

domain tree of life, which appears in most textbooks, shows eukaryotes and archaeobacteria as separate groups that share a common ancestor to the exclusion of eubacteria.

By contrast, the eocyte hypothesis has eukaryotes originating from within the archaeobacteria. We have investigated the relative support for each hypothesis from analysis of essential components of the eukaryotic nucleic acid replication, transcription, and translation apparatus. Our analyses favour the eocyte hypothesis rather than the three-domain tree of life, with important implications for eukaryotic cellular origins.

Email Address for correspondence: Martin.Embley@newcastle.ac.uk

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CSS.16

13:30 Monday 29th June 2009

Evolution of protein structure and function

Michael Sternberg (Imperial College London), Syed Nabil Ali (Imperial College London), Manuela Helmer-Citterich (University of Tor Vergata), Pier F. Gherardini (University of Tor Vergata), Keiran Fleming (Imperial College London), Lawrence A. Kelley (Imperial College London), Mark N. Wass (Imperial College London)

The evolution of the protein universe mirrors at the molecular level the evolution of species.

Proteins are formed from domains, which are the key unit of evolution. Homologous domains nearly always share similar three-dimensional structures, which tend to be far more conserved than sequence. Furthermore homologous domains can have related functions.

Based on these and other principles, groups have developed classifications of proteins into families and superfamilies including the SCOP and CATH databases. Using bioinformatics analyses, genomes of a wide range of organisms can be assigned to SCOP or CATH domains and this provides the starting point from evolutionary analyses, several of which will be reported.

First we will describe how the number of different domains and the nature of their combinations can provide insights into the evolution of prokaryotic and eukaryotic species. Next a specific study which used the presence of a domain within a species to compare different species and thereby construct an evolutionary tree. A recent analysis considered the evolution of protein function. The protein repertoire generally reuses domains to create novel functions with domain recombination being the major force behind evolving function.

The detection that two proteins are homologues also provides a powerful approach for protein modelling. Our program Phyre constructs a predicted three-dimensional model of a protein based on the experimental coordinates of a homologue. Function can be assigned to proteins using enhanced sequence analysis by a variety of algorithms including our program CONFUNC.

Email Address for correspondence: m.sternberg@imperial.ac.uk

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Using molecular phylogeny to investigate the bacteria associated with the cabbage aphid (*Brevicoryne brassicae*)

Emily L. Clark (SCRI, University of Dundee), Alison J. Karley (SCRI), Jane Wishart (SCRI), Tim J. Daniell (SCRI), Stephen F. Hubbard (University of Dundee)

Aphids harbour symbiotic bacteria that can have positive, negative or neutral effects on their survival and performance. These bacteria are split into two groups: the primary obligate endosymbiont, *Buchnera aphidicola*, and the secondary symbionts. In pea aphid (*Acyrtosiphon pisum*) the secondary symbionts have been shown to influence various fitness traits in their aphid hosts (Ferrari et al., 2004, Ecological Entomology, 29, 60–65.), but very little is known about their fitness effects in other aphid species. To investigate whether bacterial composition influences trophic interactions in other aphid species we have used molecular methods to characterise the bacteria associated with a Scottish arable pest, the cabbage aphid (*Brevicoryne brassicae*).

We found that the relative abundance of bacterial types other than *Buchnera* varied between cabbage aphid lines. A real-time PCR assay based on a maximum likelihood phylogenetic tree generated by cloning and sequencing of the bacterial 16S gene indicated there are at least three different community types in cabbage aphid: (1) aphid lines dominated by one bacterial type; (2) aphid lines dominated by a second bacterial type; and (3) aphid lines in which no bacteria other than *Buchnera* have been detected.

Based on the molecular results we devised aphid performance experiments to test the influence of bacterial composition on aphid fitness, with a particular focus on the success of hymenopteran parasitism by the wasp *Diaeretiella rapae*. The truly multi-trophic nature of cabbage aphid population dynamics in arable systems is highlighted by this study.

Email Address for correspondence: emily.clark@scri.ac.uk

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14:20 Monday 29th June 2009

Leaf movements and Darwin – A novel adaptive perspective on an old conundrum

Michael A. Woodley (Royal Holloway University of London), Paul F. Devlin (Royal Holloway University of London)

Darwin (1880) proposed a role for nyctinastic circadian driven leaf movements in the conservation of meristemic heat. We have shown that in *Arabidopsis thaliana*, a highly r-strategist weed, such movements may play a novel role facilitating competition for light between individual plants through an action characterized by leaf overtopping. Experiments have been conducted investigating the adaptive role of this mechanism, in which wild type was put into direct spatial competition with the arrhythmic circadian clock mutant, *lhy-1*. Two different light regimes (16 hour day, 8 hour night and continuous light) were used in an effort to determine under which conditions competition, as measured by image analysis of leaf area from an aerial view, was maximized. It was found that the day/night cycle regime conferred a selective advantage on wild type. It consistently out-competed *lhy-1*, acquiring a total leaf exposure area that was at least 25% greater than *lhy-1*. Under continuous light conditions the advantage was gained by *lhy-1* indicating that such an environment is negatively-selective with respect to circadian leaf movements. These experimental results compliment the findings of similar experiments conducted using arrhythmic circadian mutants of the cyanobacterium, *Synechococcus elongates* (Woelfle et al., 2004). These data are indicative of an adaptive role for circadian driven leaf movements in *A. thaliana* as a resource-seeking aid in competition.

