

figure fits well with the 70-million-year approximation, divergence times based on molecular data are usually presented as 'error-less numbers' — with proper statistical caveats added, and considered in a geological context, such estimates often appear meaningless<sup>11</sup>.

Whether or not molecular data will ever give reliable dates is a moot point, but I see no existing evidence to suggest that butterflies are older than about 70 million years, and little to imply a key role for Gondwana in their diversification. Most of the higher groups are either very widespread, or restricted to a single biogeographic region or continent<sup>12</sup>. As de Jong has wryly observed<sup>9</sup>: "We have no idea when the butterflies originated, although there is no shortage of wild guesses." Nonetheless, by applying their outstanding knowledge of riodinid systematics to the description of this remarkable find, Hall *et al.*<sup>1</sup> bring new life to the study of fossil butterflies. But their work also reminds us of many issues, both methodological and philosophical, that continue to dog the purely observational sciences. ■

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- Hall, J. P. W., Robbins, R. K. & Harvey, D. J. *Proc. R. Soc. Lond. B* doi:10.1098/rspb.2004.2691 (2004).
- Hedges, S. B. *Annu. Rev. Ecol. Syst.* **27**, 163–196 (1996).
- May, R. M., Lawton, J. H. & Stork, N. E. in *Extinction Rates* (eds Lawton, J. H. & May, R. M.) 1–24 (Oxford Univ. Press, 1995).
- Ehrlich, P. R. & Raven, P. H. *Evolution* **18**, 586–608 (1965).
- Hall, J. P. & Harvey, D. J. *Mem. Entomol. Soc. Wash.* (in the press).
- Owen, D. F. *Tropical Butterflies* (Oxford Univ. Press, 1971).
- Ross, A. J., Jarzembowski, E. A. & Brooks, S. J. in *Biotic Response to Global Change: The Last 145 million Years* (eds Culver, S. J. & Rawson, P. F.) 288–302 (Cambridge Univ. Press, 2000).
- Kristensen, N. P. & Skalski, A. W. in *Handbook of Zoology Vol. 4* (ed. Kristensen, N. P.) 7–25 (de Gruyter, Berlin, 1999).
- de Jong, R. *Invertebr. Syst.* **17**, 143–156 (2003).
- Zakharov, E. V., Caterino, M. S. & Sperling, F. A. H. *Syst. Biol.* (in the press).
- Graur, D. & Martin, W. *Trends Genet.* **20**, 80–86 (2004).
- Ackery, P. R., de Jong, R. & Vane-Wright, R. I. in *Handbook of Zoology Vol. 4* (ed. Kristensen, N. P.) 263–300 (de Gruyter, Berlin, 1999).
- Vane-Wright, R. I. in *Butterflies: Ecology and Evolution Taking Flight* (eds Boggs, C. L., Watt, W. B. & Ehrlich, P. R.) 477–513 (Univ. Chicago Press, 2003).

Evolutionary biology

## Ferns reawakened

Torsten Eriksson

The principle of the evolutionary cul-de-sac is commonly invoked to explain the apparent lingering existence of once-diverse groups of organisms. Maybe that principle itself has had its day.

Some biological concepts keep popping up, even when they have been shown, time and again, not to be generally true. One well-known example is the 'biological species concept', the idea that only those organisms that can cross and produce fertile offspring belong to the same species. This can't generally be true for many reasons, the most obvious perhaps being that some organisms are not even sexual (such as bacteria and dandelions) and yet have species.

Schneider *et al.*<sup>1</sup> (page 553 of this issue) touch on another of these favourite concepts, the 'evolutionary cul-de-sac'. This is a common explanation for why some groups that show great diversity in the fossil record still exist but are greatly diminished in diversity, remaining largely unchanged — and supposedly unable to change. The new findings tell us that ferns, at least, do not belong in this category. Schneider *et al.* conclude that ferns (Fig. 1) have attained their current diversity much more recently than had been thought, and they probably did so as a response to the diversification of flowering plants.

During evolutionary history, many groups of organism have, of course, died out entirely. Plenty of others have persisted, however, even if much diminished compared with their apparent earlier diversity. Perhaps the best-known example among

land plants is the maidenhair tree (*Ginkgo*), which is the single living species of a lineage that is almost 300 million years old according to the fossil record. Horsetails (*Equisetum*) are another example: they now consist of only a handful of herbaceous species, but they belong to a lineage that was very diverse during the Carboniferous era (300 million years ago and older) and that included large



Figure 1 Ferns — diversified later than had been thought.

