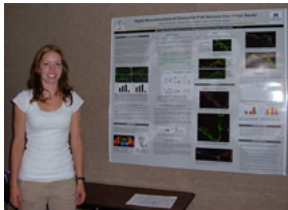


Complex Biological Systems Summer Undergraduate Research Program Summer 2007 Cohort Research Abstracts



❖ **Jessica Dorschner**

University of Wisconsin- Eau Claire

Mentor: Gwen Jacobs, Cell Biology & Neuroscience

Research Abstract:

Fragile X Syndrome (FraX) is the most common inherited mental retardation disease. The disease results from the silencing of the *fragile X mental retardation 1 (fmr1)* gene which encodes for the fragile X mental retardation protein (FMRP). FMRP is a widely expressed translational suppressor with many potential regulative targets.

In the *Drosophila* model of FraX, dFMRP has been shown to be a potent translational suppressor of neuronal complexity and synaptic differentiation. Subsequently, *Drosophila fmr1* null mutant neurons have increased dendritic elaboration and axonal branching (Fig. 1). Overexpression of dFMRP, on the other hand, results in reduced neuronal complexity.

An effective way to analyze the morphology of *Drosophila* FraX neurons is via digital reconstructions from image stacks. Digital reconstructions allow for analysis of 3D neuronal structure, and provide morphometric data such as branch number, branch order, average diameter, total path length, and total surface area.

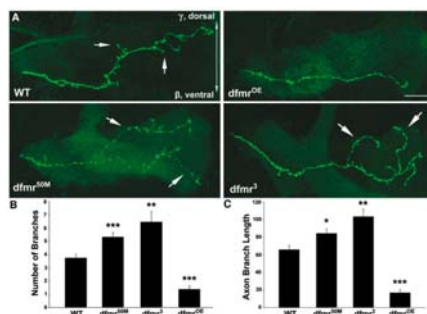


Figure 1. Data from collaborators that indicates dFMRP negatively regulates axonal branching in *Drosophila* mushroom body Kenyan cells (5). WT=wild-type; dfmrOE=dFMRP overexpression; dfmr50M and dfmr3=two types of *dfmr* deletion mutants. A) Comparison of single WT and mutant Kenyan cells labeled via the MARCM technique. Arrows indicate small branches of interest. B)/C) Branch number and axonal length comparisons. * =significance 0.001<p<0.05; **=0.0001<p<0.001; ***=p<0.0001.



❖ **Barbara (Jeannie) Hunnicutt**

Boise State University

Mentor: Charlie Gray, Cell Biology & Neuroscience

Research Abstract:

The way in which the brain stores and uses information about objects in the visual field is largely unknown. When the information is only remembered for a short period of time this process is referred to as working memory. There are three main parts to working memory; encoding is storing the information, maintenance is remembering it over some period of time, and utilization is recalling the information for use. This process is thought to involve many different cortical regions, specifically the posterior parietal and dorsolateral prefrontal cortices. The actions of these areas individually, as well as an interdependence between them, may facilitate different aspects of working memory.

The rhesus macaque monkey is used as a model for human cognition, and the neural activity recorded in them can be applied to understanding human brain functions. Figure 1 shows the areas recorded in this study from in the macaque monkey brain (left), and the homologous regions in the human brain (right). These areas have been previously shown in both macaques and human to be involved in working memory separately, but the ways in which they interact are harder to study due to limitations in current recording techniques. The experiment described here allowed for spatially and temporally precise recording from both areas simultaneously, and will hopefully allow us to understand the interactions between posterior parietal and dorsolateral prefrontal cortices during working memory tasks.

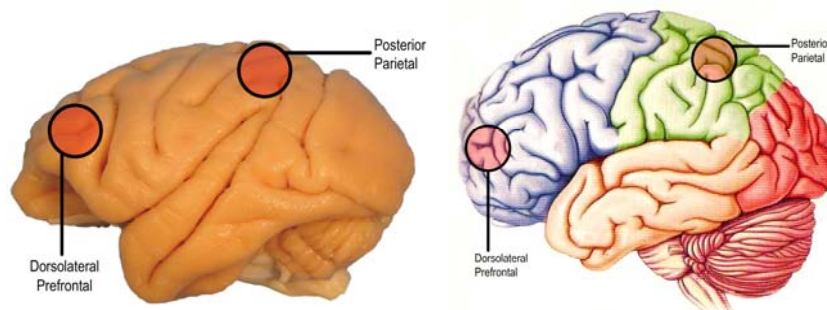
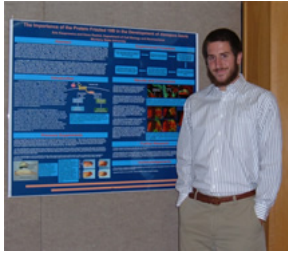


Figure 1. The areas of interest in the rhesus macaque brain are specified by the circles in over the brain on the left. The homologous regions in the human brain are shown on the right. These are the areas neural activity is recorded from in this study.



