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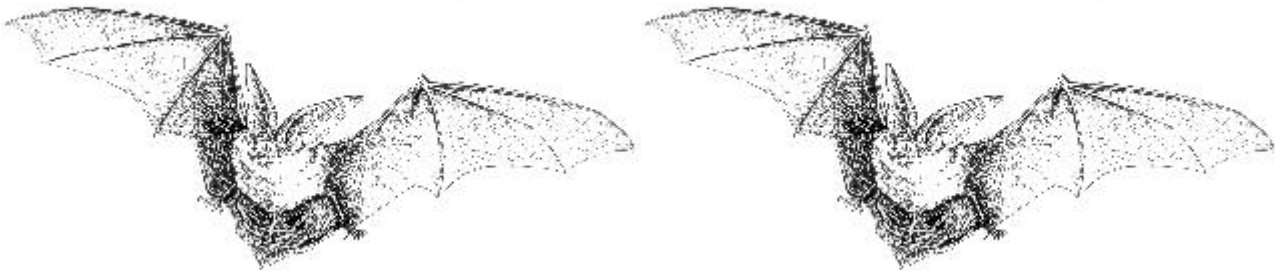
From the Editor

This is the last Newsletter before the Biennial in August, so I must take the last opportunity of reminding you to register if you haven't already done so. The meetings in Oxford, Glasgow and London were all fantastic successes and Dublin promises to exceed them all – take a look at Steve Waldren's piece below and the website.

The other main features in this newsletter are on the ATOL project, which is likely to have a substantial impact on the way we all work. Perhaps as a counterpoint to ATOL, there is also an elegant allegory on the pitfalls of molecular bioinformatics by Malte Ebach. There are also reports on the University of Reading Molecular Systematics Intensive Course, the 2002 Young Systematists' Forum and short project reports by three SA small grant holders. All of these are good examples of the way the Association supports and facilitates systematics, especially for those systematists whose careers are in their infancies.

See you in Dublin in August.

Paul Wilkin (p.wilkin@rbgkew.org.uk)

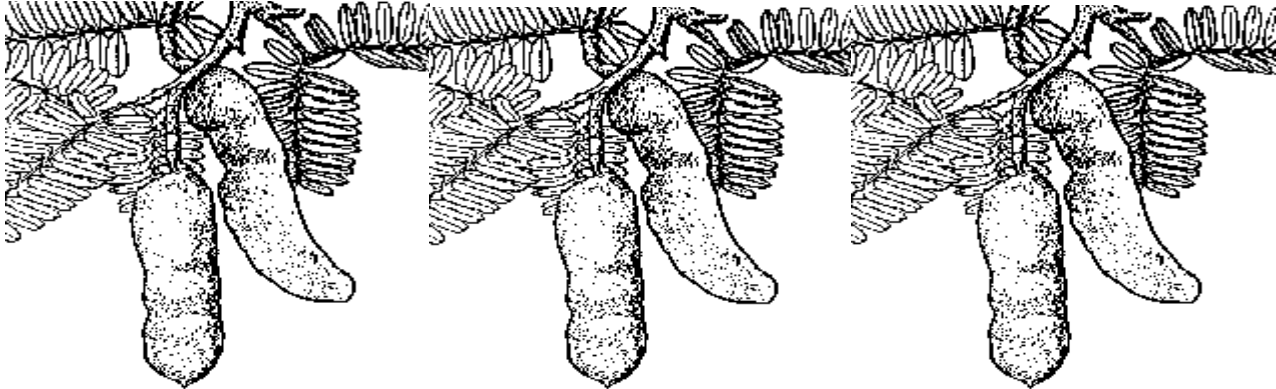


4th Biennial Meeting of the Systematics Association

Preparations for this meeting, to be held at Trinity College Dublin from 18-22 August 2003, are well underway. Delegates will register on the afternoon of Monday 18th, with plenary sessions on Tuesday, Wednesday, Thursday and Friday morning. There will be three themed sessions: *'The systematics of large and species-rich groups'* (Tuesday 19th), *'Biodiversity databases: change and challenge'* (Wednesday 20th) and *'Human evolution and environments'* (Wednesday 20th). Fifteen student bursaries have been offered by the Systematics Association, and prizes for the best student talks kindly donated by Taylor & Francis. A large number of papers have already been offered, and the meeting promises to be of very broad interest. There will be a poster viewing session on the Tuesday evening, a reception on the Wednesday

