

approach that avoids the problem of using different time series to track different phenomena. They exploit a relatively new method of measuring past changes in ocean temperature^{5,6}, the Mg/Ca ratio of the carbonate shells of surface-dwelling microplankton called foraminifera. Armed with an Mg/Ca-based estimate of changes in sea surface temperature within the Indonesian archipelago during deglaciation, they then use a venerable isotopic tracer — the ratio of ¹⁸O/¹⁶O in these same foraminiferal shells — to determine the changing volume of ice in continental glaciers. This is possible because the oxygen isotopic ratio of foraminifera records both seawater temperature and its isotopic composition (largely controlled by the growth or melting of ice sheets, which are depleted in ¹⁸O compared with sea water). An independent temperature estimate means that the foraminiferal isotopic ratios can be corrected for temperature effects, leaving a residual that is directly related to the amount of polar ice that has melted into the ocean during deglaciation.

Visser *et al.* present two important findings. They conclude that, 18,000 years ago, sea surface temperatures in the Indo-Pacific warm pool were 3.5–4 °C cooler than they are now — this is yet another piece of evidence that contradicts previous views that tropical temperature changes during glacial–interglacial cycles were much smaller, only a degree or two, than that. More notably, their work provides strong evidence that the last deglaciation was ‘felt’ first in the tropics, as shown by a rise in temperature within the Indo-Pacific warm pool, and that this warming signal propagated from the tropics to drive ice-sheet melting in the Northern Hemisphere 2,000 to 3,000 years later. The strength of the evidence lies in the recording of the lagged response of ice-sheet melting using the same foraminiferal signal carrier in the same sediment core. The authors’ views are further supported by their observation of the same sequence of events and extent of temperature change during a previous deglaciation about 130,000 years ago.

The sediment cores that Visser *et al.* analysed were also dated using radiocarbon. When compared with evidence from polar ice cores, it seems that warming in the tropics, beginning just over 18,000 years ago, is synchronous with the initial rise in atmospheric CO₂, as well as with the warming recorded during deglaciation in Antarctica. These findings are somewhat less secure, as they are based on comparisons of data obtained with different dating systems. Nevertheless, they point to deglaciation that was largely driven by tropical events, probably through the reinforcing greenhouse effects of two gases — CO₂ and water vapour. If the Indo-Pacific warm pool warmed during deglaciation, simple thermodynamic and solubility considerations

mean that the ocean would have supplied additional water vapour and CO₂ to the atmosphere, wherein an enhanced greenhouse effect would act as a positive feedback on planetary warming. Antarctic temperatures appear to have responded quickly. Ultimately, this warming led to rapid melting of ice sheets in the Northern Hemisphere several thousand years later.

Inevitably, there are caveats about this work. The foraminiferal Mg/Ca thermometer is a relatively new tool: although the temperature signal is set during the lifespan of the foraminifers, it is not yet clear to what extent it may be altered as their delicate carbonate shells settle through the ocean and are buried at the sea floor. Moreover, there are only a handful of Mg/Ca time series spanning the last deglaciation, and no others from the heart of the warm pool. Palaeoclimate scientists have learned that replication sometimes yields surprising results, and additional cores from the western Pacific should be similarly analysed. Visser *et al.* also suggest that warming of the tropical ocean by 3.5–4 °C could account for much of the 90 p.p.m. rise in atmospheric CO₂ through a direct solubility effect alone (warmer water holds less CO₂). Yet, from other estimates⁷, it seems that during deglaciation the direct effect of temperature on CO₂ levels is smaller, suggesting

that the transfer of carbon between reservoirs was more complex.

Nevertheless, the finding that temperatures in the tropics increased before the onset of melting of the northern ice sheets is consistent with several other studies^{8,9}. And if it is supported by further analyses, it will be highly significant because it suggests a way in which the tropics can amplify a small, direct radiative signal, such as that associated with long-period orbital variations, to produce a large and dynamic climate change. As we head uncertainly into a greenhouse world, we should perhaps expect that some of the climate surprises that await us will emanate from the tropics. ■

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Molecular systematics

Counting angels with DNA

Mark Blaxter

It is impossible to describe biological diversity with traditional approaches. Molecular methods are the way forward — especially, perhaps, in the form of DNA barcodes.