❖ Eric Kasporwicz

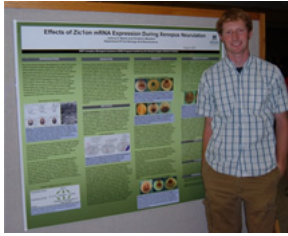
University of Virginia

Mentor: Dana Rashid, Cell Biology & Neuroscience

Research Abstract:

During embryonic development, Frizzled proteins are thought to play important roles in mediating *Wnt* pathways. These pathways are responsible for important events such as body axis specification and control of planar cell polarity. One of the Frizzled proteins found in the frog *Xenopus laevis*, frizzled-10B (*Xfz10B*), is expressed in the neural tube in the later neurula stages, which suggests it plays an important role in neural development. Research already completed by Dana Rashid has shown that down-regulation of *Xfz10B* using a morpholino severely stunts the growth of embryos and diminishes the growth of somites, branchial arches and neural tube. The effects of the *Xfz10B* morpholino on somites were shown using antibody staining and fluorescence microscopy. In these experiments, areas injected with morpholino showed no somite staining. In addition, when *Xfz10B* was over-expressed through injection of extra *Xfz10B* RNA, in situ hybridizations using a Sox-9 neural crest probe showed an expansion of the branchial arches. These results led us to believe that over-expression of *Xfz10B* in other dorsal tissues, including the somites, would lead to an increase in size of those tissues.

In order to better understand the effects of over-expression of *Xfz10B*, albino *Xenopus* embryos were injected with either *Xfz10B* RNA+GFP or GFP-only as a control at the 4-cell stage. These embryos were fixed at different stages, frozen and sectioned. The sectioned embryos were incubated in antibodies that targeted different tissues depending on where the *Xfz10B* RNA was injected. Results from the 12-101-somite stained embryos have shown that over-expression of *Xfz10B* does increase the size of the somites. Other embryos stained with Xen-1, which targets neural tube, have not yet shown any expansion when injected with *Xfz10B* RNA. Further research in these experiments will be to continue looking at the effects of over-expression of *Xfz10B* on other dorsal structures. In addition, we would like to concentrate on determining the expression patterns of *Xfz10B* in early development. Because of the results of our somite research, we believe that *Xfz10B* is expressed in mesodermal tissue during the early stages of development.



❖ Joshua Martin

Montana State University

Mentor: Christa Merzdorf, Cell Biology & Neuroscience

Research Abstract:

The time during *Xenopus* development in which the neural tube is formed is called *neurulation*. During *neurulation* several different factors within the nucleus tell cells to begin and eventually to form the neural tube. The majority of these factors are known as *transcription factors*. Different combinations of transcription factors establish which mRNA will be expressed in each cell. Zic1 is a transcription factor that contains a DNA binding domain that is made up of protein motifs known as zinc fingers. Using these zinc fingers Zic1 is able to bind to DNA. Along with several other transcription factors in different combinations, Zic1 can either up regulate or down regulate the expression of certain neural specific genes.

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❖ Richard Nzokwe

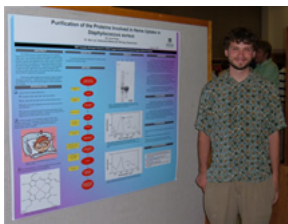
Alcorn State University

Mentor: Frances Lefcort, Cell Biology & Neuroscience

Research Abstract:

Motor neurons are part of the nervous system, and are located in the central nervous system (CNS). They project their axons outside the CNS and directly control muscles.

Like other neurons as well as other somatic cells, motor neurons undergo programmed cell death (apoptosis), which may be advantageous or disadvantageous in some cases. Motor neurons are clinically significant to study because of their role in human motor neuron diseases like Amyotrophic lateral sclerosis (ALS).



❖ Jared Page

Montana State University

Mentor: Ben Lei, Veterinary Molecular Biology

Research Abstract:

The *Staphylococcus aureus* machinery that uptakes heme as an iron source consists of the surface proteins IsdA, IsdB, IsdC, IsdH and the transporter IsdDEF. How all of these proteins interact and transfer heme to each other is unknown. The purpose of my project is to prepare the proteins to study the heme transport mechanism. I focused on the preparation of IsdA and IsdC. IsdA with bound heme (holoIsdA) was purified to above 90% purity, and heme-free IsdC (apoIsdC) was purified to apparent homogeneity.

Preliminary tests indicate that holoIsdA rapidly transfers its heme to apoIsdC. Further study of this transfer reaction will establish the roles of the two proteins in heme acquisition in *S. aureus*.



