



Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

POSTER SESSION 1

MGH 206, Easel 178

11:00 AM to 1:00 PM

Association of Allelic Variation in ERAP1 with Higher Risk of Gastric Dilatation Volvulus in Great Danes

Thanh Thanh Trinh (Sarah) Dinh, Senior, Biology, Microbiology

McNair Scholar, Undergraduate Research Conference Travel Awardee

Mentor: Michael Harkey, Transplantation Research, Fred Hutchinson Cancer Research Center

Gastric dilatation volvulus (GDV) is a life-threatening condition that occurs in large breed dogs. Previous research investigating three candidate genes of major histocompatibility complex (MHC), DLA88, DRB1 and the innate immunity gene, TLR5 found diagnostic markers that could be used to identify Great Danes at risk for GDV. The Endoplasmic Reticulum Aminopeptidase 1 gene (ERAP1), is now known to be an important up-stream component of the antigen-presentation system of the MHC, and human polymorphisms in this gene have been linked to the same inflammatory disorders. I hypothesize that Great Danes with certain ERAP1 single nucleotide polymorphism (SNP) variants on exons 3,7,12,13,16 associate with the risk for GDV in Great Danes. We conduct the experiment on two groups of Great Danes; eighty dogs are recruited for this study. Half comprise a GDV group consisting of dogs that have undergone emergency surgery for GDV, and a second age-matched gender-matched control group is dogs with no history of gastric problems. We perform polymerase chain reaction (PCR) and sequencing on subjects from both groups in the variable regions of the ERAP1, evaluating alleles from the gene for association with GDV while controlling for dog family, ages, and diet intake. The goal of this work is to establish a list of specific “risk” or “protective” alleles of ERAP1 that are associated with GDV in Great Danes. If the dominant genotype that predisposes dogs to GDV can be determined, this canine GDV model marker will provide a means to detect at-risk animals, especially in Great Danes. Early genetic testing, probiotic, drug-based approaches and gastropexy (a surgery to prevent GDV) could reduce the incidence of GDV.

POSTER SESSION 1

Commons East, Easel 69

11:00 AM to 1:00 PM

Data Analysis Methods for Multiband Gravitational Wave Astronomy

*Mi Do, Junior, Physics: Comprehensive Physics
McNair Scholar*

Mentor: Joey Key, Physical Sciences Division, University of Washington Bothell

In 2015, the Laser Interferometer Gravitational wave Observatory (LIGO) received the first gravitational wave signal, shepherding a new era of discovering the universe in general, specifically, in the field of observing gravitational waves in astronomy. LIGO detected ten binary black hole mergers, and in 2017 the collision of two neutron stars, which enabled the multi-messenger observation of the merger and associated kilonova. To maximize the discovery potential for the new era of gravitational wave astronomy, a comprehensive approach to data analysis and parameter estimation was employed to identify and characterize gravitational wave signals. Therefore, great strides will be made in data analysis methods across the gravitational wave spectrum between groups, including LIGO, the North American Nanohertz Observatory for Gravitational waves, and the Laser Interferometer Space Antenna. This work will continue to expand the Bayesian data analysis strategy, which was successfully used in the first detection of gravitational waves across the gravitational wave spectrum. Specifically, we use Markov Chain Monte Carlo (MCMC) for parameter estimation. By coordinating and combining analyses across the full gravitational wave spectrum we will be able to move science beyond what could be accomplished by any individual group, alone.

SESSION 1H

POLITICS, PARTY, & POWER

Session Moderator: Margaret O'Mara, History

MGH 242

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Disability Inclusion and the United Nations: Leading from Behind?

