COMMENTARY

Conservation prioritization in the context of uncertainty

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Human activity is causing rapid degradation of biodiversity (Mace et al., 2005). There was a failure to meet the Convention on Biological Diversity global target to reduce biodiversity loss by 2010 (Butchart et al., 2010). The latest evidence (Tittensor et al., 2014) suggests that there has since been insufficient progress making it unlikely that a revised set of targets will be met a decade later. The resources available for conservation are inadequate to prevent the loss of much of the world's threatened biodiversity; the pace of remedial action, at least to date, is too slow. Conservation planners have therefore been forced to prioritize among the many deserving cases: which species and areas should receive the most protection? They have had to do so in the context of great uncertainty – a conundrum famously referred to as 'the agony of choice' (Vane-Wright, Humphries & Williams, 1991).

Through both academic research and conservation action, it has been strongly argued that maximizing phylogenetic diversity should be one of the main goals of priority setting for conservation (Faith, 1992; Crozier, 1997; Isaac et al., 2007). The argument has been made that limited conservation resources should be focused on those species that would be most keenly missed if they were to become extinct, and the metric put forward for measuring their importance is the amount unique evolutionary history that they represent. Research has focused on several key areas: how should evolutionary history be measured (Faith, 1992; Pavoine, Ollier & Dufour, 2005), how should it be combined with measures of urgency such as extinction risk (Redding & Mooers, 2006; Isaac et al., 2007), what is the impact of changing information (e.g. risk classification and taxonomy) on prioritization decisions (Collen et al., 2011), and most recently, how should evolutionary history be prioritized spatially (Pollock et al., 2015)?

Phylogenies provide a wealth of ways to measure biodiversity, quantify evolutionary history, and discern among competing conservation priorities (Mace, Gittleman & Purvis, 2003). However, the production of species rich phylogenies of the type required to prioritize among groups of species for conservation is still relatively slow. Large-scale revisions of relationships among taxa are often separated by decades, despite the rapidity with which molecular information on species is apparently produced. To date, it has not been possible to adequately evaluate the impact of changing knowledge of phylogenetic relationships on the prioritization decisions made with such trees. In their recent article, Curnick et al. (2015) took advantage of a set of molecular-based phylogenies published in short succession, to investigate the impact of growth of knowledge of phylogenetic history on the calculation of evolutionary distinctiveness for scleractinian corals. Their main finding, that incomplete phylogenies and scores derived from expert elicitation, performed almost as well as the most recent and complete tree, lends great encouragement to prioritizing evolutionary history in less well-known groups of species. Lack of phylogenetic knowledge remains a major barrier to this type of prioritization.

Describing biodiversity patterns and understanding ecological and evolutionary processes requires careful and meticulous research. This is at odds with a discipline that requires urgent answers to pressing questions. Lack of knowledge poses many problems for biodiversity conservation, not least that managers and conservation practitioners are required to act in the face of great uncertainty. Establishing how best to make robust decisions with limited and uncertain information is therefore an important avenue of research. If the findings of Curnick et al. (2015) prove to be common to other groups with perhaps different underlying phylogenetic structures and patterns of missing species, then active conservation under a phylogenetic framework of less well-known groups of species could progress quickly.

The other side of the prioritization equation is to determine the urgency with which any species identified as being of high evolutionary distinctiveness should be attended to. Typically, this is measured using a metric of extinction risk,

such as IUCN Red List classification (Isaac *et al.*, 2007; Mace *et al.*, 2008). Assessing the extinction risk of a suite of species in a 'barometer of life' has been proposed (Stuart *et al.*, 2010) to inform us about the changing face of nature. Achieving this goal will take innovation and increased investment (Collen & Baillie, 2010; Rondinini *et al.*, 2013). The overriding problem in measuring urgency, as in measuring evolutionary history, is still one of how to account for uncertainty. Roughly one in six of the *c.* 75 000 species whose extinction risk has been evaluated, is assessed as Data Deficient (IUCN 2015) – we have no clear understanding of the extinction risk that they may face. Progress is being made to assign predicted categories of risk to such species, based on the often quite rich ecological trait and geographic data available for them (Bland *et al.*, 2015). Testing whether the high levels of prediction observed in mammals can be achieved in non-vertebrate groups of species will demonstrate whether such techniques are of use on a broad-scale.

Bringing together innovations that develop a broader understanding of phylogenetic relationships among species with more rapid ways of assessing their extinction risk will enhance our ability to prioritize for conservation. Doing so in groups of species that are currently not well known, but which provide key services, ecosystem functions and which represent the vast majority of biodiversity could bring about a step change in conservation activity. An expanded set of conservation options, including ways to prioritize outcomes from evolutionary and ecological processes, would be of great benefit to biodiversity conservation.

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