

Abstracts

Plant genomics and gene expression: the Next Generation

David Galbraith

Plants comprise the foundation of all living organisms on this planet, a consequence of their exceptional ability to perform photosynthesis. Understanding plants is critical to the survival of the human race, and cytometry has a central role to play in this advancing this understanding. Urgency is increasingly provided given largely uncontrolled growth of the human population, the impact of which is resulting in the ongoing extinction of plant species. This talk will focus on the use of cytometry, first, to examine gene expression according to cell type and at the level of single cells, and as a means to provide a complete molecular census of the angiosperms, and, second, on the ways that Next Generation sequencing strategies can be integrated in addressing these goals.

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David Galbraith received his B.A., M.A. and Ph.D. degrees in Biochemistry from Cambridge University. His research interests include biological instrumentation, developmental and tissue-specific gene expression in eukaryotes, functional genomics and proteomics, and food safety issues. Dr. Galbraith was recently elected a Fellow of the American Association for Advancement of Science.

Reference-free Analysis and Comparative Genomics of Tropical Trees

Charles H. Cannon

Completing a reference genome requires a substantial investment and is best suited for the study of model species. For many ecological and evolutionary studies, a complete reference genome is not necessary. Additionally, tropical forests are dominated by diverse genera that often possess hundreds of closely-related species. What is the most effective way to study tropical biodiversity from a genomic perspective? In this talk, I will present an analytical approach that does not require a reference but instead directly compares short nucleotide diversity in many genomes and identifies regions of interest for further study, given a particular comparative question. The comparative genomics of tropical biodiversity will provide unique and powerful insights into diversification, speciation, and phenotypic adaptation. I will conclude with a few examples for further discussion.

Charles Cannon has been working in Southeast Asia since 1987. He has participated in a wide range of research projects and training programs . Currently, he is the P.I. of the Ecological Evolution Group at CAS-XTBG, and an Associate Professor at Texas Tech University. He has a wide range of research interests and currently his research group integrates ecological and evolutionary approaches with advanced DNA sequencing technology and GIS-based analyses to develop effective strategies for managing and conserving these megadiverse forests.

Attack of the “-Omics” : Anticipating the utilization of technological advance for the study and conservation of tropical forest

Chai-Shian Kua

In this era of “omics”, we have observed rapid technological advances in sequencing technology and genome level analyses. While these breakthroughs have already ushered in a new era of medical and agricultural research, many challenges remain for their application in non-model organisms, particularly for ecological and evolutionary questions. In this talk, I will briefly review the major genomic techniques and analyses used in well-studied organisms, like humans, and try and anticipate how we can most effectively transfer these approaches to tropical forest species. Also, possibly, how we might develop novel techniques to take advantage of some of the peculiar characteristics of highly diverse forests to better understand the genomic properties of biodiversity and possibly manage them more effectively in the future.

Chai-Shian Kua is currently an Assistant Professor of the Ecological Evolution Group, CAS-XTBG. She is interested in exploring the transfer of molecular biology techniques and technology in model systems to study non-model organisms. Currently, her research

focuses on using next gen sequencing data as a tool to survey the “genomic landscape” of non-model organisms (with a focus on tropical rainforest trees).

Ficus Biology

Rhett Harrison

Ficus, or the figs, is a diverse (ca. 750 spp.) pan-tropical genus, with diverse assemblages of species (up to ca. 80 spp.) throughout the tropics. Figs have long been identified as 'keystone' species in tropical forest ecosystems, as they provide food to a wide range of frugivores throughout the year and particularly during periods of food shortage, which helps maintain animal populations. Figs also possess a complex co-evolutionary relationship with their pollinators, the highly specialized fig-pollinator wasps (Agaoninae), and a diverse assemblage of non-pollinating fig wasps (other Chalcidoidea). These symbiotic relationships have been the focus of a large amount of research on evolutionary theory, such as Local Mate Competition and sexual dimorphism. Additionally, figs possess two main sexual systems: monoecy, where unisexual flowers of both sexes are found within the same synconium, and dioecy, where unisexual flowers of each sex are found on different plants. These sexual systems impose substantially different dynamics on population level gene flow, particularly in relation to effective population size. The genus has a greater diversity of plant growth forms including, shrubs, climbers, trees, and hemi-epiphytes, than any other, and is also an important component of forest succession in the tropics. This combination of features (high species richness, diverse co-evolutionary relationships, and diverse ecologies) makes Ficus an ideal model for comparative research.

