Shanshan Zhou Defends Her Thesis

by Lauren Dembeck and Shilpa Swarup

On March 9th, Shanshan Zhou, who studied under the direction of Drs. Robert R. H. Anholt and Trudy F. C. Mackay successfully defended her doctoral dissertation. Shanshan was a doctoral candidate of the Biology Department and the W. M. Keck Center for Behavioral Biology; her dissertation is titled "Genetic Basis of Phenotypic Plasticity in *Drosophila melanogaster*". Shanshan is a native of Beijing, China. Before coming to North Carolina State University, she attended Beijing No. 4 High School (Beijing Sizhong) and subsequently earned a Bachelor's degree in Biology from Tsinghua University.

Shanshan delved into the less studied corner of the genotype-phenotype-environment paradigm by studying phenotypic plasticity - the ability of organisms to produce distinct phenotypes under different environmental conditions. Using *Drosophila melanogaster* as a model species, she researched the transcriptome and how regulatory networks are influenced by and interact with the environment. With a focus on chemosensation, she constructed customized cDNA microarrays representing all classical odorant receptor genes, gustatory receptors and odorant binding protein genes of Drosophila. She investigated their expression patterns under different developmental stages, physiological status and social conditions. Shanshan found that cytologically clustered chemoreceptor genes undergo independent transcriptional regulation during different developmental stages and between sexes. Distinct subgroups of chemoreceptor genes are sensitive to reproductive state and social interactions. Fascinatingly, simply the exposure of flies to the odor of the opposite sex alters transcript abundance of chemoreceptor genes in a manner that is different than when flies are allowed physical contact.

She then decided to broaden her study in an ambitious pursuit to measure transcriptional variation in a synthetic outbred population termed ‘Flyland’ under 20 different environmental conditions. Flyland was constructed by crossing 40 inbred lines of *D. melanogaster* derived from a natural population. This was advantageous because the progenitor lines have sequenced genomes and published transcriptome data. She associated transcriptional variation induced by the environment with the environmental variation of different fitness traits including development time, life span, chill coma recovery, and starvation stress resistance.

She found that about 15% of the transcriptome is highly responsive to environmental changes. Of the environmentally sensitive transcripts, 1249 are highly significant for treatment and responded differentially to different environments. These transcripts are associated with response to heat shock, xenobiotic and energy metabolism, immune defense, proteolysis, transcription, computationally predicted transcripts of unknown function, and non-coding RNAs. She also identified 970 environmentally sensitive transcripts with low genetic variation that showed extensive sexual dimorphism and were enriched for transcripts associated with reproductive functions. She named these two groups of transcripts Class I and Class II transcripts. Her analysis of sequence conservation across 12 Drosophila species indicated that environmentally sensitive genes, especially the Class II transcripts are more rapidly evolving than genes with robust expression under different environments.

Shanshan's research provides intriguing insights into transcriptional co-regulation and is the largest most detailed study of environmental plasticity to date. She is currently continuing as a postdoctoral associate with Drs. Anholt and Mackay. We wish Shanshan all the best with her future endeavors and will miss her greatly when she leaves the "MacAnholt" lab.