New insights into the spatial genetic structure of the Indian riverine buffalo populations

Several programmes for the genetic improvement and conservation Indian buffalo breeds have been implemented by various agencies since 1970. These programmes may have shaped the present genetic diversity and thereby the evolutionary potential of buffalo populations across India. In this study, we attempted to provide an insight into the contemporary genetic structure of buffaloes by simultaneously analyzing the genetic and geospatial data. A battery of 100 microsatellite markers was genotyped across 1055 buffalo samples representing different geographical regions of the country. Bayesian and multivariate approaches were used for analyses. Although the clustering results from the different approaches were not convergent, these methods were able to identify sub-structuring within the UP buffalo population. In our study BAPS was able to distinguish most of the buffalo breeds with better spatial distribution. The genetic structuring detected in our study is mainly characterised by isolation by distance and also reflects the effect of improvement programmes. Our analysis suggested genetic connectivity of Murrah and Nili-Ravi with several buffalo breeds, as they have been used for breed improvement. The information may be useful in identifying ecologically distinct or connected populations for future improvement and conservation programmes.
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**FeedOMICS: Systems Genomics, Transcriptomics and Metabolomics of Feed efficiency in Pigs**

The FeedOMICS project is aimed at understanding and utilizing multi-omic molecular biology information in genomic selection and breeding for Feed Efficiency (FE) in pigs. FE defined in terms of FCR or RFI had been a central focus of the pig breeding programs but in recent years there is a renewed interest to identify and utilize the genes/variants/QTLs with functional effects in an improved version of genomic prediction. FeedOMICS project conducts multi-omics experiments using high-density SNP genotyping, RRBS, RNA-Seq and NMR technologies to profile genomic, epigenomic, transcriptomic and metabolomic variations in pigs with different genetic merit (genomic breeding values) for FE in an intensive experimental setting. This project involves extensive biological sampling in experimental farm and slaughterhouse and processing of samples in labs. Project will utilize multi-omic high-throughput datasets originating from these experimental pigs; investigate multi-omic data integration methods, joint modelling, analyses and inferences. The project aims to provide systems level understanding of biology of FE, to deliver testable genetic-, epigenetic-, bio- and metabolite-markers for FE and to improve genomic prediction/selection methods for FE given the genetic architecture and biological information. Quantitative-molecular genetics, bioinformatics, bio-statistics and integrative systems biology will form a core part of this research project. This project is funded by The Danish Council for Independent Research – Technology and Production Sciences (DFF-FTP) with co-funding from University of Copenhagen for 3 years (total grant size of ~ 8.5 million Danish Kroner or 1.3 M US$). The overall project director is Professor Haja Kadarmideen.

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