this challenge but he forgets that the major hurdle is financial rather than technological.

In most countries, the scientific community simply is not prepared to allocate significant resources to taxonomic research of poorly known organism groups, not even from funds dedicated to biodiversity research [Statistics on Swedish biodiversity funding (http://www.artdata.slu.se/Svenska_artprojektet_Eng.htm)]. A glowing exception is the USA, where new generations of taxonomists have been trained in the PEET program since 1995 [5] and where the recent US$14 million Planetary Biodiversity Inventories programme (http://www.nsf.gov/pubs/2002/nsf02186/nsf02186.htm) aims to complete the world species inventory for some selected taxa.

In countries with less supportive scientific communities, separately funded national inventories could be the key to significant acceleration of the biodiversity census. The so-called Swedish Taxonomy Initiative (STI) provides a nice example (http://www.artdata.slu.se/Svenska_artprojektet_Eng.htm). It was launched in January 2002 and aims to complete an inventory of Sweden's fauna and flora of multicellular organisms within 20 years. STI is likely to expand the current list of 50 000 Swedish species considerably, both with named and previously unnamed taxa. The project will require some Euro 65 million in direct funds to taxonomic research, inventory work and outreach focused on the Swedish flora and fauna, and another Euro 65 million to support incorporation of the resulting material into existing natural-history collections, making it one of the largest biodiversity initiatives yet.

The geographical constraint is not ideal from a scientific perspective but the forte of national inventories is that they can provide society with the necessary deliverables. In addition to taxonomic research, STI will produce illustrated identification keys and basic facts concerning the distribution and biology of all species in Swedish. This will broaden the knowledge base for the identification and monitoring of biodiversity, provide a rich information source for schools, and significantly boost public awareness of local biodiversity and its conservation.

National inventories also have the potential of spreading to neighbouring countries. Indeed, other Nordic countries are now considering taxonomy initiatives of their own. The completion of the first national biodiversity map will undoubtedly be a significant event. Will the Swedes, inspired by their Linnaean tradition, be first?

References

1 Wilson, E.O. (2003) The encyclopaedia of life. *Trends Ecol. Evol.* 18, 77–80
2 Woodruff, D.S. (2001) Declines of biomes and biotas and the future of evolution. *Proc. Natl. Acad. Sci. U. S. A.* 93, 5471
3 Bisby, F.A. *et al.* (2002) Taxonomy, at the click of a mouse. *Nature* 418, 367
4 Godfray, H.C.J. (2002) Challenges for taxonomy. *Nature* 417, 17–19
5 Rodman, J.E. and Cody, J.H. The taxonomic impediment overcome: NSF's partnerships for enhancing expertise in taxonomy (PEET) as a model. *Syst. Biol.* (in press)

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Keeping taxonomy based in morphology

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The recent spate of articles and letters regarding the relative importance of DNA technology versus morphological traits in modern taxonomy and biodiversity studies [1–4] is both intriguing and frustrating. The Linnean system, based largely on morphological features, has served biology extremely well for almost 300 years. I agree with Lipscomb *et al.* [3] that taxonomy will be advanced by appropriate and prudent dependence on both DNA and morphology.

Because I am not a systematist, I approach this debate from the standpoint of a user (at a botanic garden) of such information and as a some-time educator. In the first instance, it seems ludicrous to expect that botanic garden curators, plant explorers and other garden staff will use DNA sequences in making decisions as to which taxonomic group a particular plant belongs. For the most part, we have neither the resources nor the expertise to either obtain DNA sequences or to interpret them. This is particularly true for my colleagues at gardens in the developing world. Field taxonomy is likely to continue to be based on examination and interpretation of morphological traits.

In the second instance, I cannot understand how taxonomy will be taught to students without starting first with morphology. This applies not just to university students, but also to volunteers, parataxonomists and others who are taking on the mantle of plant conservation. The first priority must be to know the organisms, to understand their features and to be able to identify a taxon visually using keys (electronic or printed). The effort that many natural history institutions are undertaking to make taxon-based collections more accessible, be they plant (e.g. http://www.vplants.org [5]) or animal [6] collections, must be morphologically based. It is difficult to see how a set of DNA sequences could be used to aid students in learning a flora or fauna, in the identification of living or herbarium specimens, or in other fieldwork.

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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.

References

1 Mallet, J. and Willmott, K. (2003) Taxonomy: renaissance or Tower of Babel? *Trends Ecol. Evol.* 18, 57–59
2 Seberg, O. *et al.* (2003) Shortcuts in systematics? A commentary on DNA-based taxonomy. *Trends Ecol. Evol.* 18, 63–65
3 Lipscomb, D. *et al.* (2003) The intellectual content of taxonomy: a comment on DNA in taxonomy. *Trends Ecol. Evol.* 18, 65–67
4 Tautz, D. *et al.* (2003) A plea for DNA taxonomy. *Trends Ecol. Evol.* 18, 70–74
5 Schaub, M. and Dunn, C.P. (2002) vPlants: a virtual herbarium of the Chicago region. *First Monday* 7 http://www.firstmonday.dk/issues/issue7_5/schaub/index.html
6 Soberón, J.M. *et al.* (2000) The use of specimen-label databases for conservation purposes: an example using Mexican papilionid and pierid butterflies. *Biodiv. Conserv.* 9, 1441–1466
7 Alberch, P. (1993) Museums, collections and biodiversity inventories. *Trends Ecol. Evol.* 8, 372–375
8 Butler, D. (1998) Museum research comes off the list of endangered species. *Nature* 394, 115–119
9 Winker, K. (1999) How to bring collections data into the net. *Nature* 401, 524

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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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