Undergraduate Research Symposium May 16, 2014 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

Commons West, Easel 25

11:00 AM to 1:00 PM

Investigation of Neutron Emission from a Farnsworth IEC Fusion Reactor

Raymond Maung, Junior, Physics: Comprehensive Physics
Rian Naveen (Rian) Chandra, Sophomore, Pre-Sciences
NASA Space Grant Scholar, UW Honors Program
Mentor: Brian Victor, Aeronautics and Astronautics

The Farnsworth-type IEC reactor was once considered to behave as a point source of neutrons with reference to the spherical central accelerating grid. This was assumed because the deuteron-deuteron fusion reaction is inherently spherically symmetric (isotropic), and current theory suggested that the vast majority of fusion events were occurring in the deepest region of the potential well (the accelerating grid, which is also the geometric center of the reactor). However, anecdotal evidence has suggested that isotropy may not be empirically accurate. Our main objective was to conclusively test the assumption by measuring deviations from uniformity in the neutron flux. To measure this we used three different types of detector: CR39 plastic, BTI bubble detectors and He-3 dosimeters. We exposed the CR39 slides to fast neutrons (2.45 MeV) at a fluence of 10^6 n/cm^2, and they indicated apparent anisotropy (p-value of .0035) with higher flux at the front and rear of the machine. The BTI bubble detectors and He-3 tubes also corroborated a higher neutron density at those sites. We then hypothesized that beam loading on the front and rear conflats by the plasma "jets" emanating from the central cathode could be responsible. Measurements with paired He-3 tubes after blocking the jets with quartz glass showed the apparent anisotropy reduced by 38% on average ($p << .001$). This quantitative confirmation of anisotropy, and the significant (but not sole) role that beam-target fusion plays therein, represents an important shift in the understanding of the Farnsworth-type reactor, which could have important implications in plasma physics and the development of fusion energy.

POSTER SESSION 1

Balcony, Easel 94

11:00 AM to 1:00 PM

Analysis of Banana Peel Headspace by Solid Phase Micro-Extraction Gas Chromatography Mass Spectrometry (SPME-GC-MS)

Khang To, Senior, Biochemistry, Chemistry
Brandyn Mannion, Senior, Biochemistry, Biology (Molecular, Cellular & Developmental)
Kyeong Min Yu, Senior, Chemistry
Trinh K. (Trinh) Hoac, Recent Graduate,
Mentor: Robert Synovec, Chemistry
Mentor: Brian Fitz, Chemistry

Gas chromatography - mass spectrometry (GC-MS) is a widely used analytical technique for separating and identifying volatile and semi-volatile compounds in complex mixtures. It is beneficial to research ways of increasing sample throughput (i.e. decreasing analysis time) while not losing any chemical information. This study investigates the change in volatile chemicals (odors) that are emitted from banana peels in varying stages of ripeness. The headspace of banana peels was first analyzed using Solid Phase Micro-Extraction (SPME) with a standard gas chromatograph and a quadrupole mass spectrometer (qMS). For demonstrating a viable platform for increased sample throughput, the samples were then analyzed on a LTM (Low Thermal Mass GC) coupled to a Time-of-Flight mass spectrometer. The banana peel analyses on the LTM-TOFMS decreases the run time by tenfold when compared with the traditional GC-qMS. A new data analysis program developed by the Synovec Lab is used to visualize the data and identify compounds.

POSTER SESSION 1

Commons West, Easel 14

11:00 AM to 1:00 PM

Electron Density Fluctuations within the HIT-SI Experiment

Taylor Keith (Taylor) Fryett, Senior, Physics
UW Honors Program, Undergraduate Research Conference Travel Awardee
Mentor: Thomas Jarboe, Aeronautics & Astronautics
Mentor: Brian Victor, Aeronautics and Astronautics

This research traces the origins of electron density fluctuations in the HIT-SI experiment. HIT-SI is a magnetic confinement experiment that uses two helicity injectors to initialize and sustain current in the confinement region. Densities of

1-10e19 m^{-}3 with density fluctuations related to the injector frequency are measured with an FIR interferometer. After spheromak formation, injector currents flow in the direction of toroidal current in the confinement volume. Peaks in the density fluctuations are seen when the injector current passes through the beam path of the interferometer. These observations are consistent with particle motion in the direction of injector current as expected by anti-dynamo action in this region. Furthermore, we have observed fluctuations that indicate that the injector current displaces the confined current. Calculating the toroidal current centroid from surface magnetic probe measurements as a function of time provides further testing of this model. Understanding density fluctuations allows a more complete description of the physics of current drive in HIT-SI.

