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Tracking animal movement by comparing trace element signatures in claws to spatial variability of elements in soils

Danielle M. Ethier [a,*], Christopher J. Kyle [b], Joseph J. Nocera [c]

[a] University of Guelph, 50 Stone Road East, Guelph, Ontario N1G 2W1, Canada
[b] Natural Resources & DNA Profiling Forensic Centre, Trent University, DNA Building, 2140 East Bank Dr., Peterborough, Ontario K9J 7B8, Canada
[c] Ontario Ministry of Natural Resources, Trent University, DNA Building, 2140 East Bank Dr., Peterborough, Ontario K9J 7B8, Canada

HIGHLIGHTS

- Trace element signatures in soils vary locally and broadly.
- Chemical profiles in claw keratin can be linked to the surrounding environment.
- Results provide evidence that movement can be discerned from claw chemistry.
- Element profiles in tissues could be used to assess geographic origin of animals.

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ABSTRACT

Biogeochemical markers in ecology have provided a useful means for indicating geographic origin and movement patterns of species on various temporal and spatial scales. We used trace element analysis to resolve spatial and habitat-specific environmental gradients in elemental distributions that could be used to infer geographic origin and habitat association in a model terrestrial carnivore: American badger (*Taxidea taxus jacksoni*). To accomplish this, we generated element base-maps using spatial principal component analysis, and assessed habitat-specific signatures using multivariate statistics from soil element concentrations in southwestern Ontario, Canada. Using canonical correlation analysis (CCA) we also test whether element variability in the claw keratin of a terrestrial carnivore could be explained by the chemical variability in the soils of the local environment. Results demonstrated that trace element signatures in soils vary locally with land use practices and soil texture type and broadly with the underlying geology. CCA results suggest that chemical profiles in claws can be linked to the surrounding chemical environment, providing evidence that geographic patterns in mammalian movement can be discerned on the basis of claw chemistry. From this, we conclude that geographic assignment of individuals based on element profiles in their tissues and referenced against soil elemental distributions would be coarse (at a spatial scale of 100–1000 km, depending on the chemical heterogeneity of the landscape), but could be used to assess origin of highly mobile animals or habitat association of individuals. Compared to stable isotope analysis, the assessment of trace elements can provide a much greater level of detail in backcasting animal movement pathways.

1. Introduction

The movement of animals over space and time is a crucial component of almost all ecological and evolutionary processes (Nathan, 2008). Movement defines an individual's interaction with its surrounding environment, thus influencing the resources it encounters and the space it occupies. However, researchers are often limited in their ability to study movement patterns, especially for species that are rare, cryptic, or long-distance migrants (Chadès et al., 2008). Therefore, our understanding of movement by such species is typically indirect and incomplete. Various extrinsic (e.g., mark-recapture and radio-telemetry) and intrinsic (e.g., genetics) makers have provided valuable insight on ecological relationships and movement histories of species, but are often burdened by low sample sizes, prohibitive financial costs, or significant logistical barriers (Webster et al., 2002). These methods also carry their own set of limitations regarding their assumptions and temporal signatures, which can therefore be used jointly to get a more complete picture of a species movement ecology. Because of this, there has been increasing interest in alternative methods for tracking animal movement, such as using intrinsic chemical indicators.

Stable isotopes have been used to determine migratory connectivity in a variety of taxa, including birds, mammals, fishes, and insects (e.g., Kelly et al., 2002; McCarthy and Waldron, 2000; Rubenstein and Hobson, 2004; Vogel et al., 1990; Wassenaar and Hobson, 1998), where movement is reflected in differences in the isotopic composition

* Corresponding author. Tel.: +1 226 923 9206.
E-mail addresses: ethier.danielle@gmail.com (D.M. Ethier), chris.kyle@nrdpfc.ca (C.J. Kyle), joe.nocera@ontario.ca (J.J. Nocera).

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of their tissues. More recently, the application of trace element analysis has provided an additional geographic marker (Burger et al., 2001; Donovan et al., 2006; Gómez-Diaz and González-Solis, 2007; Kelsall and Calaprice, 1972; Kelsall and Burton, 1979; Hanson and Jones, 1976; Parrish et al., 1983; Norris et al., 2007; Ramos et al., 2009; Szép et al., 2003; Torres-Dowdall et al., 2012). Similar to stable isotopes, trace elements are incorporated into animal's tissues during growth, in proportion to local environmental concentrations (Driessens and Verbeeck, 1990; Gartner, 1989; Szép et al., 2003). These environmental concentrations are influenced by the surface geology, soil, vegetation, and anthropogenic chemical inputs in a particular area (Bortolotti et al., 1989; Szép et al., 2003). Therefore, information on environmental condition and habitat association are integrated into animal's tissues over the period the tissues are synthesized (Bearhop et al., 2002; Chamberlain et al., 1997; Hobson and Clark, 1992; Hobson and Wassenaar, 1997). If a tissue is selected that is chemically inert once formed (e.g., shells, otoliths, hair, claws) and is grown incrementally (i.e., deposited in layers on a daily, seasonal, or annual basis), shifts in an individual's foraging environment could be captured in the chemical changes in these tissues, acting as a time-integrated indicator of geographic origin. The blade horn keratin of mammalian claws has been identified as a likely reliable tissue for such time-series analysis, as this portion of the claw is deposited linearly and is uncomplicated by the mixing of old and new keratin layers along its length (Ethier et al., 2010).

Trace element analysis presents an advantage over stable isotopes because it allows us to retrieve precise element archival information from biological samples (Outridge et al., 1995) due to its fine-scale sampling resolution (e.g., a 30–100 μm diameter beam for laser ablation), low detection limits (conservatively, <1 ppm), and multi-elemental analytical capabilities (>40 elements, Szép et al., 2003). In addition, stable isotopes typically vary regionally (>1000 km; Marra et al., 1998), whereas trace element signatures can vary in distinct patterns at relatively fine spatial scales (10–1000 km; Szép et al., 2003), allowing for a higher degree of spatial resolution for geographic assignment.