For 200 years taxonomists have recognized two living species of elephant, the African and the Indian. According to molecular evidence, however, this understanding is wrong^{1,2}. Although the details are still under discussion, two or maybe three groups of ‘African’ elephant are as distinct from each other as either is the Indian, and so may constitute distinct taxonomic groups — a finding with implications for conservation. This kind of discovery, using molecular markers, epitomizes a sea change occurring in taxonomy. It underlies a proposal, published by Hebert *et al.*³ in *Proceedings of the Royal Society*, for a DNA-based barcoding system for all animal species. This is not a new idea for some taxonomic groups. But Hebert *et al.* now formally suggest that a molecular barcode inventory should be made of known animal taxa, and that this database should become the basis of biodiversity assessment and taxon identification.

There may be over 100 million extant species on Earth, but only a tiny proportion

of them have been described⁴. The scale of the descriptive deficit varies widely for different groups of organisms (Fig. 1). For taxa with large body sizes, such as vertebrates, the catalogue may be essentially complete. For smaller taxa (with bodies 0.5–10 mm long) that is far from the case. For instance, there are some 1 million described species of arthropods (insects and allies), but estimates of actual diversity range from 3 million to 30 million. Only 20,000 species of nematode (roundworms) have been described out of a predicted million or so⁵. For the smallest organisms — the bacteria, archaea and single-celled eukaryotes — we may be ignorant of over 99% of actual diversity⁶. It is not feasible⁷ to catalogue that diversity by traditional methods based on taxon-by-taxon, specimen-by-specimen morphological description. Instead, emerging technologies must be harnessed to the task⁸.

In the 1990s, ideas about the biosphere were revolutionized by surveys of the diversity of bacteria and archaea (the prokaryotes)

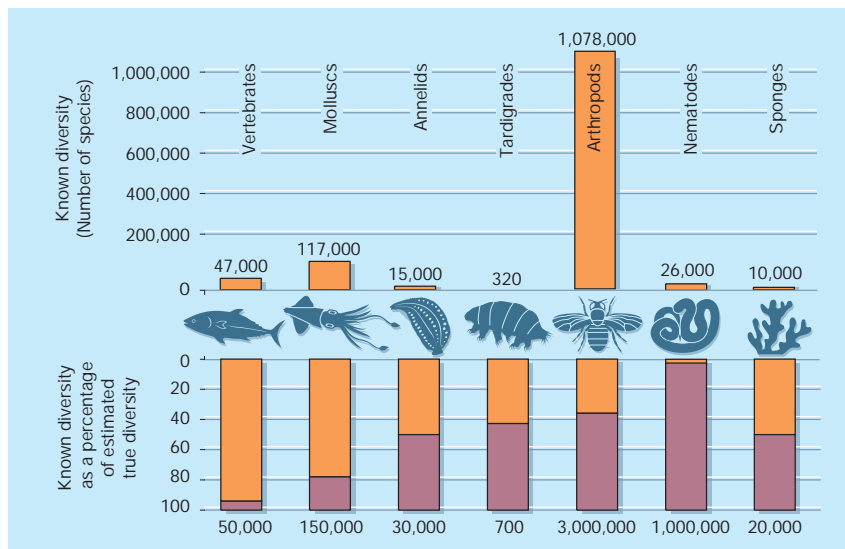


Figure 1 Known and estimated diversity of a selection of animal phyla. The histogram above each representative image indicates known diversity (in terms of number of species). That below represents known diversity as a percentage of estimated true diversity, shown by the number at the bottom. This graphic provides only a keyhole view of biodiversity and the task the systematist faces. It is confined to just a few phyla of the larger eukaryotes (loosely, organisms whose cells contain a nucleus), of which there are many more groups, including the plants and unicellular forms. And then there are the vast numbers of microscopic prokaryotes, consisting of the bacteria and archaea. Molecular barcoding methods may be the only way of charting unknown diversity.

using DNA sequences. All cellular organisms have the highly conserved small subunit ribosomal RNA (SSU) gene, which can be isolated specifically even from bulk samples of 'environmental DNA'. By surveying SSU gene sequences in a sample, it is possible to identify how many different taxa are present, and assess their relationships to previously described and sequenced groups. All environments sampled yield the same pattern: many of the constituent microorganisms come from major groups unknown to traditional microbiology, and the diversity of prokaryotes is probably 100 times higher than was previously expected^{6,9}. Similar SSU gene surveys of communities of eukaryotic microbes, such as marine picoplankton, also suggest that traditional, descriptive methods have sampled only the tip of diversity^{10–12}.

