Systematics & biogeography of sawflies

Spencer K. Monckton
Ph.D. Candidate
York University, Toronto, Canada

• Taxonomy of North American Pristiphora
• Phylogenetics & biogeography across Holarctic
• Patterns of diversity & post-glacial recolonization in Northern North America
• Phylogeography using hyRAD

Why are sawflies so diverse at higher latitudes?

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Molecular Evolution of Stomatal Regulation and Guard Cell Metabolism in Crassulacean Acid Metabolism (CAM) Plants

Daniel Cowan-Turner, Maxim Kapralov, Anne Borland

~6 Fold improvement in WUE

Adapted from Yang et al. (2015)

Heyduk et al. (2019)
Detection of LGT within bacterial species

Jackie Purdue

Investigating methods to quantify LGTs in a setting with little phylogenetic signal

Branches with low support

Many identical sequences

Thousands of Salmonella isolates

Pangenome analysis

Species Tree

Gene Trees

LGT inference

35%
91%
33%
96%
91%
33%
100%
100%
100%
Carbohydrates
Lipids
Proteins
attine ants fungus garden
Ants-Cultivar
50 Millions Years of covevolution

Parasite
Escovopsis

Analysis with three markers

Analysis with Five markers

Escovopsis

New Genus
?

New Genus
?

New Genus
?

New Genus
?

New Genus
?

Quimi V. Montoya
Department of Biochemistry and Microbiology, São Paulo State University, Sao Paulo, Brazil.
Department of Biology Emory University, O. Wayne Rollins Research Center, Atlanta, USA.
Parallel evolution of the aphid male wing polymorphism

Characterizing patterns of wing evolution
- Does wingedness evolve repeatedly?
- What impact do ecological and life history traits have?
- Are there multiple transitions?

What are the evolutionary dynamics that govern the male polymorphism?

Omid Saleh Ziabari, PhD Candidate
University of Rochester

Pea Aphid

**Winged**  **Wingless**  **Dimorphic**
Marjan Sadeghi
Ph.D. Candidate, Scientific Computing Department
Florida State University

Current Project:
- Modeling Biological Events Along the DNA Sequence Using Point Processes: Recombination Hotspots Motif Occurrences
- Estimating Population Genetic Parameters Using Coalescent with Recombination Hotspots
**Question:** What are the host-symbiont evolutionary patterns of *Bembidion* beetles and *Wolbachia* bacteria?
Transmission, ecological, geographic traits

Collaborator: David Maddison, Oregon State University

What I hope to learn: co-phylogenies and how to analyze heterogeneous infections within some hosts

20-70% of insects
Parasitic infection
Transmitted via egg
Reproductive barrier

Maddison, 2012, *Molec Phylogen & Evol*
1,200 *Bembidion* spp.
Predators
Elucidating the genome structure and phylogenetic position of Metamonada

Evan Mee
PhD student in Evolutionary Biology
Advised by Dr. Gillian Gile
Arizona State University
Genome evolution in Karyorelictea (ciliates)

Ying Yan, Postdoc
Katz lab, Smith College

- Uncultivable ciliate, “karyo-relict”
- ‘Omics: gene family evolution, genome rearrangements
- Confocal microscopy: “aging” nuclei

Cartoon of inferred genome structures

Karyorelictea have lower transcript diversity (aka paralogs) than other ciliates
Phylogenetics and Phylogeography of *Cercopithecus mitis* (Blue Monkey)

Research Interests:
- Phylogenetic analyses of mitochondrial genome
- Variation and relatedness among populations of *mitis*
- Biogeography and phylogeography
**Question:**
• How do these structurally similar voltage-gated ion channels give rise to their distinct functional behavior?

**Plan:**
• Combine ancestral protein reconstruction of HCN1 and EAG1 with electrophysiological techniques

Modified from John Cowgill et al. PNAS 2019;116:2:670-678
Modified from https://watchlearnlive.heart.org/index.php?moduleSelect=arrhyt
Alex Lewanski

Institution: University of Wyoming (Lab of Dr. Catherine Wagner)

Primary Interests:
- Genomics of speciation
- Community phylogenetics
Elisa Maria Costa-Paiva, PhD
University of Sao Paulo, Brazil
Postdoc Researcher

Physiology of Ediacaran-Cambrian modern analogues
- Interface of molecular evolution and geosciences
- Proteomic and gene expression
- Simulation chambers

Evolutionary history of oxygen-binding proteins
- Blood pigments
- Protein timetrees
- Early animals respiratory physiology

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Erik Tamre
PhD student at MIT with Greg Fournier

Current research: **phylogenetic history of cyanobacterial UV-tolerance**

Generally: Interaction of life and physical environment over geological timescales

Vincent et al. (2004), Lyons et al. (2014)
Life history evolution of brittle stars

Nicole Nakata
PhD Student
Advisor: Dr. Richard Emlet

Phylogenetic revision of Ophiuroidea

Evolution of nonfeeding, direct developing larval types
Research interest:

Evolution of regulatory and protein coding sequences of genes involved in skeletal muscle development in vertebrates

**Chicken embryo electroporation**  
*(in vivo assay to the activity of regulatory elements)*
Bacterial leaf spot of tomato and pepper (BLS)

- *Xanthomonas perforans*
- *Xanthomonas euvesicatoria*

How are demographic processes influencing the presence and distribution of virulence determinants in BLS pathogens?