POSTER SESSION 1

Commons West, Easel 40

11:00 AM to 1:00 PM

Biogeography and Phylogeny of Aigarchaeota: A Novel Phylum of Archaea

Gisele Goertz, Senior, Biology, University of Nevada Las Vegas

McNair Scholar

Mentor: Brian Hedlund, School of Lif Sciences, University of Nevada Las Vegas

Mentor: Timothy Alba, School of Life Sciences, University of Nevada Las Vegas

'Aigarchaeota' is a candidate phylum of Archaea known only by 16S rRNA gene fragments from cultivation-independent microbial surveys and a single composite genome from Candidatus *'Caldiarchaeum subterraneum'*, an inhabitant of a subterranean gold mine in Japan. Gene sequences reported in various publications were found almost exclusively in geothermal settings, but a comprehensive assessment has not yet been performed. The purpose of this study was: (i) to rigorously define the phylum; (ii) to gain insight into the phylogenetic and potential taxonomic structure of the phylum; (iii) to assess the distribution of *'Aigarchaeota'*; and (iv) to design *'Aigarchaeota'*-specific 16S rRNA gene primers. Public databases were mined for 16S rRNA gene sequences related to known *'Aigarchaeota'* and a combination of approaches were used to rigorously define the phylogenetic boundaries of the phylum and compile a neighbor-joining and maximum likelihood phylogenetic tree. Primer template gene sequences were aligned in ClustalW in order to locate regions that are suitable for targeting genus-level groups. *'Aigarchaeota'*-specific primers for the polymerase chain reaction (PCR) amplification of 16S rRNA genes were designed using sequence alignments and reviewed using the Ribosomal Database Project Probe Match tool. The analyses supported the proposed relationship between *'Aigarchaeota'*, *Thaumarchaeota*, *Crenarchaeota*, and *Korarchaeota* in the so-called 'TACK' superphylum, and identified ˜300 16S rRNA genes and gene fragments affiliated with *'Aigarchaeota'*, including those recovered from terrestrial geothermal systems on several continents and marine geothermal and subsurface samples. *'Aigarchaeota'* belonged to at least three family- to order-level groups and at least 13 genus-level groups which are represented in the resulting phylogenetic tree. All genus-level groups were recovered from geographically distant locations, suggesting a global distribution. The primers will be used to determine the presence and abundance of *'Aigarchaeota'* in a wide variety of samples from terrestrial geothermal systems in the U.S. and Asia using quantitative real-time PCR.

SESSION 1L

21ST CENTURY CRISIS POLITICS

Session Moderator: Rebecca Thorpe, Political Science

271 MGH

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Necessary Conditions: Political Party Majority Thresholds that May Need be Achieved in Order to Pass Significant Programmatic and Budgetary Legislation Recommended to Prevent Another 2008 Like Crisis

Scott Matthew (Scott) Hodges, Senior, Economics, Mathematics (Philosophy), Political Science

UW Honors Program

Mentor: Victor Menaldo, Political Science

Mentor: Rebecca Thorpe, Political Science

The 2007-2009 financial crisis and subsequent recession has brought the looming unsustainable debt and deficits of the United States to the forefront of the minds of people everywhere. This paper will delve into the puzzle of why neither dominant political party has been able to take the large legislative action needed to implement the recommendations of four well regarded institutions (Office of Management and Budget, The Federal Reserve, the Simpson-Bowles Commission, and the Domenici-Rivlin Debt Reduction Task Force) in light of their general consensus regarding goals that need be met in order to avoid a budget/currency crisis. I ask the question: Why has the Congress of the United States failed to enact the large scale budgetary reforms necessary to bring the US debt/deficit in line with the recommendations? My hypothesis is that there is some threshold of power balance that must be achieved over the opposing political party to achieve a strong enough majority in order to pass legislation that makes large program or budgetary changes. I will investigate legislation before the floor of the House and Senate in the areas of Social Security, and Medicare. First, I discuss the

