Lancaster Spring Phylogenetics Conference 2014

incorporating

Scottish Phylogeny Discussion Group 6th Meeting

15th April 2014, Lancaster University

2pm: **Professor Eddie Holmes**, University of Sydney:
"The Greatest Experiment in Evolution: Viral Biocontrol of Rabbits"

3pm: **Tea/coffee**

3.30pm: **Dr Nick Goldman**, European Bioinformatics Institute:
"Molecular phylogenetics: can we do it better?"

4.15pm: **Professor David Robertson,** University of Manchester:
"Evolution of HIV-1 envelope drug resistance: use of the drug-bound CCR5-coreceptor versus coreceptor switching"

4.45pm: **Dr Rob Gifford,** University of Glasgow-MRC Centre for Virus Research:
"Origins and evolutionary history of the small ruminant lentivirus pandemic"

5.30pm: **Close**

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Talk abstract: Lancaster Spring Phylogenetics Meeting, 15 April 2014

http://eggg.st-andrews.ac.uk/spdg

The Greatest Experiment in Evolution: Viral Biocontrol of Rabbits

Edward C. Holmes

Marie Bashir Institute for Infectious Disease and Biosecurity, School of Biological Sciences and Sydney Medical School, The University of Sydney, Sydney, NSW 2006, Australia.

The wild European rabbit (*Oryctolagus cuniculus*) was successfully introduced into Australia in 1859. By the early 1900s rabbits had crossed the borders of all mainland states spreading at a rate of about 70 km a year, the fastest of any colonising mammal. By the 1950s there may have been more than one billion rabbits in Australia. The introduction of the rabbit has irrevocably changed the Australian landscape, significantly affecting both native flora and fauna. Rabbits have therefore been vigorously targeted through the deliberate introduction of two viral control agents: Myxoma virus (MYXV) was successfully released in Australia in the 1950s, while Rabbit Haemorrhagic Disease Virus (RHDV) escaped from quarantine field trials in 1995.

Through the application of genome-scale phylogenetic methods I will describe the patterns, processes and outcomes of these unique and grand-scale experiments in evolution. In particular, I will show how viral virulence has evolved in both cases (the example of MYXV in European rabbit is the canonical study of the evolution of virulence), and how phylogenetic methods provide a valuable insight into the genomic determinants of virulence evolution. In addition, phylogenetic analysis of the spread of both MYXV and RHDV in the Australian environment provides key information on the rates, patterns and dynamics of pathogen evolution in a naïve environment, and represents a powerful analogy to cases of disease emergence following cross-species virus transmission to a novel host.

I will close by discussing the possible evolutionary consequences of the next grand viral biocontrol experiment planned for Australia: the release of Koi herpesvirus (KHV) to control the common carp that was also introduced to Australia in the 19th Century.

David L Robertson
Computational and Evolutionary Biology,
Faculty of Life Sciences,
University of Manchester.

Evolution of HIV-1 envelope drug resistance: use of the drug-bound CCR5 coreceptor versus coreceptor switching

Entry-inhibitor molecules such as maraviroc are emerging as a potent class of antiviral-drugs. These differ from other HIV-1 drugs as they target the host cell coreceptor CCR5 as opposed to a virus protein. Lack of sensitivity to an entry-inhibitor occurs primarily through emergence of pre-existing viruses that use the CXCR4 coreceptor, while 'true' resistance occurs through use of the drug-bound CCR5 coreceptor. In this talk I will present molecular phylogenies that demonstrate these two types of resistance pathways. We have applied our methods to next generation sequencing data sets and are able to detect potentially resistant virus at extremely low frequency. Virus that has switched to using the CXCR4 coreceptor is readily detectable using genotypic algorithms. However, detecting resistant R5-tropic is extremely difficult due to a lack commonality in the specific sites conferring resistance in different patients. I will present the results of recombination analysis and coevolutionary analysis that help delineate the important regions for resistance and discuss the reasons for the unpredictable nature of envelope-mediated drug resistance.

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The SPDG was created in 2011 by a grant from the former Scottish Bioinformatics Forum and the former Centre for Evolution, Genes and Genomics at the University of St Andrews.

http://www.lancaster.ac.uk/50/
http://eggg.st-andrews.ac.uk/spdg/

Local organizers: Derek Gatherer & Catherine Pennington
SPDG organizer: Daniel Barker

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