Evolutionary history
- Genome plasticity
- Recombination

Host-pathogen interactions
- Host specificity and virulence

Molecular and population biology approach
Entomological Intelligence

Silvia Andrade Justi
National Research Council Research Associate
The Walter Reed Biosystematics Unit
Smithsonian Institution - Museum Support Center
Walter Reed Army Institute of Research

*Aedes vexans*

Dermacentor variabilis, a.k.a. "American Dog Tick"

Triatoma dimidiata, a.k.a. "Kissing Bug"
Andressa Paladini from Brazil

Entomologist - spittlebugs

Finished my PhD in 2012 – spent one year in US (New York State Museum)

Got a job position in 2016

Lab of Systematic, Entomology and Biogeography

Establish a research line

Improve my knowledge, interact and establish collaborations

Contact: andri.paladini@gmail.com
My name is Kip Lacy. I’m currently interested in changes to the substrate of natural selection.
1. **Measure and map heterogeneity of recombination within different bacterial species**

   - Identify hyper-donating/receiving organisms
   - Explore frequently recombining genes
   - Track trends with metadata

2. **Nitpick all of it!**

   - Study spread of AB-resistance/virulence genes
   - Enhance understanding of mechanics behind HGT and recombination

3. **Solve Problems**

   - Study spread of AB-resistance/virulence genes
   - Enhance understanding of mechanics behind HGT and recombination

4. **Do it all over again within communities**
What are the mechanisms suppressing selfish chromosome segregation in female mammalian meiosis?

1. Asymmetric meiotic division of female gametes allows selfish chromosome segregation (meiotic drive)

2. Rapidly evolving centromeric DNA highjacks meiotic division

3. Rapidly evolving centromeric proteins may suppress selfish chromosome segregation

Finding rapidly evolving centromeric proteins

Generation of species-specific alleles

Molecular Evolution

Cell Biology

Oocyte microinjection and microscopy

Mouse-related species

Mouse egg

Rat_Sgo2

Chromosomes

Molecular Biology

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Oocyte microinjection and microscopy
Developing statistical methods to infer infectious disease virulence from complex phenotypes.
Evolutionary study of the functional switch in eukaryotic CLC proteins

Eva Fortea (PhD student)
Physiology and Biophysics Dept. at Weill Cornell Medicine
Interests: Protein evolution, Biochemistry and Biophysics

Questions: Why do some CLCs work as Channels and others as Transporters?
Approach: Bioinformatics combined with Biochemical and Biophysical characterization of ancestral proteins
Daniel Castaneda Mogollon
Microbiology & Infectious Diseases

What I do:
- Study of haplotypes and SNPs across Plasmodium species (mostly \textit{P. falciparum}) for diagnostics purposes of ‘common’ and treatment – resistant strands across symptomatic and asymptomatic cases.

What my research interests are:
- Be proficient in wet lab and bioinformatics analysis.

Purpose:
- To provide significant insight to the scientific community that could improve the life quality of individuals suffering from malaria and emerging diseases.

\begin{align*}
P. \textit{falciparum} & \quad \text{Treatment} \quad \text{P. \textit{falciparum}} \\
P. \textit{falciparum} & \quad \text{JF681166} \\
P. \textit{falciparum} & \quad \text{KJ170101} \\
P. \textit{falciparum} & \quad \text{JQ627151} \\
\end{align*}
Susette Castañeda Rico
Postdoctoral Research Fellow
Center for Conservation Genomics
George Mason University

Mitogenomes
UCEs
SNPs

Ancient DNA

Phylogenetics
Population genetics
Biogeography

• Evaluate phylogenetic relationships within and among species
• Biogeographical analyses to understand whether distributional patterns of (Foxes and rodents) coincide with widely known biogeographical patterns.
African Amphibian Diversification

Greg Jongsma

I am interested in understanding the process that drive and maintain patterns of diversity in Central Africa.

I am taking a comparative phylogeographic approach with 9 species of co-distributed frogs to test different diversification hypotheses. I will use ddRADseq data to test the following demographic scenarios:

River Barrier Hypothesis: a general allopatric model of population splitting with no gene flow (except at the headwaters). Population boundaries are delimited by rivers.

Pleistocene Forest Refugia Hypothesis: allopatric divergence in which population isolation is followed by size expansion and secondary contact. Genetic diversity will be highest at refugia and lesser outside in the intervening areas.

River-Refugia Scenario: allopatric divergence in which population isolation is followed by size expansion. Genetic diversity will be highest at river tributaries with relief. Distinguishable from PFR if populations are more similar within the same watershed than with any other watershed, regardless of geographic distance.

I have ddRADseq data for 430 frogs.
Human Life support systems
Controlled system for advanced monitoring of human subjects (and/or full recycling required for space colonies).

Research interests:
● Environmental Heterogeneity
● Epigenetic Inheritance
Paulo Manrique Valverde  
Msc. Biochemistry and Molecular Biology, UPCH-Perú.

1. Transmission surveillance.

2. Distribution and dispersion patterns of parasite populations.  
   - Identification of endemic areas and contact zones of dispersion (Malaria corridors).  
   - Distribution and dispersion of resistant parasites.

3. Identification of risk factors of malaria transmission.

4. Reconstruction of the transmission tree.

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Population genetics and molecular epidemiology of *Plasmodium* spp.

- OR = 4.33 Travel in the last month, p = 0.04
- OR = 3.35 Live with someone who has traveled in the last month, p = 0.05*
- OR = 3.65 Presence of symptoms, p = 0.03
- OR = 1.1 parasitaemia, p = 0.04
- OR = 4.33 Travel in the last month, p = 0.04
- OR = 3.35 Live with someone who has traveled in the last month, p = 0.05*
- OR = 3.65 Presence of symptoms, p = 0.08*
- OR = 6.42 Fishing in the last month, p = 0.1

*Living with someone who has left the community in the last month (OR = 4.48, p = 0.01) increased the probability of presenting symptoms.