

ABSTRACT

Domestic buffalo is a significant source of milk and meat for humans throughout the world. Buffalo milk is well known for its milk qualities as compared to cow milk because it has higher contents of fat, protein, lactose and minerals. Blood samples were collected from Buffalo Research Institute of Ravi Campus Pattoki and Sukkar Sindh. DNA was extracted from the whole blood by organic chloroform method and genomic sample was sent to Illumina GBI china for whole genome sequencing. The single nucleotide polymorphism (SNPs) that show the valuable difference between the buffalo breeds and they are associated with these SNPs analyses to further understand the Kappa Casein (*K-CSN*) as closely related to milk yield genes in buffalo breeds. The genetic variations in the Toll like receptors (*TLR*) and Interleukin (*IL*) genes have been related to several diseases in domestic and farm animals. In this study whole genome sequence to reference based mapping, functional annotation and gene analysis of two breeds of buffalo of Pakistan was performed. A total of 19,096,830 single nucleotide polymorphisms (SNPs) and insertion 1,555,118 and deletion is 1,694,057 were discovered in it. Comparative analysis using coding region and SNPs are close relation with the water buffalo. The mutational pattern were observed in a total of missense is 152,300 , Nonsense mutation 1,549 and Silence mutation is 234,758 and functional annotation identified a total of 13,716 high impact, low 300,192, and moderate 155,374 that may possibly affect economically important dairy and other traits adopted to heat tolerant of Pakistani buffalo breeds. Genome editing of farm animals has practical application and it helps to improve production traits, enhance the economic value of livestock, and increase disease resistance.