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Society for Experimental Biology Annual Main Meeting 28th June — 1st July 2009, Glasgow, UK

CSS — THE EVOLUTION OF EVOLUTION — WHAT WOULD YOU TELL DARWIN?

CSS.1
09:00 Sunday 28th June 2009
What would you, the SEB, tell Darwin?

Jeremy Pritchard (University of Birmingham)

Charles Darwin was born just over two hundred years ago; his book 'On the origin of species…' will have its 150th anniversary in November. His work and its development have influenced and directed the vast majority of the science that has gone on since. If Darwin was alive today there is little doubt that he would be a member of the SEB. As a society dedicated to experimental Biology, with interests as diverse as plant movement, cell structure, bird migration and earthworms, Darwin would have been at home in our research sessions. He would have been gratified to see our increased understanding of the adaptations that maximise organism fitness. But Darwin would have been amazed and delighted to learn about the complexity below the level of the cell that studies of proteins and genes reveal. Despite the novelty of some information, he would be content at the universal applicability of the simple processes of Darwinian Evolution at all four levels of the biological hierarchy.

To celebrate the 200th anniversary of his birth, this cross sectional session brings together topics from across the SEB remit of plants, animals and cells using systems ranging from genes, proteins, cells and organisms to ecology. Some of the most notable names in their relevant evolutionary fields are interspersed with offered talks from SEB members. There is much to tell Darwin; the two days of this session highlight the ongoing SEB contribution to those developments.

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CSS.2
09:20 Sunday 28th June 2009
The ecology, evolution and behaviour of Darwin's Finches

Peter Grant (Princeton University)

Peter Grant has intensively investigated Darwin's Finches for 30 years. The thirteen species evolved from a common ancestor in the last few million years and display striking patterns of morphological and behavioural variation, with some populations being exceptionally variable. The reasons for these patterns has been the main focus of investigation. First, there is much heritable variation in populations, partly as a result of hybridization. Second, this genetic variation is occasionally subject to the forces of both natural and sexual selection, as the climatic environment fluctuates between extreme conditions. These two facts mean that populations are currently labile, evolutionarily, which is fortunate because it has enabled estimation of the minimal forces of selection involved in the transformation of one species to another. Third, the composition of finch communities is strongly determined by patterns of variation in food supply among islands, and by competition among species for that food supply. Evolution of character displacement caused by interspecific competition has been observed and measured. Fourth, finch species recognise each other by their appearance and by their song, as demonstrated by experiments with models and tape-recorded song. Integrating all this information the primary driving forces in the adaptive radiation of the finches were ecological, with reproductive isolation between newly formed species being largely an incidental consequence of ecological divergence.

Adapted from Peter Grant web site at Princeton (http://www.princeton.edu/eeb/people/display_person.xml?netid=prgrant&display=All).

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CSS.3
10:50 Sunday 28th June 2009
Beneficial microbes have changed the course of evolutionary history

Angela E. Douglas (Cornell University)

The core reason why beneficial microbes have changed the course of evolutionary history is that the lineage giving rise to eukaryotes

was metabolically impoverished. The great evolutionary success of the eukaryotes is founded on their acquisition of various complex metabolic capabilities, including aerobic respiration, photosynthesis and nitrogen fixation. Importantly, the source of these capabilities was neither intrinsic (i.e. from pre-existing capabilities of the eukaryote) nor lateral gene transfer. The capabilities were gained by symbiosis with bacteria that possessed these metabolic traits. Overall, beneficial microbes have underpinned various major evolutionary transitions, including the origin of eukaryotes, land plants, reef-building corals and many animal herbivores, and they are crucial to the fitness of many eukaryotes. Among all the eukaryotes, the animals are especially impoverished metabolically. They lack, for example, the pathways for the synthesis of various amino acids and vitamins; and various animal groups, from corals through cockroaches and aphids to cattle thrive on otherwise inadequate diets by deriving these nutrients from symbiotic microbes.

The importance of beneficial microbes the evolutionary history of eukaryotes illustrates how natural selection does not exclusively involve antagonistic interactions. Time and again, organisms have responded to antagonists and inadequate resources by forming alliances with partners that provide nutrients or other benefits. This does not, however, mean that symbioses involving beneficial microbes are without conflict. The persistence of these associations, often over long evolutionary timescales, is founded on mechanisms that resolve conflict as well as the exchange of benefit.

