

## Origins and genetic diversity of New World Creole cattle: inferences from mitochondrial and Y chromosome polymorphisms

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### Summary

The ancestry of New World cattle was investigated through the analysis of mitochondrial and Y chromosome variation in Creoles from Argentina, Brazil, Mexico, Paraguay and the United States of America. Breeds that influenced the Creoles, such as Iberian native, British and Zebu, were also studied. Creoles showed high mtDNA diversity ( $H = 0.984 \pm 0.003$ ) with a total of 78 haplotypes, and the European T3 matriline was the most common (72.1%). The African T1a haplogroup was detected (14.6%), as well as the ancestral African-derived AA matriline (11.9%), which was absent in the Iberian breeds. Genetic proximity among Creoles, Iberian and Atlantic Islands breeds was inferred through their sharing of mtDNA haplotypes. Y-haplotype diversity in Creoles was high ( $H = 0.779 \pm 0.019$ ), with several Y1, Y2 and Y3 haplotypes represented. Iberian patriline in Creoles were more difficult to infer and were reflected by the presence of H3Y1 and H6Y2. Y-haplotypes confirmed crossbreeding with British cattle, mainly of Hereford with Pampa Chaqueño and Texas Longhorn. Male-mediated *Bos indicus* introgression into Creoles was found in all populations, except Argentino1 (herd book registered) and Pampa Chaqueño. The detection of the distinct H22Y3 patriline with the *INRA189-90* allele in Caracú suggests introduction of bulls directly from West Africa. Further studies of Spanish and African breeds are necessary to elucidate the origins of Creole cattle, and determine the exact source of their African lineages.

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