Difficult and reticent taxa will be best distinguished using molecular methods in addition to morphological data, but molecular methods cannot realistically be the first or only appropriate method, as has been proposed [4]. Furthermore, the genetic diversity of individuals within and among populations begs the question posed by Lipscomb *et al.* [3]: what are the appropriate gene sequences for objective taxonomic assessments, and the appropriate genetic/molecular dissimilarity to define 'taxa'?

We have known for almost a decade that the biodiversity crisis is resulting in the renewed relevance of natural-history collections [7], and the wider use of morphological 'data' contained in such collections has been repeatedly validated [8,9]. Perhaps this DNA versus morphology debate is largely one of each camp attempting to get 'there' first by proving greater relevance in the competition for limited funds. However, there is, and must be, room for both approaches.

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www.DNA-surveillance: applied molecular taxonomy for species conservation and discovery

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To address the full range of issues in biosurveillance and biodiversity, molecular taxonomy must encompass both traditional methods of museum curation and recent advances in bioinformatics [1]. DNA Surveillance attempts to bridge this gap for the identification of species threatened by exploitation or protected by international agreements (e.g. [2]). This web-based programme aligns a user-submitted gene sequence of unknown origin against a comprehensive set of reference sequences curated by species specialists [3]. Evolutionary distances and a phylogenetic tree with bootstrap simulations are used to judge species identity of the unknown 'test' sequence relative to the pre-aligned reference data set.

DNA Surveillance is implemented currently for identification of whales, dolphins and porpoises derived from strandings, fisheries bycatch, regulated exploitation and illegal hunting. Sequences from the highly variable mitochondrial DNA control region were chosen to facilitate identification of closely related species and evolutionarily significant units within the order Cetacea. Reference sequences were considered 'validated' only if they were derived from a voucher specimen accompanied by diagnostic skeletal material or photographic records. In cases of rare species, reference sequences were derived from holotype specimens.

The sensitivity of our taxon-specific approach is demonstrated by three molecular discoveries within the poorly described family Ziphiidae, the beaked whales. First, the discovery of a new species, *Mesoplodon perrini* [4], brought the number of species in this family to 21 and prompted clarification of the role of holotypes and genetic evidence in species descriptions [5]. Second, a match between sequences from the holotype skull of *M. bahamondi* and a tooth with partial jawbone collected in 1874 led to the resurrection of a long-forgotten species, *M. traversii* [6]. Third, previously misidentified specimens of *Indopacetus pacificus*, formerly considered the rarest of all whales, revealed the external appearance of this species for the first time [7].

Our approach of working closely with species specialists to develop an applied molecular taxonomy for a single order complements proposals to designate a universal bar code of life [8]. There is no single marker sufficient for

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identification of all taxa, given the vast differences in molecular patterns and rates, or even a single definition of species agreeable to all biologists. Ultimately, a universal molecular taxonomy will require a hierarchical suite of markers to connect root to branch and fully resolve the tips of the tree of life.

The applications used in DNA Surveillance, including instructions, sample data and plans for implementation with other threatened species, are available at http://www.dna-surveillance.auckland.ac.nz.

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The blind leading the blind: cryptic subterranean species and DNA taxonomy

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The potential for using DNA sequences to identify organisms (DNA taxonomy) has been advanced to help overcome the 'taxonomic impediment' [1,2], whilst being criticized as a 'backward step diluting taxonomy through the use of shortcuts' [3,4]. Although there will inevitably be major issues in setting up a robust, manageable and affordable system, a DNA taxonomy is unavoidably essential in some areas.

For some groups of organisms, such as freshwater Crustacea [5,6], morphology alone cannot determine species boundaries. Identifying morphologically inseparable cryptic or sibling species requires a new set of taxonomic tools, including DNA analysis. Cryptic species with inherently low gene flows, inhabiting island-like habitats, such as caves, and with low dispersal potentials, include a large number of obligate subterranean aquatic (stygobitic) animals. These organisms include some of the least well known and poorly studied groups, but almost certainly includes many taxa yet to be identified as species.

DNA taxonomy has enabled an increasing number of subterranean taxa to be identified. For example, research on the stygobitic amphipod *Niphargus rhenorhodanensis* (Crustacea) identified major genetic divergences between individual populations in spite of geographical proximity and, in one instance, hydrological connectivity between populations [7]. There are currently >200 species recognized by morphology in the genus *Niphargus* in Europe and this is almost certainly a gross underestimate of the true level of biodiversity [8].

It would be wrong to simply replace tried and tested taxonomic techniques with relatively costly DNA analysis if it is not required and we need to prevent the unnecessary fragmentation of the taxonomic discipline [9]. However, where research indicates that these traditional techniques can take us no further, and this is clear in the case of stygobitic Crustacea, DNA taxonomy and associated molecular tools might be the only way to reveal the true level of biodiversity.

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