Embracing phylogenetic uncertainty in prioritising species conservation: sensitivity of HEDGE scores to species split

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Abstract

The number of described species has been increasing rapidly over the last 30 years, a phenomenon which may result from a shift in species concept ("taxonomic inflation") and/or real taxonomic progress enhanced by the advances in DNA-based taxonomy and phylogeny reconstruction of the past decades. This increase in species numbers goes together with the split of single species into several ones. The consequences of such species split are the delineation of post-split species with restricted ranges and potentially increased extinction risks, which may have pronounced impacts on the establishment of conservation priorities based on extinction risk. Species split also leads to a re-evaluation of phylogenetic trees, with post-split trees having more species but species that are less evolutionary distinct species than pre-split trees. Therefore, species split may also impact the establishment of conservation priorities based on species phylogenetic originality. Consequently, predicting how species split will affect conservation priorities that incorporate both species extinction risk and phylogenetic originality is challenging. The HEDGE score is one of the criteria according to which such conservation priorities may be established. This score incorporates the evolutionary distinctiveness of a focal species, its extinction risk and those of its close relatives. Here, we evaluated the influence of a hypothetical species split on HEDGE scores. We showed that such split do not affect HEDGE scores for the close relatives of the split-species. However, it can dramatically increase the score of the split-species itself. These results suggest that ignoring cryptic species within a lineage underestimates its HEDGE score. In such situations, the estimated ranking does not capture the real ranking and some lineages may not receive the conservation attention they deserve. Overall, this work demonstrates the need for quantifying phylogenetic uncertainty in the establishment of species conservation priorities and challenges the use of species as relevant conservation units.

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