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CSS.4

11:20 Sunday 28th June 2009

How to make a whale: Molecular signature of myoglobin in diving birds and mammals

Michael Berenbrink (University of Liverpool), Scott Mirceta (University of Liverpool)

Extended breath-hold diving by birds and mammals is one of the most remarkable feats of physiological endurance displayed by animals. A key adaptation for sustained aerobic performance is the massive over-expression of myoglobin in aerobic muscles, a protein that is widely believed to bind oxygen and deliver it during extended dives. But using phylogenetic reconstruction techniques we now show that myoglobin in all diving animals also possesses a suite of highly derived molecular features of no known function. Here we propose that multiple evolution of long deep breath-hold diving across birds and mammals was each time associated with profound adaptive changes in Mb solubility and proton buffering that directly translate to whole organism diving performance. The role of these molecular features in dive performance and the evolution of diving lifestyles were previously completely unrecognised. This is despite myoglobin being the first protein that has been structurally characterised at the atomic level some 50 years ago. This study integrates molecular structure and function of myoglobin with whole organism diving capacity in an evolutionary context. This allows us to reconstruct the evolution of diving in birds and mammals, linking it to specific Mb substitutions, which – together with other adaptations – have allowed several lineages of endothermic vertebrates to secondarily return to the sea.

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CSS.5

11:50 Sunday 28th June 2009

Evolution and conservation

Georgina Mace (Imperial College London)

Darwin was inspired by the diversity of life and by the many intricate adaptations he observed, especially affecting species restricted to oceanic islands. 150 years ago, the impact of man on our Earth was substantially less than it is now. In particular, we now risk losing many species, and especially some of the species that proved so inspirational to Darwin. In this talk I will review the impact of people on the state of global diversity in 2009, and describe how taking an evolutionary approach could alter current conservation plans and priority activities for the next few years.

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CSS.6

13:20 Sunday 28th June 2009

The evolution of plants

John A. Raven (University of Dundee at SCRI)

The lecture does not update Darwin's preoccupations in his books about plants, but deals with major current areas of research on plant evolution: Darwin's interests would themselves evolve. Organisms which, like 'higher' plants, produce oxygen in photosynthesis include the cyanobacteria and algae, and the evolution of the capacity to produce oxygen in cyanobacteria perhaps 2.7 billion years ago was a very significant event. Not only did it provide cyanobacteria with access to an essentially unlimited supply of water as their reductant, but the accumulation of toxic oxygen transformed the chemistry and biology of the biosphere. The transfer of the capacity for photosynthesis to eukaryotes by primary and secondary endosymbioses to yield a diversity of algae greatly increased the range of life forms of photosynthetic organisms in water bodies, and set the scene for the ultimate (at least 450 million years ago) evolution of 'higher' plants on land. Palaeobotany, comparative bioechemistry and ecophysiology and molecular phylogenetics give us good hints as to the evolution of vegetative and reproductive traits of plants on land in the early Phanerozoic, with woody gymnospermous plants using seeds in reproduction present by 360 million years ago. The third topic is Darwin's 'abominable mystery', the origin of the flowering plants. Here evidence from molecular phylogenetics shows that the nearest living relatives of the ancestral angiosperm have a diversity of life forms. Despite these and other advances, many questions remain on the origin and evolution of angiosperms.

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CSS.7

14:00 Sunday 28th June 2009

The evolution of hyperaccumulation, is it adaptive and what are the molecular and physiological mechanisms?

Mark MacNair (University of Exeter)

This paper will compare the evolution and molecular machanisms of metal tolerance (an adaptation where the selective pressure is well understood) with metal hyperaccumulation (a presumed adaptaion but where the selective pressure is less well known). I will explore issues concerning the identification of selection acting on the character, and the identification of genes and mechanisms responsible.