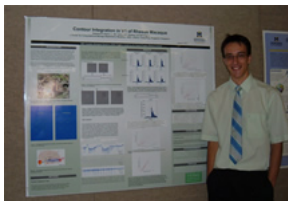
❖ **Tyler Poore**

Rensselaer Polytechnic Institute

Mentor: Alex Dimitrov, Cell Biology & Neuroscience

Research Abstract:

Neural data from female *Acheta domestica*, responding to air current stimuli, were obtained from intracellular microelectrodes located at the posterior end of the cricket. The specimen was placed in the crossroads of four sets of speakers, such that the setup used could stimulate the cricket cercal system in a multidirectional fashion; coordinated movements between the sets of speakers transmitted the waveforms into corresponding movements of air flowing across the subject's cerci.



❖ **Roberto Rojnic**

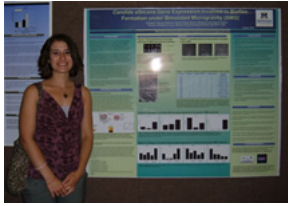
Montana State University

Mentor: Charlie Gray, Cell Biology & Neuroscience

Research Abstract:

In visual object recognition some processes require focused attention, while other processes rely on a preattentive mechanism, also called perceptual grouping. Perceptual Grouping allows various features perceived in the visual scene to be grouped according to Gestalt Criteria. Some examples of Gestalt criteria include collinearity, closure, common motion, continuity, and many more. This mechanism allows for the association and segregation of related features of an object from other objects and the background.

Much of this mechanism occurs in the early visual system. In the current study we conducted multiunit recording in V1 of a Rhesus Macaque, while it was performing a contour discrimination-direct saccade task. In the following we present the initial post-stimulus time histogram analysis of the high pass frequency of multiunit neuronal activity.



❖ Yolanda Stypula

University of Wisconsin - Madison

Mentor: Linda Hyman, Cell Biology & Neuroscience

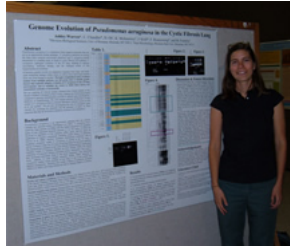
Research Abstract:

Microgravity is a condition where the effects of gravity have been greatly reduced and presents a unique stress on organisms. Studies suggest that astronauts have a weakened immune system during and immediately following space travel. Studies have also shown that several microbes experience morphological changes that might increase virulence in conditions of microgravity. It is important to study the effects of microgravity on cells (potential pathogens and human) in consideration of long-term space travel.

Studies were previously performed in the Hyman Lab on the model system *Saccharomyces cerevisiae* exposed to microgravity. Yeast were cultured in Simulated Microgravity (SMG) for at least 25 generations to examine morphology and differential gene expression. It was concluded that there were changes in polarity and budding (Purevdorj-Gage *et al* and Sheehan *et al*) and RNA microarray analysis revealed differential gene expression in genes consistent with the altered morphology.

While *S. cerevisiae* is a good model system for studying SMG, *Candida albicans* is a potential pathogen for astronauts during long term space travel. *C. albicans* is an opportunistic yeast that can form biofilms, frequently infects immunocompromised patients and is associated with a high mortality rate (40%). The advantage of forming biofilms, or communities of cells, is that they demonstrate increased resistance to external stresses, including antibiotics, which cause them to be difficult to treat in clinical infections. Therefore, it is important to study the effects of the biofilm and virulence genes in *C. albicans* under SMG.

We found that both *Saccharomyces cerevisiae* and *Candida albicans* have altered morphology in SMG (Altenburg *et al* and current study). Also, it is expected that the change in gene expression under SMG is consistent with increased biofilm formation.



❖ Ashley Warren

University of Montana

Mentor: Mike Franklin, Center for Biofilm Engineering

Research Abstract:

Pseudomonas aeruginosa is a ubiquitous Gram negative bacterium that can act as an opportunistic human pathogen. *P. aeruginosa* infections are among the three most common nosocomial infections, and *P. aeruginosa*-related pneumonia is a leading cause of death in cystic fibrosis (CF) patients. *P. aeruginosa* undergoes evolution in the CF lung, adapting to immune surveillance, antibiotic therapy, and the changing terrain of this hyperosmolar environment.

In bacteria, genetic novelty for adaptation originates from large- and small-scale mutational changes within clones as well as from lateral gene transfer from one clone lineage to another. Through a longitudinal study of clinical isolates from multiple patients, our lab group aims to identify genetic factors that underlie adaptive evolution of *P. aeruginosa* in the CF-lung environment, and to establish the extent to which these factors are transmitted vertically or horizontally.

We are studying 49 clinical isolates obtained from sixteen patients at the Necker Children's Hospital in Paris, France, making use of microarray-based comparative genomic hybridization (a-CGH) to identify gene translocations, deletions, or amplifications. We will compare genome architecture of each isolate to *P. aeruginosa* PAO1, a common laboratory reference strain, as well as to one another. We are also investigating the role of conjugative gene transfer by screening for plasmids and the presence of genes on these plasmids that may be involved in antibiotic resistance and conjugation.