WHAT WE CAN (AND CANNOT) SAY ABOUT WILDLIFE POPULATIONS USING NON-INVASIVE GENETIC SAMPLING ^{TWS}

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Non-invasive genetic sampling is emerging as a sexy new tool in the arsenal of techniques used by wildlife biologists. Like any new approach, it has promise, as well as pitfalls. I will discuss some genetic-based approaches that I am using, along with my students and other colleagues, to answer applied wildlife ecology questions. For example, abundance of elusive carnivores can be estimated using mark-recapture approaches coupled with non-invasive DNA sampling (such as hair snags), but there is a "shadow effect" that can arise from the failure to distinguish individuals based on unique genotypes. Species identification is also possible using non-invasive sampling, and we have developed diagnostic tests for distinguishing among felids (including lynx), dogs (including coyotes), bears, and mustelids (including wolverines, fisher, and marten) across the northern U.S.; these diagnostic tests are being incorporated into Nationwide sampling of lynx in collaboration with the USFS Rocky Mountain Research Station. Finally, genetic tools can be used to evaluate gene flow, as we have done with both lynx and small mammals. I will stress that genetic tools are valuable, but should not be used without validation; furthermore, the most productive avenue is to combine genetic and demographic (eg mark-recapture) approaches.