# Sarcoptic mange outbreak decimates South American wild camelid populations in San Guillermo National Park, Argentina

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## Resumen

Sarcoptic mange epidemics can devastate wildlife populations. In 2014, mange was first detected in vicuñas (Vicugna vicugna) and guanacos (Lama guanicoe) in San Guillermo National Park (SGNP), Argentina. This study describes the temporal dynamics of the outbreak, its effects on the park's wild camelid populations between 2017-2019, and investigates the potential source of the epidemic. From May 2017 to June 2018, transect surveys indicated a sharp decrease in the density of living vicuñas and guanacos by 68% and 77%, respectively. By April 2019 no vicuñas or guanacos were recorded on transect surveys, suggesting their near-extinction in the park. Clinical signs consistent with mange (e.g., intense scratching, hyperkeratosis, alopecia) were observed in 24% of living vicuñas (n = 478) and 33% of living guanacos (n = 12) during surveys, as well as in 94% of vicuña carcasses (n = 124) and 85% of guanaco carcasses (n = 20) examined. Sarcoptes scabiei was identified as the causal agent by skin scrapings, and the cutaneous lesions were characterized by histopathology (n = 15). Genetic characterization revealed that mites recovered from seven vicuñas (n = 13) and three guanacos (n = 11) shared the same genotype, which is consistent with a single source and recent origin of the epidemic. Tracing the potential source, we identified a governmental livestock incentive program which introduced llamas (Lama glama) in areas adjacent to SGNP in 2009, some of which had alopecic scaling consistent with sarcoptic mange. Though at the time of our study no llamas with mange were available for confirmatory sampling, we hypothesize that the introduction of mange-infected llamas may have triggered the outbreak in wild camelids. This unprecedented event in SGNP had devastating effects on dominating herbivores with potentially profound cascading effects at the community and ecosystem levels.

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