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Initial genomic characterization of Italian, Egyptian and Pakistani goat breeds.

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Abstract

Selection and breeding practices in goats have differed greatly among countries and populations. These processes, together with natural selection and regional drift, have shaped the phenotypic variability of goat breeds (Kim et al., 2015). The availability of improved genomic analysis tools for this species may provide useful information on the history of selection, adaptation and differentiation of goats from different areas of the world, that can be evaluated by the study of gene frequencies and length of the Runs of Homozygosity (contiguous length of homozygous genotypes, ROH; Purfield et al., 2012). In current study, we examined using a goat medium density SNP chip animals from three different countries: Egypt (with lack of selection scheme), Italy (with several standardized breeds; Nicoloso et al., 2015) and Pakistan (with several breeds showing peculiar phenotypes) to produce a genomic landscape of goats breeds in these countries. A total of 1,123 animals of 39 different populations, and 48,895 SNP markers were analyzed. Genotypes were imputed on a country-based approach, and markers without known position in the genome were excluded from the analysis. MDS and ADMIXTURE plots confirmed the good differentiation among populations from the three countries. Runs of Homozygosity (ROH) were performed for each country and population allowed the detection of genomic regions with high homozygosity levels, common in at least two out of three sampling areas. These results provide new insights into goat genome structure within and among breeds and countries. The detection of conserved regions with different lengths may explain recent selection strategies or adaptation to different, extreme environmental conditions. The research was funded by INNOVAGEN project. Support by Iowa State University and the Ensminger funds for AE and AT as well as support by the Fulbright Foundation for AE are gratefully acknowledged. Sampling from Pakistan was funded by PAK-USAID project.

References

Kim, E-S, A R Elbeltagy, A M Aboul-Naga, B Rischkowsky, B Sayre, J M Mwacharo, and M F Rothschild., 2015. Multiple Genomic Signatures of Selection in Goats and Sheep Indigenous to a Hot Arid Environment. *Heredity* 116, 255-264.

Nicoloso, L., L. Bomba, L. Colli, R. Negrini, M. Milanese, R. Mazza, T. Sechi, et al., 2015. Genetic Diversity of Italian Goat Breeds Assessed with a Medium-Density SNP Chip. *Genetics Selection Evolution* 47:62.

Purfield, Deirdre C, Donagh P Berry, Sinead McParland, and Daniel G Bradley., 2012. Runs of Homozygosity and Population History in Cattle. *BMC Genetics* 13:70.