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**EDUCATION**

2008-present Graduate: Louisiana State University, LA (PhD student)  
2003-2007 Graduate: Portland State University, OR (MS), thesis: Multivariate Morphological Analysis of Niche Partitioning Among Costa Rican Bats  
2000-2003 Undergraduate: Portland State University, OR (BS)  
1998-2000 Undergraduate: Columbia Gorge Community College, OR (AA)  
1997-1998 Undergraduate: Clark College, Vancouver, WA

**PROFESSIONAL EXPERIENCE:**

2009-present Teaching Assistant, Intro Biology for non-majors, Louisiana State University  
2008-2009 Research Assistant, Mojave Desert rodent ecology, Louisiana State University  
2005-2008 Research Assistant, Dr. Jan Zinck's genetics lab, Portland State University  
2007 Teaching Assistant, Marine Mammals, Portland State University  
2004 Teaching Assistant, Marine Mammals (Bi 4/510) and Principles of Biology (Bi 251L), Portland State University  
2004 Research Assistant, Portland State University Museum of Vertebrate Biology  
2004-2006 Research Assistant, hanta virus and small mammal ecology, Portland State University  
2001-2004 Laboratory Assistant, hepatitis C immunology, Oregon Health and Science University

**RESEARCH EXPERIENCE**

2008-2009 Research Assistant, Mojave Desert rodent ecology, Louisiana State University  
2006-present Field assistant for the Oregon and Washington Bat Grid, Portland State University and Forest Service (volunteer)  
2005-2008 Research Assistant, Dr. Jan Zinck's genetics lab, Portland State University  
2004 Research Assistant, Portland State University Museum of Vertebrate Biology  
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**GRANT SUPPORT**

2005 Forbes-Lea Research Award: \$800 for research travel

**PUBLICATIONS**

- Ormsbee, Patricia C., J. M. Zinck, J. M. Szewczak, **L. E. Patrick**, and A. H. Hart. 2006. Benefits of a standardized sampling frame: an update on the "Bat Grid", Bat Research News 47:4
- Valentine, Kim, D. A. Duffield, **L.E. Patrick**, D.R. Hatch, V. L. Butler, R. L. Hall and N. Lehman. 2007. Ancient DNA reveals genotypic relationships among Oregon populations of the sea otter (*Enhydra lutris*), Conservation Genetics, 9:933-938.

## Phylogenetic Community Structure and Morphological Overlap of Western North American Bats

Ecologists have long sought to understand the evolutionary and ecological processes that shape the structure of local communities. Local communities are likely structured by many biotic and abiotic forces and their interactions, including environmental heterogeneity, evolutionary history, dispersal ability, timing of colonization, and competition. A recent and promising approach to study the causes of community structure is the use of phylogenetic information of a regional species pool to characterize the evolutionary relationships among species in local communities.

This phylogenetic approach is based on the idea of niche conservatism, which *assumes* that species that are phylogenetically closely related will have similar phenotypes and therefore similar ecological characteristics [1]. Under this assumption, predictions about the phylogenetic relationships among species can be made that can provide insights into the effects of competitive interactions and local environmental constraints on community structure. Accordingly, local communities consisting of species that are less related to each other than expected by chance (overdispersed) would result from strong competitive interactions (i.e., other closely related species sharing similar ecological phenotypes are excluded during community assembly). In contrast, local communities possessing species that are more related to each other than expected by chance (clustered) are likely structured by habitat filtering (i.e., only those species with similar ecological phenotypes can exist under particular environmental regimes [2]). Many recent studies have taken this approach and interpreted phylogenetic structure of communities in light of multiple hypotheses proposed to account for community structure. In this study, I will infer a phylogenetic tree to use as the basis for investigating the relationship between evolutionary history and ecology in structuring local communities by examining phylogenetic community structure and using morphology to provide substantiation of the ecological processes at work.

Phylogeny in the context of community ecology is used as an estimate of overall phenotype that includes information on life history, behavior, and environmental tolerances. Nonetheless, for organisms with extremely labile phenotypes, such as *Anolis* lizards [3] and *Myotis* bats [4, 5], patterns of phylogeny and morphology may not correspond. In particular, convergent evolution could lead to big differences between ecological and phylogenetic structure of natural communities. Cases may exist where communities are phenotypically overdispersed but phylogenetically clustered, or phenotypically clustered but phylogenetically overdispersed [2, 6]. Thus, more direct measures of species ecology and interactions are necessary to complement and clarify such phylogenetic approaches. Morphology, for example, is a much better estimate for dietary differences, resource partitioning, and ultimately the competitive relationships among taxa. Because phenotypic convergence is common in the contemporary biota, phylogenetic niche conservatism cannot be assumed within clades and communities without ecological substantiation [1]. Investigating the degree of phenotypic variability within species and whether particular phenotypic characteristics are phylogenetically conserved or variable would greatly enhance our understanding of mechanisms that shape community structure.

