age at first breeding) x 100+3

Persistency Index

=(Standard Lactation Milk Yield (l))/(Peak Yield (l))

The standard uniform feeding and management practices were provided throughout the experimental period to all the animals. All the animals were maintained under stall feeding system. The main aim of present study to know the reproduction performance of Gir cattle and data calculating least-squares mean and maximum by using the fixed models given by Harvey (1975). The differences between least squares mean were tested through Duncan's multiple range tests

RESULTS AND DISCUSSION

Calf birth weight (CBW)

The overall least square means of CBW in present study 23.82±0.20 kg (Table 1). Higher BW of calves as compared to the present study was reported by many researchers (Taj, 2001). These differences might be due to breed, environmental and managerial practices that had impact on BW.

Age at puberty and weight at puberty (AP and WP)

The overall least square means of AP and WP were 979.08±12.77 days and 288.48±1.44 kg, respectively (Table 1). The present finding observed higher as compared to Mostari et al. (2007) in Red Chittagong cattle for age of puberty (458.7 days). Sandhu et al. (2011) also observed lower age of puberty in crossbred cattle (625.40±14.65 days). However, higher AP was reported by Pandit et al. (1999) in Gir cows (1116±74.7 days).

Age of first calving (AFC) and Weight at first calving (WAFC)

The overall least square means of AFC and WAFC in present study was 1254.29±12.83 day and 352.63±1.64 Kg (Table 1). The present finding found higher as compared to Kumar et al. (2016) in Frieswal cattle (980.41±8.22 days), Manjusha et al. (2016) in crossbred cattle (924.34±61.9days) and indigenous cattle (1090±192 days), Pundir et al. (2015) in Manipuri cattle (1130 days), Gaikwad et al. (2011) in Gir cattle (1401 to 1600days). Higher AFC reported by Gaur et al. (2005) and Bhadoria et al.(2003) in Gir cows as 1533±56 days and 1719.09±8.11 days, respectively. However, lower AFC was reported by Sandhu et al. (2011) in crossbred cows (655.10±10.44 days). AFC depends on various factors like the breed of animal, feeding, heat detection, animal health, breeding method etc. two and half years are considered as ideal for a cross bred cow to calve for first time Manjusha et al.(2016).

Service period (SP)

The average SP in Gir cows was 107.93±0.64 days (Table 1). The present finding is found near to the estimates reported by Pandit et al. (1999) and Bhadoria et al. (2003), who reported that 122.45±2.01 days and 138.93±5.53 days in Gir cows, respectively. Higher values for SP was observed by Umrikar et al.(1990) and Barwe et al.(2003) in Gir cattle (273.7 days and 161.44±4.85 days) and Sandhu et al.(2011)in Crossbred cattle (29.95±2.14 days). The variation in SP reported by different workers may be due to variation in the managemental practices in estrus detection and timely breeding followed in different herds (Savaliya et al., 2016).

Number of services per conception (NSPC)

The overall least squares mean for NSPC was

Table 1: Least-squares means (LSM) for reproduction performance of Gir cattle

S. N.	Traits	n	LSM±SE
1.	Birth weight (kg)	226	23.82±0.20
2.	Age at puberty (days)	226	979.08±12.77
3.	Weight at puberty (kg)	226	288.48±1.44
4.	Age at first calving (days)	226	1254.29±12.83
5.	Growth rate up to puberty (kg/day)	226	0.30±0.0034
6.	Service period (days)	1090	107.93±0.64
7.	Number of services per conception	1090	1.83±0.03
8.	Calving interval (days)	1090	387.26±0.63
9.	Gestation period (days)	1090	279.86±0.20
10.	Dry period (days)	1090	87.74±0.95
11.	Reproductive efficiency (%)	226	40.70±0.11
12.	Breeding efficiency (%)	226	89.29±0.40
13.	Persistency index	1090	184.09±0.92

SE: standard error

1.83±0.03 (Table 1). Similar findings in Gir cattle (1.8±0.3) were reported by Belay et al. (2012). Number of services per conception higher than 2.0 should be considered as poor (Mukassa Mugerewa, 1989). Higher NSPC was reported by Alemayehu et al. (2014) in indigenous dairy cows (2.0±0.65). However, lower NSPC was observed by Yifat et al. (2009) as 1.67 and Haile-Mariam et al. (1993) as 1.61. In the study area number of service per conception may be affected by time of insemination, proper heat detection and quality of semen etc.

