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Genetic Characteristics of African Breeds: An Example of Multi-Breed GWAS for Morphometric Traits in Beninese Indigenous Cattle

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Abstract

In the African livestock breeding context, routine data recording systems for performance traits especially body weight rarely exist. In contrast, morphometric traits are more easily measurable and often correlated to performance traits. They are therefore potential indicator traits for novel breeding and conservation strategies in the large but poorly studied animal genetic resources in Africa. The aim of the present study was to estimate genetic parameters and to identify functional loci underlying the variability of six morphometric traits in four indigenous breeds (Borgou, Pabli, Lagune, Somba) kept in small herds in Benin. In total, 449 cattle with morphometric records for height at withers (HAW), sacrum height (SH), heart girth (HG), hip width (HW), body length (BL) and ear length (EL), were genotyped for 36,720 SNP. This dataset was used to estimate heritabilities, genetic and phenotypic correlations, and to perform a multi-breed GWAS.

Estimated SNP-based heritabilities for the six morphometric traits ranged from 0.46 ± 0.14 (HG) to 0.74 ± 0.13 (HW). The genetic and phenotypic correlations ranged from 0.14 ± 0.10 (HW-BL) to 0.85 ± 0.02 (HAW-SH) and 0.25 ± 0.05 (HW-BL) to 0.89 ± 0.01 (HAW-SH), respectively. The multi-breed GWAS detected two genome-wide and 25 chromosome-wide significant SNP associated with the morphometric traits. The identified SNP were located near (± 25 kb) or within a total of 15 genes among which 11 genes were related to morphological, growth and carcass traits like body weight and fat deposition in cattle as well as in other livestock species and humans. The genes were additionally involved in biological processes and pathways such as hemostasis and metabolism (PIK3R6, PIK3R1), immunity or inflammatory responses (PTAFR, LYPD8), chromatin organisation (PBRM1), DNA repair (EYA3), DNA binding (SSH2), and regulation of hepatocyte growth factor receptor signaling pathway (ADAMTS12). The association between all identified genes either with feed efficiency, stress or immune response suggests that adaptability to scarce food resources, disease and extensive managements plays an important role in the phenotypic variability of the indigenous breeds. With regard to moderate to high heritabilities and the functional annotation for the associated SNP, the studied morphometric traits are suitable indicator trait candidates to develop breeding schemes for genetic improvements of the indigenous breeds.

Keywords: Genetic parameters, indigenous breeds, morphometric traits, multi-breed GWAS

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