# Trace element profiles as unique identifiers of western sandpiper (*Calidris mauri*) populations

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**Abstract:** Understanding the ecology and evolution of migratory animals requires information on how populations are geographically linked between periods of the annual cycle. To examine whether trace elements could be used to track migra-

lon™ beakers. After 2 mL of concentrated nitric acid ($HNO_3$) had been added, capped beakers were placed on a 70 °C hot plate for digestion of samples. Once the resulting liquid had cooled, 0.25 mL of hydrogen peroxide was added to digest dissolved organic compounds; samples were again dried on a 70 °C hot plate. After cooling, another 1 g of 2%

signment of individuals of unknown origin to particular geographic regions appeared unlikely.

In our study, we sampled only five wintering sites, but two of these sites were in the Bay of Panama, where 35% of the global population is estimated to overwinter (Morrison et al. 2001). It is estimated that an additional 10% of western sandpipers overwinter in Bahía Santa María. Samples from three or four more key sites in the Bay of Panama plus another three or four sites in Mexico would increase the global representation to over 75%. Based on the number of additional sampling sites needed and our current discriminatory ability, we suggest that trace element profiles could be used to accurately separate all major western sandpiper wintering sites. However, because elemental profiles appear to be highly site-specific, trace elements will likely not be useful for species with a more continuous distribution, where only a small fraction of the populations can be sampled (Donovan et al. 2006).

The key advantage of this technique is that 40 or more markers can be analyzed simultaneously from a single tissue sample (Szep et al. 2003), thereby increasing the chances that a subsample of elements will vary independently between sites. The number of elements than can be measured simultaneously by HR-ICP-MS analysis may balance out the relatively high cost (stable isotope analysis is approximately one-tenth to one-half the price). Other issues associated with these markers are likely more important to consider. Analysis of multiple stable isotopes is also possible, but these markers often show high spatial autocorrelation (e.g., $\delta^{13}C$ and $\delta^{15}N$, $\delta^{18}O$ and $\delta D$), reducing the likelihood that the geographic resolution of assignments will improve with the addition of only one or two more isotopes. The combination of stable isotopes with genetic markers has proven useful (e.g., Kelly et al. 2005; Boulet et al. 2006) and will undoubtedly improve as more genes can be screened. However, genetic markers are constrained to assigning individuals to breeding areas where genetic structuring occurs and cannot account for adult dispersal within a season because they can only link individuals with their place of birth.

We emphasize that trace elemental markers, like other intrinsic markers, should ideally be verified using known-origin birds (Hanson and Jones 1976; Bortolotti et al. 1988). In addition, there is some evidence that the chemical composition of feathers can change after growth (Hanson and Jones 1976; Bortolotti and Barlow 1988; Bortolotti et al. 1988), implying that assigning individuals of unknown origin to geographic areas in previous periods of the annual cycle could be problematic. Further experimental tests are required to determine whether chemical changes after feathers are fully grown are specific to certain mineral types, habitats, and (or) species. However, our results provide evidence that trace elements can be used to identify shorebird populations with high geographic resolution and provide the potential for tracking individuals between breeding and non-breeding areas.

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