Calving interval (CI)

The average CI observed in present study was 387.26±0.63 days (Table 1) which is near to the estimates of Khirari et al. (2014) in non-descript cows (381.23±3.27 days) and Manjusha et al. (2016) in crossbred cow (389.46±13.49 days). The estimated value was desirable for profitable milk production. The higher findings for calving interval was observed by Manjusha et al. (2016) in indigenous cattle (405.78±15 days), Kumar et al. (2015) in Frieswal cattle (423.05±12.24 days), Pundir et al. (2014) in Hill cattle (432 days), Dangi et al. (2013) in Rathi cattle (427±12.3 days), Pundir et al. (2013) in Uttara cattle (456 days).

Gestation period (GP)

The overall least squares mean for GP was 279.86±0.20days (Table 1). This average value of GP in the present study is near to the estimates of first GP reported by Singh et al. (2012) in Gir cattle (279.8±0.69 days). Similar value of first gestation period were also reported by Sharma et al. (1989), Babu Rao, (1990) and Norman et al. (2009) in Gir cattle and Raja, (2010) in Sahiwal cattle, whereas lower value reported by Mondal et al. (2005) as 275±4.11, 276±4.26, 274±4.41, 275±3.95 and 277±3.31 days with overall average 275±4.11 days in Jersey cross, Sahiwal cross, Sindhi cross, Holstein cross and Red-Chittagong cattle of Bangladesh and Patel et al. (1999) in Gir cows (273.12±1.96 days) and greater value in Gir cattle reported by Gaikwad et al. (2011), Malik and Ghei, (1977)and Casian D'Souza et al. (1978)as 284 to 286 days, 286.60±12.80 and 283.8±0.9 days gestation period and Camargo et al. (2005) by in Zebu cattle (284.4±1.1), respectively. The gestation length is a species characteristic. The variation of gestation length is genetically determined. Variation may be due to maternal influence. A little variation in gestation length within the individual may be contributed mainly by maternal and foetal factors. Ages of dam, nutritional body condition of the dam are the maternal factors. On the other hand, foetal factor include the sex of the foetus, twining and hormonal functions of the foetus. Environmental factors such as season, temperature, feeding and management may also contribute to some extent Mostari et al. (2007).

Dry period (DP)

The overall least squares mean for DP was

87.74±0.95 days. Similar findings in Gir cattle were reported by Sandhu et al. (2011) in crossbred cattle (87.06±1.63 days). Higher DP was reported by Gaikwad et al. (2011) in Gir cattle (91-120 days), Bhutkar et al. (2014) in Deoni cows (211.93±26.23 days). Nanavati et al. (2004) and Younas et al. (2008) also reported DP as 145.32±3.46 days and 137.94±4.04 days, respectively in Gir cattle.

Reproductive efficiency, breeding efficiency (%) and persistency index

Breeding efficiency (BE) is an important reproductive parameter that reflects the regularity of calving and the adaptability of the breed to its environment. The overall mean for reproductive efficiency and breeding efficiency was 40.70±0.11 and 89.29 ± 0.40 per cent. The overall mean persistency index of Gir cattle was 184.09±0.92. The mean RE and BE reported in this study was comparable with those reported by Berhanu et al. (2011) as 81.90 per cent for BE in crossbred cattle. Lower breeding efficiency by Deshpande et al. (1984) in Gir cattle (87.14%), Shelke et al. (1992b) in Red Kandhari cattle (74.77±71.0%), Getinet et al. (2009) in crossbred cattle (69.6%).

CONCLUSION

From the investigation, it was revealed that Gir cow has lower values age at puberty (979.08±12.77 days) and age of first calving (1254.29±12.83 days) in present study. Other parameters also have large quite satisfactory values in case of dry period (87.74±0.95 days), weight at first calving (352.63±1.64 kg), service period (107.93±0.64 days), number of services per conception (1.83±0.03), calving interval (387.26±0.63 days), gestation period (279.86±0.20 days) with reproductive, breeding efficiency and persistency index, 40.70±0.11 per cent, 89.29±0.40 per cent and 184.09±0.92, respectively. Therefore, it may be concluded that Gir cattle give optimum reproductive performance under Konkan Region of Maharashtra.

