UNIVERSITY of WASHINGTON

Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

Poster Session 1

Commons West, Easel 30

11:00 AM to 12:30 PM

Does Early Replication of Centromeres Prevent Genetic Instability?

Seungbeen (Steven) Lee, Junior, Biochemistry
Mentor: Bonita Brewer, Genome Sciences
Mentor: Thomas Pohl, Molecular and Cellular Biology Program

DNA replication is vital for cell division as it produces exact copies of all chromosomes for the two daughter cells. During S-phase of the cell cycle, DNA replication begins at specific, defined locations within a chromosome known as origins of replication. Interestingly, some origins activate in early S-phase while others activate late. The biological significance of this temporal control of replication is largely unknown. In multiple species, centromeric DNA, the site of recruitment for proteins required for separation of chromosomes during mitosis, has been found to be early replicating. The Brewer/Raghuraman lab has recently shown that centromeres in the budding yeast *Saccharomyces cerevisiae* promote their own early replication by advancing the activation time of their neighboring origins. The conservation of early centromere replication coupled with the Brewer/Raghuraman lab's recent finding suggests that early centromere replication may be important for chromosome maintenance. We set out to determine the consequences of a late replicating centromere by artificially delaying its replication time in *S. cerevisae*, through replacing its nearby origins with drug resistant markers. To enhance sensitivity of the experiment, I impaired the activity of the spindle checkpoint that monitors correct chromosome segregation. I also constructed a control chromosome with an early replicating centromere and the same markers. I will then compare the degree of chromosomal instability, as measured by survival on drug plates, of the control cells to those that contain a late replicating centromere. We expect the experimental group to show an increase in the number of cells that have lost the chromosome compared to the control cells. Even if the effect is small we will perform long-term growth experiments to analyze how the cells cope with reduced genetic stability. The results of this study will provide a better understanding of the biological importance of the temporal replication program.

Session 1L

Quantifying the Effects of Humans on the Environment

Session Moderator: Bonnie Becker, Academic Affairs (Tacoma)

271 MGH

1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Oh Deer! Unexpected Beneficiary of Wildlife Passage Structure in Granite Falls, WA

Jane Ann (Jane) Hutchinson, Senior,
Mentor: Thomas Murphy, Anthropology, Edmonds Community College
Mentor: Terri Wentworth-Davis, Environmental Services, Snohomish County Public Works

Combining wildlife tracking skills with motion-sensitive cameras, environmental anthropology students can provide practical results for stakeholders who are seeking to provide sustainable solutions to human-wildlife intersections and inform land management decisions. In 2010, the Learn and Serve Environmental Anthropology Field (LEAF) School at Edmonds & Everett Community Colleges partnered with Snohomish County Public Works to monitor a wildlife passage: a 4'x4' box culvert installed in a new road alignment in Granite Falls, WA. The passage connects a five-acre wetland, a mitigation site for the County, with a larger wetland complex associated with the floodplains of the South Fork of the Stillaguamish River, designated critical habitat for Puget Sound Chinook Salmon (*Oncorhynchus tshawytscha*) and Coastal-Puget Sound Bull Trout (*Salvelinus confluentus*). Research results show the culvert being utilized by targeted low-mobility species and Columbian Black-tailed Deer (*Odocoileus hemionus columbianus*), who was thought to be too large to access the passage. July 2011 photos show the first does with their fawns using the passage to cross between the wetland and the riparian corridor. Summer 2012 data shows the return of the does as well as two adolescent bucks accessing the passage. Two years of data appear to show the black-tailed deer are willing to adapt to and use this size of culvert. Through the application of a service-learning strategy students are investigating the effectiveness of the structure and considering whether current land use is-

sues may compromise the long term viability of the wildlife corridor. This research sets the stage for continued citizen science and community outreach projects in Granite Falls. These citizen-science projects become even more critical as populations push into the rural areas of the Pacific Northwest.