Darwin, C.R., 1880. The Power of Movement in Plants. John Murray, London.

Woelfle, M.A., Ouyang, Y., Phanvijhitsiri, K., Johnson, C.H., 2004. *Current Biology*, 14, 1481–1486.

Email Address for correspondence: m.a.woodley@rhul.ac.uk

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Teaching evolution: Practical resources to teach tricky issues

Jeremy Pritchard (University of Birmingham)

Evolution can be an emotive subject, but underpins all biology. All biologists should be fully engaged with Evolution and understand its mechanisms and consequences. Training and engagement of all students in the initial stages of their University education is of central importance, whether they are molecular biologists or ecologists. A range of resources are being designed to directly address specific evolutionary issues including counter-views. Many of the resources involve data collection and analysis and so develop skills in all areas of science. All are freely available on the web. The projects include:

1) Taking a historical perspective to diffuse subjective critiques; 2) Human Evolution: providing context; 3) Problem-based learning of taxonomy; 4) Plant growth demonstrating variation and adaptation ;5) The evolution of complexity by random variation and selection; 6) Directly confronting creationist arguments.

The presentation will briefly introduce the major issues. Evolution theory is often criticised for being unable to explain how chance can generate complex organs such as the eye. However Evolution by Natural selection is not the product of change alone but is a combination of random mutation and non-random differential survival. The practical Evolution of Complexity will be demonstrated. It is an 'Excel' exercise to show how complexity can be rapidly produced by chance plus selection. Its implementation will be discussed.

Email Address for correspondence: j.pritchard@bham.ac.uk

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Teaching evolution: A discussion of the use of classical characters and sequence data in the teaching of evolution

John Newbury (University of Worcester)

The concept of phylogenetic trees is central to an understanding of evolution and the diversification of life on earth. Most students can grasp the general principles of such trees. However, they may not have a thorough understanding of the designation of the classical characters that are considered to be most important in developing trees within a taxon. Alongside this, they may not understand the ways in which information about sets of characters can be manipulated by computer software to create phylogenetic trees. A key concept in such processes is that of parsimony – which here means the least complex proposed pattern of evolution that fits the data. Once parsimony is understood, it becomes easier to explain the tremendous value of DNA and protein sequence data and their use for establishing phylogenies. A key, and obvious, advantage of sequence data is that all taxa share the same characters (the same 4 bases and 20 amino acids) greatly facilitating studies into deep phylogeny. Brief reference will also be made into

studies that have allowed the acquisition of sequence data from fossil material, thereby linking two previously unconnected sources of data for the analysis of the evolutionary process.

Email Address for correspondence: j.newbury@worc.ac.uk

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Teaching evolution: The continuity between humans and other primates

Bill Sellars (Manchester)

Darwin's theories of Natural Selection building on Malthus' Principle of Population have found a rather unexpected utility in the fields of Computer Science and particularly in Artificial Intelligence. This profitable cross-fertilisation of disciplines has come full circle and these computational techniques are now proving to be extraordinarily useful in trying to understand the evolutionary scenarios of modern humans. Evolutionary Computing provides a tool that enables the researcher to explore a range of different solutions to complex problems. One such problem is trying to recreate the likely locomotor patterns of extinct animals based on their fossil morphology and trackway information. This is of particular importance in human evolution since the adoption of upright, walking gait is the defining feature of the hominin clade and considerably predates any brain size increase. Finding the reasons for this change in locomotor pattern may hold the key to understanding the divergence of chimpanzees and humans from their most recent common ancestor. These techniques have been used to identify the locomotor pattern of the famous Laetoli footprint trail and also to predict running speeds in a range of other bipeds. However there are some intriguing issues where the predictions made by simulations do not match up with established wisdom and we are forced to question whether it is our understanding of the fundamentals that is wrong or simply that our computational approaches are in some way inadequate. Simulations generate testable predictions and allow an evidence based approach to investigate palaeontological questions.

Email Address for correspondence: William.Sellars@manchester.ac.uk

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Poster Session – Monday 29th June 2009

Amino acid experimental research supporting origin of living cells incubated between muscovite laminae; the evolution of evolution

Gary C. Vezzoli (Lebanon College), Idalina Williams (Dartmouth-Hitchcock Medical Center)

Experimental research using amino acids to explore whether living cells incubated between layers of mica showed that using lysine, injected between muscovite layers and exposed to elevated pressure and to a geochemical/geophysical bath, we observed, starting at 37.5 °C, black particles that showed motility, phototaxis, and swimming action of ameba.

Email Address for correspondence: vezzoli2005@yahoo.com

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