evening, and the conference dinner on the Thursday evening- a busy schedule! Apart from the conference dinner, no other midday or evening meals have been booked, allowing delegates the opportunity to sample the varied restaurants and bars in the city centre, a few minutes walk from Trinity College. Accommodation is available on-campus, in the very centre of Dublin. Many delegates are staying extra days to sample the varied delights of Dublin or to travel further afield in Ireland. There is still time to register for the meeting, but if you would like to book accommodation within the College we urge you to do so as soon as possible, as availability is limited. Further details may be found on the web site (www.systass.org) or by contacting Steve Waldren.

Steve Waldren
Botany Department, Trinity College, Dublin (s.waldren@tcd.ie)



Assembling the Tree of Life – Europe (ATOL)

This “umbrella” strategic project will have a major impact on European systematics over several decades should it receive the EC funding sought. An introduction to the ideas and strategy of ATOL is given below. There are already 140 group leaders from 76 institutes in 20 countries involved, including virtually all the phylogeneticists in Europe. It is hoped that as many systematists as possible will be able to play a part in the project.

What are the ideas behind ATOL?

Phylogenetic approaches now underpin biological research in biodiversity, conservation, genomics, and health. We are entering a new phylogenomic and phyloinformatic era. There are growing numbers of national initiatives, and a European project is vital to lead and integrate European research, to spread expertise among EC countries, and to co-ordinate with other global biodiversity initiatives. The key scientific and societal challenges require a major integrated effort to obtain data and tools needed for a comprehensive, world-leading resource; ATOL is this major integrated effort.

Assembling the Tree of Life (the phylogeny of all organisms) is a priority for describing and understanding biodiversity and its broad exploitation for human purposes. A comprehensive Tree of Life is essential for a predictive understanding of biodiversity and tightly linked to successful expansion of post-genomic knowledge. It will generate new knowledge on biodiversity, address gaps in taxonomic research, sample a significant portion of the biodiversity in targeted marine and terrestrial groups, produce massive phylogenetic data and new bioinformatic tools to assemble a large portion of the phylogeny of all organisms, and co-ordinate the European systematics community’s contribution to the global taxonomic effort, training the wider research community in phylogenetic approaches.

What are ATOL’s main objectives?

The scientific strategy for ATOL is to generate knowledge on a massive, integrated scale, linking European taxonomic expertise and biodiversity collections to molecular phylogenetics and bioinformatic expertise. Teams will conduct detailed studies on target taxa of scientific importance, and with high impact on society (e.g. health, genomics, etc), and the

environment (e.g. conservation). A network of specialist laboratory centres will be set up across Europe to integrate research and training.

ATOL offers enormous potential for innovation in, for example, DNA taxonomy/identification service for agriculture, forensics and other users; a phylogenome service generating genome data for pests, invasive species, soil biota; a phyloinformatics service to identify candidate genes for drug development etc.

ATOL will train a generation of workers to be fluent in the tools of systematics, phylogenomics, and phyloinformatics. Emphasis will be on mobility among countries and disciplines. Lab centres will host interdisciplinary visitor programs at all levels with special attention to support for training programs.

What will the main foci of the project be?

