Genetic and evolutionary history of South American camelids
(Historia genético-evolutiva de camélidos sudamericanos)

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Four South American Camelid species are actually known, two of them are wild, the guanaco (*Lama guanicoe*) and the vicuña (*Vicugna vicugna*), and two forms are domestics, the alpaca (*Vicugna pacos*) and the llama (*Lama glama*), however the origin of the domestic species is still debated. In order to investigate the origin of the domestic forms and the genetic diversity and structure we analised the variation in two mitochondrial gene sequences, the G banding pattern of chromosomes and 14 microsatellite markers.

All analyses grouped guanacos with llamas and vicuñas with alpacas. The phylogenetic analyses showed *Vicugna vicugna* and *Lama guanicoe* as monophyletic groups. The analysis of both gene sequences showed two clades within vicuñas. Nevertheless, the results of the guanaco populations did not reflect the four proposed subspecies. The structure of chromosome bands showed fine and consistent differences on the short arm of chromosome 1, separating camels, guanacos and llamas from vicuñas and alpacas. This pattern was consistent even in a hybrid guanaco x alpaca.

Vicuña genetic structure is demographically mediated and the product of low variation within populations produced by a past population reduction which in turn has contributed to the existence of highly distinct geographic populations. We found that genetic diversity in the northern subspecies was low within populations but that populations on average were highly differentiated. In contrast, the subspecies of the Andean guanaco studied showed evidence of limited structure using microsatellite allele frequency and mitochondrial DNA.

Today our knowledge on the genetics of these wild and domestic species is limited in many aspects. However, it is clear that the structure and genetic differentiation between wild guanaco and vicuña, among populations and herds of llamas and alpacas, presents an opportunity to contextualize, expand, and apply on the rapid progress being made in camelid genomics. Increased emphasis is needed on the unique evolutionary history of each of these groups, and using differences in population structure and phenotypic variation to better characterize and explore the camelid genome.