

## Characterization of the complete mitochondrial genome of the black Alpaca breed of *Vicugna pacos* (Mammalia, Artiodactyla, Camelidae) from Puno, Peru

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### ABSTRACT

The domestic South American camelid *Vicugna pacos* L. is distributed along Peru, Chile, Bolivia, and Argentina. Here, we contribute to the bioinformatics and evolutionary systematics of the Camelidae by performing high-throughput sequencing analysis on the black Huacaya breed of *V. pacos* from Puno, Peru. The black Huacaya breed mitogenome is 16,664 base pairs (bp) in length and contains 37 genes (GenBank accession MT044302). The mitogenome shares a high-level of gene synteny to other Camelidae (*Camelops*, *Camelus*, *Lama*, and *Vicugna*). The mitogenome of the black Huacaya breed of *V. pacos* situates it in a clade with *V. vicugna* Molina, sister to *Lama*. We anticipate that further mitogenome sequencing of different breeds from *Vicugna pacos* will improve our understanding of the evolutionary history of this taxon.

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Black Huacaya alpaca; mitogenome; Peru; phylogeny; *Vicugna pacos*



Alpacas (*Vicugna pacos*) and llamas (*Lama glama* L.), domestic South American camelids, are the basis for livestock production in the High-Andean zones of Peru (Paredes et al. 2014). More than four million of alpacas in Peru positioned it as the first camelids fiber producer worldwide (90% of world production, Paredes et al. 2013). This alpaca population is composed of the Huacaya (more than 85%) and Suri breed (Quispe et al. 2009, Paredes-Peralta et al. 2011). Although selection pressures during many generations for fiber and color traits possibly lead to the loss of genetic variability mainly in the Huacaya alpaca breeds (Presciuttini et al. 2010, Paredes et al. 2013), there is limited genomic information about their genetic differences. To contribute to the evolutionary systematics of the Camelidae and to advance the understanding of the taxonomy of the black Huacaya alpaca breed, this study characterized the complete mitochondrial genome of a male specimen of *Vicugna pacos* from Quimsachata Germplasm Conservation Center at the Illpa, Puno, Peru (15°47'43"S, 70°37'22"W).

DNA was extracted from blood of the black Huacaya alpaca breed (Specimen Voucher: INIA150129) using the Quick-DNA Plant/Seed kit (Zymo Research, California, USA) following the manufacturer's instructions. The 150 bp PE Illumina library construction and sequencing was performed by myGenomics, LLC (Alpharetta, Georgia, USA). The genomes were assembled using default de novo settings in MEGAHIT (Li et al. 2016) and Sanger sequencing to close

