



## ORIGIN AND DISTRIBUTION OF MITOCHONDRIAL HAPLOTYPES IN AMERICAN NATIVE CATTLE BREEDS (*Bos taurus*): PHYLOGENETIC NETWORK ANALYSIS.

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American native cattle breeds have their common root on the European taurine cattle introduced by Iberian conquerors. They populated America mainly following human migrations. Diversity within the control region of taurine cattle mtDNA can be clustered into two main haplogroups, namely the African and European. Other minor haplogroups have been reported including T, considered the root of all extant taurine cattle. We report in this work the nucleotide sequence of a mitochondrial DNA control region fragment (240bp) from 182 individuals belonging to 10 native cattle breeds from 6 American countries. Along with sequences from African, Near Eastern and European taurine cattle, we estimated the nucleotide diversity and reconstructed a phylogenetic network in order to make inferences about the origin, distribution and age of mitochondrial lineages within native American cattle breeds. From an alignment of 675 mtDNA sequences using CLUSTALX, we estimated  $p_{st}$  ( $\pi$ ) with the TN93 correction for multiple hit allowing heterogeneity rates among sites with the ( $\alpha$ ) value (0.30) obtained from these data. Then, using a relative rate test we obtained a substitution rate  $\mu = 3.8764 \times 10^{-7}$ , equivalent to 1Ts / 10.748 years. Reduced Median Networks, which include most or all most parsimonious trees, were reconstructed using NETWORK software. Phylogenetic networks reproduce multifurcations and resolve parallelisms. Assuming a correct tree, we can estimate  $\rho$  ( $\rho$ ), an unbiased estimator of the coalescence time to the specified root. We confirmed the presence of a highly divergent lineage (AA, African-derived American sequence) defined by T16050, C16053, C16113, C16122, T16139, A16196 and C16255 (TCCCTAC), rooted on African taurine cattle, as the most frequently observed haplotype within Brazilian and Guadeloupean native cattle. Most of the 30 remaining haplotypes were similar or linked to both, the European and African consensus sequences. Estimates of expansion dates of the haplogroup AA was coherent with colonization times, but its coalescent time to the general root of taurine cattle was much older than coalescent times published for any other extant taurine mtDNA haplogroups. The hypothesis suggesting a Near Eastern sequence as the ultimate root of all the extant taurine domestic cattle was tested. We propose a modification in the order by which substitutions connecting the sequence of the common ancestor of all taurine cattle breeds (root) and the African consensus sequence should be represented. This work contributes to the characterization of native cattle breeds, providing information valuable for conservation programs.

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