Spatial and Socio-Economic Factors Shaping the Genetic Diversity of Indigenous Cattle Breeds in Benin

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Abstract

Do ecological factors shape the genetic structure of the Beninese cattle population? Are the indigenous taurine (Somba and Lagune) and hybrid (Borgou, Pabli-Kerou) breeds in Benin endangered by ongoing indicine introgression? What is the role of transhumance movements in this context? These are critical questions for the development of effective management policies for the conservation of indigenous cattle genetic resources in Benin, a country regularly influenced by transboundary transhumance movements of zebu herds.

We developed a balanced sampling design based on the distribution of the agro-ecological zones and the socio-economic factor transhumance to study the genetic diversity of the four indigenous Beninese cattle breeds. 461 animals (Borgou 181, Pabli-Kerou 61, Lagune 157, Somba 62) were phenotyped for conformation traits based on FAO guidelines and genotyped with a 50k SNP chip. SNP genotypes were used for basic measures of genetic diversity, unsupervised k-means clustering in the framework of a discriminant analysis of principal components (DAPC) and estimation of ancestry coefficients using DAPC, TESS and ADMIXTURE. The diversity analysis is complemented with linear regression-based genome-wide association studies (GWAS) for conformation traits and selection signature analysis (SSA).

Unsupervised clustering using DAPC identified 6 genetic clusters in the dataset. The two hybrid breeds Borgou and Pabli-Kerou built two nearby mixed clusters reflecting a close relationship and admixture between the two breeds. The taurine Somba breed built a highly homogeneous distant cluster, whereas the Lagune breed is more diverse with 2 separated heterogeneous clusters reflecting local transhumance effects. A separate sixth cluster reflected potential crossbreeding with non-indigenous breeds of unknown origin. The clustering results were supported by the basic measures of diversity and the admixture analysis. The main drivers of genetic diversity are spatial and socio-economic factors such as transhumance. The multi-breed GWAS revealed 9 and 23 highly conserved SNPs associated with Heart Girth and Hip Width. Similarly, we identified several significant loci across breeds, and breed specific loci for the 10 other phenotypic traits investigated. GWAS and SSA shed light on functional gene-networks shaping the genomic architecture of body conformation traits in light of environmental adaptation and artificial selection.

Keywords: Agro-ecological zone, animal genetic resources, conservation, taurine, transhumance, zebu introgression

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