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Optimizing procedures for genomic analyses of Beaver Hills canid scat

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Poster Presentation Abstract:

There are significant economic and ecological motivations to study the recently recolonized wolf (*Canis lupus*) population in the Beaver Hills region of Alberta, Canada. The reappearance of an apex predator presents challenges for land management. Competing claims for both agricultural and environmental priority necessitate an accurate description of the wolf population to inform an effective management solution. Faecal analysis presents a non-invasive technique for obtaining estimates of the population size, habitat use and genetic structure of wolves and coyotes (*C. latrans*). As a preliminary step, we sought to develop a procedure for obtaining and analyzing genetic material from canid scat. Ultimately this protocol will be applied to a 500-sample collection gathered in the Cooking Lake-Blackfoot Recreation Area and Elk Island National Park between May 2015 and January 2016. We compared and assessed protocols for scat storage and handling, DNA extraction and diagnostic molecular analyses. Extractions performed on scat samples stored at -20°C using the QIAmp Stool protocol produced DNA that could be successfully amplified using Scat ID primers. Diagnostic restriction digests match published fragment patterns for Alberta canids (i.e., dog and wolf). Based on these findings we present a protocol for species identification from canid scat collected in the Beaver Hills region.

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