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Evaluation of genetic architecture and mutation drift equilibrium of Marathwada buffalo population in Central India

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ABSTRACT

In the present study, microsatellite data on 24 loci were generated and utilized to evaluate the genetic architecture and mutation drift equilibrium of Marathwada buffaloes, a Central Indian population maintained under low input system. Sufficient allelic diversity was observed with a total of 109 alleles across different loci. The genetic diversity analysis of Marathwada buffaloes displayed moderate level of within breed variability in terms of mean number of alleles per locus (4.48) and heterozygosity values (Ho = 0.532, He = 0.624). The studied Indian buffalo population showed considerable heterozygote deficiency (F_{IS} = 0.138) and deviation from HWE at many investigated loci. Three quantitative tests viz. sign test, standardized difference test and Wilcoxon sign rank test and a qualitative test for mode shift distortion of allelic frequencies were employed to evaluate mutation drift equilibrium under three different models of microsatellite evolution. The population was found to deviate significantly under IAM and TPM, while it was reverse under SMM. The qualitative test for mode shift supported the results under SMM indicating the absence of genetic bottleneck in the recent past in Marathwada buffaloes.

1. Introduction

Indian riverine buffaloes contribute immensely to the rural economy by producing more than 50% of the total milk in the country. These buffaloes have adapted to the existing ecosystem over the years and have gained prominence as an important dairy animal. There are ten well defined breeds viz. Murrah, Nili-Ravi, Jaffarabadi, Surti, Mehsana, Bhadawari, Nagpuri, Pandharpuri, Marathwada and Toda which have been classified into five different groups based on geographic location (Cockrill, 1974). However, approximately 70% of the total 94 million heads have been grouped into non-descript type (Acharya and Bhat, 1984). All the above breeds have evolved over the years as a result of traditional animal breeding practices of small and marginal farmers in the respective areas. Buffaloes in North and North West India like Murrah, Nili-Ravi and Mehsana were developed for high milk production. Murrah, the best dairy type buffalo is widely used for grading up the non-descript as well as other local breeds (George et al., 1988). This has resulted in the dilution of many distinguished breeds which have adapted to their respective agro-climatic conditions and having been used for many other purposes like draught, hide and dung.

To design rational breeding strategies for optimal utilization and conservation of available genetic variability in Indian buffaloes, it is essential to understand their genetic architecture and relationship between them. Molecular markers like microsatellite markers can help in studying the population structure of a descript population. These markers, by virtue of being highly polymorphic, codominant, evenly distributed and neutral in nature, have been extensively used for genome characterization and diversity analysis in many species (Soysal et al., 2005, Navani et al., 2002, Pandey et al., 2006).

Marathwada breed of buffaloes represent a very ancient indigenous type characterized with lighter built and long flat horns. These buffaloes are found in the Marathwada

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region of Central India especially in Parbhani, Nanded, Bid, Hingoli and Latur districts of Maharashtra state. Marathwada buffaloes are reared in low external input system mainly due to their low maintenance cost, feed conversion efficiency, moderate production and ability to thrive in harsh climatic conditions. The breed is primarily maintained by small and marginal farmers and landless labourers mostly for their moderate milk production which vary from four to eight kg per day. Breeding of these animals is highly unorganized and is either by means of natural service with available bulls or by grading up with Murrah semen. This calls for urgent action to improve genetically as well as to conserve these buffaloes. In the present study, population structure, genetic variability and mutation drift equilibrium of Marathwada buffaloes have been evaluated using 24 microsatellite markers originally identified in cattle but tested subsequently for diversity analysis in buffaloes (Navani et al., 2002; Arora et al., 2004).

2. Materials and methods

2.1. Blood samples and DNA isolation

Unrelated animals with typical phenotypic features were selected from several villages in the breeding tract. Although no parentage records were available, to ensure unrelatedness, animals were selected from distinct villages after interviewing the farmers in detail. Blood samples were collected from jugular vein into EDTA containing vacutainer tubes. Genomic DNA was extracted from whole blood following standard phenol — chloroform extraction method (Sambrook and Russell, 2001).