There will be four major areas of activity:

- (a) **Phyloinformatic facility**
This project component will cover five elements: data structures, data storage & management, online submission, building of phylogenetic trees and uses of trees in broad multidisciplinary science. The Phyloinformatic facility may be a virtual centre; it will combine genomic and biodiversity data in innovative ways as required by the very large-scale world ambition to recover the Tree of Life.
- (b) **Reconstructing the Tree of Life incl. addressing taxonomic gaps** This project component might consist of three interrelated elements: compiling DNA data (generate new data and data mining; phylogenetics for tree building; and taxonomy of relevant groups incl. building links to existing taxonomic databases). The choice of the target taxa will imply the application of a variety of criteria: data collection and phylogeny reconstruction for better-known groups, viz. large scale demo projects for the utility of assembling a Tree of Life in terms of meeting broad scientific and societal needs (for example invasive species or relevance in medicine), and data collection for gap-filling and provision of a backbone for all life (taxonomic expertise already exist for the latter but phylogenetic work is needed).
- (c) **Capacity building**
This component has two aspects. Firstly to develop universal standards and procedures for all aspects of the ATOL programme, and address aspects of DNA and other data curation, through to curation of physical collections including DNA, other biomolecules and tissue samples. Secondly to improve the capacity and facilities in the regions in Europe. Several NAS countries have a relative good taxonomic capacity, but can improve their effectiveness and quality by promoting phylogenetic developments.
- (d) **Training**
It will be critical that the ATOL resource is set up for a range of users with different levels of knowledge, including biologists in fields other than systematics and evolution and non-biologists. Special emphasis on training of PhD students in relation to phyloinformatic projects and prioritized taxonomic groups.

Are there similar projects elsewhere?

The US National Science Foundation has set up a 15-year program on the Tree of Life, awarding 17 million US dollars to 7 projects in 2002. Yet, due to the funding structure, the different projects are not strongly integrated, for example a central phyloinformatic resource was seen as vital but has not yet been funded.

Europe has major biodiversity collections, taxonomic, phylogenetic and molecular expertise, and a formidable expansion in bioinformatics. There is considerable momentum to start an ATOL Europe project. There have been four meetings (Patras, Paris, Kew, London) attended by a large section of the European phylogenetics community, and we are ready to compete and collaborate with global initiatives. The Program Director of the US AToL programme, Diana Lipscomb, attended three of these meetings and is keen to foster EC-US links.

Who will manage the project?

A host consortium of Royal Botanic Gardens Kew, Imperial College, and the Natural History Museum in London, with the coordination of the Royal Botanic Gardens Kew, will take charge of building the project plan with key European partners. The Project Science Coordinator and Project Administrative Manager will direct the Steering Committee (which includes the Science Council and the office for administration, legal issues and support).

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Systematic Tales: Bioinformatics and Puffins

The plight of the molecular systematist, molecular data and the underlying theories of systematics can be retold as a little tale involving puffins and sea eels.

Molecular data are quite common and admired by a great many researchers in systematics. Molecular systematists collect data in large quantities, like the way in which Neolithic man collected roots and shoots after a hard day hunting mammoths. Just as Neolithic man was a hunter gather, molecular systematists are data-gatherers. Another form of gatherer is the humble puffin (*Fratercula corniculata*), a sea bird that is abundant in arctic regions.

Unlike the molecular systematist, the puffin collects sand eels (*Ammodytes tobianus*) to feed to its young that are incubated and hatched in abandoned rabbit burrows. The adults spend most of day collecting sand eels and depositing the morsels near the entrance of the burrow. The puffin chick feeds on the eels over a period of two months until it has grown its wings. Once the young bird is able to fly it leaves the burrow and starts life searching for what it knows and loves best; sand eels. Unfortunately, the adults gather food for most of the day and rarely see the young bird fly the coop. Unaware, the parents continue to collect the morsels and deposit them near the entrance of the burrow, forming a little pile of uneaten fish. Over time the pile grows. It takes many months for the parents to figure out that the young bird has either flown away or is buried behind the rotting molehill. Finally they stop stuffing the hole with eels, and fly off to sea.