SESSION 1N

MCNAIR SESSION - EXPLORING THE NATURAL WORLD: FROM NUMBERS TO NANOPARTICLES AND BATS TO BACTERIA

Session Moderator: Todd Sperry, Office of Minority Affairs & Diversity
287 MGH
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Comparative Lipid Synthesis and Acyl Saturation of Psychrophilic and Psychrotrophic *Geomyces* Fungi
Hannah Blair, Recent Graduate, Wildlife Ecology & Management, Arkansas State University
McNair Scholar
Mentor: Thomas Risch, Biological Sciences, Arkansas State University

Geomyces destructans is a psychrophilic (cold-loving) fungus that causes cutaneous infections in cave dwelling bats and high mortality in North American populations. *Geomyces pannorum* is a closely related psychrotrophic (cold-tolerant) species that is a rare skin pathogen of vertebrates. Cold-adapted organisms adjust lipid synthesis to lower membrane viscosity and thus survive unfavorable habitats. Lipid profiles, or lipid class composition, may partially explain ecological niche and *G. destructans* pathogenicity to bats. Additionally, profiles are species specific and may be utilized to differentiate closely related species and detect disease. We incubated *Geomyces* at 5, 8, 15, 18, and 22 C and isolated fungal lipid content. Broad lipid classes were determined to be primarily sterols, free fatty acyls (FFAs), and triacylglycerides (TAGs). *Geomyces destructans* produced higher proportions of unsaturated 18 carbon TAGs than G. pannorum. *Geomyces* produced more 18:3 (18 carbon, 3 double bonds) TAGs at five degrees than at higher temperatures. *Geomyces destructans* made higher proportions of TAGs at its growth limits, suggesting alterations in lipid synthesis to decrease cellular toxicity and reproductive effort. Furthermore, these results indicate *Geomyces* alter lipid structure to survive cold temperatures by increasing lipid unsaturation. Future studies should focus on temperature optima of enzymes involved in TAG synthesis and disruption of lipogenic metabolic processes. Lipid profiles among multiple *Geomyces* species should be further investigated as a method of disease detection.

SESSION 1N

MCNAIR SESSION - EXPLORING THE NATURAL WORLD: FROM NUMBERS TO NANOPARTICLES AND BATS TO BACTERIA

Session Moderator: Todd Sperry, Office of Minority Affairs & Diversity
287 MGH
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

Degradation of Bat Wings by *Geomyces destructans*
Cheyenne Gerdes, Senior, Wildlife Ecology and Management, Arkansas State University
McNair Scholar
Mentor: Thomas Risch, Biological Sciences, Arkansas State University

White-nose Syndrome (WNS) is a wildlife disease caused by the pathogenic fungus *Geomyces destructans* that has resulted in the mass mortalities of North American cave bats. One clinical sign of WNS is wing necrosis. *Geomyces destructans* may secrete proteases that degrade tissue, thus reducing wing strength and elasticity. We isolated *Geomyces destructans* extracellular enzymes from an in vitro system and applied enzyme solution to bat wing tissue. The toughness, strength, and elasticity of tissues was assessed with tensile testing. Protease activity was assessed with SDS-PAGE and peptide mass fingerprinting by MALDI-TOF MS. Protein profiles generated by SDS-PAGE indicate higher solubilized protein in treated samples. Major bands were identified as integumentary proteins by MS. Tensile testing did not detect damage, but *Geomyces destructans* proteases may cleave host integument.

SESSION 1R

SYNTHETIC BIOLOGY AND MOLECULAR BIOTECHNOLOGY

Session Moderator: Daniel Ratner, Bioengineering
022 JHN
1:15 PM to 2:45 PM

* Note: Titles in order of presentation.

A Molecular Tether Design for von Willebrand Factor Protein Constructs

Tessa Olmstead, Senior, Bioengineering, Dance: Creative Studies
Mary Gates Scholar
Mentor: Wendy Thomas, Bioengineering
Mentor: Emilie Clemmens, Bioengineering

