BIOGRAPHICAL SKETCH
Junior Trainer

NAME: Bret A. Payseur

eRA COMMONS USER NAME: PAYSEUR

POSITION TITLE: Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Colorado, Boulder	B. A.	05/1996	Molecular, Cellular, and Developmental Biology; Anthropology
Northwestern University, Chicago	M. S.	05/1998	Evolutionary Biology
University of Arizona	Ph. D.	12/2003	Ecology and Evolutionary Biology
Cornell University	Postdoctoral	05/2005	Population Genetics

A. Personal Statement

Members of my lab use genetics and genomics to understand mechanisms of evolutionary change. Topics of particular interest include speciation, evolution of the meiotic recombination rate, extreme phenotypic evolution in island populations, and population genetics when the mutation rate is high. I offer a stimulating training environment with the following features: (1) weekly one-on-one meetings in which students articulate and benchmark research and training goals; (2) opportunities to meaningfully integrate and synergize computational biology with data collection at the bench; (3) interaction with leaders in statistical genetics through collaboration; (4) an emphasis on conceptual understanding, including the history of scientific ideas; (5) guidance specifically tailored to each student; (6) annual participation in national scientific meetings; (7) weekly lab meetings to discuss research and literature. I devote most of my time and effort to training graduate and postdoctoral students. Among the four graduate and two postdoctoral students to graduate from my lab, four are faculty members at universities, one is a postdoctoral student, and one leads a research team at a biotechnology company.

B. Positions and Honors

Positions and Employment

2004-2005 Postdoctoral Research Associate, Department of Molecular Biology and Genetics, Cornell University (Advisor: Andy Clark)
2005-2011 Assistant Professor, Laboratory of Genetics, University of Wisconsin – Madison
2011-2016 Associate Professor, Laboratory of Genetics, University of Wisconsin – Madison
2016- Professor, Laboratory of Genetics, University of Wisconsin – Madison

Other Professional Experience

2011- Associate Editor, *PLoS Genetics*
2011- Associate Editor, *Genetics*
2011, 2014 Advisory Panelist, NIH Genetic Variation and Evolution
2009, 2014 Advisory Panelist, NSF Evolutionary Genetics
2013 Co-Organizer (with Karl Broman), Complex Trait Community Annual Meeting
2016 Co-Organizer, Genetics Society of America 100th Anniversary Meeting

Honors

2006	University of Wisconsin Medical Education and Research Committee New Investigator Award
2007, 2008	David and Lucile Packard Foundation Fellowship Finalist
2011	U. S. National Academy of Sciences Frontiers of Science Invited Participant
2016	University of Wisconsin Vilas Faculty Mid-Career Award

C. Contribution to Science

1. Speciation – the process through which one species becomes two – is a primary determinant of biodiversity. Using closely related subspecies of house mice as model systems and a diverse array of approaches, I have made several influential contributions to the field of speciation. In my dissertation research, I was the first person to use patterns of gene flow in a natural hybrid zone to pinpoint genomic regions involved in reproductive barriers between nascent species. This approach has since been used to identify genetic determinants of speciation in a variety of organisms. With my graduate student Michael White, I demonstrated dramatic, fine-scale variation in the phylogeny of subspecies across the entire genome. This result vividly shows that accurate phylogenetic inference in closely related groups requires consideration of loci from throughout the genome. In a rare evolutionary comparison of the genetic architecture of a major reproductive barrier, White and I discovered that the genetic loci responsible for hybrid sterility differ between two pairs of subspecies, despite their recent divergence time. This finding demonstrates the power of comparative genetic mapping, an approach I have taken a lead in advocating. My postdoctoral student, Leslie Turner, and I showed that the same genomic regions that confer hybrid sterility phenotypes also control global patterns of gene expression. This was the first time genome-wide patterns of gene expression and genetic mapping had been combined to understand the process of speciation.

Payseur, B. A., J. G. Krenz, and M. W. Nachman (2004). Differential patterns of introgression across the X chromosome in a hybrid zone between two species of house mice. *Evolution* 58:2064-2078.

White, M. A., C. Ané, C. N. Dewey, B. R. Larget, and **B. A. Payseur** (2009). Fine-scale phylogenetic discordance across the house mouse genome. PLoS Genetics 5: e1000729.

White, M. A., M. A. Stubbings, B. L. Dumont, and **B. A. Payseur** (2012). Genetics and evolution of hybrid male sterility in house mice. Genetics 191:917-934.

