



Category: Animal genomics

Identification of genetic variant in buffalo genome using ddRAD sequence

A.K. Pradhan^{1,2*}, S.R. Martha¹, D.C. Mishra² and K.K. Chaturbedi²

¹Orissa University of Agriculture And Technology, Bhubaneswar, INDIA

²Indian Agricultural Statistics Research Institute, New Delhi, INDIA

*Corresponding author: akkumaranjan@gmail.com

Abstract

Bubalus bubalis (water buffalo) is an agro-economically important livestock species due to its multipurpose use in India and other Asian countries. Among the total of 13 recognized breeds of water buffalo, majority are milch breeds in India and some of them have been listed on a state-level conservation plan by the Ministry of Agriculture, Government of India. As buffalo milk occupies the highest share in Indian dairy sector, the future improvement in traits of economic importance is dependent on genetic variation present within and between the breeds. Even though they have an important role in Indian agricultural economy, most of the breeds have not been exploited for their full genetic potential. Molecular markers like single nucleotide polymorphisms (SNPs) can play a significant role in livestock improvement through conventional breeding programmes. The aim of this study is to identify single nucleotide polymorphisms (SNPs) from buffalo genome using ddRAD sequencing through STACKS pipeline. Here we have used double digest restriction-associated DNA sequencing (ddRAD) for identification and annotation of genetic variant from three traits of buffalo such as Milk yield, Lactation period, Age at first calving. The Stacks pipeline is used to create genetic maps and conduct population analysis. It assembles loci from an individual's sequence reads by using a reference sequence. The total SNPs found in buffalo for three important traits Milk yield, Lactation period and Age at first calving are 25802, 9218 and 17914, respectively. The total genotypes, genotype frequencies and genotype map have been calculated in the population. For computation of population genetic measures (The inbreeding coefficient of an individual) F_{IS} and (An estimate of nucleotide diversity) π within populations and (A measure of population differentiation) F_{ST} between populations has been found.

Citation: Pradhan, A.K., Martha, S.R., Mishra, D.C. and Chaturbedi, K.K. Identification of genetic variant in buffalo genome using ddRAD sequence [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 20. <https://doi.org/10.24870/cjb.2017-a8>