**Microbiome Analysis Enables Future Non-Invasive Wildlife Monitoring of Rocky Mountain Elk Populations

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Rocky Mountain Elk (*Cervus canadensis*) seasonal migration, body-condition and sex ratios are important parameters for characterizing populations at high risk of disease or population decline but, so far, have been outside the scope of currently available non-invasive methods. Fecal microbiomes can be surveyed non-invasively and model systems indicate that microbiome compositional differences are associated with changes in diet, stress, disease and physical condition of the host. With this in mind, we set out to examine the host-microbiome connection in scat samples from 4 populations of elk in western Montana. The elk sampled, varied geographically (i.e. by population/herd), by body condition and by sex. We built a supervised-machine learning classifier on bacterial taxa with cross validation (CV) to predict each fecal microbiome's affiliation to known host categories. The microbiome classifier predicted host population, sex, and body-condition measurements with promising CV results for each classifier. The fecal microbiome classifier developed here may be useful for detecting the sex and relative body condition of elk from other populations or tracking variations within the sampled populations across years. Monitoring wildlife fecal microbiomes would represent a breakthrough for non-invasive conservation biology, and we provide proof of concept for obtaining low cost, fine scale, management-relevant information from scat samples that can be expanded to non-invasive applications and other animal species in the future. Future efforts may also explore training new classifiers to detect wildlife diseases such as Brucella, Anthrax, Tuberculosis or Chronic Wasting Disease that may also be associated with microbiome composition.