Turner, L. M., M. A. White, D. Tautz, and **B. A. Payseur** (2014). Genomic networks of hybrid sterility. PLoS Genetics 10:e1004162.

2. Most population genetic theory and analysis assumes that mutation rates are low, but genomes are littered with rapidly mutating variants. Using microsatellites as a model, I developed a combined empirical and theoretical framework for understanding variation at loci that mutate rapidly and recurrently. I described the landscape of microsatellite variation in an unbiased manner and discovered a complex relationship between microsatellite variation and single nucleotide polymorphism (SNP) across the human genome. With graduate student Ryan Haasl, I developed the first quantitative model of the fitness surface of a microsatellite with realistic mutational characteristics. This advance paves the way for the characterization of natural selection targeting microsatellites from patterns of variation, a goal whose importance is evidenced by the known roles of microsatellites in severe diseases and phenotypic evolution.

Payseur, B. A., M. Place, and J. L. Weber (2008). Linkage disequilibrium between STRPs and SNPs across the human genome. American Journal of Human Genetics 82:1039-1050.

Payseur, B. A., P. Jing, and R. J. Haasl (2011). A genomic portrait of human microsatellite variation. Molecular Biology and Evolution 28:303-312.

Haasl, R. J., and **B. A. Payseur** (2013). Microsatellites as targets of natural selection. Molecular Biology and Evolution 30:285-298.

Haasl, R. J., R. C. Johnson, and **B. A. Payseur** (2014). The effects of microsatellite selection on linked sequence diversity. Genome Biology and Evolution 6:1843-1861.

3. The rate of meiotic recombination varies despite functional constraints imposed by the role of recombination in ensuring proper chromosomal segregation. Using house mice and other mammals as model systems, I characterized evolutionary divergence in this fundamental genomic parameter as well its genetic basis. Graduate student Beth Dumont and I were the first to identify genomic regions that control global recombination rate differences between nascent species. We also discovered genomic regions with divergent local rates of recombination and reported that recombination rate shows a phylogenetic signal across mammals.

Dumont, B. L., and **B. A. Payseur** (2008). Evolution of the genomic rate of recombination in mammals. Evolution 62:276-294.

Dumont, B. L., M. A. White, B. Steffy, T. Wiltshire, and **B. A. Payseur** (2011). Extensive recombination rate variation in the house mouse species complex inferred from genetic linkage maps. Genome Research 21:114-125. PMCID: PMC3012918.

Dumont, B. L., and **B. A. Payseur** (2011). Evolution of the genomic rate of recombination in murid rodents. Genetics 187:643-657. PMCID: PMC3063662.

Dumont, B. L., and **B. A. Payseur** (2011). Genetic analysis of genome-scale recombination rate evolution in house mice. PLoS Genetics 7:e1002116. PMCID: PMC3111479.

Complete List of Published Work in MyBibliography
http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/40429223/?sort=date&direction=descending

D. Research Support

Ongoing Research Support

R01 GM100426 Payseur (PI) 9/10/12-2/28/21 NIH/NIGMS
Genetics of the island rule
The goal of this study is to identify the genetic causes of rapid and extreme body size evolution in an island population of house mice.
Role: PI

R01 GM120051 Payseur (PI) Award letter pending NIH/NIGMS
Evolution of the genome-wide recombination rate in mice
The goal of this study is to document natural variation among individuals in the genome-wide recombination rate and its cellular determinants.
Role: PI

NSF DEB1353737 Payseur (PI) 8/1/14-7/31/17 NSF/DEB
Identifying the genetic determinants of speciation from genomic maps of ancestry in hybrid mice
The goal of this study is to develop a new ancestry-based framework for understanding the genomic consequences of hybridization and speciation.
Role: PI

Completed Research Support

NSF DEB 0918000 Payseur (PI) 7/15/09-7/14/12 NSF/DEB
The genetics and evolution of hybrid male sterility in house mice
The goal this study was to understand the genetic and evolutionary basis of a major reproductive isolating barrier between subspecies of house mice.
Role: PI

R01 HG004498 Payseur (PI) 8/15/08-2/31/15 NIH/NHGRI

Integrating SNPs and STRPs in population genetics
The goal of this study was to develop new population genetic methods to interpret microsatellite variation and its relationship to SNP variation.
Role: PI