Affecting nearly 1% of the human population, von Willebrand Disease (VWD) is the most prevalent inherited bleeding disorder worldwide. VWD is caused by impaired platelet adhesion due to low plasma von Willebrand Factor (VWF) concentration, or dysfunction. The largest plasma glycoprotein, VWF's function is to mediate attachment of platelets to the exposed collagen on blood vessel walls at sites of injury. This interaction is sensitive to changes in flow forces or shear stress. To facilitate the study of VWF, the Thomas Lab is developing a single-molecule force measurement platform called magnetic tweezers; a tool capable of performing multiple single-bond force measurements in parallel. To use magnetic tweezers, VWF protein domains of interest are adsorbed to a glass surface on one end, and to a magnetic bead on the other. Electromagnets are then placed above the slide, applying an upward force to the VWF domains. The design and optimization of the VWF domain tethers is the focus of this research project. At present, a tethering scheme is being tested that utilizes the strength and longevity of the biotin-streptavidin non-covalent bond and the fimH lectin domain to mannose interaction. An alternative tethering scheme employing histidine tags instead of fimH is also being explored. While both types of tethers have been expressed successfully, tested in the magnetic tweezers, and shown to bind beads to the surface under force, recent data has shown that non-specific adhesion between protein-functionalized magnetic beads and the coverslip is an issue. Using immunoassays such as ELISA and the Western Blot, tether designs will be optimized using magnetic tweezers. With the capability to more accurately mimic physiologic conditions than immunoassays alone, coupled with the intrinsic ability to multiplex, the quantity and quality of data that could be acquired is impressive.

SESSION 2J

INFECTIOUS DISEASES

Session Moderator: James Mullins, Microbiology
254 MGH
3:45 PM to 5:15 PM

* Note: Titles in order of presentation.

Molecular Mechanism of Human CD1A-Deficiency

Meera Kerki (Meera) Shenoy, Senior, Microbiology
Mary Gates Scholar
Mentor: Thomas Hawn, Medicine
Mentor: Chetan Seshadri, Medicine

Mycobacterium tuberculosis infection is a leading cause of death worldwide, but the full details of how the human immune system responds to these bacteria are not known. Our lab studies CD1 proteins, which allow T-cells to recognize and respond to lipids which are the major constituents of the mycobacterial cell wall. We recently discovered that low expression of CD1A on dendritic cells is present in ˜10% of the population and is associated with increased susceptibility to tuberculosis in Vietnam. In addition to low surface protein expression, CD1A transcription is also impaired in CD1A-deficient individuals. The molecular mechanism of CD1A-deficiency is unknown. I hypothesized that CD1A expression is regulated by a single nucleotide polymorphism (SNP) that alters transcription factor binding. I cloned and analyzed the CD1A 5' untranslated region (UTR) from four CD1A-deficient and five control individuals. There was one SNP, rs366316, that showed an association with CD1A-deficiency. I genotyped 163 individuals and examined the association of the rs366316 genotypes with CD1A expression. I found that the C/C genotype (N=9) was associated with CD1A-deficiency in comparison to the C/T and T/T genotypes (N=154, $p<0.01$). Based on this association, I examined whether the C/C genotype regulated transcriptional activity. I isolated 5'UTR sequences in normal and deficient individuals that were identical except for rs366316. I used site-directed mutagenesis to generate C to T mutants and T to C mutants. I made separate luciferase expression vectors for each of the four 5'UTR constructs and found that the normal and mutated 5'UTRs with a C allele showed 44% less expression than the normal and mutated 5'UTRs with a T allele ($p<0.001$). These data show that a SNP in the 5'UTR of CD1a is causally associated with human CD1A-deficiency. Together, these data suggest that CD1A-deficiency is common, regulated by a SNP, and important in MTB pathogenesis.

POSTER SESSION 3

Commons East, Easel 49
2:30 PM to 4:00 PM

The Human NLRC4 Inflammasome and Immune Defense against *Pseudomonas aeruginosa*

Kelsey Christine (Kelsey) Nebeck, Non-Matriculated,
Mentor: William Berrington, Medicine
Mentor: Thomas Hawn, Medicine
Mentor: Glenna Peterson

Pseudomonas aeruginosa (*P. aeruginosa*) is a ubiquitous species of pathogenic bacteria and a major cause of hospital-