Rhett Harrison is an associate professor of the Co-Evolution Group, CAS-XTBG. He is an expert of conservation biology, ficus ecology and evolution. He has directed numerous field courses throughout the Asian tropics.

Evolutionary Analysis As The Basis For Interpreting, Comparing, And Presenting Genomes: The GATOR And PHRINGE System

Jeffrey L. Boore

We anticipate a great acceleration in whole genome sequencing over the next few years. Current tools for interpreting, comparing, and presenting these data cannot handle the expected pace, lack integration, require extensive IT support and computational expertise, and do too little to facilitate biological discovery. In particular, the standard “browser” format is anachronistic, with the genome assembly, rather than the biological information, being the organizing principle. It requires great manual effort to identify any particular gene or biochemical pathway. Fortunately, two new developments are enabling a better approach. First, next generation sequencing technology allows very deep sequence coverage of the set of expressed genes. For example, 200-fold mean sequence coverage can be obtained on a typical transcriptome for under \$4,000. This means that genes can be modeled with much greater accuracy, so even the early stages of analysis can focus on biological discovery instead of manual gene curation. Second, we have

developed an effective tool (“PHRINGE”, for Phylogenetic Resources for Interpreting Genomes) for assigning orthologous and paralogous relationships among genes based on phylogenetic analysis of complete gene sets. In the absence of biochemical characterization, the best inference of gene function is by inferring that orthologous genes retain the same function. This is incorporated into the “GATOR” (Genome Analysis Tools and Online Resources) system under development, a “gene-centric”, user-friendly, streamlined approach to genome interpretation, comparison, and presentation. The entry point is the gene catalog itself, sortable by many categories, including domain content, intracellular location, SNP content, biochemical pathway, protein characteristics, number of members in any gene family, and many others. Users can view evolutionary trees, gene colinearity maps, and links to protein structures for all genes in multiple sequenced genomes.

Jeff Boore is an Associate Adjunct Professor at the University of California, Berkeley. He is also the Chief Executive Officer, Genome Project Solutions, Inc. His research centers on bringing high-throughput genomic techniques to questions of evolutionary biology, including reconstruction of the evolutionary history of all gene families in sequenced genomes (see <http://oomycetes.genomeprojectsolutions-databases.com/>), comparisons of mitochondrial and chloroplast genomes (e.g., using gene rearrangements as a character for reconstructing evolutionary relationships) and Hox gene clusters (e.g., identifying the phylogenetic footprint of gene regulatory signals).

Population genomics and adaptation from standing genetic variation

Christian Lexer

I will outline evolutionary genomic approaches to address the role of admixture in the origin of functionally relevant variation in plants. I will introduce our current model system for addressing these topics, *Populus alba* and *P. tremula*, two ecologically divergent, hybridizing Eurasian tree species related to *P. trichocarpa*, the first completely sequenced forest tree. I will cover studies of both, *intra*-specific admixture and its role in local adaptation, and *inter*-specific recombination and its impact on these species’ genomes. This will include both, established molecular ecology and “next generation” approaches based on Restriction site Associated DNA (RAD) and whole genome-resequencing. I will discuss how these approaches may be applied to evolutionary studies of non-model species in tropical or sub-tropical biodiversity hotspots.

Christian Lexer (CL)’s group is primarily interested in the genetics of plant adaptation, speciation, and of traits involved in range shifts. We study these phenomena using a combination of molecular ecology and evolutionary genomics approaches and experimental work. In previous projects, CL has contributed to several text book examples of the genomics of speciation in the face of gene flow. More recently, CL’s group has pioneered the use of genomic approaches to understanding the genetics of adaptation and speciation in natural hybrid zones of plants. Research in CL’s lab makes use of the model system

***Populus* and of other plant radiations in highly structured and species-rich environments in South America, Southern Africa and Southeast Asia.**

Sequencing Suids: the biogeographic component to the genomic variation landscape of *Sus scrofa* and related species revealed by whole genome re-sequencing.

