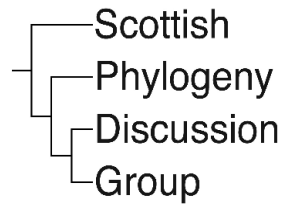


CEGG



Scottish Phylogeny Discussion Group

University of Edinburgh,
26 October 2011

Programme



THE UNIVERSITY *of* EDINBURGH

Locations

Registration, lunch and tea/coffee breaks are in the Micheal Swann building. Take the lift up to the 7th floor; we are in the Upstairs Cafe.

Lectures will take place in the adjacent Darwin building, room G10.

For more information on getting to the Swann & Darwin buildings, see here:

<http://www.wcb.ed.ac.uk/findus>

Dinner

The meeting will be followed by dinner at a restaurant in Edinburgh. Dinner is open to anyone registered for the meeting, but requires separate booking in advance. If you would like dinner, please tell Martin Jones (martin.jones@ed.ac.uk) before Tuesday 25th October. Dinner will be charged at cost.

Edinburgh meeting organizer

Martin Jones

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SPDG organizer

Daniel Barker

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Further Information

The Scottish Phylogeny Discussion Group is funded by a grant from the Scottish Bioinformatics Forum and by the Centre for Evolution, Genes and Genomics at the University of St Andrews. For information on the Scottish Phylogeny Discussion Group and its activities, please see:

<http://biology.st-andrews.ac.uk/cegg/spdg>

1.30 pm

Buffet lunch and registration

2 pm

Opening remarks

2:10 pm

Signal exploration and the affinities of the ecdysozoans

Omar Rota Stabelli, Istituto Agrario San Michele

Ecdysozoan is the newly recognised clade including arthropods, nematodes and other gloriously unfamiliar beautiful phyla. Although they encompass the vast majority of animal diversity, their evolutionary history still remain unclear. Using phylogenomics and an accurate exploration of the phylogenetic signal we recently show that some long lasting evolutionary problems in ecdysozoa phylogeny were due to systematic errors. With a hopefully robust tree of Ecdysozoa at hand, it is now time to explore other aspects of their evolution such as genome evolution and chronological history. Water bears, velvet worms and terrestrial arthropods reveals unexpected and interesting scenarios.

3:15 pm

Freshwater Fish biodiversity in Thailand: patterns, endemism and conservation status

Salinee Khachonpitsak, University of St. Andrews

Thailand is a country with a high diversity of fish species – but also somewhere where the fish fauna is incompletely characterized. The aim of this project is to assess the biodiversity of freshwater fish in Thailand using data extracted from museum collections, the scientific literature and unpublished sources. These data are used to create a new species inventory database that can be used to explore patterns in species richness, endemism and uniqueness of freshwater fishes in Thailand. Eight hundred and fifty-four species in 15 orders, 52 families and 227 genera of freshwater fishes are reported from Thailand, 8.3% and 22.1% of which are globally and nationally threatened, respectively.

3:35 pm

Tea/Coffee

4 pm

Duplication and evolution of a key sporulation gene in the differentiating bacterium, *Streptomyces coelicolor*

Paul Hoskisson, University of Strathclyde

Actinomycete bacteria represent up to 30% of the prokaryotic organisms in any niche on earth. They exhibit remarkable morphological and physiological diversity. Here I will report the duplication of a key metabolite responsive transcription factor, which has led to diversification and novel roles for each duplicate in the formation of spores in *Streptomyces*.

4:20 pm

Hacking the PDF/JPEG tree file format

Joseph Hughes, University of Glasgow

We have been illustrating the relationships between species and genes as trees for over a century. Whilst in the early years of morphological and molecular phylogenetics, embedding illustrations into manuscripts might have been the most appropriate way to disseminate knowledge, this has resulted in the locking up of phylogenetic hypotheses into the pages of journals and books without an easy way to access this information. As a result, most phylogenetic knowledge is lost upon publication. I will explain the reasons for re-using published trees, discuss ways to liberate this information and avoid these problems in the future.

4:40 pm

Exploring angiosperm pollen diversity in the context of molecular phylogenies

Alexandra Davey, Royal Botanic Garden Edinburgh

Recent advances in phylogeny reconstruction, microscopy and statistical techniques, make this an ideal time to explore morphological characters in the context of evolutionary relationships. This talk describes an ambitious, international study to investigate the diversity and evolution of pollen grain morphology in angiosperms, exploring potential methods and presenting preliminary results.

5:20 pm

Meeting ends

Speakers

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