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CSS.8

14:30 Sunday 28th June 2009

Bacteria and multicellularity

Stu West (Department of Zoology, Oxford University)

Darwin's theory of natural selection provides a general explanation of adaptation in all organisms. Much interest has focused on how natural selection can explain cooperation, where individuals perform behaviours that benefit others. Whilst this area has long been dominated by work on humans, other vertebrates and the social insects, recent work has unearthed a range of social and cooperative behaviours in bacteria and other micro-organisms. This work has provided excellent opportunities for testing fundamental aspects of evolutionary theory, but also helps illustrate many misunderstandings of evolutionary theory applied to humans.

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CSS.9

15:30 Sunday 28th June 2009

Evolution of eyes and photoreceptors

Walter Gehring (University of Basel)

Recent experiments on the genetic control of eye development have opened up a completely new perspective on eye evolution. The demonstration that targeted expression of one and the same master control gene, that is, Pax6 can induce the formation of ectopic eyes in both insects and vertebrates, necessitates a reconsideration of the dogma of a polyphyletic origin of the various eye types in all the animal phyla. The involvement of Pax6 and six1 and six3 genes, which encode highly conserved transcription factors, in the genetic control of eye development in organisms ranging from planarians to humans argues strongly for a monophyletic origin of the eye. Because transcription factors can control the expression of any target gene provided it contains the appropriate gene regulatory elements, the conservation of the genetic control of eye development by Pax6 among all bilaterian animals is not due to functional constraints, but a consequence of its evolutionary history.

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CSS.10

16:00 Sunday 28th June 2009

On the 'imperfection of the geological record': Recent palaeontological discoveries to delight Darwin

Jennifer A. Clack (University of Cambridge)

Two chapters of 'On the Origin of Species' addressed arguments related to the fossil record and its sparse and spotty nature, and the lack of many 'intermediate forms'. Darwin's explanations have largely been proved correct, and since 1859, a vast amount of corroborating data and information has accumulated, both in the geological and palaeontological realms, that would have delighted him. This lecture focuses on a few of the palaeontological advances that have been made recently in some of the areas of his concern, in terms of the wealth of specimens discovered and the use of new techniques to interpret them. In 1859, few if any fossil organisms older than the Silurian were known: since then, vertebrates, invertebrates and even animal embryos have been discovered from earlier deposits, some with soft parts represented. Other areas that concerned Darwin included the distinction between 'fish and reptiles', and how large groups like these arose. Transitional fossils between 'fish' and 'tetrapods' are now well documented, as are those between 'reptiles' and 'birds'. The former have been discovered almost worldwide, represented by three-dimensional fossils, and the latter are represented by the late Mesozoic localities in China preserved in rich lake bed deposits. A lament from Darwin over the lack of lake deposits from the Mesozoic has been magnificently overcome. These deposits have yielded early mammals, also on his wish-list. The origin of whales and the origin of teleosts were other concerns, equally of interest and importance today, and about which recent discoveries offer fundamental insights.

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CSS.11

16:30 Sunday 28th June 2009

Chromosome diversification between floral specialized and non-specialized groups of the genus *Crotalaria* (Leguminosae-Papilionoideae)

Mateus Mondin (Departamento de Genética - ESALQ - Universidade de São Paulo)

In the classical Stebbins's book Chromosomal Evolution in Higher Plants, he presented some cases where the chromosomal morphology and number showed high relationship to floral specialization. A similar case occurs in the genus *Crotalaria* (Leguminosae-Papilionoideae), where the species with floral specialization present the shortest chromosomes, while species without floral specialization have bigger and symmetrical ones. The use of chromosome banding and FISH of the 45S and 5S rDNA allowed to investigate the aspects of chromosome organization other than those of classical karyotypes. Every species studied present pericentromeric heterochromatin, however, those with floral specialization have bright CMA bands that quenched in combination with distamycin A while those without specialization does not have binding sites to any fluorochrome, and the heterochromatic blocks can be seen only after chromosome denaturation. The differences on binding fluorochromes by the pericentromeric heterochromatin occur early in the group diversification that probably resulted from a turnover in the repetitive motifs, since the species with and without floral specialization are completely separated. All species presenting 45S and 5S rDNA sites at chromosome 1 have been considered ancient, since that secondary inversion, translocation and transposition events involving rDNAs are associated with diversification inside the botanical groups. Moreover, an inversion changing the positions of 45S and 5S rDNA detected in chromosome 1, separates the specialized from the non-specialized groups. Two polyploids of specialized group showed typical characteristics of polyploid evolution like 45S and 5S rDNA reduction size, number

and inactivation, chromosomal length reduction and structural rearrangements. The results showed a close association between floral specialization and chromosome diversification.