Table 1
List of microsatellite loci studied, their primer sequences, annealing temperature, observed allele size and their location in bovine chromosome

Locus	Primer sequence	Annealling temperature	Size of observed alleles	Location (bovinechromosme)
ILSTS058	F-5′ gccttactaccatttccagc 3′ R-5′ catcctgactttggctgtgg 3′	55	126, 136, 140, 144, 146, 148	17
CSSM066	F-5′ acacaaatccttttctgccagctga 3′ R-5′ aatttaatgcactgaggagcttgg 3′	55	170, 174, 180, 184	14
ILSTS025	F-5′ gttacctttatataagactccc 3′ R-5′ aatttctggctgacttggacc 3′	55	115, 117, 125, 129, 135	2
HEL013	F-5′ taaggacttgagataaggag 3′ R-5′ ccatctacctccatcttaac 3′	55	165, 169, 175, 179, 181, 183, 187	11
ILSTS052	F-5′ ctgtccttaagaacaaacc 3′ R-5′ tgcaacttaggctattgacg 3′	55	145, 153, 157, 163, 165, 167, 185	21
ILSTS029	F-5′ tgttttgatggaacacagcc 3′ R-5′ tggatttagaccagggttgg 3′	55	162, 164, 166, 168	3
ILSTS089	F-5′ tgcaaagagttggatggggc 3′ R-5′ aaggttgctgcctcatatcc 3′	55	114, 116, 118, 120, 122,	20
ILSTS061	F-5′ aaattataggggccatacgg 3′ R-5′ tggcctaccctaccatttcc 3′	55	144, 148, 152, 156, 164	15
CSRM060	F-5′ aagatgtgatccaagagagaggca 3′ R-5’ aggaccagatcgtgaaaggcatag 3′	55	96, 112, 122, 124, 130, 132	10
ILSTS056	F-5′ gctactgagtgatggtaggg 3′ R-5′ aatatagccctggaggatgg 3′	55	143, 153, 157, 171, 191	12
ILSTS028	F-5′ tccagattttgtaccagacc 3′ R-5′ gtcatgtcataccttgagc 3′	55	140, 144, 150, 170	11
ILSTS045	F-5′ ttctggcaaactattccacc 3′ R-5′ catgaaagacacagatgacc 3′	55	161, 169	11
ILSTS030	F-5′ ctgcagttctgcatatgtgg 3′ R-5′ cttagacaacaggggtttgg 3′	55	153, 157, 159, 163	2
ILSTS073	F-5′ agggcaggagtaatctttgg 3′ R-5′ aacagagagtatggtggtgg 3′	55	152, 154	19
ILSTS026	F-5′ ctgaattggctccaaaggcc 3′ R-5′ aaacagaagtccagggctgc 3′	55	138, 142, 144, 148	2
ILSTS019	F-5′ aagggacctcatgtagaagc 3′ R-5′ actttggaccctgaagtgc 3′	55	172, 176, 182, 186	29
ILSTS095	F-5′ gaaagatgttgctagtgggg 3′ R-5′ attctcctgtgaacctctcc 3′	58	185, 189, 195, 199, 201	21
ILSTS036	F-5′ gagtattatgcttgggaggc 3′ R-5′ agacaggatgggaagtcacc 3′	55	138, 140, 142, 148, 152, 156	11
ILSTS017	F- 5’ gtccctaaaatcgaaatgcc 3′ R-5′ gcatctctataacctgttcc 3′	55	104, 116, 122	X
ILSTS060	F-5′ taggcaaaagtcggcagc 3′ R-5′ ttaaggggacaccagccc 3′	63	188, 190, 194, 198, 202	28
ILSTS031	F-5′ aattctaggtgaacagcagc 3′ R-5′ aagacatactctcagactcc 3′	60	220, 224, 228, 236	24
ILSTS033	F-5′ tattagagtggctcagtgcc 3′ R-5′ atgcagacagttttagagcc 3′	55	135, 139, 143, 149	12
ILSTS068	F-5′ aattccgtggactgaggagc 3′ R-5′ aaggaactttcaacctgagg 3′	55	162, 170, 178, 182, 186	29
BM1818	F-5′ agctgggaatataaccaaagg 3 R-5′ agtgctttcaaggtccatgc 3′	55	237, 255, 267, 271	23