acquired pneumonia. Immune responses to *P. aeruginosa* infection in mice are mediated by a cytosolic multiprotein complex called the NLRC4 inflammasome. The NLRC4 inflammasome assembles upon ligand recognition leading to the release of the pro-inflammatory cytokine interleukin (IL)-1β and culminating in cell death. *P. aeruginosa* elicits a flagellin-dependent release of IL-1β and cell death in mouse macrophages, but research has not found human macrophages to recognize flagellin. This immune response is evoked in human macrophages by needle protein, an element of the type three secretion system (T3SS) infection apparatus used by *P. aeruginosa*. The mechanisms human macrophages use to regulate immune response to *P. aeruginosa* have not been fully established. We hypothesize that NLRC4 regulates immune response to *P. aeruginosa* in humans and therefore, NLRC4 deficient macrophages infected with *P. aeruginosa* will have impaired cell death and IL-1β production compared to normal NLRC4 expressing cells. Small interfering RNA (siRNA) will be used to knock down mRNA and protein expression of NLRC4. Macrophages treated with non-specific siRNA and NLRC4 targeted siRNA will be infected with live *P. aeruginosa*. We will then assay for IL-1β with ELISA and cell death using a lactate dehydrogenase (LDH) release assay. We expect NLRC4 knockdown cells to release less IL-1β and LDH compared to cells treated with non-specific siRNA thus indicating that in humans, the NLRC4 inflammasome is associated with defense against *P. aeruginosa* infection. Upon establishing the function of human NLRC4 during *P. aeruginosa* infection, we will proceed to investigate the roles of NLRC4 inflammasome subunits in ligand recognition and initiation of an immune response. Defining these roles could further our understanding of mechanisms behind immunity or susceptibility to *P. aeruginosa* and potentially lead to novel treatments for infection.

POSTER SESSION 3

Commons East, Easel 69

2:30 PM to 4:00 PM

Feasibility of Transferring Gallium Phosphide to Diamond Using PDMS

Edward Payne Roberts, Junior, Mat Sci & Engr: Nanosci & Moleculr Engr

Mary Gates Scholar

Mentor: Kai-Mei Fu, Physics/ECE

Mentor: Nicole Thomas, Electrical Engineering

The overall project that I work in is to see how quantum states can be used to process information. To realize this, we utilize crystal defects in diamond that exhibit quantum properties. We then network the defects using GaP as a photonic waveguide. GaP is used because at the wavelength of the defect, it is transparent and its index of refraction is higher than diamond. My contribution to this project is to investigate the feasibility of using polydimethylsiloxane (PDMS), a material similar to rubber, as a way to transfer gallium phosphide (GaP) on to the diamond. Using PDMS allows the amount of GaP transferred to be easily scaled due to the surface area of PDMS. I will first use more widely available silicon on insulator substrates to develop a general process flow. The silicon will be patterned as 50 by 50 micrometer squares using photo-lithography and plasma etching. The squares are then transferred to a secondary substrate using a PDMS stamp. We expect then to be able to apply the processing scheme developed for silicon to the transfer of GaP onto diamond.

POSTER SESSION 3

MGH 241, Easel 143

2:30 PM to 4:00 PM

Perch-Type Characteristics in Overwintering Red-Tailed Hawks (*Buteojamaicensis*) and American Kestrels (*Falcosparverius*)

Alexander Worm, Senior, Wildlife Ecology and Management, Arkansas State University

McNair Scholar

Mentor: Thomas Risch, Biological Sciences, Arkansas State University

Mentor: Melissa Bobowski

Red-tailed Hawks (*Buteojamaicensis*) and American Kestrels (*Falcosparverius*) are sit-and-wait predators that rely on perch-sites to forage efficiently. Overwintering Red-tailed Hawks and American Kestrels use available perches (i.e., utility poles and wires, trees, fences, gates, etc.) to hunt for prey items in the agricultural fields in Northeast Arkansas. Observations were made from December 2011 to the present on three representative cover types: short rice stubble, soybean stubble, and fallow areas including roadsides in order to determine which perch-sites were used by Red-tailed Hawks and American Kestrels the most. Prey density and vegetation cover were also estimated in each cover type. Utility pole crossbeams at a height of 6.3 meters are the main perch-site used by Red-tailed Hawks, demonstrating the use of man-made structures as perch-sites. These perches were generally in or near short rice stubble fields, which were found to have the lowest amount of vegetation cover, and low prey density. Conversely, American Kestrels most used utility wires at a height of 4.9 meters from the ground, over fallow roadsides as perch-sites, representing an area with high prey density and vegetation cover. Although there have been documented cases of inter-specific competition between these two species, Red-tailed Hawks and American Kestrels may limit direct interaction via differential uses of perch-sites. The study gained insight into the behavioral ecology of two competing raptors in northeast Arkansas.

