

# Fossilized records of past seas

Chris Wade & Kate Darling

The planktonic foraminifera (Fig. 1) are globally distributed across the world's oceans, forming an important part of the zooplankton. The calcitic shells of this fascinating group of organisms are readily preserved in the ocean sediments as microfossils (Fig. 2). They form one of the most complete fossil records on earth, stretching across some 130 million years. The record is used to date sedimentary rocks and study evolutionary processes, and is one of the most important archives of past climate. The species, abundance and shape of shells are used to reconstruct sea surface temperatures. Environmental parameters can also be deduced from the chemical composition of the shells. The planktonic foraminifera are therefore used extensively as indicators of climate change.

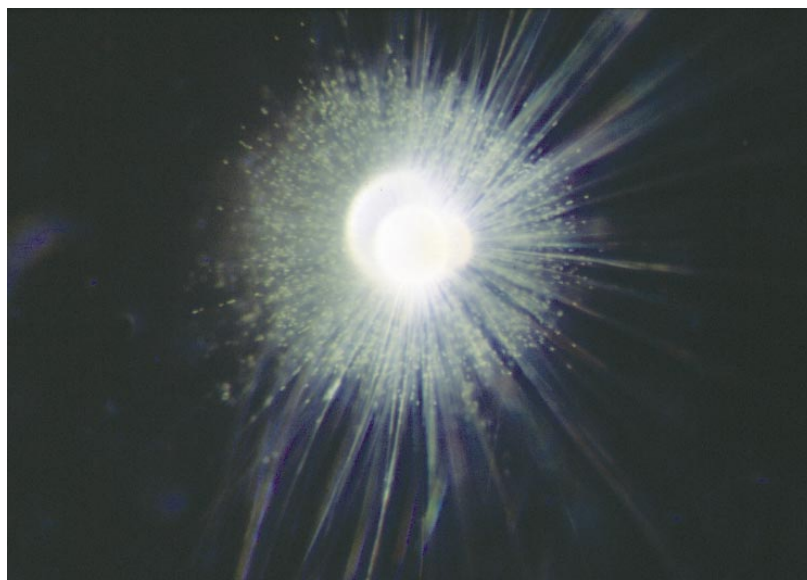
With the advent of molecular biological techniques, it has become possible to study the evolutionary relationships between species of planktonic foraminifera living in the oceans today. These studies have led to the discovery of previously unrecognized genetic diversity, providing the potential to enhance the role of the foraminifera as indicators of past climate. Furthermore, in combination with their fossil record, planktonic foraminifera provide a unique and ideal tool for addressing important questions regarding the mechanisms of plankton speciation and evolution through time.

## ● Origins of the foraminifera

It is possible to discover the evolutionary relationships among organisms by comparing their DNA sequences. These relationships are typically shown in the form of an evolutionary tree (a phylogeny). To date, most studies of the foraminifera have focused on comparing the ribosomal (r)RNA genes. When their small subunit (SSU) rRNA genes are compared with those of other eukaryotes, they seem to form one of the earliest diverging eukaryote lineages in the 'tree of life' (Fig. 3). This placement is interesting because it means that the foraminifera could provide information about events early in eukaryote evolution. However, more work is needed because the foraminifera show an exceptionally fast rate of evolution in their rRNA genes. Lineages with high rates of evolution are notoriously difficult to place in evolutionary trees, and it has been suggested that the foraminifera may in fact have a far less ancient origin.

## ● From ocean floor to planktonic life

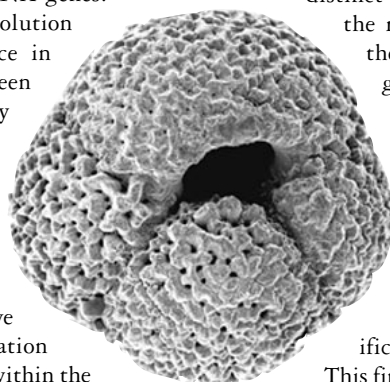
Despite the reservations about external relationships, studies of foraminiferal SSU rRNA genes have provided a great deal of information about evolutionary relationships within the



foraminifera. As well as planktonic forms, there are benthic species that live on the ocean floor. The evolutionary transition between benthic and planktonic forms is of considerable interest. Planktonic species first appear in the fossil record long after the benthic forms, and arose from the adaptation of a benthic species to life in the plankton. Since this has been considered to be a major evolutionary step, it was concluded that all planktonic species arose from a single benthic ancestor. This hypothesis is not supported by the genetic data; instead of the planktonic species clustering in a single group, they occupy three separate locations in the molecular tree (Fig. 4), suggesting that the planktonic way of life has evolved from at least three independent benthic lines. The planktonic spinose species (foraminiferans with spines) cluster separately from the planktonic non-spinose species, which are located in two separate regions of the benthic cluster.

