

obtained from single specimens, often without compromising subsequent morphological identification; (2) morphologically indistinguishable taxa can be separated; (3) all stages and morphs of taxa are accessible; and (4) a single technique is applicable to all taxa. Sequence data can be used in phylogenetic analyses to derive testable hypotheses of OTU interrelatedness. This concept is not new: it has been applied to bacterial and viral typing for many years and has been extended revealingly to eukaryotic protists [7,8]. The commonest MOTU sequence target in microbes is the small subunit ribosomal RNA gene (SSU), which might also be useful for other groups: there are >6600 metazoan SSU gene sequences (full length and partial) in GenBank (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>). The chloroplast *rbcL* gene might be useful for plants, and cytochrome oxidase I [9], and large subunit ribosomal RNA (M. Markmann, PhD Thesis, Ludwig Maximilians Universität, 2002) genes have also been proposed for Metazoa.

Currently, the time taken to identify taxa scales inversely with body size [10] and thus an efficient method for micro- and meiobiota is sorely needed. Nematodes, like other meiofauna, are abundant, speciose and 'difficult' because of the microscopic size of distinguishing morphology. We have used an SSU-based MOTU method to measure soil nematode biodiversity [6]. In ~2000 sequences from individual nematodes from one terrestrial site, we discerned >150 MOTU (R. Floyd *et al.*, unpublished). By testing biological and morphological taxon diagnoses on a set of closely related, cultured isolates, we found that the MOTU corresponded to taxa defined by interisolate fertility, and that morphological identification was at best equivocal (and required SEM data, a significant additional time burden) [11]. We have applied the same method to other meiofaunal groups (tardigrades) and environments (marine nematodes) with similar success.

A MOTU method by itself only yields a division of individuals into taxa that do not have any other biological attributes. However, by comparing MOTU sequences with sequences derived from specimens identified by traditional methods, a taxonomic assignment can be achieved. For the Nematoda, there are only ~350 SSU sequences from identified taxa available (out of an estimated 1 million nematode species), but we have been able to assign most of our soil nematode MOTU to named species or genera [6]. Alignment of sequences is not particularly problematic

as most are between relatively closely related taxa. Once a link between sequence and traditional taxon is made, biological properties can be assigned to the MOTU, and linked in with extensive accumulated knowledge.

Importantly, the MOTU method will not, as has been claimed, impoverish the rich field of systematics. As the MOTU method is independent of the research worker, it will be possible for systematists worldwide to use shared data sets in their analyses. In the case of novel sequences, molecular phylogenetics can be used to investigate the probable relationships of the taxon, and thus direct biologists to search for and study possible taxonomic novelties. Further prospecting might be stimulated by the definition of two MOTU where a single morphological taxon is described. As DNA extracts can be archived stably, it is possible to return to a problem OTU and investigate relationships and composition using multiple additional markers with different evolutionary rates. Taxonomic and other biodiversity surveys need to turn to molecular tools to tackle realistically the abundance around us, and the methods are in place to do so.

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# Taxonomy and biodiversity inventories: time to deliver

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Increasingly, the completion of a full inventory of the Earth's biota stands out as a vitally important and urgent task.

Experts think that it could be virtually completed in 25 years [1] but this requires a 30-fold increase in the current species discovery rate [2]. As many others have, Wilson [1] focuses on information technology [3,4] that might help taxonomy face

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<http://tree.trends.com>

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](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](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?

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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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