**Phylogenomics of African clawed frogs (*Xenopus*): implications for evolutionary dynamics of sex chromosomes**

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I am working with high-throughput sequencing data (RNAseq) as a first step in understanding evolutionary transitions (“turnovers”) of sex chromosomes in amphibians, focusing on African clawed frogs (*Xenopus*). Amphibians represent an interesting model for studying sex chromosome evolution because, unlike mammals, the sex determining regions or genetic triggers have changed dozens of times, and sex chromosomes tend to be minimally diverged with genetic recombination occurring over most of their length. These ‘homomorphic’ sex chromosomes are thought to be the ancestral state of all sex chromosomes, including those of humans. The first step in this project is to resolve the phylogenetic relationships among the *Xenopus* genus. I have sequenced the transcriptomes of 5 individuals representing the major clades within the genus. One of the challenges of working with a polyploidy species is that it is necessary to sort out which sequences have an orthologous relationship (representing speciation events) and which sequences have a paralogous relationship (representing duplication events). We have designed a pipeline to ensure that only orthologous comparisons are made and I have conducted Bayesian phylogenetic analysis to resolve the phylogeny. Broader implications of this work include furthering our understanding of the evolutionary history of the only known master sex determining gene in Amphibians (DM-W). In addition, will be able to explore the evolution of polyploidy genomes, looking at rates of pseudogenization and the evolution of gene expression following a whole genome duplication event.