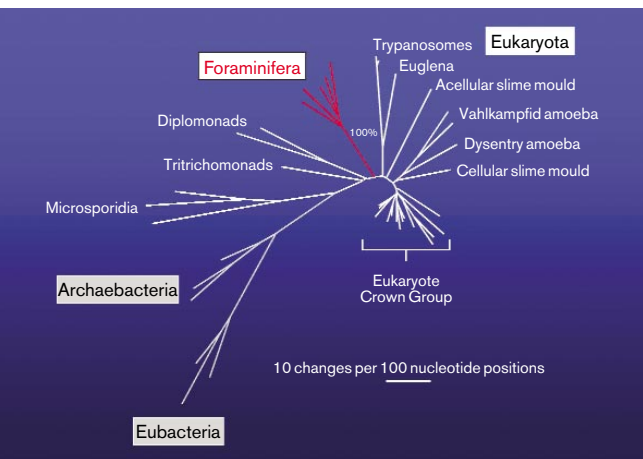
## ● Hidden diversity and the implications for reconstructing past climate

The planktonic foraminifera are divided into distinct types ('morphospecies') based upon the morphology of their shells. One of the most interesting outcomes of genetic studies concerns the extent of differentiation within these morphospecies. Most of them show an exceptionally high level of genetic diversity in their SSU rRNA genes, and many include more than one genetically distinct entity (Fig. 5). Some of these genetic types may warrant classification as separate 'cryptic' species. This finding is important because of the role



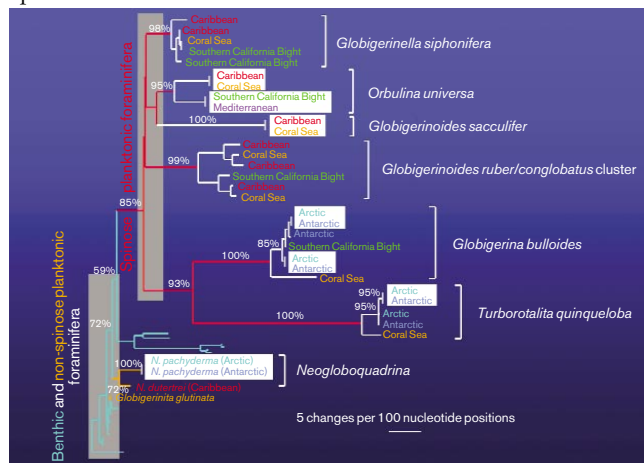
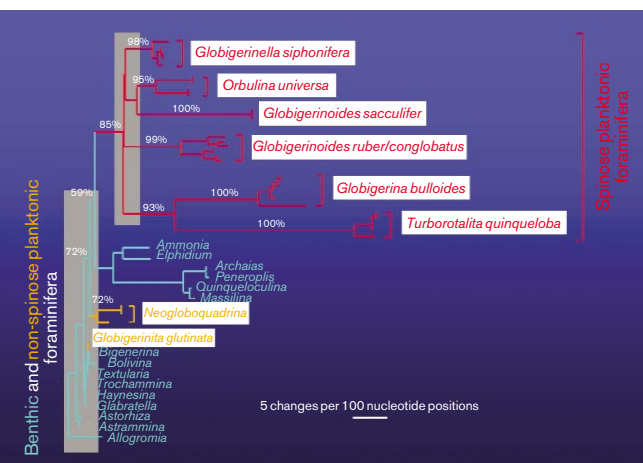
ABOVE:  
**Fig. 1.** The planktonic foraminiferan *Globigerinoides sacculifer*. The cell is enclosed within a calcitic shell, which has a series of interconnecting chambers. This species has an array of spines that serve as a 'net' for snaring prey. Energy is also generated by photosynthesis and this species contains a large number of algal symbionts, which are distributed out along the spines to maximize light. COURTESY DR K. DARLING, DEPARTMENT OF GEOLOGY AND GEOPHYSICS/ICAPB, UNIVERSITY OF EDINBURGH

BELOW:  
**Fig. 2.** A microfossil of the planktonic foraminiferan *Neoglobobadrina pachyderma*, obtained from marine sediments. COURTESY DR M. KUCERA, DEPARTMENT OF GEOLOGY, ROYAL HOLLOWAY, UNIVERSITY OF LONDON



of foraminiferal microfossils in reconstructing past climates. For climate reconstruction it has been assumed that each morphospecies is a single entity with a specific ecological (and thus climatic) preference. If the distinct genetic types within morphospecies are in fact adapted to different habitats, and exhibit different ecological and climate preferences, then the assumption that each morphospecies is characteristic of a particular climate would be wrong. If this is so, there may be significant errors in current models of climate reconstruction. Recent work suggests that different genetic types are indeed associated with different environments. If it does become possible to distinguish these newly recognized genetic types in the fossil record, the role of the