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Comparative study of pre and post Artificial Insemination after antibacterial drugs infusion in repeat breeding crossbred cows

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ABSTRACT

The study was conducted on 144 normal and repeat breeder cows. In the case of normal cow higher conception rate (63.63 %) was observed with pre Artificial Insemination Amoxicillin -Cloxacillin treatment than the Ceftriaxone sodium treatment, 53.84 %, while in post Artificial Insemination treatment higher conception rate 57.14 % was recorded with Ceftriaxone than Amoxacillin-Cloxacilin. In repeat breeding cow, pre and post A. I. treatment with Amoxacillin-Cloxacilin showed higher conception rate 60.60 % and 63.63 % respectively as compared to 50.00 % and 50.41 % in the case of Ceftriaxone infusion.

Keywords: Amoxacillin-cloxacilin, ceftriaxone, crossbred cows, repeat breeder
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INTRODUCTION

One of the most important and commonly encountered sub fertility conditions in cattle which play a vital role in dairy economics is repeat breeding efficient dairying and breeding demand that an animal shall give birth of a healthy calf every 12 months and be in the milk for at least 300 days per lactation. Effort should therefore be made to enhance fertility in dairy animals by narrowing down their dry period to be minimum range of 80 to 90 days. Thus, fertility of milch animals appears to plays a major role in dairy economics. Repeat breeding is one of the most vexing problems in dairy cattle and account for huge economic loss to the farmer. The reason for repeat breeding are tow fold viz. failure of fertilization (39.7%) and early embryonic mortality (93.2%) most due to infection of female genitalia (Tanabe and Casida, 1949). In the present experiment, single dose of Ceftriaxone sodium (Vetaceph) and Amoxicillin-Cloxacillin (Crilmox) were tried through intrauterine route for improving conception rate in repeat breading cows.

MATERIALS AND METHODS

The trial was carried out on 144 cross bred repeat breeding cows belonging to private organized farms at Ranchi. The cows which failed to conceive for three or more than three either naturally or artificially bred were included in the trial. All these animals had normal estrus cycles estrus periods, and had clear & transparent cervical mucus discharge hanging from vulva. The experimental animals were grouped into two treatment and control group and treated as pre the following protocol (table 1).

The animals under all the treatment and control groups were observed and efficacy of each treatment schedule was judged on the basis of pregnancy diagnosis by rectal palpation on D50-60 post artificial insemination. The comparative efficacy of

Table 1: Treatment profile for different groups

Groups	Drugs	Doses	Routes
Group-I	Ceftriaxone sodium	1 gm, dissolved in 30 ml distilled water	infused I/U 8-12 hrs pre or post insemination
Group II	Amoxycillin+ Cloxacillin	1.25 g, dissolved in 30 ml distilled water	infused I/U 8-12 hrs pre or post insemination
Group III	Distilled water	only 30ml of distilled water	infused I/U 8-12 hrs pre or post insemination

medicine was worked out by comparing the conception rate in treatment groups with the control one.

RESULTS AND DISCUSSION

The Conception rate with intrauterine infusion of ceftriaxone sodium and Amoxicillin –Cloxacillin during pre or post A.I. in normal and repeat breading animals have been presented in table 2. The table shows that the conception rates both in pre & post A. I. ceftriaxone sodium and Amoxicillin –Cloxacillin treated animals were significantly higher in repeat breeder & normal animals.

Though higher conception rates obtained in normal cows in the case of pre A..I. amoxicillin–Cloxacillin infusion (63.53%) and post A.I. Ceftriaxone sodium (57.14%) infusion, the difference was statistically non- significant. In the repeat breeding cows, conception rate was higher (60.00%) in pre A.I treatment with Amoxicillin –Cloxacillin than with Ceftriaxone sodium (50.00%). Where as in post artificial insemination treatment with amoxicillin –Cloxacillin showed higher (63.63%) conception rates than the ceftriaxone sodium (50.00%) table 1. When the ceftriaxone sodium was done either pre or post A.I. in repeat breeding cows, the conception rate was almost equal (50.00 and 50.14%). The present observation is comparable to the reports of Mutiga (1978), Purbey and Umashankar (1985), Saha and Chaudary (1987), Panchal et al. (1991), Rao and

Table 2. Comparative effect of intra –uterine (Pre and post) Ceftriaxone sodium and Amoxicillin–Cloxacillin infusion on conception rate in normal and repeat breeding cases

