

2nd International Conference on Animal & Dairy Sciences

September 15-17, 2014 Hyderabad International Convention Centre, India

Genomic information a tool for assessment of genetic diversity in Mithun

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The Mithun (*Bos frontalis*) according to Phanchung and Roden (1996) is believed to have its origin from Gaur (*Bos gaurus*). The Mithun looks more like a transition between cattle and buffalo, but genetic analysis of the Mithun's chromosomes by Winter et al.(1984), Gupta et al. (1995) and Mukherjee et al. (2012) shows a diploid number 58 (2n) compared to 60 in cattle and 48+ in buffalo. Mithun is specifically reared by the tribal community and is reared on free range, grazing at altitudes of between 1000-3000m AMSL.

The currently available HD Genotyping Bead Chip panel provides extensive genome coverage and map resolution and has the potential to perform beyond other molecular markers resulting in much improved accuracy in exact QTL identification. The prime objective is to determine the diversity and variation existing in the Mithun population so as to generate information for future conservation and utilization of the animal.

Mean MAF ranges from 22.4 (Manipur) to 27.7 (Nagaland). At MAF $p \geq 0.05$ (common allele), Nagaland population markers exhibited lowest minor allele frequency of 85%, while all other populations had no MAF. Identity by state (IBS) was least among Mizoram strain and highest among Manipur mithun. The majority of polymorphic SNPs were found to be in HWE, Percentage SNP deviation from HWE ($p \leq 0.05$) was least among Manipur mithun and highest among Nagaland mithun.

The level of polymorphism in mithun population has not been known and analyzed. Prior to this study, no SNPs have been described for these populations. In this study, we report the first preliminary findings on SNP variation in the population of *Bos frontalis* (mithun) in north-east region of India. Determination of the population structure of the mithun based on the 770k Illumina Bovine HD chip was first step in genomic improvement programme.

The low number polymorphic loci (167,215) derived on outgroups (water buffalo, yak and gaur) corroborate our finding in this work (127,432). This means a successful use of bovine SNP chip will not be achieved. This preliminary study being the first of its kind on mithun has been able to show that 80% of the SNPs on the array have MAF < 0.05 , so approximately 20% are polymorphic (1/5).

The Inclusion of mithun genome in future design will aid enough to infer as a tool for selection purpose in mithun improvement program. For the purpose of conservatory program of the mithun it is recommended that genome wide SNP analysis can be successful along with a whole-genome sequence.

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