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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 cameld *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.

Alpacas (*Vicugna pacos*) and llamas (*Lama glama* L.), domestic South American camels, 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 during many generations for fiber and reproduction in any medium, provided the original work is properly cited.

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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**

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