Stable Isotope Analysis Of Summer Wolf Diet In Northwestern Montana

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When distinct δ13C and δ15N values of potential prey are known, stable isotope analysis (SIA) of wolf (*Canis lupus*) hair can be used to estimate diet variability at the individual, pack, and regional levels. Our objectives were to estimate intra-population diet variability, and determine proportions of prey consumed by wolves. We collected guard hairs of 45 wolves from 12 packs in northwestern Montana and temporally matched scats from 4 of the same packs, summer 2008 and 2009. We used hierarchical Bayesian stable isotope mixing models to determine diet and scales of diet variation from δ13C and δ15N values of wolves, deer (*Odocoileus* spp.), elk (*Cervus canadensis*), moose (*Alces alces*), and other prey. We calculated percent biomass of prey consumed from scats, and used bootstrapped scat data,

and Markov Chain Monte Carlo simulation data from stable isotopes to estimate confidence intervals of difference between results from each technique for the 4 packs with matched samples. Differences among packs explained most variability in diet based on stable isotopes, and moose was the most common prey item for 11 of 12 packs. From scat data, deer was the most common prey item for 3 of 4 packs, and estimates of moose consumed were significantly different from SIA estimates for the same 3 packs. The proportion of moose in wolf diet may have been overestimated by SIA because wolf-specific fractionation values were not available. Stable isotope analysis has the potential to efficiently provide useful management information, but experimentally derived fractionation values for wolves would likely improve the accuracy of estimates in future studies.