## Population structure analysis of the New World Creole cattle

G. Mészáros<sup>1</sup>, M. Naves<sup>2</sup>, R. Martínez<sup>3</sup>, C. Lucero<sup>3</sup>, J. Sölkner<sup>1</sup>

<sup>1</sup>University of Natural Resources and Life Sciences, Vienna, BOKU, Austria; <sup>2</sup> Institut National De La Recherche Agronomique, INRA, Guadeloupe, France; <sup>3</sup>Colombian Corporation of Agricultural Research, CORPOICA, Colombia

gabor.meszaros@boku.ac.at

The Creole cattle are a group of Bos Taurus breeds, originating from Spain, first imported to the New World in the 16<sup>th</sup> century. There were later influenced by local selection processes, herd management, and complex admixtures, during the historical period. The genotype data of 200 Creole cattle from Colombia (Blanco Orejinegro (BON, n=50), Costeño con cuernos (CCC, n=50), Romosinuano (ROM, n=50), Sanmartinero (SAM, n=50)) and 223 Creole cattle from Guadeloupe was analyzed to assess within and between breed genetic diversity. Total of 41,011 autosomal single nucleotide polymorphism (SNP) markers, after standard quality control, were used for the analysis. The population structure was analyzed via logistic factor (LFA) and principal component analysis (PCA). Both confirmed well separated, non-overlapping clusters for all breeds. The first principal component explained 10% and the second 7.7% of the variance. The Fst values between breeds were in the range of 0.09 to 0.12. While most of the animals between breeds were unrelated, some non-zero IBD coefficients were found between animals from different Colombian breeds. The within breed genetic distances were fairly similar in all cases, with slightly higher values for ROM, confirming the LFA and PCA results. The genomic inbreeding coefficients assessed via runs of homozygosity (ROH) were computed with restrictions of minimal ROH lengths of 2, 48 and 16 Mb. The longest ROH segments denoted recent inbreeding up to 3 generations ago, with the highest values in the GUA population (F<sub>ROH</sub>=0.04, sd=0.05). When considering ancestors up to 25 generations ago via minimum ROH length of 2Mb the ROM population was the most inbred (F<sub>ROH</sub>=0.12, sd=0.04). The ROH segments were distributed across the whole genome, with notable exceptions of several breed specific ROH islands. These regions of excessive homozygosity indicate differentiation in selection pressure in various Creole populations.