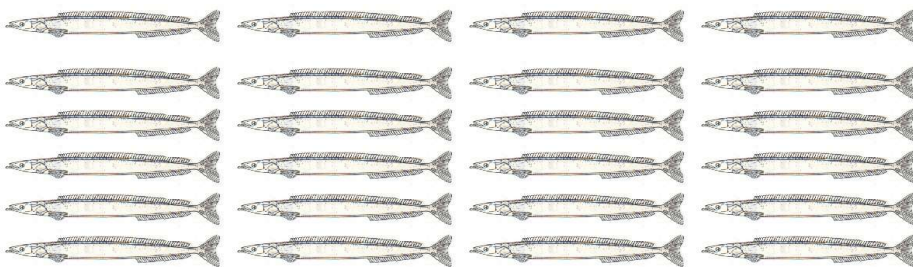
The puffin is not unlike the molecular systematist. The systematist extracts sequences, and many trees are found. The systematist then sends morsels of gathered data to a burrow called a 'genbank' where it feeds a hungry biological evolutionary theory. The burrow is dark and deep and the molecular systematist rarely sees the theory inside. The theory however, happily eats the data and yields complex hypotheses about phylogeny and biogeography. Unlike the young puffin, the theory never leaves its coop. In fact it never sees the light of day, as the influx of data outweighs the ability of the theory to digest it all. Over time the burrow hole is covered by the increasing mass of undigested data. The parent systematist, unaware of their theories' demise in the dark burrows depths beneath, gathers more data. Slowly the data grows into a large pile that has much in common with our huge mountain of rotting sand eels.

This act of building large rotting mounds is termed bioinformatics and is practiced by many molecular systematists. One day, however, the molecular systematist may also realize the immensity of the data and the unfortunate demise of its theory. These enlightened systematists leave the roost, fly south for winter and attend Willi Hennig and SSB conferences.

The moral to this cautionary tale is plain. A fledgling puffin happily progresses in its industry - to collect sand eels. It grows into an adult, finds a mate and returns to the breeding grounds to gather sand eels for its young. The molecular systematist, however, never progresses in its industry: bioinformatics. It keeps gathering data until it has buried underlying theories under a mountain of rotting data.

Dr. Malte C. Ebach

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Report: University of Reading Molecular Systematics Intensive Course

The University of Reading ran a Molecular Systematics Intensive Course between 8th and 18th March this year. The Systematics Association awarded two bursaries of £150 each, which were put towards the attendance the costs of Kadri Poldmaa, a fungal systematist from Estonia and Anne Krämer from Germany, who works on flowering plants. The short report below was supplied by Kadri Poldmaa.

The course of Molecular Systematics was held at the University of Reading from 18th to 28th of March, 2003. Today's systematics, i.e. the description and explanation of origin of biological diversity, is largely based on analyses of molecular data. Though being a very young field of science, molecular systematics is developing very quickly with many new methods and software emerging every year. In this regard, I think, the expectations of many participants of the course us where similar to those phrased by one of us at the dinner table, before the start of the course: "I've been trying to create

phylogenies for the group I'm studying but I'm not sure whether I have done it right or whether it is the best way to analyze my data?"

As if anticipating our expectations, the course organizers, Dr. Julie Hawkins and Dr. Alastair Culham, had emphasized data analysis rather than the acquisition of sequence data while compiling the program. Altogether, 10 lecturers came to tell us about their understanding of which algorithms are the best and how and for what kind of data are they suited for. We were amazed to realize that none of the speakers was dogmatic about his ideas. Rather, the main message in most of the talks was not to use the blackbox method but to understand things you are doing and explain your way of thinking in the papers you publish. One of the reasons to thank the organizers is that we not only listened the lectures but could practice on the Macs in the lab.