It is now accepted in bacteriology that taxa can be identified using sequence data, and rules of thumb for defining taxa based on sequence difference are developing¹³. The taxa so defined have been termed 'phylo-types'¹⁰ or 'molecular operational taxonomic units'¹⁴. Thus a DNA sequence can be used to both identify and classify an organism, much as a barcode identifies supermarket products.

Hebert *et al.*³ extend this idea to non-microbes, and propose that a database of DNA barcodes for identification of all animal taxa should be established. They test the use of the mitochondrially encoded cytochrome oxidase I (COI) gene in assigning specimens to different taxonomic levels — phylum, order and species. The COI gene

is a good target, as it is present in all animals, in many identical copies per cell, and is known to evolve relatively quickly. It carries sufficient 'signal' to allow differentiation between closely related taxa, and in a survey of moths collected around Guelph, Ontario, the authors show that the COI barcode can in most cases yield a reliable assignment to previously identified and sequenced species. Other insect specimens were correctly assigned to the superfamily level, and Hebert *et al.* claim that in general the approach can identify which phylum a sequence derives from.

This is indeed a promising approach. Many potential barcode sequences already exist in public databases: about 12,000 COI sequences, over 20,000 SSU gene sequences (from all organisms)¹⁵, and more than 50,000 sequences from the 'ribosomal internal transcribed spacer segment' (from higher eukaryotes). Plant systematists have also extensively surveyed the photosynthetic *rbcL* gene¹⁶. My group has used the SSU gene to successfully barcode soil nematode biodiversity¹³, and the large subunit ribosomal RNA gene has been used for identifying freshwater fauna¹⁷. It is not necessary to limit data collection to one gene, as sensitive amplification techniques allow the isolation of several sequences from one specimen. Given technological advance and genome-scale sequencing, sequencing of several barcode genes for large numbers of specimens could be achieved rapidly and cheaply.

A major unresolved issue is how closely these molecular taxa correspond to what



100 YEARS AGO

The unfortunate fatal accident which occurred at the Fulham Public Baths on December 23 serves to show how dangerous an electric shock may be when the conditions are such that really good contact is made. In this case, two bathers were killed by standing up in their baths and putting their hands on a metal rail running along the top of the partition between the baths; on top of this rail ran the iron pipes containing the electric-supply leads. It seems that there was leakage, possibly in a faulty lampholder, to these pipes, which were insufficiently "earthed". The bathers therefore completed the earth through their bodies to the bath itself, and thus received a shock which, in spite of the fact that the pressure could only have been something like 170 volts, had fatal results on account of the very good contacts which existed. The circumstances of the case are altogether exceptional, and there is absolutely no need for users of electric light to take any alarm.

From *Nature* 8 January 1903.

50 YEARS AGO

Gregorio Ricci-Curbastro, inventor of the tensor calculus, was born at Lugo, in Italy, on January 12, 1853. The absolute differential calculus, as he himself called it, gained little attention until Einstein used it for the formulation of general relativity, even though it had reached a mature form by 1895, after some ten years of growth. It was so little thought of, indeed, that in 1901 Ricci was denied the Italian Royal Prize in mathematics on the ground that the calculus was "useful but not essential for the treatment of some mathematical questions". Nevertheless he himself retained a belief in its value... In 1912 Einstein's attention was directed to it by his colleague, Marcel Grossmann, and the outcome was the relativistic theory of gravitation published in 1916... The relativistic principle of covariance, namely, that the general laws of physics can be expressed in a form which is independent of the co-ordinate system, has a meaning only in so far as there exists a way of expressing them in such a form. The Ricci calculus provides a means of doing so... The tensor calculus is fully established as one of the main instruments of modern mathematics, and gives to its inventor a permanent place in the history of the subject.

From *Nature* 10 January 1953.

traditional biologists would recognize as a species. Species concepts are difficult to apply to bacteria and protozoa, where sexual isolation (the cornerstone of the original biological species concept) is not relevant. A bewildering abundance of species concepts have been proposed and, practically, there are many cases that fall between different sets of criteria^{18,19}; molecular taxon concepts may add to the confusion. This problem is properly the domain of systematists, but a useful compromise will be achieved by extensive sampling from within recognized species and across known species 'flocks'; and developing rules of thumb that can be used to associate molecular differences with useful biological categories¹².

