

An International Symposium for biodiversity and bioGENESIS research

Organized by **Tetsukazu Yahara** and **Michael Donoghue**

November 1, 2006

Lecture room 3, Department of Biology, Kyushu University

Programme

- 10:30-10:50 **Tetsukazu Yahara** (Kyushu University, Japan)
Welcome address
- 10:50-11:10 **Motomi Ito** (University of Tokyo, Japan)
Molecular basis of innovative events in plant evolution
- 11:10-11:30 **Yoshihisa Shirayama** (Kyoto University, Japan)
Census of Marine Life: An international research project to assess the marine biodiversity
- 11:30-11:50 **Mutsumi Nishida** (University of Tokyo, Japan)
Reconstructing comprehensive molecular phylogenies
- 11:50-1:00 Lunch
- 1:00-1:20 **Hidenori Tachida** (Kyushu University, Japan)
Genetic diversity, its maintenance and evolution
- 1:20-1:40 **Joel Cracraft** (American Museum of Natural History, USA)
Linking rates of diversification to Earth history
- 1:40-2:00 **Rafael Zardoya** (Museo Nacional de Ciencias Naturales, Spain)
Molecular systematics of Metazoa
- 2:00-2:20 Break
- 2:20-2:40 **Susana Magallon** (Universidad Nacional Autonoma de Mexico, Mexico)
Angiosperm evolution from the point of view of floral morphology, timing and rate of diversification.
- 2:40-3:00 **Daniel Faith** (The Australian Museum, Australia)
Biodiversity, phylogeny, and the 2010 biodiversity target
- 3:00-3:10 **Elena Conti** (University of Zurich, Switzerland)
From the Mediterranean to the arctic through the Alps: an integrative perspective on the origin of biodiversity
- 3:10-3:30 Break
- 3:30-3:50 **Lúcia Lohmann** (Universidade de São Paulo, Brazil)
Untangling Diversity Patterns in Neotropical Lianas: A Phylogenetic Approach
- 3:50-4:10 **Christoph Hauser** (State Museum of Natural History, Stuttgart, Germany)
Biodiversity data for conservation – a new approach by the EDIT ATBI+M project
- 4:10-4:30 **Anne-Hélène Prier-Richard** (DIVERSITAS, Paris, France)
DIVERSITAS – International Programme of Biodiversity Science
- 4:30-4:50 Break
- 4:50-5:10 **Michael Donoghue** (Yale University, USA)
Explaining geographic gradients of species richness
- 5:10-5:20 **Tetsukazu Yahara** (Kyushu University, Japan)
Red Queen, speciation and biodiversity
- 5:20-6:00 Discussion
- 6:00-7:30 Mixer

Abstracts

Molecular basis of innovative events in plant evolution

Motomi Ito, University of Tokyo, Japan

The plants (land plants) are evolved from the ancestor of green algae, with several evolutionary innovations. We are now taking a comparative genomic strategy for understanding the evolution in the clade of Streptophyta (land plants + Charophyta), focusing major innovative events, such as evolution of multi-cell organism, differentiation of organs, and evolution of sporophytes.

Census of Marine Life: An international research project to assess the marine biodiversity

Yoshihisa Shirayama, Kyoto University, Japan

The Census of Marine Life is a ten-year initiative to assess and explain the diversity, distribution, and abundance of marine life in the oceans -- past, present, and future. It is also a growing global network of researchers in more than 70 nations engaged in. It consists of four major elements, i.e. History of Marine Animal Population to know the past of the ocean, 14 Field projects to understand the current status of marine life, Future of Marine Animal Population to predict the ocean to come, and Ocean Biogeography Information System to be database of all marine organisms. In this presentation, I will summarize the project with emphases on the relationships to the study of marine biodiversity.

Reconstructing comprehensive molecular phylogenies

Mutsumi Nishida, Ocean Research Institute, University of Tokyo, Japan

Our main area of research interest is the evolution of biodiversity in aquatic animals, mainly fishes. During these years, we have been trying to estimate reliable phylogenetic frameworks of ray-finned fishes, the largest group of vertebrates, by using large data sets of complete mitochondrial genome sequences. Resulting sequence data have been incorporated into a fish mitochondrial database (*MitoFish*) we developed, which provides a user-friendly platform facilitating mitochondrial DNA data search as well as fish species identification. My talk will present an outline of results of these works, emphasizing importance of comprehensive molecular phylogenies for analyzing and understanding biodiversity.

