

Report from the First Snake Genomics and Integrative Biology Meeting

Todd A. Castoe^{1†}, Edward L. Braun², Anne M. Bronikowski³, Christian L. Cox⁴, Alison R. Davis Rabosky⁵, A.P. Jason de Koning¹, Jason Dobry⁶, Matthew K. Fujita^{7,4}, Matt W. Giorgianni⁸, Adam Hargreaves⁹, Christiaan V. Henkel¹⁰, Stephen P. Mackessy¹¹, Denis O'Meally¹², Darin R. Rokyta¹³, Stephen M. Secor¹⁴, Jeffrey W. Streicher⁴, Kenneth P. Wray¹³, Ken D. Yokoyama¹, and David D. Pollock¹

¹Department of Biochemistry & Molecular Genetics, University of Colorado School of Medicine, Aurora, CO, USA

²Department of Biology, University of Florida, Gainesville, FL, USA

³Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA, USA

⁴Department of Biology, University of School of Biological Sciences, University of Northern Colorado, G

A community using snakes as model systems

Snakes are gaining importance as model systems for a diversity of research. They are valued models for studying extreme physiological and morphological plasticity, evolutionary ecology, molecular evolution, developmental biology, and venom evolution. Despite the importance of snakes as models for basic and biomedical research, there is little known about the genomes of snakes, and there are minimal genomic resources currently available. These limitations, however, will soon be lifted as numerous groups are making progress in establishing complete snake genomes and genomic resources, thereby enabling numerous new areas of research utilizing snakes.

The first Snake Genomics and Integrative Biology meeting was held October 5-8, 2011 in Vail, Colorado USA to bring together an international collection of researchers from diverse backgrounds that share a common interest in snake genomics and comparative biology. A core aim of the meeting was to showcase ongoing and potential projects that utilize (or aim to utilize) snake genomic and transcriptomic data for integrative and comparative biology. The meeting was organized around the goals of catalyzing collaborative research, identifying shared interests in research and data collection, and coordinating among research groups to maximize scientific impact, collaboration, fundability,



Snake (*Sonora semiannulata*). They then presented an ongoing transcriptomics project to identify expression differences of color genes in multiple color morphs of mimetic species across the snake radiation. These comparative genomic and transcriptomic projects will be key to identifying the genes that underlie color pattern in snakes, furthering our understanding of how and why color pattern evolves over time and space. Jeffrey Streicher (University of Texas at Arlington, USA) discussed the difficulties in identifying evolutionary lineages and population differentiation in brightly colored coral snakes from the United States and Mexico. He demonstrated the use of next-generation sequencing to identify microsatellite loci rapidly, and by combining these data with DNA sequences, venom variation, and morphological data, was able to better define evolutionary lineages in these venomous snakes.

Anne Bronikowski (Iowa State University, USA) presented data for the differential life history patterns among proximal populations of garter snakes, and how she was using these to study the tradeoffs between and consequences of these strategies at the molecular level using transcriptomic data. Stephen Secor (University of Alabama, USA) discussed the adaptive rela-