Despite these advantages, some research has suggested that trace element signatures show no geographic gradients in their distribution (Donovan et al., 2006), unlike those of stable isotopes (e.g., δD; Hobson and Wassenaar, 1997), possibly limiting our ability to assess geographic origin of samples transported across large spatial scales. Having little *a priori* information on trace element variability in terrestrial systems, it is not surprising that these markers have not been used to study movement history in terrestrial mammals. In terrestrial systems, soil is the major source of biologically available elements (Kabata-Pendias and Mukherjee, 2007), yet spatial patterns in soil element concentrations are poorly defined. Although there is a considerable amount of literature on element behavior in soils (e.g., Sauvé et al., 2003) and the impact of point-source contamination (e.g., Nriagu et al., 1998), there is comparatively little information on ambient background trace element concentrations (McKeague and Wolynetz, 1980; Sheppard et al., 2009) and their relative spatial distributions (Atteia et al., 1994; Facchinelli et al., 2001; McGrath et al., 2004; Saby et al., 2009). How element concentrations vary with biogeographical gradients is unclear and data regarding patterns of variation are lacking (Gómez-Diaz and González-Solis, 2007). Free of human interference, the element content of the soil is largely dependent on the parental rocks from which the soil was derived through weathering (Kabata-Pendias and Mukherjee, 2007). In highly altered agro-ecosystems, other factors, including the input of fertilizers, pesticides, sewage effluents, and biosolids (e.g., animal wastes, paper pulp sludge) can affect element and macronutrient concentrations (Kabata-Pendias and Mukherjee, 2007). Ideally, to indicate an animal's origin and track movement, a map of elemental signatures should be developed for the area in which the tissue was synthesized (Donovan et al., 2006). Mapping of multiple chemical signatures has been used to interpret natural and anthropogenic factors affecting their distribution (e.g., Fong et al., 2008; Saby et al., 2009; Tao, 1996), but such effects have yet to be applied to biogeochemical application in wildlife ecology.

Here we address the issue of geographic gradients in trace elements in relation to animal movement by examining the spatial distribution and habitat-specific patterns of soil trace element signatures across a terrestrial agro-ecosystem of southwestern Ontario to facilitate the determination of geographic origin of a model terrestrial carnivore. We approached this investigation by first quantifying the spatial variation in elements to generate "base-maps" of elemental occurrences in soil. Element base-maps have been generated in few ecological studies and have, until now, been limited to stable isotopes (e.g., Hobson and Wassenaar, 1997). We also used multivariate statistics to describe the relationships between soil element composition and various treatments (i.e., land use practice and soil texture type) since element profiles are suggested to be site-specific, reflecting habitat characteristics rather than reflecting broad-scale geographic gradients (Bortolotti et al., 1989; Donovan et al., 2006). Our objectives were to assay soils so as to: (1) quantify the relative variability among 11 elements (Ca, Mg, K, Al, Ba, Cr, Cu, Fe, Mn, Sr, and Zn), (2) determine how environmental factors influence their distribution, and (3) describe the spatial relationships of these elements. To determine if element base-maps can be useful for geographic assignment, we quantify the level of association between trace element signatures in the claws of a model terrestrial carnivore and those from the soils of the local environment. This work follows that of Ethier et al. (2013), where trace element signatures in the blade horn keratin of American badger (*Taxidea taxus jacksoni*) claws could be attributed, in part, to endogenous uptake of trace chemicals from the local environment. Given these research findings, the logical next step in this field of study is to determine if these claw chemical signatures are in fact associated with those of the local soils.

We conducted this study in the summer of 2009 in the agriculturally dominated landscape of southwestern Ontario, Canada (Fig. 1). Our sampling structure was designed to create a trace element base-map to compare to the elemental constitution of claws from an endangered population of American badgers. Badgers are difficult to study using conventional methods due to their secretive nature, low population densities, and nomadic behavior. The application of trace element analysis, therefore, lends itself well to the study of this elusive carnivore. Badgers maintain large territories (range 13–513 km^2; Newhouse, 1998), have a high dispersal capability (upwards of 100 km; Messick and Hornocker, 1981), and broad foraging niche (Azevedo et al., 2006) making it highly probable that an individual will encounter a variety of chemically distinct environments throughout the course of its daily, seasonal, or annual cycle.

2. Materials and methods

2.1. Soil sampling

We selected study sites to facilitate corresponding element analysis of claw samples collected from American badgers. Therefore, we concentrated soil sampling around collection locations of eleven male (sampling radius = 10 km, area = 314 km^2), nine female (sampling radius = 5 km, area = 78.5 km^2), and five un-sexed (sampling radius = 10 km, area = 314 km^2) archival badger specimens, with site centroids on the location of claw collection (Fig. 1). Sampling diameters were selected to approximate home-range sizes for male (292–513 km^2) and female badgers (2–82 km^2) based on published literature (Newhouse, 1998). Within each study site, we selected 21 points randomly, of which a range of 6–17 was sampled based on site access and landowner permission. At each sampling point, we collected 20 soil profiles from a 10 m × 10 m area, which were pooled to form a composite for each sampling point (de Zorzi et al., 2008). We sampled the subsoil (10–20 cm depth) to reduce the effects of surface contaminants and variable organic content in the topsoil on ambient element concentrations (Sastre et al., 2001). We collected and analyzed a total of 367 (pooled to 25 study sites) soil samples. At each sampling point, we recorded additional information on land use practice and soil texture. Land use was divided broadly into five categories: forest