

From hunters to herders in the central Andes

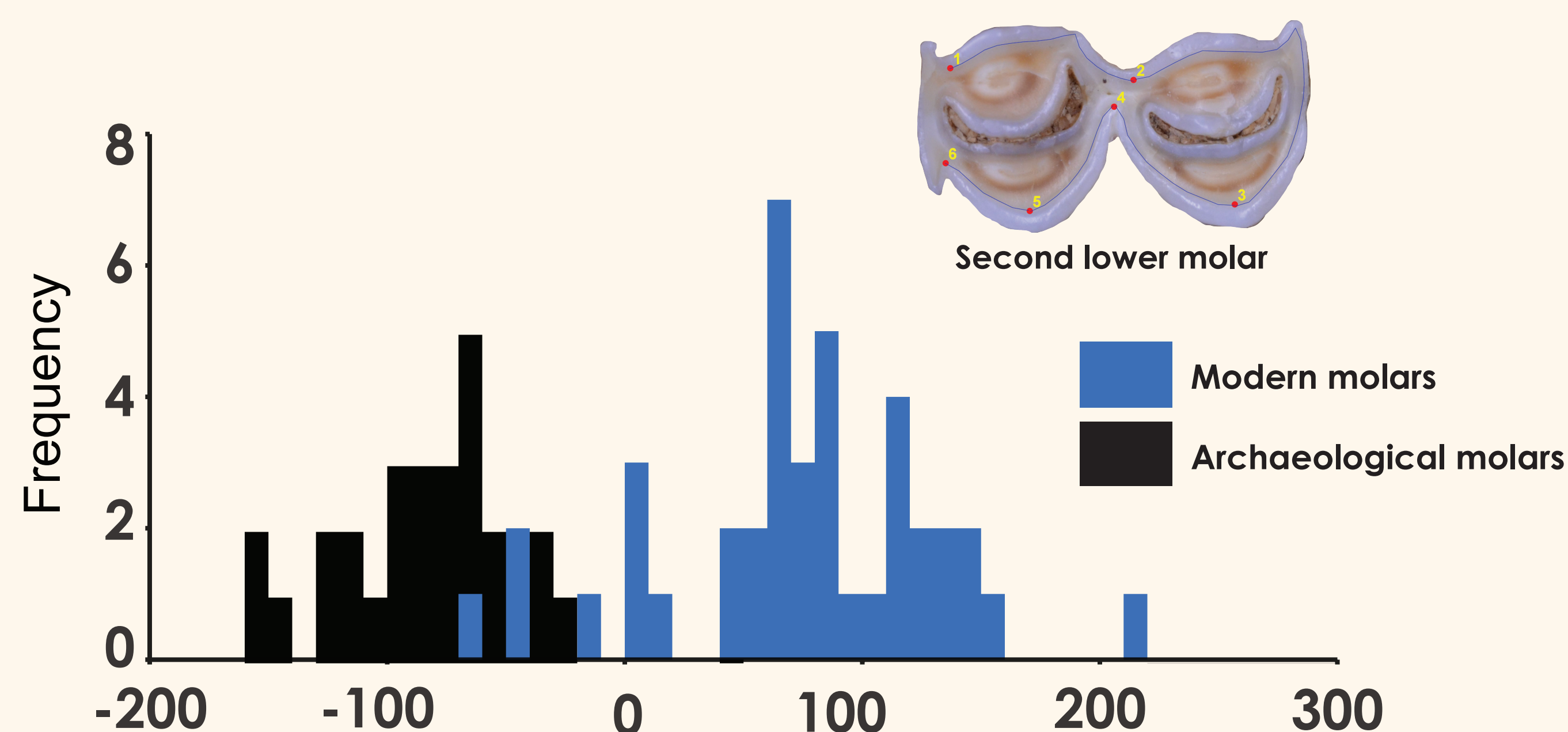
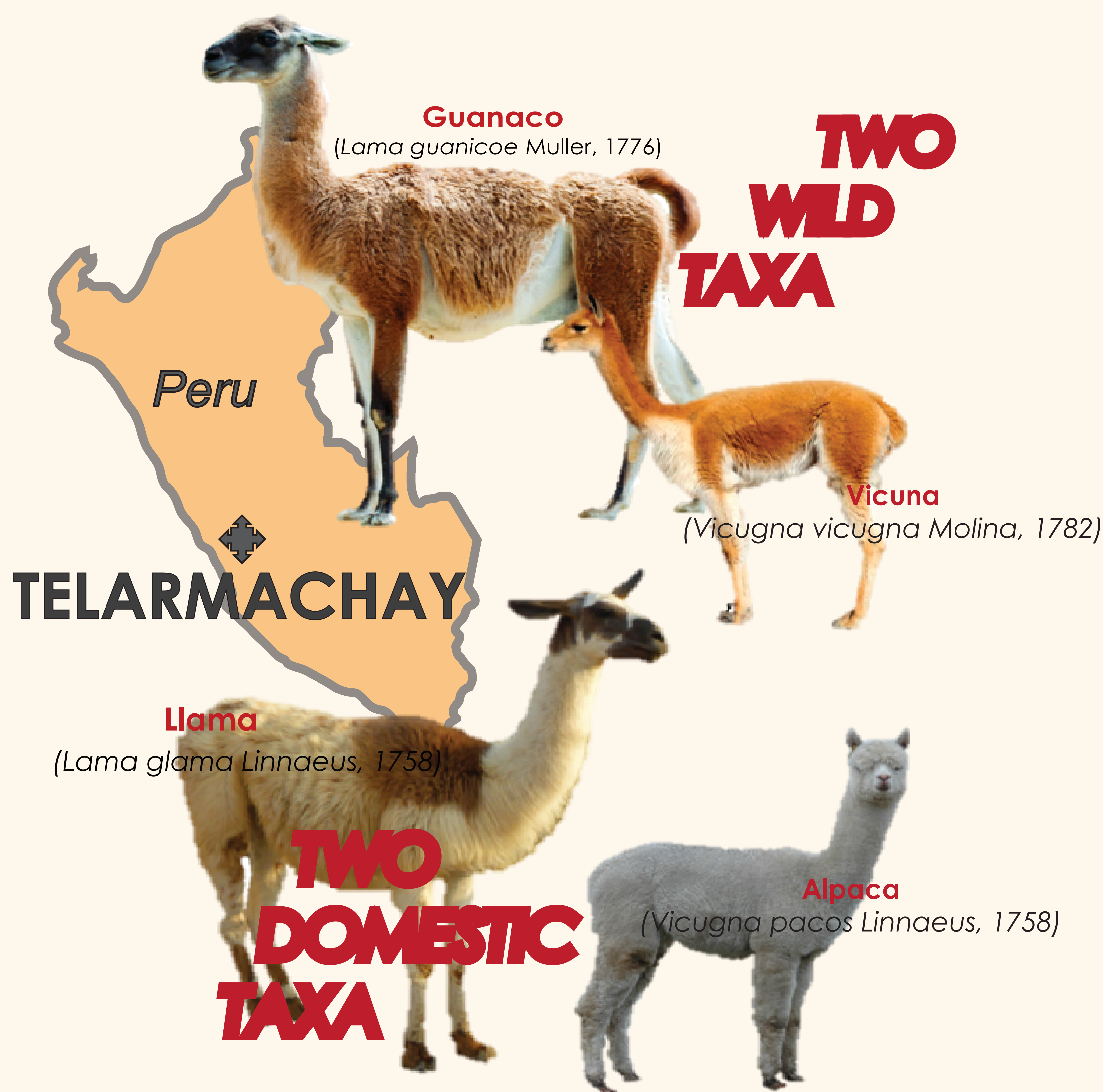
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Context