POSTER SESSION 4

Commons West, Easel 23

4:15 PM to 5:45 PM

Petals' Shape and Growth in Blooming Lilies

Peter Nathaniel (Peter) Holmes, Junior, Biology (Molecular, Cellular & Developmental)
Mentor: Thomas Portet, Chemistry
Mentor: Sarah L. Keller, Chemistry

Lily blooming has recently been suggested to result from differential growth of the petals. The tissue expands along the edges, making them longer than the midrib. To accommodate for this excess length, the petal reverses its curvature, causing the bud to open. This is the growth driven mechanism for lily blooming. We inquired into the shape of the ripples resulting from edge growth and if we could observe direct evidence of the growth. We first investigated rippling, another consequence of edge growth. When the growth rate is high enough, lily petals ripple and their edges adopt their characteristic wavy shape. Using time-lapse imaging, we observed lily petals' edges rippling. We monitored the formation of several generations of ripples, with a fractal-like pattern of smaller waves superimposed onto larger ones. We also measured the temporal evolution of the ripples' wavelength, amplitude and arc length. We found that these quantities could be related using a geometric argument. Agreement between our prediction and observations is excellent. This indicates that in addition to biology, physics plays a significant role in determining the shape of lily petals. Second, we sought to quantify edge growth. We took quantitative measurements of the different growth rates, by tracking the positions of marks along the edge and along the midrib. We found that the growth rate is 35% larger along the edge than along the midrib, supporting the edge growth driven blooming model. We now want to measure the growth rates of different lily species, and investigate whether smaller growth rates can correlate to the absence of ripples. The purpose was to understand the 3D shape resulting from growth in a 2D sheet to supply knowledge leading to understanding plant development. It will also lead to applications in the packaging industry where flat shapes are made into 3D objects.

POSTER SESSION 4

MGH 241, Easel 155

4:15 PM to 5:45 PM

The Application of Quantum Dot Technology for Protein Localization in Breast Cancer

Rachel Victoria (Rachel) Lucero, Junior, Bioengineering
Mentor: Tania Vu, Biomedical Engineering, Oregon Health and Sciences University
Mentor: Thomas Jacob, BME, Oregon Health and Sciences University

Understanding the complex signaling pathways that lead to tumor formation is essential for developing methods the diagnosis, prognosis and treatment of cancer. As the proteins implicated in these pathways are often overexpressed or constitutively activated, the technology for detecting these proteins is necessary for this area of research. Recently, studies have suggested the importance of subcellular localization of these proteins in diagnosing cancer subtype and survival rate. However, the current analytical methods for detecting specific proteins do not provide enough spatial or quantitative information for single-molecule resolution. Quantum dots are nano-sized fluorescent crystals that can label single molecules and be more accurately quantified than fluorescent dye, which is currently used. Quantum dot labeling technology offers the high spatial and temporal resolution that is needed to study the localization of cancer-relevant proteins. We studied the correlation of the protein Akt, which has previously been suggested to preferentially localize in the nucleus or cytoplasm depending on the breast cancer subtype. We used a combination of quantum dot labeling and cellular compartment staining on a breast cancer cell line, and stimulated with insulin to activate Akt for varying amounts of time. Cells were imaged via fluorescent microscopy and the localization of proteins was conducted through MATLAB. Our results showed increased activation of Akt in the stimulated cells over non-stimulated cells, as measured with our quantum dot probe. We also showed an insulin stimulation-dependent localization of Akt. This project suggests that quantum dots can effectively label Akt in breast cancer cell lines at a high spatial and temporal resolution and offer a new platform for studying the mechanisms of cancer signaling proteins.