I found the course incredibly valuable for proceeding with my research and started to experiment with my data right after returning from the course. For a systematist who is devoting half of her time sitting behind the microscope it feels almost impossible to grasp the whole array of methods available for understanding how one group of organisms has evolved. The course held at the University of Reading definitely helped us in keeping track of the latest ideas and programs developed. It also encouraged us to spend more effort in analysing the data, an idea most explicitly expressed by one of my favourite lecturers of the course, Dr. Mark Wilkinson from the Natural History Museum: "In systematics we can't set up replicable experiments, the experiment is in the form of multiple analyses of data."

Dr. Julie A. Hawkins

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Small Grants

Details of the eight recipients of grants in the 2002-3 small grant awards can be found on the SA website (<http://www.systass.org/awards/gr0203.html>)

Project Reports: 2001-2 Small Grant Awards

Field trial of Automated Identification Software: Digital Imaging of Belize Hawkmoths

In June to August 2002 I spent seven weeks light-trapping and photographing hawkmoths (Sphingidae) in the Maya Mountains of Belize. The Systematics Association funded my airfare for this important fieldwork. I aimed to collate image banks representing 20 individuals of each hawkmoth species. These image banks will be used to train and test DAISY (Digital Automated Identification SYstem), new software that applies pattern recognition to the identification of biological specimens. Hawkmoth wings, rich in species-specific pattern variation, are ideal material for DAISY.

Having had my generator confiscated in Miami airport (to finally reach Belize Airport the day fieldwork ended!) my light-trapping was limited to the main clearing of Las Cuevas Research Station. A golf umbrella, net curtain, sticks, rocks and two mercury vapour light bulbs were held together with staples and parcel tape to form the 'Umbrella Trap', a bizarre sight but extremely effective. Moths, attracted by the bright light, settled on the outer surface of the net curtain. I photographed them at rest then collected specimens for the NHM pinned and frozen tissue (DNA) collections.

I imaged 66 Sphingid species, taking over a thousand photos, and I was thrilled to encounter three species new to Belize: *Hyles lineata*, *Manduca barnesi* and *Stolidoptera tachasara*. *Manduca barnesi* was previously thought to be limited to Western dry forest. How it got to the Maya Mountain forests is a biogeographic mystery.

Image identifications have been confirmed and the images will now challenge the DAISY system. Living moths vary in resting posture and have often lost wing scales; such non-informative variation must be tolerated if DAISY is to become a useful tool for field taxonomy. The outcome of the Belize field trial is eagerly awaited.

The Umbrella Trap. Two bulbs shine light out through the walls, attracting moths from all sides to settle on the curtain for imaging.



Manduca florestan, a common hawkmoth species at Las Cuevas.



Anna T Watson, Fern House, Colne Road, Trawden, Colne, Lancs. BB8 8PF

Investigation of CYCLOIDEA-like genes in the Leguminosae

The increase in knowledge of the molecular mechanisms controlling the development of morphological features will help answer one of the fundamental questions in systematics: what is the origin of novel characters that distinguish species? Developmental genes have been isolated in distantly related model organisms such as *Arabidopsis*, maize and *Antirrhinum* (snapdragon), but little is known about the genetic changes that lead to morphological variation in other groups of flowering plants, or between closely related species.

Floral characters in particular are important in understanding plant evolution, and the control of these characters is now being studied at the molecular level. One trait which has received much attention is floral symmetry, which is believed to affect pollination specificity. The developmental gene CYCLOIDEA (CYC) has been shown to be crucial for the control of floral symmetry in *Antirrhinum* (Verbenaceae, Lamiales). In the Leguminosae, the third largest plant family, floral symmetry is an important taxonomic trait and has been used in traditional interpretations of character evolution in this family. The Papilionoideae is the most species-rich subfamily (containing 2/3 of legume species) and its members are characterised, with a few notable exceptions, by highly bilaterally symmetric flowers. Elucidating the genetic control of floral symmetry in legumes will allow to test whether homologous genes play a similar role in distantly related taxa, and could provide a new perspective on the evolution of flower shape in this family.

