

Congenital Consequences of Two-Founder Effects on Guanacos Inhabiting a Small Island for 70 Years

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Abstract: The objective of this study was to determine what reproductive and congenital consequences, if any, resulted from intensive inbreeding in a closed-wild population of guanacos (*Lama guanicoe*) starting with a small nucleus of founding individuals. In the late 1930s 15 guanacos from southern Patagonia of South America were introduced to Staats Island in the Falkland Islands (see Franklin 2005, Franklin and Grigione 2005, Franklin et al. 2005). Although small in size (5 km²), the island contained equivalent plant communities to the Patagonia including highly favorable forage for guanacos. The population grew 16 to 18% per year for the next 25 years when nearly 400 animals were removed by hunting, leaving just 10–20 animals in the late-1950s. Over the next 45 years the population grew reaching 413 in 2004. Behaviorally, only one to two breeding males may have monopolized mating at each population bottleneck. Thus, twice the genes of a few animals became the future population. During four-partial birth seasons 23 abnormal guanacos were encountered on the island: newborn deaths (39%), limb deformities (22%), facial deformities (choanal atresia) (17%), stillborns (17%), and dystocia related (4%). All died except one adult female with partially collapsed pasterns. Abnormal newborns represented 18% of all young-of-the-year. It is suspected that unavoidable inbreeding depression resulted in a genetic driven, high rate of congenital defects and deaths seen today. Ironically, the population of guanacos on Staats Island with its finite resources is unlikely to have survived without this mortality impact of repetitive-close inbreeding created by two-founder effects. Preliminary genetic analyses reveals heterozygosity and number of alleles by locus is not significantly different than Patagonia guanaco populations, despite the fact that there is a reduction in haplotypic richness and changes in haplotypic proportions. Results from this island population have management implications for guarding against inbreeding in introduced and remnant populations on the mainland. Findings also raise the question do the South American camelids have a propensity for congenital defects caused by genetic variants that have been carried through their evolutionary and/or man-made histories?

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