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The pig (*Sus scrofa*) is among the most important domesticated animal species, and is subject of breeding for improved growth rates, feed conversion, meat quality, but also for enhancing animal welfare issues such as disease resistance and adapting to more animal friendly housing conditions. Breeding is done on standing variation, and for utilization of that variation it is of vital importance that it is adequately characterized and understood. While many studies have focused on genetic variation in pig and wild boar in the past decades, much remains unclear about the genomic variation landscape in the species. With current developments in Next-Gen sequencing, and with the genome of *Sus scrofa* to be published later in 2011, we now finally have the opportunity for a full characterization of variation in individual pig and wild boar genomes throughout its geographic range. In our project we aim to re-sequence up to 300 individual pigs, wild boar, and individuals from several other species of Suids, to address the questions above. Here we present preliminary analyses of the first 55 individuals that were sequenced at a sequence depth of 8 to 25x. To investigate the temporal component, we included whole-genome sequence data of several related species, such as *Sus celebensis*, *Sus verrucosus*, *Sus barbatus* and the African Warthog (*Phacochoerus africanus*). We investigated patterns of sharing of polymorphisms (single nucleotide polymorphisms – SNPs, copy number variants – CNV, and transposable elements) between species as a function of time and genomic recombination rates. Sequence divergence was found to be ~0.9% between *Sus scrofa* and the other species of *Sus*, and ~2% between *Sus* and African Warthog. Low level of SNP sharing was observed between species, with both sharing and degree of differentiation being positively correlated to genomic recombination rates.

Furthermore, the pigs and wild boar, sampled from the extremes of the distribution area (Europe and China), and representing two independent domestication events, were characterized for SNP variation within and between individuals, and between biogeographic areas. The biggest differences in SNP compositions was between the European and Chinese *Sus scrofa*, highlighting the importance of fully understanding the geographic component for animal

breeding and conservation. In addition, signatures of hybridization of European and Asian pigs were found, corroborating historical records that have suggested this to have happened in the 18th and 19th century. However, further investigation of the biogeographic component in East and Southeast Asia revealed that *Sus scrofa*, both wild and domesticated, showed various genomic regions with contradictory coalescent patterns. These contradictory patterns demonstrate both the importance for good understanding of the biogeography as well as sequence-based, whole genome characterization of variation to fully understand patterns of variation in the domesticated species.

Hendrik-Jan Megens is a member of the Groenen lab at The Animal Breeding and Genomics Center, Wageningen University, Wageningen, Netherlands. He was instrumental in the development of a high-density SNP chip for *Sus scrofa*, which has been used as a platform for biodiversity studies of wild and domesticated *Sus scrofa*.

Adaptive Evolution in Louisiana Irises: Phenotype to Genetics to Genomics and Back Again

Mike Arnold

In this talk, I will illustrate the development of one plant species complex, the Louisiana Irises, into a ‘model system’ for investigating hybrid fitness and the role of genetic exchange in adaptive evolution and diversification. In particular, I will argue that a multitude of approaches, involving both experimental and natural environments, and incorporating both manipulative analyses and surveys of natural populations, are necessary to adequately test for the evolutionary significance of introgressive hybridization. An appreciation of the variability of hybrid fitness leads to the conclusion that certain genetic signatures reflect adaptive evolution. Finally, I will discuss some of the newer experiments our group is establishing using a variety of genomic and transcriptomic approaches to decipher the basis of reproductive isolation and adaptation.

Members of Mike Arnold’s lab have tested evolutionary hypotheses in a wide array of organisms – including fungi, plants and animals. In spite of the taxonomic diversity reflected in this work, there is a unifying theme. This theme is well described by the title of a 1954 *Evolution* paper authored by the plant evolutionary biologists, Edgar Anderson and Ledyard Stebbins – “Hybridization as an Evolutionary Stimulus”. Thus, our group has examined a range of phenomena associated with the process of gene exchange between organisms in nature. The data collected have derived from analyses of population genetics, phylogenetics, reproductive biology, pollinator behavior, eco-physiology, molecular evolution and, most recently, linkage/QTL mapping of fitness traits.