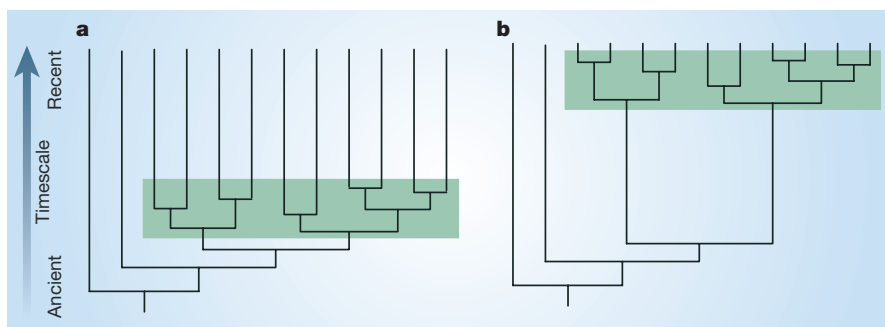
trees. The cycads are a further case: the 120 or so living species of palm-like seed plants are the meagre remnant of a much more diverse group that is at least 250 million years old.

There are many more examples, and in textbooks the extant members of such groups are invariably described as having remained virtually unchanged for several hundred million years. Even if it is not stated explicitly, the implication is that these poor plants were forced into an evolutionary cul-de-sac by more successful plants, or by becoming too specialized.

In this context, however, the ferns are a special case. The fossil record shows them to be an old group (one type, the leptosporangiate ferns, which contain the majority of extant ferns, is more than 250 million years old). But with more than 10,000 extant species they remain fairly numerous. It has been proposed that these species are not just an ancient remnant, but the consequence of a more recent expansion. Did the ferns diversify relatively recently? Or are they just dwindling more slowly than some other groups?

To resolve these questions, several methods and data have to be used in combination. Schneider *et al.*<sup>1</sup> make good use of them. First, there must be a sufficiently detailed evolutionary tree — that is, a cladogram with branch lengths — depicting relationships and distances between the relevant groups. Second, a method for estimating the age of branches in the tree has to be available. Third, appropriate fossils are necessary to calibrate the tree, and make it a 'chronogram'; that is, a direct timescale is needed. Fourth, to have confidence in the age estimates, the analysis should indicate the margin of error in the estimates. At the extremes, combining all these requirements would be expected to show the extant lineages as old (long terminal branches; Fig. 2a) or much more recently diverged (short terminal branches; Fig. 2b).

Before evolutionary trees were in use, it was hard to establish even the order of events in evolution. When 'traits', such as the occurrence of mitochondria or flowers, were placed in their most optimal position on the evolutionary trees, it became possible to determine on which branches the traits evolved (and sometimes their order). But correlation of other kinds of events, and in particular correlations between lineages, are much more difficult. Such correlations usually involve time comparisons, which are problematic because evolutionary rates are commonly different among different lineages, and a general molecular clock — that is, one based on molecular changes and ticking at a constant rate — cannot be applied. So the goal of putting absolute times on the branches of the tree of life has been hampered by the lack of methods that use a variable molecular clock. Such methods do now exist<sup>2–4</sup>, and the one used by Schneider *et al.* allows both for variation in evolutionary rates and inference of the level of



**Figure 2** The long and the short of it. Two extreme outcomes following the time calibration of an evolutionary tree for a hypothetical group of organisms (shown in green). Diversification of the group was earlier in chronogram a than in chronogram b. As far as ferns are concerned, the results of Schneider *et al.*<sup>1</sup> indicate that the extant fern diversification pattern is more like that in b, whereas the traditional expectation would be that in a.

variability to accept from the data<sup>4</sup>. This may be a good compromise between enforcing a general molecular clock (which is still most commonly done) and allowing random variation of evolutionary rates.

What about the progress in analysing evolutionary trees? Until recently, it has been computationally almost impossible to reliably analyse the relationships of large numbers of species using model-based methods, such as 'maximum likelihood', which aims to find the statistically most likely tree. Model-based estimates of the amount of evolution on the trees (branch lengths) seem preferable, and new software with the 'bayesian inference of phylogeny' — as applied by Schneider *et al.* — is becoming increasingly used<sup>5,6</sup>. This is partly because such methods can deal with the really large data sets that are

now being assembled, and still give information on how reliable the trees are. But there are also other reasons<sup>7,8</sup>. One is that a bayesian-inference analysis yields not only a tree, but a sample of trees and model parameters, and this sample can be analysed to investigate various aspects of evolution. Schneider *et al.* used this sample in a novel way for the crucial purpose of obtaining standard deviations for their age estimates.