various recommendations regarding the debt and deficit. Second, I review the literature regarding theories of legislative gridlock. Third, I research and analyze the passage or failure of bills before the House and Senate floor in terms of size of the legislative change in budget and program, as well as compare this to the party balance of power present. Finally, I speculate as to what would be necessary for Congress to pass the large budget/programmatic changes recommended. Having done so, it is our hope that we can provide policy makers and constituents with a deeper understanding of the debt/deficit problem that the country faces.

SESSION 1N

MCNAIR SESSION - STRESS, EMOTION, AND INEQUALITY IN PARENTING, EDUCATION, EPISTEMOLOGY, AND PUBLIC HEALTH DOMAINS

Session Moderator: Gabriel Gallardo, Geography
287 MGH
12:30 PM to 2:15 PM
* Note: Titles in order of presentation.

Global Health Betrayal? Reproduction of Unequal and Uncaring Exchanges
Cynthia Simekha, Senior, Public Health-Global Health
EIP Scholar, Presidential Scholar, McNair Scholar
Mentor: Victoria Lawson, Geography
Mentor: Matthew Sparke, Geography, UCSC

There has been growing scholarly attention to the fact that most global health projects/research are disproportionately focused on specific locales resulting in temporary restricted interventions. This approach is, in some significant sense a 'betrayal' of the very idea of global health. This study asks how Seattle's various global health institutions and organizations approach Global health in Kenya. I hypothesize that most global health projects promote the production of inequity, unequal and uncaring exchanges between donor institutions and the recipients. I analyze the sociohistorical, economic and political histories and ties between Kenya and global health institutions in Seattle drawing on political-economy analysis and feminist care ethical analysis. I also thematically code and analyze ethnographic interviews to investigate the relationship between the responses and the main research topic. I expect to find that global health projects may not necessarily achieve their intended goals because they do not fully consider the four phases of care, which involve attentiveness, responsibility, competence and responsiveness. Understanding the factors influencing the production of unequal and uncaring exchanges in global health is essential as it will impact how global health projects should be conducted.

POSTER SESSION 2

Commons East, Easel 48
1:00 PM to 2:30 PM

Residual Stress of a Carbon Fiber Reinforced Epoxy Double Box Beam
Russell Kilgannon, Senior, Mat Sci & Engr: Nanosci & Moleculr Engr
UW Honors Program
Mentor: Brian Flinn, Materials Science & Engineering

In the past few years there have been large amounts of research done on the benefits of adding metallic nanoparticles into carbon fiber reinforced epoxy composites. The goal of this study is to estimate the effect of nanoparticle additives on the residual stress development in a Double Box Beam carbon fiber reinforced composite structure. Carbon fiber composites are being used in many aerospace applications as a means of weight savings due to their high strength to weight ratio. If residual stress can be reduced, the carbon fiber composite will have increased strength, fatigue resistance, and allow for more precise manufacturing tolerances. The through-hole drilling method is used to test for residual stresses induced by the thermal curing process. Using ASTM Standard Test Method E 837, the test shows the strains before and after the hole was drilled which is associated with the relaxation strain. Working backwards from this relationship and using the equations associated with this method, a value for residual stress was found. Looking at the effect nanoparticles have had on previous research, we can estimate the amount of residual stress present in the Double Box Beam structure with nanoparticles. If time permits values will be validated experimentally by a Double Box Beam with nanoparticles incorporated. Compiling this data gives a clear understanding of how nanoparticles will affect the curing cycle and the residual stress.

SESSION 2N

MCNAIR SESSION - THE CHALLENGES OF SOCIAL TRANSFORMATION: NAVIGATING CHANGE IN SCHOOL AND COMMUNITY ENVIRONMENTS

Session Moderator: Rick Bonus, American Ethnic Studies
295 MGH
3:30 PM to 5:00 PM

* Note: Titles in order of presentation.