Animals	No. of Animals treated		No. of Animals conceived		C.R.(%)		χ^2 Value
	Ceftriaxone sodium	Amoxicillin–Cloxacillin	Ceftriaxone sodium	Amoxicillin–Cloxacillin	Ceftriaxone sodium	Amoxicillin–Cloxacillin	
Normal							
Pre A.I.	13	11	7	7	53.84	63.63	0.235^{NS}
Post A.I.	14	11	8	6	57.14	54.54	0.342^{NS}
Repeat breeder							
Pre A.I.	12	10	6	6	50.00	60.00	0.220^{NS}
Post A.I.	14	11	7	7	50.14	63.63	0.465^{NS}

NS= Non –significant

Table3. Comparative effect of intra –uterine (8-12 hrs Pre and post insemination) Ceftriaxone sodium and Amoxicillin–Cloxacillin infusion on conception rate in normal and repeat breeding cases.

Animals	No. of Animals treated	
	Ceftriaxone	Amoxicillin–Cloxacillin
Normal		
Pre A.I.	13	11
Post A.I.	14	11
Repeat breeder		
Pre A.I.	12	10
Post A.I.	14	11

Naidu (2000) and Das et al. (2002).

In the present study, a difference in conception rates in different treatment groups was observed Amoxicillin–Cloxacillin combination (1.25 g) has given satisfactory results. Therefore, it can be concluded that the (8-12 hours) pre or post insemination intra-uterine infusion can be preferred in such cases where the exact causes of repeat breeding is difficult to be ascertained.

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Effect of genetic and non genetic factors on pre-weaning growth of broiler rabbits and their crosses†

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ABSTRACT

The data on 847 bunnies of purebred Flemish Giant (FG) and two synthetic breeds namely APAU Fawn (FN) and APAU Black (BL) and their crosses born during October 2012 to September 2013 were analyzed to study the effect of genetic group, season of birth and litter size at birth on pre-weaning body weights and average daily gain. The genetic group significantly influenced the pre-weaning body weights at all the ages except at 4th week of age whereas the average daily gain was influenced at all the pre-weaning ages. The least squares mean body weights were 50.20 ± 0.48, 111.05 ± 1.26, 154.83 ± 1.97, 203.86 ± 2.90 and 406.81 ± 6.01g at birth, 1, 2, 3 and 4 weeks of age, respectively. The synthetic APAU Black proved its superiority over the other purebreds and crossbreds. The FG, heaviest breed of rabbits, recorded lowest body weights at all the pre-weaning ages while the highest average daily gain showed by it at 4th week of age. Season of birth had a highly significant (P≤0.01) effect on the pre-weaning body weights and average daily gain (ADG). Bunnies born in summer had higher body weights than those born in rainy and winter seasons. As the litter size increased the body weights as well as average daily gain were significantly decreased. In conclusion, based on body weights and average daily gain the synthetic pure breeds APAU Black and APAU Fawn performed well whereas purebred FG was the least performing among all the genetic groups studied.

Key words: Rabbit, cross breeding, growth trait.

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INTRODUCTION

Rabbits have potential as a meat producing animal in developing countries to meet ever increasing demand for animal protein. They have several advantages as meat producing animals as they can thrive on high fiber feed stuffs, can be bred throughout the year and can not compete with humans for the food resources. The meat is rich in protein low in fat and has no religious taboos for its consumption. The pre-weaning growth phase of broiler rabbits has more impact on meat production at finisher stages of production. Growth traits in growing rabbits are important because heavier marketable bodyweight promotes the economics of rabbit production (Rashwan et al., 1997). The pre-weaning body weights are affected by different factors such as breed, season of birth and litter size at birth. Hence the present study was undertaken to study the effects of these factors on pre-weaning body weights of rabbits.

MATERIALS AND METHODS

Data on body weight at birth, at weekly intervals up to 4 weeks of age on - 847 bunnies belonging to Flemish Giant (FG) and synthetic breeds of APAU Fawn (FN) and APAU Black (BL) and their crosses born during the year October 2012 to September 2013 maintained under "Rabbit production for meat" Scheme of the Department of Animal Genetics and Breeding, College of Veterinary Science, Hyderabad were utilized for the present study. Both the synthetic breeds were developed in the University by crossing New Zealand white, Grey Giant and local white Rabbits which are now breeding true to their type. The effect of genetic group, season of birth and litter size at birth on pre-weaning body weights and average daily gain (ADG) were studied. Data were analyzed by least squares technique Harvey (1979) as the frequencies of observations were unequal among the different subgroups.