Hebert *et al.* approach this problem by showing that anonymous specimens were robustly associated with their correct morphological species, but it is likely that different rules may have to be implemented for different animal groups with different evolutionary rates. Until a comprehensive database is assembled, it is not clear how helpful the system using COI will be: for example, the nematode samples in Hebert and colleagues' data set were not well resolved, and there were significant problems with speciose taxa such as beetles.

Nonetheless, a taxonomic genomics programme should yield huge benefits for biodiversity science and ecology, much as the sequencing of genomes has benefited other areas of biology. As was the case with the initial work of Hebert and colleagues, the first stages of such a programme will need identified specimens to represent known diversity and link barcodes to biology. Subsequently, barcoding of environmental samples or collections of unidentified specimens will reveal novelties: flocks of taxa where one

species was expected, or divergent taxa with possible novel biology. One of the advantages of this approach is that the raw data — the DNA sequence — can be stored in databases and accessed through the Internet for comparison and reanalysis. Another is that debate about what usefully defines a taxon, how many taxa there are and what taxon diversity means will become a data-rich science, rather than resembling theological speculation as to how many angels can dance on the head of a pin. ■

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example of a fluid so resistant to flow that it 'remembers' its past history and produces forces within it that are proportional to the spatial inhomogeneities in its stretching. This resistance tends to make the incursions into these materials narrow and crack-like, similar to the hairline fractures in a brittle material. Experimentally, this kind of behaviour has been seen in wet clays² and in dilute solutions containing long-chain polymers³.

Levermann and Procaccia's technique builds on the work of Hastings and Levitov⁴, who developed methods based on the theory of analytic functions of complex variables to describe situations in which the retreating fluid was an ordinary, 'newtonian' viscous fluid. The pressure in this kind of fluid obeys the partial differential equation called Laplace's equation. Mathematicians would say that the pressure is a harmonic function. Laplace's equation provides a precise statement of the condition that the pressure within a region varies as smoothly as it can, given its values at the boundaries of the region. Complex-variable methods provide a natural framework and convenient language to describe any situation possessing planar geometry, and particularly harmonic functions. From the coordinates x and y in a plane, the complex variable $z = x + iy$ (where i is the square root of -1) can be defined. As if by magic, the maths tells us that any analytical function of z obeys Laplace's equation. These functions can then be used to build a computer model to calculate the pressure in a system.

For an elastic, rather than a viscous, material, the equation to be solved is more difficult. Levermann and Procaccia have used complex-variable analysis to solve the equations for the elastic material. They obtain the displacement of the material and the forces within it, given only the shape of the crack.

But how can the shape of the crack be determined? Here is the novelty of Levermann and Procaccia's work. In the past, it has mostly been assumed that the motion at the boundary between the two materials is smooth. Instead, Levermann and Procaccia divide the motion into little bursts of activity, with each burst localized in a small region of the interface between the two materials. The probability that a burst will happen depends on the forces in that region of the material boundary. Bursting could be explained by the material being so dirty that the motion takes the form of successive events of sticking and slipping, a chaotic jittering motion. This same motion was assumed by Witten and Sander⁵. Their idea was later applied to viscous flow, and then extended⁶ to problems of fracture in amorphous solids.

To make their calculation predictive, Levermann and Procaccia choose a particular model for calculating the probability of a burst at each point on the interface. They roll the computer's dice to figure out where the

Materials science

Bursting apart

Leo P. Kadanoff

When a low-viscosity fluid is injected into an elastic material, it forces its way through by making slender cracks, in a random, fractal pattern. The spreading of the cracks can be modelled through a series of 'bursts'.

Nature abounds in branched objects possessing random, fractal structures: the pattern of air vessels in our lungs, or the branched structure of a river and of the streams and rivulets that feed it. Such patterns arise when the branching process occurs easily and is sensitive to small, random features in the environment. A laboratory example is the pressure-driven expansion of one low-viscosity fluid into another, more viscous fluid. As the fingers of low-viscosity material push outwards, they create high pressure-gradients, and their motion becomes unstable. As a result, little bits of

'dirt', or some other randomness, can considerably affect the flow. The dirt effects show up both in the details of the pattern and also in its gross appearance.

Writing in *Physical Review Letters*, Anders Levermann and Itamar Procaccia¹ describe a calculational procedure that can predict the shape of these patterns. The authors have extended the theories and simulations developed for two-dimensional viscous fluids to the extreme case in which the retreating medium flows elastically. Elastic materials such as rubber resist stretching and deformation. They may be considered to be the extreme