Communicating Climate Change in Rural Communities
Sarra Zebra (Sarra) Tekola, Senior, Environmental Science & Resource Management
Mary Gates Scholar, McNair Scholar
Mentor: Richard Fenske, Environmental and Occupational Health Sciences
Mentor: Victoria Breckwich Vasquez, Dept of Environmental and Occupational Health Sciences

Pew Research found that 77% of Democrats believe in climate change compared to 43% of Republicans. This project aimed to measure the impact of community led climate change education on individuals in a traditionally Republican district. This was done with a new approach in bridging the communication gap by bringing together community leaders to discuss climate change in the hope of disentangling the climate conversation from partisan arguments and to promote a dialogue that considers the inter-generational nature of this public health concern. I hypothesized that people will accept information about climate change when it is presented by a community member or relative. I, along with my research team, hosted a community-wide educational forum in Maple Valley and Granger, small rural towns in Washington. The Maple Valley forum was led by a city council member, with five local students who taught their community about climate change using the stories collected from regional farmers and the knowledge they learned in their high school science class. We surveyed the participants (N = 30) before and after the forum to assess whether their perceptions have changed as a result of the forum. After coding the surveys into quantitative data, the effectiveness of the forum was analyzed using a paired t-test. This research will help us assess and refine educational methods for communicating the science and impacts of climate change to rural communities.

SESSION 2P

FOOD, SLEEP AND LIFE: INSIGHTS

Session Moderator: Ian Sweet, Medicine
022 JHN
3:30 PM to 5:00 PM

* Note: Titles in order of presentation.

Elucidating the Link between Tyrosine Metabolism and Aging in *Caenorhabditic elegans*
Farzin Eshaghi, Senior, Biochemistry, Biology (Molecular, Cellular & Developmental)
UW Honors Program
Mentor: Matt Kaeberlein, Pathology
Mentor: Victor Pineda, Pathology

Tyrosinemia Type II is a genetic disorder caused by a mutation in the enzyme tyrosine aminotransferase (TAT), which leads to an elevated level of tyrosine in the blood. If untreated, individuals with tyrosinemia develop life-threatening clinical symptoms that include an increased tendency to bleed, damage to the nervous system, damage to the eyes, and organ failure. Unexpectedly, mutation of TAT in the nematode Caenorhabditis elegans results in animals that are long lived in comparison with wild-type (WT) worms. This study aims to elucidate the cellular mechanism and workings of TAT in the mitochondria, its role in the pathology of the disease, and its possible links with aging in C. elegans. Thus far, we have developed a simple method to measure the CO2 output of the worms and shown that the TAT mutant's metabolism is about 50% compared to WT. This significant decrease in CO2 output was matched comparable to a strain deficient for mitochondrial Cytochrome C Oxidase, which served as a positive control. Cytochrome C Oxidase, or Electron Transport Chain Complex IV, is one of the three complexes that create the proton gradient inside the mitochondrial matrix upon accepting electrons. Notably, mutation of the gene acting downstream to TAT in the tyrosine degradation pathway, which causes Tyrosinemia Type III in people, or any other mutation in tyrosine metabolism that we have tested, causes no significant change in CO2 output of C. elegans. Furthermore, through our preliminary metabolomics assay we have identified three metabolites that are accumulated to extremely high levels in comparison to positive and negative controls. The future steps will include determining whether these metabolites play a direct role in the effects of TAT mutation on mitochondrial function and aging.

POSTER SESSION 3

Commons West, Easel 30
2:30 PM to 4:00 PM

Characterization of Mutations in the Mitochondrial Rieske Iron-Sulfur Protein
Nathan Cole (Nathan) Schurman, Senior, Biochemistry, Biology (Molecular, Cellular & Developmental)
Mary Gates Scholar
Mentor: Matt Kaeberlein, Pathology
Mentor: Brian Wasko, Department of Pathology