Genetic diversity, its maintenance and evolution

Hidenori Tachida, Kyushu University, Japan

Maintenance and evolution of the genetic diversity of species are affected by the geographical structure of the population, extents of selection, mutation and other genetic factors. Because such factors are considered to differ among species, we expect to find various patterns of genetic diversity in nature. In this talk, I summarize my research on several species in this respect and discuss how species-specific diversity patterns arise.

Linking rates of diversification to Earth history

Joel Cracraft, American Museum of Natural History, USA

Many causal explanations have been proposed regarding the rate-control of speciation. Current evidence suggests that most new species arise in allopatry in most groups of organisms, therefore it follows that the drivers of allopatry, to the extent we can identify them, would seemingly constitute something like a "null model" with which to examine alternative causal explanations of diversification. My talk will illustrate the ways in which the causal linkages between speciation and Earth history can be investigated by applying the most appropriate analytical tool, historical biogeographic analysis of basal taxonomic units (phylogenetic species). The primary example will show how mountain building, leading to vicariance and allopatry, is a primary first-order cause of diversification in South American and New Guinea birds.

Molecular systematics of Metazoa

Rafael Zardoya

Departamento de Biodiversidad y Biología Evolutiva, Museo Nacional de Ciencias Naturales, Madrid, Spain

We have a general interest in understanding the evolutionary mechanisms that are involved in the generation of animal biodiversity. Our research interests include (1) questions about the tempo and mode of DNA and amino acid sequence evolution, and (2) the establishment of phylogenetic relationships using molecular data sets. I will present an outline of our latest results in these two main lines of research, including the development of a bioinformatic tool to estimate best-fit models of amino acid evolution, and several phylogenies of vertebrates and mollusks based on complete mitochondrial genome sequence data.

Angiosperm evolution from the point of view of floral morphology, timing and rate of diversification.

Susana Magallon, Universidad Nacional Autonoma de Mexico, Mexico

My main research interests are (1) evolution of floral structure during the early diversification of eudicots (tricolpate angiosperms); (2) timing and rate of diversification of angiosperms and angiosperm clades; (3) the phylogenetic context and environmental correlations of plant biodiversity in Mexico.

Biodiversity, phylogeny, and the 2010 biodiversity target

Daniel Faith, The Australian Museum, Australia

Much of my research at the Australian Museum focuses on how we can use our valuable collections, and key products such as phylogenies, for biodiversity assessments. I also link my research to economics, policy, and other disciplines. As an example, I will describe our work exploring how biodiversity measures based on phylogenetic pattern may help us use the potential explosion of new data from DNA barcoding. Here, phylogeny may allow us to side-step endless debates about species definitions, and address quickly the major information gaps we face in biodiversity assessment. Noting that Japan is expected to host the 10th meeting of the Conference of the Parties to the Convention on Biological Diversity (COP10) in 2010, I will link this research to an important policy context: the 2010 biodiversity target for a significant reduction in the rate of loss of biodiversity • Some initial case studies suggest a pathway to actually achieving this difficult target.

From the Mediterranean to the arctic through the Alps: an integrative perspective on the origin of biodiversity

Elena Conti, University of Zurich, Switzerland

I will summarize my current projects on the origin of biodiversity in Mediterranean and arctic/alpine biota, which are characterized by very different environmental conditions and levels of species richness. Within the Mediterranean basin, I am studying the biogeography and diversification of plants endemic to the Corso-Sardinian microplate, because its geologic history is both complex and well-known, providing a temporal framework for hypotheses of vicariance, migration through land bridges, and over-water dispersal. For this project, I selected groups with rich fossil record and low dispersability of propagules, including endemics in Rutaceae, Araceae, and Boraginaceae. Within arctic/alpine plants, I am focusing on the patterns and processes of diversification in *Primula*, because of its high species number (425 spp) and alternation between distyly and homostyly. We are investigating the association between breeding systems, ploidy levels, and patterns of distribution in relation to the influence of Pleistocene glaciations. We also started to examine the diversity of floral scents in primroses and how they affect pollinators' floral constancy in connection to distyly. Within the Alpine mountain range, I am studying the origin of paleo- and neo-endemics in the Maritime Alps.

