THOMAS JOSHUA MEYER

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SUMMARY

- Postdoctoral Researcher, Lab of Dr. Lucia Carbone (Department of Behavioral Neuroscience, Oregon Health and Science University)
- Ph.D., Lab of Dr. Mark Batzer (College of Science, Louisiana State University)
- Experience with a broad array of computational, molecular, and field biological techniques
- Diverse teaching experience and student mentoring
- Proven track record of problem-solving and team-building

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher (Oregon Health and Science University): Dec. 2011 – Present
- Advisor: Dr. Lucia Carbone
- Bioinformatics support for ongoing comparative genomics projects
- Repetitive element detection and phylogeny derivation from next-gen data
- Installation and administration of bioinformatics Linux server

Postdoctoral Associate (Louisiana State University): Jan. 2011 – Dec. 2011
- Advisor: Dr. Mark Batzer
- Bioinformatics support for ongoing comparative genome projects
- Repetitive element detection and phylogeny derivation from next-gen data
- Installation and administration of Illumina GAIIx Linux server
- Training and supervision of undergraduates

Co-Instructor (Louisiana State University): Spring 2011
- Team taught Human Molecular Genetics (BIOL 4753) with Dr. Mark Batzer

Graduate Teaching Assistant (Louisiana State University): 2005 – 2010
- Human Molecular Genetics (BIOL 4753) – Dr. Batzer, 3 semesters (2007, 2009, & 2010)
- Microbiology Lab for Majors (BIOL 2051) – Dr. Brininstool, 6 semesters (2008 – 2010)
- Introductory Biology Lab for Majors (BIOL 1209) – Dr. Wischusen, 4 semesters (2005 – 2007)
- Evolution (BIOL 3040) – Dr. Pollock, 1 semester (Spring 2005)

Graduate Mentor (Louisiana State University): Aug. 2008, 2009, & 2010
- Supervisor: Dr. Wischusen
- BIOS: Biology Intensive Orientation for Students
- Mentor for incoming undergraduate Biology majors

Instructor: 2002 – 2004
- Supervisor: Dr. David Rodvien, Remington College, Mobile, AL
- Designed and taught courses on Anatomy & Physiology, Communications, and Ethics

Teacher: Spring 2002
- Employer: Alabama School of Math and Science, Mobile, AL
- Designed and taught lecture, lab, and field components of Field Botany course

Lab Instructor (University of South Alabama): 2000 – 2002
- Introductory Biology Lab for Majors (BLY 121 & 122) – Dr. Freeman
- Introductory Biology Lab for Non-Majors (BLY 101 & 102) – Dr. Freeman
- Anatomy and Physiology I (BLY 151) – Dr. Shardo
- Earth History (GY 112) – Prof. Davis

Research Technician (University of South Alabama): 1997, 1999 – 2001
- Advisor: Dr. David Nelson
- Field research studying Alabama redbelly turtle life history, loggerhead sea turtle nesting, coastal bird nesting, and riverine and estuary fish communities
- Maintenance and piloting of research boats and off-road vehicles, deployment and repair of traps, species identification, and collection of morphometric, feeding, radio telemetry, and nesting data

EDUCATION

Ph.D. Biological Sciences: Louisiana State University, College of Science (2005 – 2010)
- Advisor: Dr. Mark Batzer
- Retrotransposon-mediated genomic dynamism
- Computational data mining and analysis of retrotransposons in primate genomes
- Characterization of variant twin-priming retrotransposon insertion mechanism
- *Alu* element-based phylogenetic reconstruction of gibbons

B.S. Biology: University of South Alabama, College of Arts and Sciences (1994 – 1999)
- Undergraduate Advisor: Dr. David Nelson
- Life history of the Alabama redbelly turtle
- Nesting study of the loggerhead sea turtle
- Myology and osteology of the forelimb of the Florida manatee

PROFESSIONAL SKILLS

Laboratory Techniques:
- PCR
- Gel electrophoresis
- Gel extraction
- Transformation, cloning, and colony PCR
- DNA sequencing