The Rieske iron-sulfur protein (Rip1) is a nuclear encoded protein that assembles into the cytochrome bc1 complex of the electron transport chain in budding yeast, Saccharomyces cerevisiae. The iron-sulfur cluster bound by this protein facilitates the flow of electrons during cellular respiration in the inner membrane of the mitochondrial matrix. In the nematode worm, Caenorhabditis elegans, a mutation in a conserved residue of the Rieske iron-sulfur protein has been found that delays development and extends the lifespan of this organism. Mutagenesis experiments from our laboratory have identified suppressors of this C. elegans developmental phenotype that

are due to secondary mutations in conserved residues within a flexible hinge region of the Rieske iron-sulfur protein. The primary mutation and secondary suppressing mutations were introduced to the yeast Rip1 gene through site directed PCR mutagenesis. Transgenic yeast have been created expressing the mutant forms of Rip1 homologous to those identified in C. elegans. The next stages of my project will entail the characterization of these mutations in yeast. I plan to assay the replicative lifespan, growth rate, respiratory efficiency, as well as sensitivity to variance in temperature, reactive oxygen species and carbon source in an effort to understand how this mutant's lifespan extension fits into the larger picture of known aging pathways. The extrapolation of the mechanisms found in these model organisms serve as the basis for understanding our own complex aging process.

POSTER SESSION 3

Commons East, Easel 62

2:30 PM to 4:00 PM

Regulation of Yeast Replicative Life Span: VMA Mutants Response to Supplemental Iron and Antioxidants

Grace Bora (Grace) Kim, Junior, Biology (Molecular, Cellular & Developmental)
Mentor: Brian Wasko, Department of Pathology

The budding yeast, Saccharomyces cerevisiae is a single-celled eukaryote that provides many advantages for use as a model organism, including the ease of genetic and environmental manipulation. The replicative lifespan assay is a commonly used method for quantifying the lifespan of yeast by measuring the number of times an individual mother cell can divide. My laboratory has found that yeast lacking genes encoding subunits of the vacuolar ATPase (V-ATPase) have an extremely short replicative lifespan. The V-ATPase is a multisubunit protein complex that pumps protons across membranes and acidifies intracellular organelles, such as the lysosome-like vacuole in yeast. Lysosomes are organelles in eukaryotic cells containing digestive enzymes that break down and digest macromolecules and waste products. Yeast provides an ideal model for the study of disruption of the V-ATPase as they are able to survive loss of this complex, which is essential in most other eukaryotes. Vma21 is a protein required for the assembly of the V0 subunit of the V-ATPase. I have observed that vma21 mutants are short-lived, have a respiratory growth defect, and are sensitive to low iron levels. My experimental model demonstrates that supplemental iron and antioxidants, such as sodium ascorbate (vitamin C), dramatically increase the shortened lifespan of vma21 mutants. Supplemental iron also rescues the respiratory defect of vma21 mutants. My data supports a model where loss of V-ATPase function results in disrupted iron homeostasis leading to loss of mitochondrial function and shortened lifepsan, which can be rescued by supplemental iron and antioxidants.

POSTER SESSION 4

Commons East, Easel 72

4:00 PM to 6:00 PM

Screen of Human Tau Expressing *Caenorhabditis elegans* for Suppressors of Phenotypes

Landis Kwong, Junior, Biology (Molecular, Cellular & Developmental)
Mentor: Brian Kraemer, Medicine

In neurodegenerative diseases, such as Alzheimer's disease, tau protein aggregation is observed. In Alzheimer's disease and related conditions, accumulation of insoluble tau impairs physiological function that ultimately leads to neuron loss. Using a transgenic *Caenorhabditis elegans* model that expresses human tau protein in neurons, we are able to see accumulated, insoluble, phosphorylated tau, and uncoordinated movement (Unc) phenotypes in these organisms. To identify genes participating in aggregated tau and Unc phenotypes, we conducted a mutagenesis; an estimated 20,000 worm genomes were screened and we isolated seven promising strains of *C. elegans* that carried loss of function genes suppressing the tau-induced phenotypes. These strains are currently being sequenced to determine the identity of the loss of function genes, which may represent novel suppressors of tau pathology. Currently, the Kraemer lab has identified two genes suppressing tau-induced Unc phenotype and called them suppressor of tau 1 (*sut-1*) and suppressor of tau 2 (*sut-2*). Animals with *sut-1* and/or *sut-2* mutations are resistant to the negative effects of tau, meaning that the proteins made by these genes are necessary for tau phenotypes. With this knowledge and the additional information to be gained from the sequencing of seven novel *sut* alleles, we hope that potential neuroprotective approaches for treatment can be developed.