PROJECT SUMMARY

Intellectual Merit: Polyploidy, the possession of extra full sets of chromosomes, is a major driver in genome evolution. Patterns of gene silencing in response to polyploidy are very predictive of which genes will be maintained through time (Josefsson et al. 2006, Ha et al. 2009) and are therefore interesting in the context of genome evolution. The fate of the duplicates is well described (Innan and Kondrashov 2010) but immediate response to these sudden spikes in genome size is largely unknown. Genomic disturbance often occurs, particularly in polyploids that are formed through hybridization (allopolyploids). New allopolyploids must coordinate two competing gene sets and regulatory networks in order to thrive. Recent research supports that disturbances in epigenetic factors contributing to chromatin integrity are a major contributor to the conflict between genomes (Michalak 2009). Despite polyploid events being important to vertebrate genome evolution, little is known about the immediate impact of polyploid formation upon genomic function.

Overview: The purpose of this study is to identify the variability of genomic response in an allopolyploid vertebrate complex and define epigenetic mechanisms driving expression change. Disease stress changes the response significantly, even when polyploids do not differ from diploids under control conditions. As such, I include disease exposure in my analysis of variability in genomic response.

Aim 1) Characterize the variability of expression response in the polyploid complex.

Research Question: How do genomes respond to different genomic and environmental stress?
Hypothesis: Allopolyploids will have larger deviations from parent species' transcription response when transcribing both parent genomes, especially in disease conditions.
Outcome: I will evaluate the pattern of genome silencing in a larger portion of an allopolyploid complex. I will compare findings with dissertation data to define variability in expression throughout the complex, with particular focus on gene silencing patterns in normal and disease conditions.

Aim 2) Identify epigenetic mechanisms that correlate to changes in expression.

Research Question: How do small RNAs respond to genomic shock in vertebrates?
Hypothesis: As a result of expressing both parental genotypes, allopolyploids will exhibit high transposons activity (evidence of genomic shock), rRNA will be expressed from both parental genomes, and microRNAs will correlate with number of copies from each parental genome. Infection will perturb the epigenetic mechanisms to cause down regulation of most genes as seen in Ching et al. 2010.
Outcome: I will identify mechanisms that correlate to the patterns of expression in my dissertation and in Aim 1. I will correlate transposon response to divergences in parental expression patterns. I will characterize the role of microRNA and rRNA in buffering genome shock in vertebrates.

Broader Impacts: I am generally interested in increasing the accessibility of genetic research, particularly in amphibian systems, by reducing cost and expanding the availability of training. I will:

- Continue to work with management groups, such as Partners in Amphibian and Reptile Conservation (PARC) and Herpetological Research Management, presenting on chytrid response, risk factors in populations, and protocols that decrease time and cost of salamander surveys (Sanders et al. in prep).
- Develop a workshop for teachers and high school students on basic molecular techniques while highlighting the local study system. I will work with the University of Notre Dame's new DNA Learning Center and data collected will be used to define local salamander demographics.
- Continue to help adapt the cost effective methods into undergraduate research projects at colleges with limited genetic resources and funding (St. Joseph College, Northland College, Hanover College).
- Continue to work with local outreach programs in supporting ecology (Fernwood Botanical Gardens) education by providing high quality imagine of amphibian development and live education animals.
- Extend my current assistance in different next generation sequencing analysis within our research group to the development of a whole new module for small RNA analysis, to be part of our public workshop the University of Notre Dame Genomics and Bioinformatics Core is developing.