Computational Techniques:
- System Administration: Linux, Windows, MacOS X
- Programming languages: Perl, Shell scripting
- Administration and installation of RepeatMasker analysis suite
- Whole-genome repetitive DNA annotation
- Orthologous sequence retrieval and analysis (BLAT, LiftOver, custom Perl scripts)
- Primer design
- Multiple sequence alignment creation and editing
- Molecular evolution analyses (MEGA, ClustalX/W, Arlequin, custom Perl scripts)
- Phylogenetic Tree Building (Mesquite, PAUP*)
- Motif-based analysis using custom Perl scripts
- Mapping and annotation of sequence data to Genome Browser (UCSC) and Galaxy
- Next-gen sequencing data analysis

PROFESSIONAL SERVICES

- Website development, design, and content management – Batzer Lab, http://batzerlab.lsu.edu/
- Server and personal workstation acquisition, configuration, administration, and maintenance – Batzer Lab, LSU
- Illumina server administration – Genomics Facility, Scott Herke, LSU
- Undergraduate and Graduate training and mentoring
- Community outreach and education – Museum of Natural History, LSU

PUBLICATIONS

Meyer, T. J., A. T. McLain, J. M. Oldenburg, C. Faulk, M. G. Bourgeois, E. M. Conlin, A. R. Mootnik, P. J. de Jong, C. Roos, L. Carbone, and M. A. Batzer. (2012) An *Alu*-based phylogeny of gibbons (Hylobatidae). *Mol. Biol. and Evol*. **29**: 3441-3450. **HTML PDF**

A. T. McLain, **T. J. Meyer**, C. Faulk, S. W. Herke, J. M. Oldenburg, M. G. Bourgeois, C. F. Abshire, C. Roos, and M. A. Batzer. (2012) An *Alu*-based phylogeny of the lemurs (Infraorder: Lemuriformes). *PLoS ONE* **7**: e44035. **HTML PDF**

Lee, J., S. Mun, **T. J. Meyer**, and K. Han. (2012) High levels of sequence diversity in the 5' UTRs of human-specific L1 elements. *Comparative and Functional Genomics* **2012**: 129416. **HTML PDF**

Meyer, T. J.*, D. Srikanta*, E. M. Conlin, and M. A. Batzer. (2010) Heads or tails: L1 insertion-associated 5' homopolymeric sequences. *Mobile DNA* **1**: 7. **contributed equally.* **HTML PDF**

Lee, J., K. Han, **T. J. Meyer**, H.-S. Kim, and M. A. Batzer. (2008) Chromosomal inversions between human and chimpanzee lineages caused by retrotransposons. *PLoS ONE* **3**: e4047. **HTML PDF**

Han, K., J. Lee, **T. J. Meyer**, P. Remedios, L. Goodwin, and M. A. Batzer. (2008) L1 recombination-associated deletions generate human genomic variation. *Proc. of the Natl. Acad. of Sci., USA* **105**: 19365-19370. **HTML PDF**

Han, K.*, J. Lee*, **T. J. Meyer**, J. Wang, S. K. Sen, D. Srikanta, P. Liang, and M. A. Batzer. (2007) *Alu* recombination-mediated structural deletions in the chimpanzee genome. *PLoS Genetics* **3**: 1939-1949. **HTML PDF**

Han, K.*, M. K. Konkel*, J. Xing*, H. Wang*, J. Lee, **T. J. Meyer**, C. T. Huang, E. Sandifer, K. Hebert, E. W. Barnes, R. Hubley, W. Miller, A. F. A. Smit, B. Ullmer, and M. A. Batzer. (2007) Mobile DNA in Old World monkeys: a glimpse through the rhesus macaque genome. *Science* [cover article] **316**: 238-240. **HTML PDF**

Nahum, L. A., M. T. Reynolds, Z. O. Wang, J. J. Faith, R. Jonna, Z. O. Jiang, **T. J. Meyer**, and David D. Pollock. (2006) EGenBio: a data management system for evolutionary genomics and biodiversity. *BMC Bioinformatics* **7** (Suppl 2): S7. **HTML PDF**

Nelson, D. H. and **T. J. Meyer**. (2001) Nesting of the loggerhead sea turtle (*Caretta caretta*) on Dauphin Island, Alabama. *J. of the Alabama Acad. of Sci.*, **Jan. 1, 2001**.

