

Próximas conferências científicas sobre informação genética do gado bovino na Época Romana, com inclusão de amostras do Castro de Chibanes (Palmela)



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“Genomic variability of Western Mediterranean Roman cattle”

Variabilidade genética do gado bovino do Mediterrâneo Ocidental na Época Romana

Abstract

Cattle mitochondrial DNA (mtDNA) is geographically structured. It is therefore possible to associate maternal lineages to specific regions. Thus, the T1 and T3 haplogroups predominate in Africa and Europe, respectively. Genetic studies of both past and extant domestic cattle indicate chronological continuity over time between cattle populations from the same location, with strong maternal founder effects resulting from initial colonization. However, there is considerable mtDNA diversity in Western and Southern Europe: the phylogenetic analysis of complete mitochondrial sequences in extant Iberian breeds showed a high occurrence of ~17% of T1-matrilines. Ancient DNA of cattle bones from well-characterized archaeological sites enables tracking changes in genomic diversity associated with mobility and animal production traits. In Roman times an increase in cattle size is more apparent in the Roman Empire and less so in the periphery. Our aim is to understand whether the Roman state enhanced cattle genetic diversity in the Western periphery? A PCR-based analysis of a few short mtDNA sequences indicates presence of various lineages in Roman Spain. We used whole-genome shotgun resequencing (Illumina HiSeqX) to analyse ancient DNA from 9 Roman Portuguese cattle specimens. They include a metacarpal and a humerus from S. Miguel de Odrinhas (Sintra), a metacarpal and two molars from Chibanes (Setúbal), an astragalus from Monte dos Castelinhos (Vila Franca de Xira), an astragalus from Conimbriga (Coimbra), and two metacarpals from Alcáçova de Santarém. Mitochondrial genome coverages were between 2x and 60x. These cattle from Roman Iberia carried mostly the T3-matriline, but the T1-African lineage was also observed in two specimens from Chibanes. We interpret these findings from a population genomics perspective to model genomic variation over time and investigate genetic relationships between past and extant cattle from this region.

Keywords: Roman Iberian Cattle; Osteometry; Archaeogenetics; Mitogenomes

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Mitogenome analysis of cattle from the Roman Republic fortification of Chibanes, Palmela, Portugal

Abstract

The expansion of the Roman Empire had a big impact on the culture and economy of Lusitania, despite its peripheral location. There has been an intense debate about the role played by animal husbandry and livestock trade during the different phases of the Roman Period. For example, there are zooarchaeological evidences showing the Romans improved their cattle for larger body sizes, in newly founded cities of the province of Lusitania (such as *Emmerita Augusta* and *Ammaia*). However, in some early settlements, dated to the Roman Republican (2nd/1st cent. BC), a significant increase in the size of cattle was not observed, suggesting that local resources were not improved. Still, some sites, such as Chibanes and Mesas do Castelinho, did show higher averages of widths and lengths in cattle bones, than contemporaneous settlements such as Alcáçova de Santarém. This study is focused on Castro de Chibanes, in Palmela, a fortification occupied by the Romans in the 1st century BC. We combined zooarchaeological and archaeogenomic data to determine if new stock was introduced by the Romans or if, alternatively, local cattle were improved. We generated whole-genome shotgun resequencing data (Illumina HiSeqX) for cattle remains collected in Chibanes (one metatarsal and two inferior third molars). Endogenous DNA content ranged between 1.03% and 25.86% and the depths of coverage obtained for the mitogenomes of these specimens were between 99.26x and 100x. We present and discuss preliminary results of this study, particularly the analysis of cattle mitogenomes to infer major haplogroups and investigate genetic relationships between past and extant cattle from this region. We will try to understand if the increase in the size of cattle bones is associated to the introduction of new genetic lineages.

Tópico: Ciências Biológicas/Ciências Agrárias

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