RESULTS AND DISCUSSION

The least squares means for body weights and average daily gain according to genetic group, season of birth and litter size at birth at different pre-weaning ages were presented in the Table 1.

Effect of Genetic group: The genetic group had significant influence on all the pre-weaning body weights except at 4 weeks of age. The pre-weaning average daily gains were significantly influenced at all the ages studied in the present investigation. The overall least squares mean body weights were 50.20 ± 0.48, 111.05 ± 1.26, 154.83 ± 1.97, 203.86 ± 2.90 and 406.81 ± 6.01g at birth, 1, 2, 3 and 4 weeks of age, respectively. The results of present investigation were in accordance with the findings of Prakash and Gupta (2008) who reported the mean body weights at birth and weaning as 51.6 g and 403.24g, respectively. Kumar et al. 2006) and Sarin (2013) reported higher pre-weaning body weights at birth and weaning than obtained in present investigation, while Obike and Ibe (2010) reported lower pre-weaning body weights at birth and weaning.

Genetic group exerted a significant effect on all pre-weaning ADGs in the present investigation. These findings concur well with the findings of Ozimba and Lukefahr (1991), Gupta et al. (1999) and Sarin (2013). The synthetic APAU Black proved its superiority over the other purebreds and crossbred genotypes. The FG rabbits recorded lowest body weights at all the pre-weaning ages indicating the importance of the APAU black in meat production.

Table 1. Least squares means (g) of pre-weaning body weights

Attributes	n	Birth		1 week		2 weeks		3 weeks		4 weeks	
		Mean	S.E	Mean	S.E	Mean	S.E	Mean	S.E	Mean	S.E
Overall	847	50.20	0.48	111.05	1.26	154.83	1.97	203.86	2.90	406.81	6.01
Genetic groups											
BL × BL	95	51.59^{b}	1.05	118.37^{a}	2.78	171.20^{a}	4.32	217.50^{a}	6.43	417.06	13.35
BL × FN	115	51.30^{b}	0.98	114.68^{ab}	2.40	163.43^{ab}	3.81	213.85^{a}	5.61	423.29	11.50
BL × FG	89	47.92^{d}	1.06	112.73^{abc}	2.80	152.81^{c}	4.57	201.29^{b}	6.76	397.40	13.76
FN × BL	84	52.14^{b}	1.11	107.14^{d}	2.90	155.04^{bc}	4.49	206.10^{b}	6.58	398.91	13.63
FN × FN	75	49.00^{cd}	1.20	116.19^{ab}	3.16	151.32^{c}	4.85	201.65^{b}	7.11	438.38	14.57
FN × FG	111	50.52^{bc}	0.96	109.05^{cd}	2.35	146.22^{c}	3.68	177.37^{d}	5.48	409.32	11.09
FG × BL	81	55.06^{a}	1.12	111.84^{bcd}	2.79	163.86^{de}	4.33	214.26^{a}	6.62	397.85	13.54
FG × FN	35	48.86^{cd}	1.70	112.26^{abc}	4.51	156.22^{bc}	7.08	217.26^{a}	10.38	369.46	21.40
FG × FG	162	45.43^{e}	0.82	97.23^{e}	1.92	133.38^{e}	3.15	185.48^{e}	4.84	409.61	11.07
Season of birth											
Summer	326	49.169^{a}	0.63	115.10^{b}	1.69	156.29^{b}	2.66	206.10^{b}	3.92	435.86^{b}	8.03
Rainy	245	49.669^{a}	0.70	111.11^{a}	1.80	148.33^{a}	2.80	186.38^{a}	4.18	399.25^{a}	8.86
Winter	276	51.768^{b}	0.71	106.96^{a}	1.76	159.88^{b}	2.83	219.11^{c}	4.21	385.32^{a}	8.78
Litter size at birth											
1 – 3	70	52.22^{b}	1.18	116.82^{b}	3.14	161.84^{b}	4.91	219.25^{b}	7.19	473.43^{c}	15.00
4 – 6	390	50.64^{b}	0.52	112.59^{b}	1.28	154.74^{b}	2.04	200.21^{b}	3.06	407.56^{b}	6.34
7 - 9	387	47.74^{a}	0.52	103.77^{a}	1.35	147.91^{a}	2.13	192.13 a	3.17	339.44^{a}	6.55