Shirlee Sophia Helena (Sophie) Watson, Senior, Law, Societies, & Justice

Colin L. Newton, Senior, International Studies

Zu Zinyang Tan, Senior, Sociology

Mentor: Megan McCloskey, School of Law

With the adoption of the 2030 Agenda for Sustainable Development, United Nations Member States committed to ensure international development that “leaves no one behind,” and pledged to reach “the furthest behind first.” Recognizing that globally persons with disabilities as a group are often among those left furthest behind, the Executive Office of the UN Secretary General and the Special Rapporteur on the Rights of Persons with Disabilities are reviewing how UN operations can better integrate and promote the rights of persons with disabilities. To support that review, a study was commissioned to assess the current state of disability inclusion within UN operations at the headquarters and country levels. In December 2018, a research team led by the School for Global Inclusion and Social Development at the University of Massachusetts and supported by undergraduate students at the University of Washington completed a baseline assessment of disability inclusion within the 40 UN agencies, funds and programs which are members of the UN Sustainable Development Group, and 40 UN Country Teams. Although the assessment is not currently public, this presentation discusses the results of our research which focused primarily on evaluating UN entity disability inclusion through public sources alongside staff survey responses.

POSTER SESSION 2

Commons East, Easel 59

1:00 PM to 2:30 PM

Modeling Pulsar Red Noise to Detect Gravitational Waves

Min Young Kim, Junior, Statistics, Physics: Comprehensive Physics

Mentor: Joey Key, Physical Sciences Division, University of Washington Bothell

Mentor: Jeffrey Hazboun, Physical Sciences Division

The North American Nanohertz Observatory for Gravitational Waves (NANOGrav) uses an array of galactic millisecond pulsars to search for low frequency gravitational waves. The stability of millisecond pulsars allows their pulse time of arrival (TOA) to be used as precise clocks. Gravitational waves will produce timing delays that are correlated across pulsars. In order to detect such correlations in TOAs, we must also understand the noise processes in the pulsar signal. Noise model selection aims to produce custom noise descriptions for each pulsar. Using NANOGrav’s search code

enterprise a Markov Chain Monte Carlo (MCMC) algorithm is used to search for the most favored model. A hyper model framework is used to explore across a set of models, which have different red noise and dispersion measure (interstellar medium effect) processes. The posterior odds ratio is then represented by the relative amount of time the chain spends in a model. An iterative approach is taken, where one model selection analysis is used to inform the next set of models from which to choose. The resulting noise descriptions will aid in mitigating its effects within the pulsar signals, increasing chances of gravitational wave detection.

POSTER SESSION 4

MGH 206, Easel 175

4:00 PM to 6:00 PM

Determining the Presence of Streptomycin Resistance Genes in *Escherichia coli* from Crow Feces and Water Runoff in the University of Washington Bothell Wetlands

Megan Christine Fridge, Senior, Biology (Bothell Campus)

Mentor: Keya Sen, School of STEM, UW Bothell

In this study we looked at the presence of streptomycin resistance genes, *strA*, *strB*, and *aadA* and the insertion sequence IS133 for the bacteria *Escherichia coli* obtained from the wetlands located within the University of Washington Bothell. The wetlands serve as a roost for more than 15000 crows all through the autumn and winter months. The hypothesis of this study was that the presence of antibiotic resistance may be able to spread through the vector of American crows. The genes tested in this study encode for factors that play a role in streptomycin resistance (Sugiyama, Masanori, and Osamu Nimi). The IS was tested because it would indicate presence of transposon TN5393 which in turn would suggest the presence of *strAB* genes on conjugative plasmids (Zhao, J., and H. Dang) and thus capable of horizontal gene transfer among the bacteria. The samples were collected from crow feces and water runoff within the wetlands. 23 water samples and 37 fecal samples, were tested by TaqManTM quantitative PCR for the presence of the three streptomycin resistance genes, *strA*, *strB*, and *aadA*. Once the streptomycin genes were detected, the samples were tested to see whether the genes were located on a plasmid by testing for IS133 insertion and the TN5393 transposon. Our results show that 53% of the isolates tested were positive for *strA*, 57% were positive for *strB*, 5% were positive for *aadA*, 22% were positive for IS133, and 22% were positive for both *strA* and *strB*. Plasmids isolated from one water runoff sample and a fecal sample showed the presence of *aadA* and *strB*. The plasmids were successfully transformed into DH5 Alpha *E. coli* and were ampicillin resistant but not streptomycin resistant. These results indicate that there may have been other plasmids in the cell that rendered the samples resistant to ampicillin.

