UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

Poster Session 1

Commons West, Easel 25

11:00 AM to 12:30 PM

Gene Expression Analysis of Human-Specific Duplications of *ARHGAP11*

Kenneth Munn Keung (Kenneth) Mark, Senior, Biochemistry
Mentor: Evan Eichler, Genome Sciences
Mentor: Megan Y. Dennis, Genome Sciences

A significant proportion of the 23 known human-specific duplicated genes are implicated in neurological processes. The Rho GTPase activating protein 11 (*ARHGAP11*) is one such gene that is also found in an area associated with schizophrenia, intellectual disability, and autism. We determined that the human-specific duplicated copy (*ARHGAP11B*) duplicated 5.3 million years ago (mya) shortly after the human-chimpanzee divergence (˜6.5 mya). The human-specific duplicated copy is not found in all humans, and represents an incomplete version of *ARHGAP11A*, suggesting a potentially alternative function. The goal of my project was to identify sequence differences between A (ancestral) and B (duplicated) paralogs (i.e., genes related by duplication within the same species) and use these differences to assess gene variation and expression. By sequencing 64 different transcripts (i.e. protein coding regions) we found nine "paralog-specific variants" (or PSVs) allowing us to distinguish between A and B. We assessed the level of gene expression (how much a gene is "used") for each paralog in human fetal brain samples and found that A was expressed approximately two times more than B. Interestingly, we found similar results from other tissue types including blood. Further, we have used these PSVs to identify potentially pathogenic mutations of *ARHGAP11A* from targeted large-scale sequencing data of a collection of children with intellectual disability. We are using these data to understand the function of different members of the ARHGAP11 gene family both on neurological development and potentially on the evolution of traits that make us uniquely human.

Session 1H

Aquatic Ecology and Biodiversity

Session Moderator: Julia Parrish, Aquatic & Fishery Sciences

248 MGH

1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Indices of Nutrition with Depth from Two Seasons in the Green Urchin, *Strongylocentrotus droebachiensis*

Katie (Kate) Olson, Senior, Aquatic & Fishery Sciences
Mary Gates Scholar
Mentor: Megan Dethier, Biology
Mentor: David Duggins, Friday Harbor Labs
Mentor: Aaron Galloway

Drift algal material is expected to play a significant trophic role in ecosystems adjacent to kelp beds. The contribution of drift algae to the overall nutritional state of various invertebrates can be assessed using phenotypic traits such as gonad index (larger gonad mass with better nutrition) and for sea urchins, jaw diameter (larger jaws with inconsistent food supplies). In this study, we collected green urchins (*Strongylocentrotus droebachiensis*) within kelp beds (5m depth) in the shallow subtidal photic environment (SSPE) and outside of kelp beds in nearby deep subtidal environments (DSE; 100m depth) during spring and winter seasons. SSPE and DSE sampling stations were less than 1 km apart. In the initial spring analyses, urchins in the DSE had significantly larger gonads but also larger jaws than SSPE animals. Winter gonad indices showed a reverse pattern, in which SSPE urchins had larger gonad indices, but still had smaller jaw indices than the DSE urchins; gonads in all urchins on this sampling date were much larger than those in the previous spring. These results suggest that food supplies may vary among seasons, especially in deep habitats, where the subsidy of algal material exported from shallow water may be inconsistent; the jaws from DSE urchins concur with this hypothesis. Gut content analyses from winter samples will be used to evaluate the types of foods available to deep vs. shallow-water animals.

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Fatty Acid Signatures and Growth in Juvenile *Idotea wosnesenskii* Respond to Differing Macroalgal Diets

Morgan Elizabeth Eisenlord, Senior, Biology (Ecology, Evolution & Conservation)
Mary Gates Scholar
Mentor: Megan Dethier, Biology
Mentor: Aaron Galloway

Fatty acids (FA) are commonly used as biomarkers to infer contributions of different basal energy sources to consumers. However, modification, catabolism, and storage of dietary FA are poorly understood for most animals. Controlled feeding experiments are critically needed to determine the appropriate use of FA as dietary tracers. We conducted two such experiments with juvenile isopods to investigate their use as a model organism for FA signature analysis in a direct herbivore. Newly hatched *Idotea wosnesenskii* were raised for 10 weeks on five different macroalgal diets at two different temperatures. Broods were raised from hatching on a single food source. Highest growth rates were on *Ulva* spp., fresh *Nereocystis luetkeana*, and aged *N. luetkeana*. Animals grew significantly slower on diets with chemical (*Fucus distichus*) and structural (*Mazzaella splendens*) anti-herbivore defenses. Temperature did not substantially affect growth rates. Preliminary analyses indicate that FA in *Idotea* tissues reflect those of their diets, and that FA driving the patterns include common biomarkers for the algae consumed. Juvenile *Idotea* are a promising model organism for FA trophic ecology because they generally thrive in a laboratory setting and can be hatched and quickly grown on a variety of diets.