Table 2. Least squares means (g) of pre-weaning average daily gain

Attributes	n	1 week		2 weeks		3 weeks		4 weeks	
		Mean	S.E	Mean	S.E	Mean	S.E	Mean	S.E
Overall		8.44	0.17	6.11	0.22	7.00	0.28	29.17	0.85
Genetic groups									
BL × BL	95	8.99^{a}	0.38	7.37^{a}	0.49	6.73^{b}	0.61	28.50^{bc}	1.87
BL × FN	115	8.91^{a}	0.33	6.69^{a}	0.43	7.19^{ab}	0.53	29.86^{ab}	1.60
BL × FG	89	8.90^{a}	0.38	5.46^{b}	0.52	6.95^{ab}	0.64	28.02^{bc}	1.92
FN × BL	84	7.60^{bc}	0.40	6.75^{a}	0.51	7.40^{ab}	0.63	28.17^{bc}	1.90
FN × FN	75	9.20^{a}	0.43	4.98^{b}	0.55	7.18^{ab}	0.68	33.40^{a}	2.03
FN × FG	111	8.23^{ab}	0.32	5.30^{b}	0.42	4.35^{c}	0.52	33.37^{a}	1.55
FG × BL	81	8.02^{b}	0.38	7.34^{a}	0.49	7.30^{ab}	0.64	26.03^{c}	1.89
FG × FN	35	8.70^{a}	0.61	6.13^{a}	0.82	8.74^{a}	0.99	24.06^{c}	3.28
FG × FG	162	7.39^{c}	0.26	4.98^{b}	0.36	7.15^{ab}	0.46	31.08^{ab}	1.54
Season of birth									
Summer	326	9.20^{c}	0.23	5.85^{b}	0.30	7.24^{b}	0.37	32.91^{c}	1.12
Rainy	245	8.46^{b}	0.24	5.29^{b}	0.32	5.42^{a}	0.40	30.03^{b}	1.24
Winter	276	7.65^{a}	0.24	7.21^{a}	0.32	8.34^{c}	0.40	24.56^{a}	1.26
Litter size at birth									
1 – 3	70	8.94^{b}	0.43	6.16	0.56	8.25^{b}	0.68	36.32^{c}	2.10
4 – 6	390	8.62^{ab}	0.17	6.06	0.23	6.52^{ab}	0.29	29.53^{b}	0.89
7 - 9	387	7.75^{a}	0.18	6.12	0.24	6.23^{a}	0.30	21.65^{a}	0.95

The FN x FN recorded highest ADG (33.40g) while FG x FN (24.06g) recorded lowest ADG at weaning. The results of present investigation were in accordance with the findings of Sarin (2013) who reported the mean ADGs from birth to one week and weaning as 8.66 and 29.52g, respectively. Lower values are reported by Reddy et al. (2001), Devi et al. (2007) and Sivakumar et al. (2013).

Effect of Season of birth: Season of birth had a highly significant (P≤0.01) effect on the pre-weaning body weights and ADGs, which is in agreement with the reports of Gupta et al. (1999) and Sarin (2013). In contrary Devi et al. (2007) reported non-significant effect. Summer born rabbits recorded significantly higher body weights and average daily gain at most of the pre-weaning ages. Gupta et al (1999) and Prakash and Gupta (2008) also found that bunnies born in summer had higher body weights than those born in rainy and winter seasons. The difference associated with the season of kindling can be attributed to the prevalent environmental conditions and to stress factors affecting feed intake (Eberhart, 1980).

Effect of litter size at birth: Bunnies born in small litters recorded significantly (P≤0.01) higher pre-weaning body weights and average daily gain. As the litter size increased, the body weights as well as average daily gain were decreased. Similar results were also reported by Gupta et al. (1999), Reddy et al. (2001) and Sarin (2013).

In conclusion, based on body weights and average daily gain the genetic groups ranked in descending order as follows: BL X BL, BL X FN, FN X FN, FG X BL, FN X BL, FG X FN, FN X FG, BL X FG, and FG X FG. The synthetic pure breeds APAU Black and APAU Fawn performed well whereas purebred FG was the least performing among all the genetic groups studied.

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