So, what about the results? Schneider *et al.* have added data on ferns to the huge database of sequence information on plant DNA that has built up during the past two decades. In their initial analysis, they dated the diversification of extant ferns as later than expected — around 80 million years ago, rather than perhaps three to four times that age. But they also went further to try to explain what made

that relatively recent diversification possible. By performing the same analysis on the flowering plants (angiosperms), they were able to correlate the age of the evolutionary 'radiations' of ferns and flowering plants, and they conclude that the extant ferns diversified after the angiosperms. The chronograms they produced appear on page 556.

Schneider and colleagues' explanation for fern diversification adds credibility to their conclusion: they argue that the expansion of flowering plants, and in particular the forests they created, increased environmental complexity and thereby the variety of habitats that could be explored by opportunistic organisms. Among such organisms were ferns, which in consequence underwent an evolutionary reawakening. It seems reasonable to assume that this could happen in any group when the opportunity arises, and it has indeed been shown to occur in certain tropical clubmosses (lycopods) that grow on trees<sup>9</sup>. Perhaps the whole idea of the evolutionary cul-de-sac is basically flawed. ■

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1. Schneider, H. *et al.* *Nature* **428**, 553–557 (2004).
2. Thorne, J. L., Kishino, H. & Painter, I. S. *Mol. Biol. Evol.* **1**, 1647–1657 (1998).
3. Sanderson, M. J. *Mol. Biol. Evol.* **12**, 1218–1231 (1997).
4. Sanderson, M. J. *Mol. Biol. Evol.* **19**, 101–109 (2002).
5. Rannala, B. & Yang, Z. *J. Molec. Evol.* **43**, 304–311 (1996).
6. Huelsenbeck, J. P. & Ronquist, F. *Bioinformatics* **17**, 754–755 (2001).
7. Lewis, P. O. *Trends Ecol. Evol.* **16**, 30–37 (2001).
8. Huelsenbeck, J. P., Rannala, B. & Masly, J. P. *Science* **288**, 2349–2350 (2000).
9. Wikström, N. & Kenrick, P. *Mol. Phylogeny. Evol.* **19**, 177–186 (2001).

## Nanoscale physics

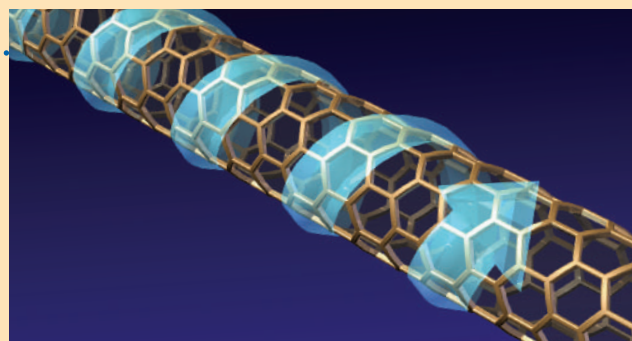
### Big moment for nanotubes

As an electron whizzes around the nucleus of an atom, it develops a magnetic signal known as an orbital magnetic moment. The size of the moment depends on the outer diameter of the electron's orbit, which is fixed by the size of the atom. Electrons orbiting around the walls of a carbon nanotube (right) should also have an orbital magnetic moment, but this had previously never been detected. In this week's issue, E. D. Minot *et al.* are at last able to show that the resulting magnetic signal is exactly what's predicted (*Nature* **428**, 536–539; 2004).

Magnetic signals have been picked up in carbon nanotubes before, but because nanotubes come in several flavours (from metallic to semiconducting) and can have several layers (like a rolled cigar), it was not clear where the

magnetic moment was coming from. Minot *et al.* address this problem by using individual 'quasi-metallic' carbon nanotubes — which means that, although the nanotubes are not strictly metallic, it still takes only a small amount of energy to excite an electron so that it becomes a moving conduction electron.

Electrons on the threshold of freedom can orbit around the nanotube in a clockwise or anticlockwise direction; the orbital magnetic moments have the same magnitude for both directions, although their orientations are opposite. But when a magnetic field is applied, the electron energies are shifted. The clockwise orbits now have a different energy from the anticlockwise ones: half the electrons are shifted closer to the



conducting 'edge', while the others become harder to kick free.

The value of the energy shift depends on the strength of the applied field and on the orbital magnetic moment of the electrons, and Minot *et al.* were able to determine this precisely by measuring the conductance of a single nanotube suspended between two electrodes. The orbital magnetic moment derived for an electron traversing the waistline of a nanotube is about 10 to 20 times larger than that

for an electron in an atom — consistent with the difference in their diameters.

Minot and colleagues' conductance measurements are clear proof that orbital magnetic moments influence a nanotube's electron-energy levels in a magnetic field. They also raise the possibility of controlling the energy levels through an external magnetic field, opening the door to further studies of the fundamental properties of nanotubes, as well as technological applications. **May Chiao**