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Genomic sequencing for variant detection in buffalo breeds

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DESCRIPTION

Buffaloes are India's most common milk-producing domestic animals, with milk fat content range between7% to 11% depending on breeding. The water buffalo is the domesticated animal with the most promise and potential for productivity. Buffalo has exceeded all others as the country's premier dairy animal, with excellent milk, meat, fuel, draught power, and farm manure production potential. Water buffalos are mostly cultivated for milk production. Milk production varies greatly between breeds, ranging from 600 to 3500 kg each lactation. Water buffalo have 25 pairs of chromosomes, 24 pairs of autosomes and 1 pair of sex chromosomes, according to cytogenetic studies. A total of 5 sets of chromosomes are metacentric, with the remaining 20 pairs are including pair of sex chromosome are acrocentric.

The water buffalo is used by more people than other domestic animal species. With 168 million buffalo reported, water buffalo make up 11.1 percent of the world's bovid population. Water buffalo milk contains more fat, lactose, protein, and minerals than cow milk, accounting for more than 5% of global milk production. Water buffalo are less susceptible to ticks and other ectoparasites due to their wallowing actions. Mastitis inhibits milking water buffalo less than dairy cattle, which could explain why buffalo milk output has increased.

In the last twenty years, the global population of water buffalo breeds has expanded by around 2% per year. Given India's yearly population growth of 1%, there is a window for species improvement through breeding programs based on genomic selections. In India, there are 13 recognised breeds of water buffalo, the majority of which are milk breeds, and some of which have been included on a state-level conservation plan by the Ministry of Agriculture. Because buffalo breeds accounts for the largest proportion of the Indian dairy farms, future developments in economically important features will be dependent on genetic variation within and across breeds. Despite their significance in the Indian agricultural economy, the majority of breeds have not been utilized genetically.

To improve genetic improvement in cattle, genomic selection has recently been applied extensively. Moreover, different farm animal's genetic resources are used to investigate molecular genetic diversity in river buffalo. SNPs (single nucleotide polymorphisms) are molecular markers that can help enhance livestock through traditional breeding procedures. However, river buffalo genetic resources are still scarce. Given the strong evolutionary link between cattle and water buffalo, and the availability of fully sequenced cattle genomes and other associated genetic data. There is a potential to investigate the river buffalo genome on a broad scale to find genetic variants, particularly large-scale SNP discovery, which could open a new door for river buffalo genomics in terms of genetic enhancements.

Single-Nucleotide Polymorphism

A single-nucleotide polymorphism occurs when a particular nucleotide in the genome — A, T, C, or G — differs between members of a biological species or paired chromosomes in an individual. SNPs are the most common sort of sequence polymorphism found in the genome, making them ideal for genetic research such as linkage analysis and gene typing, which are significant in animal and plant breeding programs. Because of the identification and screening of a significant number of SNPs using next-generation sequencing technology, SNP databases have been greatly enriched. SNPs (single nucleotide polymorphism) are the marker of choice right now because they are found in almost everyone in the population. SNPs have been used in a variety of fields, including human forensics and diagnostics, aquaculture, marker assisted dairy cattle breeding, agriculture development, wild animal conservation, and fisheries resource management. SNPs found in regulatory genes,

transcripts, and Expressed Genome Tags are used in functional genomics studies (ESTs).

Exome Capture

Individual laboratories are now able to sequence an entire eukaryotic genome because to the invention and widespread use of massively parallel sequencing. However, it is too expensive to analyze significant sections of genomes in a large number of people, which is necessary for population research. The "exome" is a term that refers to all exons in the eukaryotic genome in a specific tissue at a specific time. Exome are short, functionally significant DNA sequences that indicate the sections of genes that are translated into protein, as well as the translated area on each side (UTR).

Exome investigations typically exclude UTRs:

- The exome is the most functionally important section of the genome in terms of protein coding, and it is thus the most likely to influence an organism's phenotype.
- Exome is a group of genes that are found in the human genome. Exome is made up of 2% of the typical eukaryotic genome.

The genome is estimated to make up 1% (30 Mb) of the overall genome. It is estimated that 85 percent of disease-causing mutations occur in the human genome's protein-coding regions. Exome sequencing has been used to accurately discover the functional variation that causes Mendelian disorder and other prevalent disorders like Miller syndrome. Exome sequencing in *Bos Taurus* (taurine cow), *Bos indicus* (water buffalo cattle), and Buffalo was started performing in Cosart by using Illumina Genome Analyzers (GA) I and II (American bison). Exome can be captured and sequenced using a variety of approaches, including PCR, Molecular Inversion Probe (MIP), Microarray (Hybrid capture), NGS techniques, and others.