

# Utility of genetic variation in coat color genes to distinguish wild, domestic and hybrid South American camelids for forensic and judicial applications

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## Abstract

A molecular genetic protocol for distinguishing pure and hybrid South American camelids was developed to provide strong, quantifiable, and unbiased species identification. We detail the application of the approach in the context of a criminal case in the Andes Mountains of central Chile where the defendants were alleged to have illegally hunted three wild guanacos (*Lama guanicoe*), as opposed to hybrid domestic llama (*Lama glama*)/wild guanaco crosses, which are unregulated. We describe a workflow that differentiates among wild, domestic and hybrid South American camelids (*Lama* versus *Vicugna*) based on mitochondrial cytochrome b genetic variation (to distinguish between *Lama* and *Vicugna*), and *MC1R* and exon 4 variation of the *ASIP* gene (to differentiate wild from domestic species). Additionally, we infer the population origin and sex of each of the three individuals from a panel of 15 autosomal microsatellite loci and the presence or absence of the *SRY* gene. Our analyses strongly supported the inference that the confiscated carcasses corresponded with 2 male and 1 female guanacos that were hunted illegally. Statistical power analyses suggested that there was an extremely low probability of misidentifying domestic camelids as wild camelids (an estimated 0 % Type I error rate), or using more conservative approached a 1.17 % chance of misidentification of wild species as domestic camelids (Type II error). Our case

report and methodological and analytical protocols demonstrate the power of genetic variation in coat color genes to identify hybrids between wild and domestic camelid species and highlight the utility of the approach to help combat illegal wildlife hunting and trafficking.