

NESCent Graduate Fellowship Application

Heath Blackmon

NESCent Working Group: Tree of Sex – A comprehensive synthesis of sex determination systems in eukaryotes

**Title:** Comprehensive analysis of the rates and patterns of sex chromosome evolution in arthropods.

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**Project Summary:** The evolutionary dynamics of sex chromosomes are unique because they have smaller effective population sizes than autosomes and do not spend equal time in males and females. However, our understanding of the rates and patterns of sex chromosome evolution come from very few model organisms. The Proposed research will synthesize data from decades of cytogenetic work and phylogenetic studies and will use Bayesian comparative phylogenetic methods to estimate the rate at which sex limited chromosomes decay and how frequently sex chromosome systems experience turnover. This project will allow us to determine how broadly applicable our understanding of sex chromosome evolution is and how variable the rate of sex chromosome turnover and decay is across some of the most speciose groups of animals, and which groups exhibit patterns that may be worthy of further research. Completion of this project will also lead to useful comparative phylogenetic tools that can be used to perform posterior predictive simulations of discrete characters.

**Public Summary:** Many organisms develop distinctly different male and female forms. The gender of an individual is often determined by which sex chromosomes they inherit from their parents. The genes on sex chromosomes experience different evolutionary forces since they are found in different proportions in males and females. Many of our observations about how species arise and evolve assign a special role to sex chromosomes, often it seems that genes on the sex chromosome keep organisms from hybridizing. However, our understanding of the rates and patterns of sex chromosome evolution are based on very few species. The proposed research will synthesize data from 1,000s of species and use phylogenetic trees to model the evolution of sex chromosomes. The proposed research will help us to understand the similarities and differences in the way that sex chromosomes evolve across the majority of multicellular organisms.

**Introduction and Goals:** The canonical view of sex chromosome evolution is that a sex determining mutation arises and converts homologous autosomes into sex chromosomes (Rice 1996). Theory predicts that the presence of linked sexually antagonistic loci (i.e. those that benefit one sex at the expense of the other) will lead to selection for reduced recombination around the sex-determining locus (Charlesworth 1991). Once recombination is reduced the sex limited chromosome is subject to a variety of processes that lead to the accumulation of mutations and a reduction in the relative fitness of the chromosome (Charlesworth and Charlesworth 2000). Depending on the density of genes on the sex limited chromosome different forces such as Mueller's ratchet, genetic drift, selective sweeps, and background selection are expected to be dominant in driving the decay of the chromosome (Bachtrog 2008). Over time these processes often lead to heteromorphic sex chromosomes and possibly even inevitable loss of the Y chromosome (born to be destroyed hypothesis) (Steinemann and Steinemann 2005). The process of sex chromosome evolution has been studied primarily in model systems by sequence analysis of young sex chromosomes (Bachtrog 2004), or by the creation of artificial sex determination alleles (Rice 1994). This project will use a new approach to discover when and if sex limited chromosomes are destined for loss and determine how much variability exists in the evolutionary rates and patterns of sex chromosome evolution.

**Proposed Activities:** I will use novel phylogenetic methods to study sex chromosome evolution, synthesizing a large sex chromosome database with phylogenies from across the

**arthropods.** The Tree of Sex working group has collected sex chromosome data for over 18,000 arthropod taxa (of which 4,726 were contributed by me, and stem from my dissertation work on Coleopteran sex chromosomes: [www.uta.edu/karyodb/](http://www.uta.edu/karyodb/)). This wealth of data offers a unique opportunity to examine turnover and decay of sex limited chromosomes under a variety of conditions. Specifically I will be able to compare processes acting in XY and ZW systems as well as groups with holocentric vs metacentric chromosomes, and implicitly test the “born to be destroyed” hypothesis across arthropods. The taxa that will be used in the proposed analysis are:

| Order       | Sex Chromosome System | Centromeres |
|-------------|-----------------------|-------------|
| Lepidoptera | ZW                    | Holocentric |
| Coleoptera  | XY                    | Monocentric |
| Mantodea    | XY                    | Monocentric |
| Orthoptera  | XY                    | Holocentric |
| Odonota     | XY                    | Holocentric |

Existing phylogenies (Mutanen et al 2010, Svenson and Whiting 2004, Fenn et al 2008, Dumont et al 2009) will be used to build supertrees for each group. I will use the sex chromosome data in concert with the phylogenies to infer the rates at which sex limited chromosomes are gained and lost and to determine the rate of sex chromosome turnover. I will use Bayes’ factors in model selection and posterior predictive simulations to evaluate model adequacy. This research will determine how variable the rates and patterns of sex chromosome evolution are across some of the largest groups of eukaryotic life.

**Rationale for NESCent support:** My project depends on extracting large amounts of data from the Tree of Sex database that NESCent personnel are actively developing. I believe that having an end-user who is also familiar with databases could insure that the Tree of Sex database is a success. My research is also highly synthetic taking results from cytogenetic and phylogenetic studies and applying comparative phylogenetic methods to learn about sex chromosome evolution in a novel way. As the center for synthetic studies NESCent will be an excellent environment to pursue this work. Due to the broad nature of my research I believe that I will also benefit from the opportunities to interact with the variety of scholars in residence and who visit NESCent.

**Collaborations:** While at NESCent I will interact closely with members of the working group via skype, specifically Doris Bachtrog and Laura Ross who are both interested in and responsible for a large amount of the arthropod data. I will also have weekly skype meetings with my advisor Jeffery Demuth, and make one short trip back to Texas for a meeting with my advisor.

**Proposed Timetable:** If this application is successful I plan to begin working from NESCent in August 2013 and remain until December 2013. I plan to reside at NESCent for the duration of the fellowship (see Collaborations for brief exceptions). I plan to spend the first month of my time preparing the data for analysis. In the second month I anticipate beginning analyses. Finally, the remainder of my time will be spent with follow-up analyses and manuscript preparation.

**Anticipated IT Needs:** The only IT need that I anticipate is access to the Tree of Sex database. I will use my own laptop for most analyses access one of the servers in my advisors lab.

**Anticipated Results:** A variety of products will be produced as a result of this fellowship: 1) an R package with functions facilitating PPS of discrete data; 2) a synthetic analysis comparing the results in each arthropod group and discussing the possible causes of any differences that are found between the groups. Perhaps most importantly this fellowship will maximize the understanding that this existing data offers and will point us to those clades that exhibit divergent patterns worthy of more intense study in the future.

## References

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