Seas (Fig. 5), and also in individuals from the Eastern Pacific and Mediterranean in *O. universa* (Fig. 5). These findings are important because they suggest that gene flow is occurring on a global scale, with genetic intermixing between populations as far apart as the Arctic and Antarctic, or the Pacific and Atlantic. This is at odds with the observation that many morphospecies have high levels of genetic diversity and include more than one genetically distinct entity. For diversity to arise, it is generally considered that there must be some form of barrier to gene flow. It is therefore unclear how diversity arose in the planktonic foraminifera when there are apparently no effective barriers to gene flow. The planktonic foraminifera raise intriguing questions concerning the process of speciation in the oceans.



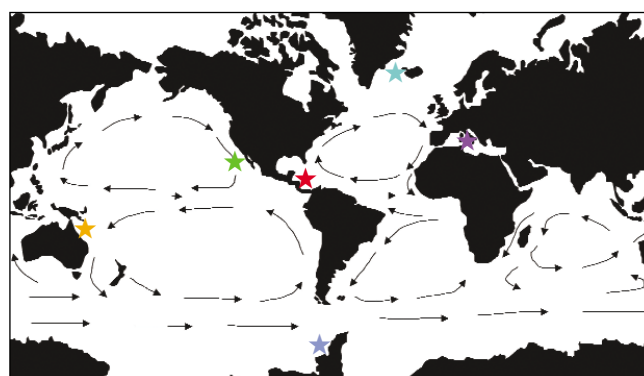
ABOVE TOP:  
**Fig. 3.** Evolutionary tree showing the origins of the planktonic foraminifera. The eukaryote crown group includes all multicellular eukaryotes (including plants, animals and fungi) and several other groups of unicellular protists. Percentages indicate the level of support for branches in the tree.

ABOVE BOTTOM:  
**Fig. 4.** Evolutionary tree showing the relationship between planktonic (red and orange) and benthic foraminifera (blue). The planktonic species can be further subdivided into species with spines (spino-se; red) and those without spines (non-spino-se; orange). Percentages indicate the level of support for branches in the tree.

foraminifera as indicators of past climate could be greatly enhanced.

### ● Global gene flow and the implications for the origin of new species

Genetic studies of the planktonic foraminifera have also begun to illuminate the processes of speciation in the oceans. Despite the high degree of genetic diversity observed in their SSU rRNA genes, identical sequence types (genotypes) have been found in individuals collected at opposite ends of the globe in several morphospecies (white boxes, Fig. 5). Perhaps most remarkable is the discovery of identical rRNA genotypes in individuals collected from the Arctic and Antarctic subpolar regions within each of the cool-water morphospecies *Globigerina bulloides*, *Turborotalita quinqueloba* and *Neogloboquadrina* (Fig. 5). This is surprising, as these morphospecies are only found in the high latitudes and are absent from the tropical regions, which are considered a formidable barrier to gene flow. Similarly, identical rRNA genotypes have been found within the warm-water morphospecies *Orbulina universa* and *Globigerinoides sacculifer* in individuals collected from the Caribbean and Coral



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# Archives matter!

## Peter Harper

### Further reading

Darling, K.F., Wade, C.M., Kroon, D., Leigh Brown, A.J. & Bijma, J. (1999). The diversity and distribution of modern planktic foraminiferal small subunit ribosomal RNA genotypes and their potential as tracers of present and past ocean circulations. *Paleoceanography* 14, 3–12.

Darling, K.F., Wade, C.M., Stewart, I.A., Kroon, D., Dingle, R. & Leigh Brown, A.J. (2000). Molecular evidence for genetic mixing of Arctic and Antarctic subpolar populations of planktonic foraminifers. *Nature* 405, 43–47.

de Vargas, C., Norris, R., Zaninetti, L., Gibb, S.W. & Pawlowski, J. (1999). Molecular evidence of cryptic speciation in planktonic foraminifers and their relation to oceanic provinces. *Proc Natl Acad Sci USA* 96, 2864–2868.

Wade, C.M., Darling, K.F., Kroon, D. & Leigh Brown, A.J. (1996). Early evolutionary origin of the planktic foraminifera inferred from SSU rDNA sequence comparisons. *J Mol Evol* 43, 672–677.

### UPPER LEFT:

**Fig. 5.** Evolutionary tree showing hidden diversity in planktonic foraminiferal morphospecies. Sequences are coloured according to where they were collected (see Fig. 6 for details of collection sites). Identical sequences are highlighted in white. Percentages indicate the level of support for branches in the tree.

