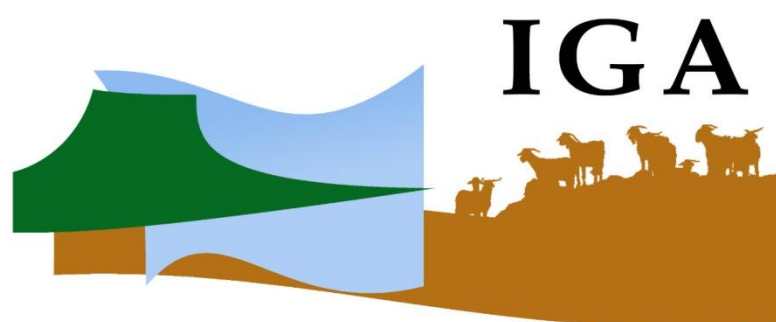


BOOK OF ABSTRACTS

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CONBIAND network: scientific cooperation for biodiversity studies in goat breeds from Ibero-America

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The CONBIAND network is a scientific society integrated by researchers involved in biodiversity, sustainability and conservation biology. A research consortium was established within this network to investigate the genetic relationships among Iberian and Creole goats, and how they relate to colonization history. The main objective of the BioGoat Project is to study the genetic signatures of Iberian breeds, primarily taken to the Americas through different dispersion routes which covered the territory from the Caribbean Islands and South-Western United States all the way down to Patagonia. In this study, Iberian, African and commercial goat breeds were included in different analyses to assess their influence on Creole goats. Overall, 65 goat populations from different origins, represented by 2,500 animals, were analysed with twenty-four microsatellite markers. The genetic differentiation between populations was moderate, with a mean F_{ST} of 0.13. The neighbour-net constructed with the DA genetic distances indicates that Creole populations from Argentina, Bolivia and the goat populations from USA group in the same cluster integrated by Iberian populations (from Spain and Portugal). Cuban Creole goats grouped with the populations from the Canary and Cabo Verde Islands, closer to the African populations cluster. Clustering of populations and estimates of the proportions of individual genomes deriving from their inferred clusters were obtained using the model-based clustering program Structure. Assuming the existence of two ancestral clusters, the populations from the Iberian Peninsula and most Creole goat populations grouped in the same cluster, while the Brazilian, Canarian, Cuban and Arapawan populations formed another cluster. With three ancestral clusters, the Canarian, Cuban and Arapawan populations grouped in the same cluster. Assuming a higher number of ancestral clusters led to further division and grouping of the populations. The results obtained in our study suggest a clear influence of the Iberian populations on Creole goats, while the Cuban Creole goat is more influenced by Canarian breeds. The ANOVA and Factorial Correspondence Analysis results showed that the proximity of most Creoles to their Iberian ancestors is stronger than their relation to the commercial goat breeds. Despite the time frame since the end of the colonization period, the genetic influence of Iberian breeds in Creole goats is still very evident.