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CSS.12
10:20 Monday 29th June 2009
Darwin in silico: Computational approaches in human evolution

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.

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CSS.13
10:50 Monday 29th June 2009
Evolution of bipedalism

Susannah Thorpe (University of Birmingham)

Darwin famously evaded the issue of human evolution in Origin of Species, noting only that “light would be shed on the origin of man and his history”. But, in Descent of Man, he touched, albeit unknowingly, on what was to become the defining feature of humans; our locomotion. Darwin clearly saw the link between the locomotion of the other primates and humans, noting that “monkeys exhibit a manner of progression intermediate between that of a quadruped and a biped, but…the anthropomorphous apes approach in structure more nearly to the bipedal than to the quadrupedal type”. Two hundred years on, debate on the origins of human locomotion remains intense.

The traditional hypothesis argues that the common ancestor of chimpanzees and humans descended to the forest floor and knuckle-walked, much like the modern chimpanzee, before our ancestor developed a bipedal gait about 6 million years ago. However, recent paleontological evidence suggests that adaptations for bipedalism actually arose in an arboreal context, and genetic evidence has suggested that bipedalism predates the chimpanzee–human split. Nevertheless, the adaptive benefit of arboreal bipedalism remains unknown. Here we show that it allows the most arboreal great ape, the orangutan, to access supports too flexible to be negotiated otherwise. We find that human bipedalism is less an innovation than an exploitation of a locomotor behaviour retained from the common great-ape ancestor. This brings into question the use of bipedalism as the defining feature of the hominin clade.

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CSS.14
11:20 Monday 29th June 2009 (SEB Education and Public Affairs Section President's Medallist 2009)
On the physiology of mammalian life-history strategies

Teresa G. Valencak (Veterinary University Vienna)

Charles Darwin, considered reproducing animals to be limited by food. However, recent studies on mammals and birds have demonstrated that, even when food is abundant, energy intake of animals with high nutrient demands, such as lactating females, may reach a limit. It is not fully understood what the nature of physiological ceilings is, and which factors influence these limits. Two main approaches can explain limits to energy turnover. The first suggests that certain morphologically imposed constraints might be limiting. In this view, physiological limits would represent constant traits that have evolved as an adaptation to average resource availability and reproductive investments. The other framework refers to life-history strategies. Ever since Fisher followed by the work of Lack, Cole and, particularly, Williams, it has been suggested that investment into current reproduction may conflict with future reproduction and survival. Assuming that operating at peak rates of energy turnover has a physiological cost, it will serve the interest of an individual to approach physiological limits during reproduction only if the reproductive value of the offspring is relatively high. To date, we however do not know whether reproducing mammals regularly operate at their physiological limit, or well below in order to not overly compromise their own survival and reproduction. In the latter case, reproducing females may maximise their fitness by evaluating costs and benefits of each reproductive event before approaching metabolic ceilings.

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CSS.15
11:40 Monday 29th June 2009
The archaebacterial origin of eukaryotes

Martin Embley (University of Newcastle)

The origin of the eukaryotic genetic apparatus is central to understanding the evolution of the eukaryotic cell. Disagreement about the source of the relevant genes has spawned competing hypotheses for the origins of the eukaryote nuclear lineage. The iconic rooted three-

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

By contrast, the eocyte hypothesis has eukaryotes originating from within the archaebacteria. 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.

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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.

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CSS.17

14:00 Monday 29th June 2009
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 (*Acyrthosiphon 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 multitrophic nature of cabbage aphid population dynamics in arable systems is highlighted by this study.

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CSS.18

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.

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CSS.19
15:40 Monday 29th June 2009
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.

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CSS.20
16:00 Monday 29th June 2009
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.

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CSS.21
16:20 Monday 29th June 2009
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.

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CSS.22
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.

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