### LOWER LEFT:

**Fig. 6.** Sites of collection. Planktonic foraminiferans have been taken from the Coral Sea (off Australia), the Caribbean, the Southern California Bight in the Eastern Pacific, the Mediterranean, the Arctic and the Antarctic.

Archives are fundamental to our understanding of the past, showing us and future generations how we as nations, communities and individuals came to be what we are. In the UK we have an unrivalled archival legacy whose potential as a rich learning resource for all is increasingly being realized. Archives of the science that has transformed our lives over the last century must be preserved as part of that legacy. In this way the contributions of leading scientists to the national life will take their place alongside those of politicians and military and literary figures in the archival record.

Science archives may not receive as much publicity as other aspects of our archival heritage, but they are not a neglected area. Since 1973 a specialized archives project, sponsored by the Royal Society and now based at the University of Bath, has made an indispensable contribution to preserving the archives of eminent British scientists. The National Cataloguing Unit for the Archives of Contemporary Scientists (NCUACS) locates the archives, brings them to Bath for cataloguing and then finds homes for them in established, usually university, repositories. In this way 225 archives of British scientists have been saved and made accessible to those wishing to explore the country's modern scientific heritage.

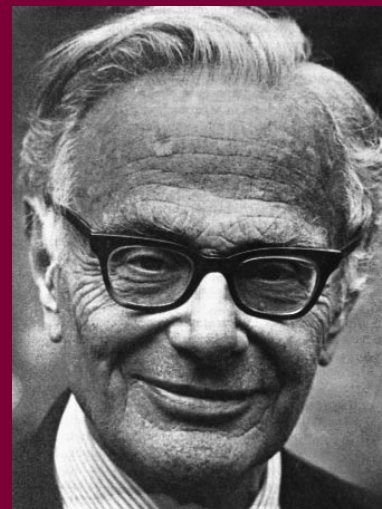
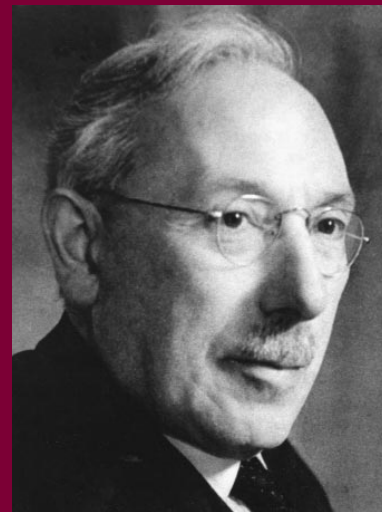
Although the remit of the NCUACS covers all the sciences, it has catalogued a very respectable number of archives of scientists of interest to the SGM. These include, from the list of the Society's original members: Sir Frederick Bawden, Norman Heatley, Edward Hindle, David Keilin, Sir Hans Krebs, Kenneth M. Smith, Richard L.M. Syngé and Donald D. Woods, while the archives of two further original members, Norman W. Pirie and Martin R. Pollock are current projects. The archives themselves may take many forms: research notebooks, correspondence with distinguished colleagues, lectures and teaching material tracing the development of a discipline over time, photographs from laboratories and symposia, and records of professional affiliations and of public service and advisory roles.

The internet has transformed the way information about archives can be accessed, and the NCUACS has sought to ensure that science archives are fully represented in national developments. Almost all the catalogues compiled since 1973, some 14,000 pages in total, have been contributed to *Access to Archives* (A2A), the English component of a scheme for a UK-wide online archival network, and are thus searchable and browsable via the A2A website (<http://www.a2a.pro.gov.uk>). Searches on microbiology and related sciences, the Society for General Microbiology and the names of individual scientists give some idea of the Unit's contribution to preserving the original source materials for the field and securing its representation on a major online educational resource.

The NCUACS is an entirely externally funded Unit whose work is supported by varying periods by grants from scientific societies, trusts and foundations and special project funding. Next April the scientific archives project will be celebrating 30 years of preserving the archives of modern British science. To place the funding of the work on a firmer foundation the Unit is establishing a development fund and launching an appeal. Those wishing to make a donation in support of this important work should send their cheques (payable to the 'University of Bath') to the Director, NCUACS, University of Bath, Bath BA2 7AY, UK.

Further information about the work of the Unit and the development fund and appeal is available from the Unit's website (<http://www.bath.ac.uk/ncuacs>) or directly from the Director.

● Peter Harper,  
Director, NCUACS



RIGHT:  
Some original members of the SGM whose archives have been catalogued by the NCUACS.  
From top to bottom:  
David Keilin (1887–1963),  
Sir Frederick Bawden (1908–1972)  
and Sir Hans Krebs (1900–1981).  
PHOTOS SGM