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The effect of genetic relatedness and diversity on parasite load in the North American raccoon (*Procyon lotor*)

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The influence of genetic relatedness and diversity on parasite transmission and diversity was examined in raccoons (*Procyon lotor*) from mid-Missouri. Relatedness and diversity of individuals was measured using 12 polymorphic microsatellite loci that were amplified using the polymerase chain reaction (PCR). Fragment analysis was used to determine the alleles of the individuals at each locus. Using the computer analysis program Kinship, relationship probabilities were calculated between individuals and populations. Heterozygosity, internal relatedness, and d_2 values were also calculated. Parasite similarity indices did not differ among pairwise comparisons of animals with first order, second order, and no detected relationships. We are currently investigating if correlations exist between ectoparasite or endoparasite loads and heterozygosity, internal relatedness and d_2 values. The data generated in this preliminary study will be used in a larger study of patterns of disease/parasite occurrences in artificially aggregating raccoons.

This project was completed to fulfill a Capstone requirement.