MEMBERSHIPS, HONORS, AND AWARDS

2009 – Present	AAAS Member
2005 – 2009	Vice Chancellor's Graduate Enhancement Award ($20,000 over 4 years), LSU
2009	Graduate School Travel Award ($350), LSU
2009	BioGrads Travel Award ($300), LSU
2009	BioGrads Research Award ($300), LSU
Spring 2007	Research Assistantship provided by Dr. Batzer, LSU
1999 & 2001	Alabama Academy of Science
1997	Outstanding Freshman of the Year, Dept. of Geology, U. of South Alabama
1994 – 1998	Presidential Scholarship, U. of South Alabama

ACADEMIC PRESENTATIONS

May 8–12, 2012	An *Alu*-based Phylogeny of Gibbons (Hylobatidae) (*Poster*) Cold Springs Harbor Laboratory Biology of Genomes Meeting. Syosset, NY.
Aug. 11, 2011	Gibbon (Hylobatidae) Phylogeny Through the Lens of Mobile Elements (*Presentation*) FASEB Summer Conference on Mobile Elements in Mammalian Genomes, Snowmass, CO.

Mar. 11, 2011	Study in Primate Evolution: Constructing a Gibbon Phylogeny Using Mobile Genetic Elements (*Presentation*) Department of Geography and Anthropology Friday Forum. LSU, Baton Rouge, LA.
Nov. 13, 2009	The 5' Stretch: Simple T Repeats Found at the Ends of Retrotransposon Insertions (*Poster*) BioGrads Symposium. LSU, Baton Rouge, LA.
Jul. 5 – 10, 2009	The 5' Stretch: Simple T Repeats Found at the Ends of Retrotransposon Insertions (*Poster*) FASEB Summer Conference on Mobile Elements in Mammalian Genomes. Snowmass, CO.
Nov. 7, 2007	The Use of SINEs in Phylogenetics and Population Analyses (*Presentation*) BioGrads Symposium. LSU, Baton Rouge, LA.
Sep. 17, 2007	Genomic Fluidity Through Recombination: How Mobile Elements Have Shaped the Genome (*Presentation*) Graduate Seminar. LSU, Baton Rouge, LA.
Oct. 22, 2005	Snakes: Nature's Most Misunderstood Children (*Presentation*) Snakes Alive! Program. LSU, Baton Rouge, LA.
Mar. 2001	Hoop Trap Survey of Freshwater Fish Communities Along Coastal Alabama (*Presentation*) Meeting of the Alabama Academy of Science.
Mar. 1999	Myology and Osteology of the Forelimb of the Florida Manatee (*Trichechus manatus latirostris*) as Revealed by Computerized Tomography and Magnetic Resonance Imaging Scans (*Presentation*) Meeting of the Alabama Academy of Science.

RESEARCH SUMMARY

My research has focused on the effects that the proliferation of two retrotransposon families, LINE-1 and *Alu* elements, have had on the primate genomes in which they have proliferated. While initially learning the basics of this field, I was part of a team of researchers that characterized the mobile DNA content of the then-newly sequenced rhesus macaque genome, a project during which I learned the value of computational skills. I further developed these skills in continued projects with my collaborators that investigated several mechanisms by which non-allelic homologous recombination between mobile element insertions produce deletions, duplications, and inversions. Next, I helped lead a team that unraveled the possible mechanisms behind the origins of an unusual subpopulation of L1 insertions found throughout the primate order. We computationally data mined all available primate genomes to screen for the non-canonical genomic architecture we had observed, and then characterized the insertions using molecular techniques. My current projects include the use sequencing data and orthologous genomic comparisons to detect lineage-specific *Alu* element insertions among both gibbons (Hylobatidae) and lemurs (Lemuriformes). These insertions are then used to generate robust phylogenies of these groups.

REFERENCES

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