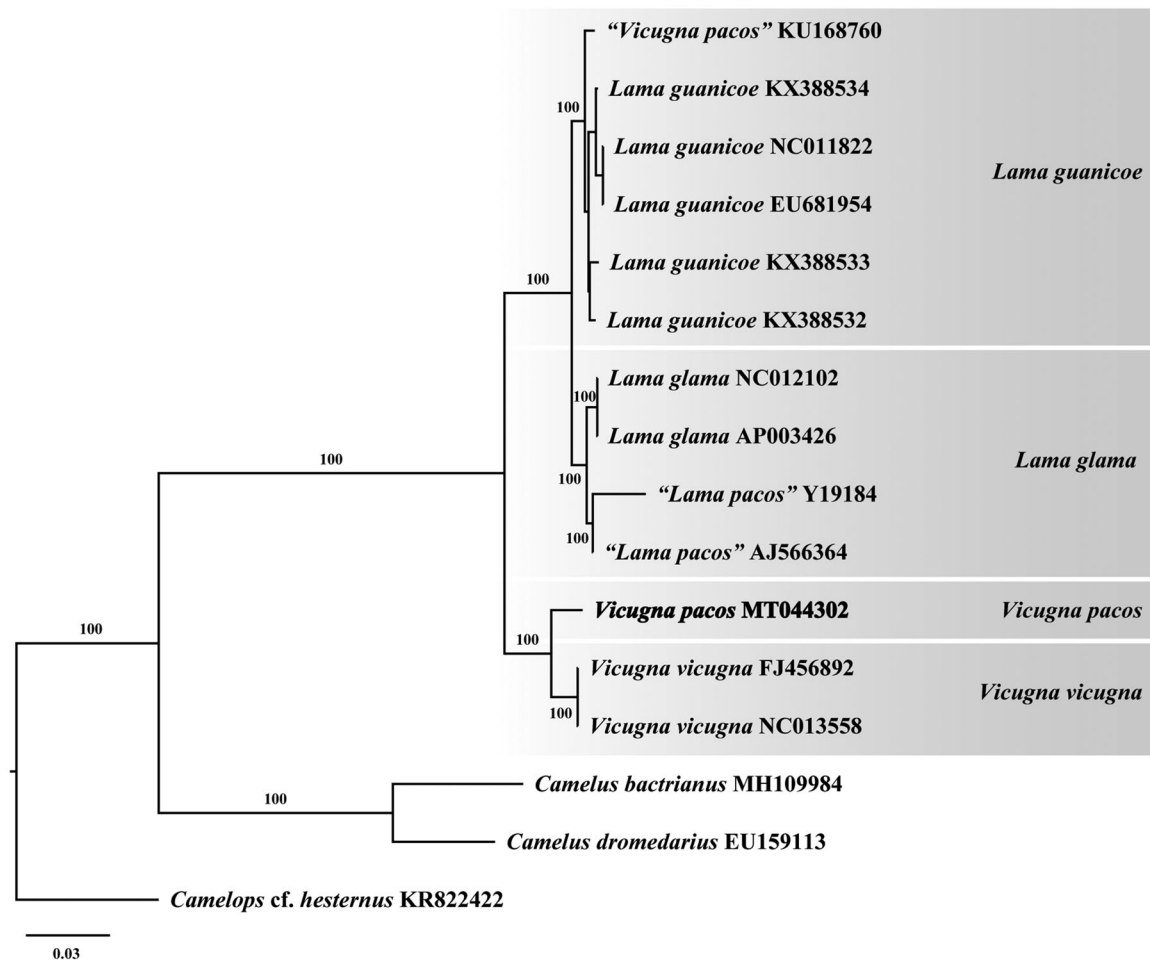
the gap in the control region using primers 16,107F 5'-CCCGCATCATAACAACCATAAAGG-3' and 48R 5'-CCATCTAGGCATTTTCAGCGC-3' following the protocol of Bustamante et al. (2017). The mitogenome was confirmed using default mapping settings in Geneious Prime (Biomatters, Ltd, Auckland, New Zealand). The genes were annotated with MITOS (Bernt et al. 2013) and manually using ORFfinder. The Huacaya breed mitogenome was aligned to other mitogenomes using MAFFT (Kato and Standley 2013). The phylogenetic analysis was executed with RAXML-NG (Kozlov et al. 2018) with the GTR+gamma model and 1000 bootstraps. The tree was visualized with TreeDyn 198.3 at Phylogeny.fr (Dereeper et al. 2008).

The mitogenome of the black Huacaya alpaca breed is 16,664 bp in length and contains 37 genes. It has a slight A+T skewed (59.1%) and includes 22 tRNA (tRNA-Leu and tRNA-Ser occur in duplicate), 2 rRNA (rnl, rns), 13 genes involved in electron transport and oxidative phosphorylation, and 1 control region (CR). The mitogenome of the Huacaya breed is similar in length, content, and organization to other 14 Camelidae belonging to the genera *Camelops* Leidy, *Camelus* L., *Lama*, and *Vicugna* (Di Rocco et al. 2010, Westbury et al. 2016).

Phylogenetic analysis of the black Huacaya breed of *V. pacos* resolved it in a fully supported clade with *V. vicugna*, sister in position to the genus *Lama* (Figure 1). A similar evolutionary relationship for Camelidae was reported by

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**Figure 1.** Maximum likelihood phylogram of black Huacaya alpaca breed (*Vicugna pacos*) (MT044302) and related camelids. Numbers along branches are RaxML bootstrap supports based on 1000 nreps. The legend below represents the scale for nucleotide substitutions.

Westbury et al. (2016) and Díaz-Maroto et al. (2019) based on mitogenome data. Further complete mitogenome sequencing of different breeds from *Vicugna pacos* (i.e., Suri breed) will help improve our understanding of the phylogenetics of the South American camelids.

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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