

How Reliable are Morphological Criteria for Species Identification: a case study using ants of the *Lasius* genus

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The species concept defines a species as a group of potentially interbreeding populations. However, many species are described only by their morphological characteristics. This can make identification time intensive and cause inconsistencies with indistinguishable or intermediate phenotypes. Now, molecular methods of identification have begun to be used in conjunction with morphological methods as sequencing techniques become more accessible. These can be used to evaluate the consistency of morphologically identified species and true reproductively isolated populations. However, molecular methods can pose their own challenges, such as contamination from non-target species during the DNA extraction process, making the contaminated sequence data unusable for most analyses. Here, we use a dataset of over 1,000 RAD-seq and COI-gene sequenced individuals that were morphologically identified in the *Lasius* ant genus to investigate the congruence between genetic and morphological species identification and identify interspecific hybrid individuals. We developed a method based on minor allele-depth and competitive mapping to detect and remove sequence contamination from non-target species. We were able to find consistent agreement between the morphological and genetic identifications, as only 1.9% of individuals were incongruous. We could also identify 49 likely hybrid individuals across 6 species. Therefore, using genetic marker analysis of *Lasius* individuals within the surveyed geographic range can be a reliable method to quickly and accurately identify them to the species level. Perfecting these techniques of species identification is imperative for accurate analysis across the fields of ecology, evolution, and conservation biology.