

Tomorrow's taxonomy: collecting new species in the field will remain the rate-limiting step

I am writing this as one of five contributions of 'short thoughts', by way of introduction to this issue dedicated to deeper thoughts on the major challenges facing taxonomy and systematics in the twenty-first century. I have seen one of my co-thinker's short essays (Wilson 2004) and I have a slight fear that these essays/forewords will exhibit an authorial form of the synonym problem that so besets estimates of numbers of species: the same thoughts expressed under different patronyms!

This issue contains an excellent and timely set of papers, on a hugely important subject. It cannot be emphasized too strongly that taxonomy and systematics are NOT stamp collecting. (Indeed, we may do well to remember that the famous nineteenth-century physicist who said they were, also said 'heavier than air flying machines are impossible'; even given the inadequate knowledge of his time, this statement is not as ridiculous as the stamp-collecting one.) Taxonomy provides the bricks, and systematics the plan, with which the house of the biological sciences is built. Taxonomic and systematic knowledge underpin everything in evolution and ecology as such, and thereby are the basis for applied responses to climate change and other environmental problems.

Currently, we are adding roughly 10 000 distinct new species each year to the library of the scientifically known, discounted for resolution of past synonymies. The rate at which we are completing the task of cataloguing life on Earth—or more particularly eukaryotic species—can indeed be greatly accelerated. Over the next decade or so advances in molecular biology accompanied by appropriate technologies will, I believe, provide us with widgets such that we can put a piece of a newly collected specimen into them, have appropriate bits of DNA sequenced, and then have the machine give us information about whether this species is indeed new to us (and, if so, where it belongs at least on a molecular phylogeny). However, the leap from such a vision of progress, along with corresponding visions of digitizing relevant knowledge bases, in my view stops a long way short of the notion that a complete catalogue of life on Earth will be available within the next 25 years or so, as suggested by the study group at Harvard referred to by Ed Wilson. I am inclined to wonder what these people had been smoking! Even if the task of keying out a collection were reduced effectively to zero time (in contrast to the present circumstance where it typically takes longer to key out a collection than to put it together in the field), and even if we took the more conservative estimates of eukaryotic species totals which I favour (in the range 5–10 million, with a best guess towards the lower

rather than the higher end of the range), the rate-limiting step in the task will remain the craft of collecting specimens in the field. Even if the Harvard group's estimate were allowing for completion to be interpreted as more like 90% complete—recognizing the growing problems of capturing the tail end of the sample once it is almost complete—I still think 25 years must be very optimistic, unless some entirely new methods of collecting potential new species in the wild are created. Just reflect: if the global total of eukaryotic species is approximately seven million, then completing the task (up to the 90% level) within the next 25 years implies adding approximately 200 000 newly collected, but previously unknown, specimens each year. Assuming zero time for keying out and full comparison with all existing knowledge (which activity currently consumes about half the total time and effort in finding and identifying new species), this still represents a roughly 10-fold speeding up over current rates of progress. To do this within less than one scientific generation really seems a bit unrealistic to me. I take no pleasure in this, and hope the Harvard group might, against the odds, be correct.

Of course, perhaps this 25 year estimate was allowing extravagantly for the rate at which species are currently being extinguished! However, despite some overheated estimates (27 000 species extinct per year is one of the sillier, with its two digit illusion of precision), and although there is a clear indication that extinction rates have, over the past century, accelerated by factors of 100–1000 above background rates (averaged over the sweep of the fossil record), such increased extinction is unlikely to make any truly major impact on global species numbers within the next 25 years.

In this issue, Oren (2004) has given a thoughtful account of prokaryote diversity and taxonomy, outlining the current state of play and some future challenges. It is, however, really important to recognize that the taxonomic hierarchies that serve us well, and which are meaningful bases for quantifying diversity, simply do not apply to bacteria and other such prokaryotes. For instance, different strains of what is currently classified as a single bacterial species, *Legionella pneumophila*, have nucleotide-sequence homologies (as revealed by DNA hybridization) of less than 50%; this is as large as the characteristic genetic distance between mammals and fishes. The higher rates of genetic exchange among bacteria put them in a wholly different realm of taxonomic discourse than that for eukaryotes, on which most of our intuition about 'biodiversity' is based. This applies even more strongly to viral species, many of which are best regarded as 'quasispecies swarms'. Indeed, even among what might politically incorrectly be called the 'lower eukaryotes', there are arguably groups where 'functional units', rather than species, are the more biologically meaningful units.

One contribution of 19 to a Theme Issue 'Taxonomy for the twenty-first century'.

Be all this as it may, this collection of papers, will, I hope, help in bringing about the methodological—and funding—revolution that taxonomic science needs and deserves. Future generations will look back with sorrow and justified anger if we fail.

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REFERENCES

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