As part of a study of the evolution and function CYC-like genes in the Leguminosae, homologues of CYC have been isolated in a wide range of legume taxa using a PCR and cloning-based approach. The Systematics Research Grant has allowed me to clone and sequence 136 cloned PCR products from 17 legume taxa representing the range of this family. Gene fragments were amplified using primers located in the two conserved regions (known as the TCP and R domains) characteristic of members of this gene family. Taxa were sampled extensively from the entire range of the Papilionoideae, including species such as *Cadia purpurea* with unusual radially symmetric flowers. A few species from the Caesalpinioideae and Mimosoideae were also included in the study.

Multiple copies of CYC-like genes (up to four) were isolated in most taxa. Sequence analysis revealed that all fragments were putatively functional CYC-like genes, even those from taxa with radially symmetric flowers. Fragments were highly variable in length and sequence so that unambiguous alignment was only possible in the conserved TCP and R domains. Phylogenetic analyses using parsimony, maximum likelihood and Bayesian methods were congruent, and suggest this gene family has undergone repeated duplication events early in the evolution of the Papilionoideae. These results form a framework for testing functional hypotheses.

The apparent rapid of evolution of these genes, and the potentially complex pattern of gene duplication and loss, do not make them suitable for phylogenetic analysis of distantly related taxa. However, these genes are potentially good sources of phylogenetic data at the species level. A paper (Citerne H., Luo D., Pennington R.T., Coen E., Cronk Q.C.B.. A Phylogenomic Investigation of CYC-like TCP genes in the Leguminosae) presenting these results has been accepted for publication in the special legume issue of *Plant Physiology* released in March 2003.

Hélène Citerne
Royal Botanic Gardens, Edinburgh



Bat Programme in Myanmar

After years of government imposed isolation, the universities of Myanmar (Burma) are now actively seeking to collaborate with the international scientific community in a range of research and training programmes. The Harrison Institute has been working with staff and students of the University of Yangon (Rangoon) since 1999. To date, the emphasis has focused on the study and conservation of Myanmar's rich biodiversity, and in particular the bat fauna.

In March, 2002, a grant was received from the Systematics Association towards our Myanmar bat programme. The aim of the programme was to develop an active in-country bat research group with strong regional links within South-east Asia. The travel grant of the Systematic Association allowed Christine Fletcher of the Forest Research Institute, Malaysia to make two visits to Myanmar. During the first, sponsored by the Systematics Association, she conducted training in a range of bat related studies at Yangon University and with students in the field. The success of this, prompted Myanmar Airways International and TotalFinaElf to sponsor her a second visit to a small international workshop organised by the Harrison Institute/Yangon University, which was held in Myanmar in October, 2002.

The Systematics Association grant also helped with the purchase of a computer programme and books relating to the study of bat echolocation. This allowed two students from Yangon University to take part in the first ever bat survey in Myanmar using acoustic identification techniques. This project, initially supported by the Systematics Association and Kent Bat Group has now developed in to a Darwin Initiative project, and has a very promising future.

The Harrison Institute and the Zoology Department, Yangon University are extremely grateful for the support of the Systematics Association. The commitment of the Association has been a catalyst which has led to the rapid development of the project. We are also most grateful to Christine Fletcher for her time, enthusiasm and support of our bat project.

Dr Paul Bates
Harrison Institute, Centre for Systematics and Biodiversity Research, Sevenoaks, Kent

Young Systematist's Forum 2002 and 3

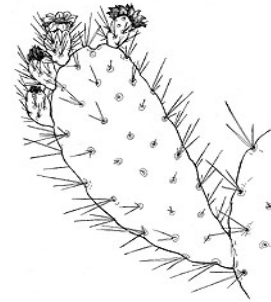
NB Abstracts from the 2002 YSF are available on the website (<http://www.systass.org/ysf/youngsystem02.html>)

2002 Report

The Young Systematist's Forum has continued to gain in popularity, so much so, that before the final programme was decided, the number of available slots for the 14 oral presentations was already oversubscribed by mid-October.