I will focus on an ecologically and economically important taxon: western North American bats. In the western United States (US), there are four families, sixteen genera, and thirty-three species of bats [7]. Bats are integral to ecosystem functioning wherever they occur; in the western US they serve as pollinators of several plant species [8] and consume economically important pest insects [9]. It is therefore important to understand mechanisms that structure bat communities for both ecological and economic reasons. To explore whether and how deterministic processes have structured bat communities in different regions, and if patterns are shared between regions, I propose to estimate a regional phylogeny to compare phylogenetic community structure and morphology of bats within and between the four great desert regions of the American west: Mojave, Great Basin, Sonoran, and Chihuahuan deserts. These deserts each host distinct floral assemblages and were formed at different times by various geological processes [10], potentially leading to discrete evolutionary histories of the fauna residing therein.

This study requires a reliable estimation of the phylogeny of the regional species pool. There are many phylogenetic trees for US bats (e.g., [4, 5, 11-13]); however none of them have the same genes or taxa in common, creating the need to build a phylogenetic tree myself. The most common genes on Genbank for these taxa are mitochondrial cytochrome b, 12S rRNA, tRNA<sup>Val</sup>, and 16S rRNA genes and the nuclear RAG2 gene. Of the thirty-

one species of bats in the western US, nine have all aforementioned gene sequences on Genbank, seventeen are missing sequences for one or more genes, and five are lacking these genes or even any representation on Genbank altogether. To complete the regional phylogeny, I propose to sequence the missing genes and species from tissues preserved in museum collections or collected during my own fieldwork using previously published primers [5, 11]. This molecular work is what I am asking the Society of Systematic Biologists to fund. I will use Modeltest [14] and MrModeltest [15] to determine the most appropriate models of evolution for both partitioned and un-partitioned datasets. I will then use GARLI [16] and MrBayes [17] to infer phylogenies using maximum likelihood and Bayesian inference. The resulting tree will provide a better estimation of the phylogenetic relationships of species in the western US than previous studies, helping to disentangle some of the previously problematic relationships among these taxa. This tree will also be useful for other studies, like mine, where species relationships can be used to understand processes responsible for community assembly.

At least four local communities in each of the four deserts (sixteen local communities total) will be used to make comparisons within and between regions. Species composition of local communities will be based on vouchered specimens collected at sites that have been surveyed at least ten times. Data will be gathered from previously existing museum collections and my own field collections. Net relatedness index and nearest taxon index (measures of the degree of phylogenetic clustering and overdispersion of taxa [18]) will be calculated using Phylocom [19] for each local community. In order to detect non-random patterns of community structure, 10,000 randomly generated communities from the regional species pool will be simulated for and compared to the empirical phylogenetic structure. To assess morphological overlap within and between local communities, I will examine twenty specimens (ten males and ten females) of each species from each of the sixteen local communities. Cranial, wing, and general body measurements will be based on their known or suspected ecological functions (e.g., [20, 21]). I will use geometric morphometrics to disentangle the size and shape components of morphological community structure. Morphological and phylogenetic structure will be compared to assess roles of competition and habitat filtering in shaping local bat communities in these four deserts.

If competitive interactions are structuring bat communities in western North America, I expect sympatric species to exhibit little morphological overlap. On the contrary, if habitat filtering is occurring, then I expect to find that there is little morphological distinction among co-existing species. While most mammalian assemblages studied thus far are phylogenetically overdispersed [22], for *Myotis*, I expect to find that phylogeny and morphology are decoupled, manifested either by phylogenetically clustered, morphologically overdispersed assemblages (indicating competition) or by phylogenetically overdispersed, morphologically clustered assemblages (indicating habitat filtering).

Patterns of phylogenetic overdispersion and clustering need to be substantiated with more direct functional ecological approaches to more rigorously demonstrate the importance of competitive interactions and habitat filtering in community organization [23]. However, these inferences are only as rigorous as the phylogenetic tree used to investigate these patterns. Several of the species in the regional species pool have little to no representation in Genbank, hampering comprehensive phylogenetic and systematic studies. To date, there are few studies of phylogenetic community structure of vertebrate communities [24], particularly those of bats [22]. And even less have integrated phylogenetic and morphological information. Furthermore, given projected range shifts of many species due to climate change [25], it is important to have a comprehensive understanding of community dynamics to better predict the impact of shifting species ranges on community assembly. This is particularly important for bats given their economic importance in ecosystem function and pest control [8, 9]. This study will make a contribution to evolutionary ecology in general and bat community ecology in particular by investigating mechanisms responsible for community assembly from two different but complementary perspectives.

I began my degree program in Spring of 2008. I will begin my fieldwork for this project spring and summer 2010, fall 2010 I will gather the morphological and molecular data, and will analyze and write up the results winter and spring 2011.

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Item	Quantity	Price
Qiagen tissue extraction kit	1 50 kit	\$135
Qiagen PCR purification kit	2 50 kit	198
illustra PuReTaq Ready-To-Go PCR Beads (0.5 ml tubes)	1 100 rxn/bag	151
Ethanol, tubes, tips, other consumables		150
Sanger sequencing and dye	\$10 x 82 samples	820
Primers	\$10 x 6	60
<b>Total</b>		<b>\$1514</b>