

Individual genotypes from environmental DNA: fingerprinting snow tracks of three large carnivore species

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Abstract

Continued advancements in environmental DNA (eDNA) research have made it possible to access intraspecific variation from eDNA samples, opening new opportunities to expand non-invasive genetic studies of wild animal populations. However, the use of eDNA samples for individual genotyping, as typically performed in non-invasive genetics, still remained unachieved. We present the first successful individual genotyping of eDNA obtained from snow tracks of three large carnivores: brown bear (*Ursus arctos*), European lynx (*Lynx lynx*) and wolf (*Canis lupus*). DNA was extracted using a protocol for isolating water eDNA and genotyped using amplicon sequencing of short tandem repeats (STR) and, for brown bear, a sex marker, on a high-throughput sequencing platform. Individual genotypes were obtained for all species, but genotyping performance differed among samples and species. Multilocus genotyping success for individual identification was higher for brown bear samples (6 over 7), than for wolf (7 over 10) and lynx (4 over 9) samples. The sex marker was genotyped in 5 out of 7 brown bear samples. Results for three species show that reliable individual genotyping, including sex identification, is now possible from eDNA in snow tracks, underlining its vast potential to complement the non-invasive genetic methods used for wildlife. To fully leverage the application of snow track eDNA, improved understanding of the ideal species- and site-specific sampling conditions, as well as laboratory methods promoting genotyping success are needed. This will also inform efforts to retrieve and type nuclear DNA from other eDNA samples, thereby advancing eDNA-based individual and population level studies.

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