Archaeological evidence suggests that South American Camelids (SAC), llamas (*Lama glama*) and alpacas (*Vicugna pacos*), were domesticated from potential wild ancestors, guanacos (*Lama guanicoe*) and vicunas (*Vicugna vicugna*), around 6000 years ago in the Andes. However, their domestication process is still poorly understood. Their taxonomic identification in the archaeological records remains challenging for zooarchaeologists due to their morphological similarity. A clear distinction between the four species is highly required to further document their domestication process.

First results

We first investigated how much tooth morphology could contribute to identify the taxonomic diversity of SAC using 2D Geometric morphometrics (GMM) of teeth. This approach proved unable to distinguish current wild and domestic taxa. However, we found a great divergence between the archaeological and modern variation of SAC, suggesting that the camelids Pre-hispanic diversity could not be explored using modern SAC as comparatives.



Bivariate diagrams with scores projection of the different discriminant axis, composed of archaeological molars group and modern M/2 group

New investigations

To bring new insights into the SAC domestication process, my PhD research project will focus on the unique site of Telarmachay (Peru) where evidence of a domestication process, 2000 years before the rest of Andean area, has been proposed. We will use a multidisciplinary approach combining 3D geometrics morphometrics on post-cranial bones and isotopics geochemistry analyses to unrevealing the domestication process.