Untangling Diversity Patterns in Neotropical Lianas: A Phylogenetic Approach

Lúcia G. Lohmann, Universidade de São Paulo, Brazil

My primary interest is in understanding patterns of diversification in Neotropical lianas. I am currently working on the systematics, biogeography, ecology, and evolution of Bignoniaceae (Bignoniaceae), the most diverse group of lianas in the Neotropics. I have used a broad-scale phylogenetic framework to explore evolutionary explanations for contemporary patterns of morphological diversity in this group. I am now beginning to explore the broad patterns and respective underlying processes in more depth through analyses of smaller clades. My long-term goal is to use this liana group as a model to help evaluate patterns of geographic distribution and morphological diversity for lianas more generally and also other non self-supporting plants such as epiphytes and parasites. My talk will summarize some of my findings and future directions

Explaining geographic gradients of species richness

Michael J. Donoghue, Peabody Museum of Natural History, Yale University, USA

Why are there more species in some areas than there are in others? In part this has to do with where the lineage in question originated and how long it has occupied different areas (i.e., historical biogeography). But it also reflects shifts in the rate of diversification, either due to "key innovations" or to the extrinsic factors associated with different regions. I will briefly describe our attempts to sort out the relative importance of these factors in the plant clade Dipsacales.

Red Queen, speciation and biodiversity

Tetsukazu Yahara, Kyushu University, Japan

I briefly summarize my findings in three research topics. (1) Molecular divergence of geminiviruses infecting asexual populations of Eupatorium, (2) Molecular phylogeny of sexual and asexual lineages of Mexican Stevia, and (3) Patterns of species diversity in a local plant community. I will discuss a possibility to integrate community ecology with molecular phylogeny.

DIVERSITAS: International Programme of Biodiversity Science

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Plants, animals, their genetic diversity and their diverse habitats are being threatened as never before by factors such as habitat loss, overexploitation of resources or climate change—all of which result from human activities. These changes in biodiversity will have far-reaching and often unanticipated consequences on our Planet's life-support systems and on the services that humans derive from ecosystems.

DIVERSITAS provides an international framework for scientists around the world to address the questions posed by biodiversity loss.

The **missions** of DIVERSITAS are:

- Promote an integrative biodiversity science, linking biological, ecological and social disciplines in an effort to produce socially relevant new knowledge
- Provide the scientific basis for the conservation and sustainable use of biodiversity
- Draw out the implications for policies for conservation and sustainable use of biodiversity

DIVERSITAS seeks to

- Develop common international frameworks for collaborative research
- Form research networks to tackle focused scientific questions
- Promote standardised methodologies
- Guide and facilitate construction of global databases
- Facilitate efficient patterns of resource allocation, and undertake analysis, synthesis and integration activities on particular biodiversity themes
- Promote practical application of cutting-edge science to support policy and contributing to the Convention on Biological Diversity

DIVERSITAS Core Projects encourage global investigation of four key aspects of biodiversity research:

- *bioGENESIS*: To provide an evolutionary framework for biodiversity science
- *bioDISCOVERY*: To monitor biodiversity changes and understand the causes of these changes
- *ecoSERVICES*: To study the consequences of biodiversity changes for ecosystem functioning and for the delivery of ecosystem services
- *bioSUSTAINABILITY*: To guide policy and decision making that supports the conservation and sustainable use of global biodiversity

DIVERSITAS also coordinates four **Cross-cutting Networks** that focus on specific ecosystems or issues:

- *Global Mountain Biodiversity Assessment (GMBA)*: To explore and explain the great biological richness of the world's mountains
- *agroBIODIVERSITY*: To provide a common framework for biodiversity science within agricultural landscapes

- *freshwaterBIODIVERSITY*: To provide a common framework for freshwater biodiversity assessment
- *Global Invasive Species Programme (GISP)*: To conserve biodiversity and sustain human livelihoods by minimising the spread and impact of invasive alien species