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Identification of novel SNPs in differentially expressed genes and its association with horn cancer of *Bos indicus* bullocks by next-generation sequencing

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The use of polymorphic markers like SNPs, promises to provide comprehensive tool for analysing genome and identifying genomic regions that contributes to cancer phenotype. Horn cancer is the most common cancer among *Bos indicus* animals. Increased expression of some genes due to polymorphisms increases risk of HC incidence. We successfully amplified 91 SNPs located in 69 genes in 52 samples, each of HC and HN. Equimolar concentration of amplicons from 69 PCR products of each samples were pooled and subject to sequencing using Ion Torrent PGM. Data obtained were analysed using DNASTAR software package and case control analysis using SAS software. We found SNP present in BPIFA1 gene of *B. indicus* shows association with event of HC which reflects its potential to be a genetic marker. Bioinformatic analysis to detect structural and functional impact nsSNP of BPIFA1 added another layer of confirmation to our result. We successfully identified SNP associated with HC as well as demonstrated efficient approach for limited number of SNPs discovery and validation in targeted genomics regions in large number of samples combining PCR amplification and Ion Torrent PGM sequencing which suits to small scale laboratories with limited budget.

Biography

Koringa P G is working as an Assistant Professor at Department of Animal Biotechnology, College of Veterinary Science and Animal Husbandry, Anand Agricultural University since last 9 years. He was gold medallist/university first during his UG and PG studies and looking to his bright educational career, Honourable Vice. Chancellor has selected him as Assistant Professor at the age of 26 years only. He has completed his PhD under guidance of Dr. C G Joshi. He has published more than 28 papers in reputed journals and has wide on hand expertise in NGS data generation and analysis related to animal cancers and metagenomics. .

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