POSTER SESSION 4

MGH 206, Easel 176

4:00 PM to 6:00 PM

Multilocus Sequence Typing of *Campylobacter jejuni* Isolates from Crow of Two Different Geographical Regions

Nidhi Patel, Junior, Biology (Bothell Campus)

David Mateo Ricci, Senior, Biology (Bothell Campus)

Mentor: Keya Sen, School of STEM, UW Bothell

Campylobacter jejuni is a Gram-negative spirochete bacteria that colonizes the guts of many bird species. They are pathogenic to humans and typically consumed with undercooked poultry or contaminated water. In this study, two species of crow, separated by 7,000 miles, have been examined for their ability to carry *C. jejuni*. Crow fecal samples were collected from Bothell, Washington (WA) and Kolkata, India (KK). All of the crow *Campylobacter* isolates were confirmed by qPCR and PCR methods to be *C. jejuni*. No other species are isolated. We compared these isolates by method of MLST (Multilocus Sequence Typing) and searched for known allelic profiles on the PubMLST database. Thirteen isolates were analyzed for seven housekeeping genes: *aspA*, *glnA*, *glyA*, *gltA*, *pgm*, *tkt*, *uncA*. Using primers specified in the PubMLST database portions of the genes were amplified by PCR, verified by gel-electrophoresis and sent to Eurofin Genomics for sequencing. Once the sequence files were returned, they were aligned and assembled using Mega7 software. An allele number was obtained for each sequence for each sequence from PubMLST database. The allelic profile of the 7 genes for each isolate was used to obtain the Sequence type (ST) of the isolate. MLST of 15 crow isolates that represented different phylogenetic clusters based on fla-SVR sequencing, showed a majority of the WA isolates to belong to sequence types ST2678, ST9271, ST3322, ST5472. The Kolkata isolates were ST8288 and ST5472. All types were shown to occur in wild birds. One crow's ST3174 from Kolkata has been shown to occur in human stool, while 4 isolates including Kolkata and Washington were of unknown ST's. Although Kolkata and WA isolates belonged to different ST's, majority were from wild birds that have rarely been isolated from humans.

POSTER SESSION 4

Commons East, Easel 58

4:00 PM to 6:00 PM

Finding the Lineage of *Escherichia coli* (*E. coli*) Isolates from UW Bothell Wetland

Babak Taheri, Non-Matriculated,

Mentor: Keya Sen, School of STEM, UW Bothell

Beside its academia, University of Washington Bothell (UWB) is also known for its phenomenal nature where more than 15,000 crows roost every evening, especially during the autumn and winter months, in the wetlands. Since these crows have infested these wetlands, and because free living birds can be significant contributors of antibiotic resistant (AR) bacteria to the environment they were chosen for this study. *E. coli*, which lives as a harmless commensal in the gut of all animal and birds, has proved to be not only an indicator of fecal coliform but also of antibiotic resistance present in the environment. This study seeks to find out the different sequence types (STs) of *E. coli* found in UWB wetlands using the Multi Locus Sequence Typing (MLST) technique, to find out about the lineage, and potentially how these isolates have ended up in the UWB wetlands. Antibiotic resistance possessed by the isolates was performed against 13 different antibiotics by other students in the laboratory. MLST was performed according to methods specified in the EntroBase database; Specifically 7 housekeeping genes, were amplified and sequenced. Extended spectrum beta lactamase (ESBL) and non-ESBL containing isolates were found. Two non-ESBL isolates, one from water and one from the fecal samples collected on the same date, with the same antibiotic resistant pattern, turned out to be from the human isolated clone ST 58, suggesting a link between crow and water. ESBL *E. coli* isolate ST 131, a highly virulent, and multi drug resistant isolate was found in 6 fecal and 1 water isolate. Therefore it is concluded that crows are potential vectors of spreading multiple drug resistant strains in wetlands, which poses health risk since these strains may be carried further during the winter months.