



Genomic sequencing and its variant discovery in buffalo breeds

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DESCRIPTION

Buffaloes are the most prevalent domestic milk-producing animals in India, with milk fat content ranging from 7% to 11% depending on breeding. The tamed animal with the highest promise and potential for productivity is the water buffalo. Buffalo has surpassed all others as the country's top dairy animal, producing great milk, meat, fuel, draught power, and farm waste. Water buffalos are usually raised for their milk. Each lactation, milk production varies substantially between breeds, ranging from 600 to 3500 kg.

According to cytogenetic studies, water buffalo have 25 pairs of chromosomes, 24 pairs of autosomes and 1 pair of sex chromosomes. Five sets of chromosomes are metacentric, whereas the remaining 20 pairs including a pair of sex chromosomes, are acrocentric. More people use water buffalo than any other domestic animal type. Water buffalo account for 11.1 percent of the world's bovid population, with 168 million reported. Water buffalo milk is higher in fat, lactose, protein and minerals than cow milk and it accounts for more than 5% of global milk output. Because of their wallowing behaviour, water buffalo are less susceptible to ticks and other ectoparasites. Mastitis affects water buffalo milk production less than dairy cattle which could explain why buffalo milk output has grown. Over the last two decades the global population of water buffalo breeds has grown at

a rate of about 2% each year. Given India's 1% annual population growth there is an opportunity for species improvement *via* breeding programmes based on genomic choices. There are 13 recognised water buffalo breeds in India, the bulk of which are milk breeds and have been listed on a state-level conservation plan by the Ministry of Agriculture. Because buffalo breeds make up the majority of Indian dairy farms, future advancements in commercially essential traits will be reliant on genetic variation within and across breeds. Despite their importance in the Indian agricultural economy, the bulk of breeds have not been genetically utilised. When a single nucleotide in the genome — A, T, C, or G — differs between members of a biological species or paired chromosomes in an individual, this is referred to as a single-nucleotide polymorphism. SNPs are the most prevalent type of sequence polymorphism found in the genome, which makes them suitable for genetic studies such as linkage analysis and gene typing both of which are important in animal and plant breeding programs.

SNP databases have been considerably enriched as a result of the detection and screening of a large number of SNPs using next-generation sequencing technologies. SNPs (Single Nucleotide Polymorphisms) are the preferred marker at the moment because they are found

in nearly everyone in the population. SNPs have been employed in several domains, including human forensics and diagnostics, aquaculture, and marker assisted dairy farming. Genomic selection has recently been widely used to increase genetic improvement in cattle. Furthermore, genetic resources from various farm animals are being employed to examine molecular genetic variety in river buffalo. SNPs (single nucleotide polymorphisms) are molecular markers that can aid in the improvement of livestock through traditional breeding methods.

However, genetic resources for river buffalo are still sparse. Given the close evolutionary relationship between cattle and water buffalo, as well as the availability of fully sequenced cattle genomes and other genetic data. There is the possibility to explore the river buffalo genome on a big scale in order to detect genetic variants, particularly large-scale SNP discovery, which could open up new avenues for river buffalo genomics in terms of genetic upgrades.