Applications came in from USA, SE Asia and Europe and it was therefore decided to increase the number of available spaces for poster presentations cater for those wishing to attend.

Changing venues from the Palaeontology Demonstration Room to The Flett Lecture Theater within The Natural History Museum proved to be very advantageous for the increased numbers. Moreover, The Flett is equipped with excellent audio visual aides and all participants very ably showed what Powerpoint could do when put through its paces. Talks and posters were of a very high standard with molecules, methods, plants and animals, all getting a look in. A select panel of judges took the difficult decision to award of the oral and poster prizes to only two attendants. The award of best poster entitled "Tropical diversity - the problem of large genera: *Cyrtandra* (Gesneriaceae)" was made to Gemma Bramley, while that for best presentation entitled "Opuntioid cactus evolution and systematics; inferences from DNA sequence data" was made to Patrick Griffith, who had traveled from California to attend.



At the end of the meeting an open discussion across the floor highlighted funding problems associated with systematic research and also aired various views as to where further research should take us - more on methods, less on molecules and vice versa. In addition the need for alpha-taxonomy (whilst few talks presented such data) was enforced. The President Chris Humphries gave a short summary of the position of the Systematics Association regarding the House of Lords document on the future of taxonomy and systematics within UK universities. The somber note on which the meeting closed quickly dispersed to a jovial atmosphere. All attendants enjoyed the provided dinner and talked to colleagues. No doubt new friends and contacts were made, an essential aim of the Forum.

2003

A date for all your diaries – the YSF 2003 will take place on 4 December at the Royal Botanic Gardens, Kew - see the website and the November Newsletter for further information. The organisers will be Russell Seymour at the NHM and Paul Wilkin and Bill Baker at Kew.

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Systematics Association Special Volumes
from Taylor & Francis



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Telling the Evolutionary Time Molecular Clocks and the Fossil Record

Philip Donoghue and Paul Smith,
both at the University of Birmingham, UK

- Pulls together the various strands of the science of systematics into one cohesive text
 - Takes an historical and forward thinking perspective
- Written specifically to encourage further debate and discussion
 - Highlights a controversial area of evolutionary biology
- Provides a thorough assessment of the strengths and weaknesses of both molecular clock theory and the fossil record

Understanding the timing of major evolutionary events is important, not only in itself, but critical also to our understanding of the tempo and implied mechanism of evolutionary change. *Telling the Evolutionary Time* represents a discussion between molecular biologists and palaeontologists, in which they investigate the significance of competing sources of data, explain the nature of molecular clocks and the fossil record, and attempt to develop compromise models that incorporate conflicting opinions. These are presented as a series of case studies dealing with many of the most important groups of complex organisms. Research scientists and advanced undergraduates across the field of evolutionary biology will find this a stimulating volume, bringing new insight and perspective to a thorny debate.

Contents:

1. Molecular Clocks: Whence and Whither 2. The Quality of the Fossil Record and Reconciling Differing Molecular and Morphological Dates 3. Ghost Ranges: Real or Imaginary? 4. Towards an Integration of Molecular Clocks, Earth History, and the Fossil Record 5. Episodic Evolution in *foraminifera*, Evidence from Molecular and Fossil Data 6. Molecular Clock Calibration from Comparing Molecular and Stratophenetic Phylogenies of *coccolithophores* 7. Dating the Origin and Early Diversification of Land Plants: Evidence from Fossils and Molecules 8. The Origin of Flowering Plants 9. Angiosperm Divergence Times: What Use are Molecules? 10. Comparing Molecular and Palaeontological Estimates for the Divergence of Animals 11. Whitten in Stone? Fossil Evidence for the Origin of Animals 12. Origin and Early Evolution of Chordates: Reconciling Molecules and Fossils 13. Bones, Clocks and Crown Tetrapod Origins 14. Molecules Clocks and the Fossil Record: The Radiation of Modern Birds 15. Origin and Spread of Anatomically Modern Humans

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