

## Genomic Adaptation to Local Climate Conditions in Native Cattle Using Whole Genome Sequencing Data

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**Abstract :** In this study, we generated whole-genome sequence (WGS) data from 110 native cattle. Together with whole-genome sequences from world-wide cattle populations, we estimated the genetic diversity and population genetic structure of different cattle populations. Our findings revealed clustering of cattle groups in line with their geographic locations. We identified noticeable genetic diversity between indigenous cattle breeds and commercial populations. Among all studied cattle groups, lower genetic diversity measures were found in commercial populations, however, high genetic diversity were detected in some local cattle, particularly in Rashoki and Mongolian breeds. Our search for potential genomic regions under selection in native cattle revealed several candidate genes related with immune response and cold shock protein on multiple chromosomes such as TRPM8, NMUR1, PRKAA2, SMTNL2 and OXR1 that are involved in energy metabolism and metabolic homeostasis.

**Keywords :** cattle, whole-genome, population structure, adaptation

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