POSTER SESSION 4

Balcony, Easel 88

4:15 PM to 5:45 PM

Discovering the Inner Oort Cloud

Jesse Velasquez, Senior, Astronomy, Physics: Comprehensive Physics
NASA Space Grant Scholar
Mentor: Thomas Quinn, Astronomy

The discovery of 2003 VB12, or "Sedna", far beyond Pluto has suggested a new class of Solar System objects. These objects are not members of the Kuiper belt, a large disk of icy objects spanning roughly 30 AU to 50 AU from the sun;

nor do they reach far enough to be considered members of the Classical Oort Cloud, which is comprised of Long Period Comets (LPCs) and distant objects that may take millions of years to orbit the sun. Both of these groups and this new class of objects are likely debris from the planets' formation, making them surviving "fossils" from the Solar System's early history that can be directly examined. Despite the great numbers of this population, however, the vast majority is undetectably dim, a problem that observers hope to address by peering deeper than ever with the upcoming Large Synoptic Survey Telescope (LSST). Sedna-class objects may be unique in that they provide clues about the Solar System's interaction with the Galaxy over its history. Because they orbit beyond the boundaries of planetary perturbations, they could have resulted from the sun's migration close to the galactic center. I, along with Alexia Lewis, ran simulations of the Solar System's formation with this migration model. I then analyzed them alongside "static" model simulations, which could be compared to past survey data and be used to predict the numbers of comets and Sedna-like objects that will be seen by the LSST. Later verification by the LSST will constrain models of the inner Oort cloud (where LPCs are expected to be abundant) and the region of Sedna-like objects, provide exciting new clues toward our models of how the Solar System was formed, and whether it has migrated from the center of the Galaxy over its history.

POSTER SESSION 4

Commons West, Easel 41

4:15 PM to 5:45 PM

Unexpected Stories: Nikkei Concerns Oral History Project

Crystal (Crys) Donovan, Sophomore, Anthropology, Edmonds Community College
Mentor: Thomas Murphy, Anthropology, Edmonds Community College
Mentor: Marshall Kramer

The Learn and Serve Environmental Anthropology Field (LEAF) School at Edmonds Community College has partnered with Nikkei Manor and the Wing Luke Museum to develop the Nikkei Concerns Oral History Project. Through this project, students have the opportunity to serve as both mentors and mentees. Eight students have undergone training, interviewed and recorded the experiences of Japanese Americans who were interned during World War II. From these survivors we are learning more than the easy to record factual history, we are learning about experience, about the diversity of coping strategies, adaptive solutions, and emotional struggles these Americans lived. We found unexpected stories relating to aspects of control and freedom within the camps, as well as humor, acceptance, bitterness and forgiveness. The hope in a project such as this is to develop a greater understanding of the experience of these people, to record their stories and create awareness of what they faced. This is a unique opportunity for students to hear firsthand accounts from internment survivors and participating students will continue to learn about the internment era while transcribing the stories shared by Nikkei residents, and mentoring their classmates in the transcription process. While there has been much research elsewhere, the story of internment in the Northwest has received less attention. This project has allowed for student engagement and development as well meeting the needs of the Nikkei residents who wished to share their stories. Recordings will be kept both by the Wing Luke museum and Edmonds community college.

POSTER SESSION 4

MGH 241, Easel 140

4:15 PM to 5:45 PM

Developing Magnetic Tweezers for Multiplexed Single Molecule Force Measurements to Quantify Biomechanical Function of Von Willebrand Factor

Hani Jason (Hani) Mahmoud, Senior, Bioengineering
Mary Gates Scholar
Mentor: Wendy Thomas, Bioengineering
Mentor: Emilie Clemmens, Bioengineering

Single-molecule force spectroscopy is a powerful tool for studying mechanical forces on proteins and other biological molecules. Magnetic tweezers (MT), optical tweezers, and atomic force microscopy (AFM) are specific examples of high-resolution tools that allow users to investigate how changes in the biomechanical function of a single protein, for example, can lead to larger effects in the complete organism. We have chosen to develop and implement an MT apparatus due to its unique potential to expand our current capabilities by allowing many single-molecule measurements in parallel. In this system, molecules are tethered to a glass surface and to magnetic beads, and a magnetic field is applied to pull on the beads and thus the molecules. We then used a bead-tracking algorithm to derive quantitative force measurements. We hope that multiplexing will allow for a more efficient study of how mechanical forces regulate molecular structure and function. Ultimately, this knowledge can be applied to both engineering innovative materials and designing therapeutic interventions. For example, we are using our MT to investigate how mutations in a blood clotting protein called von Willebrand factor (VWF) can lead to bleeding disorders. We intend to accomplish this by measuring how VWF's sensitivity to forces comparable to those in the blood affect its roles in platelet binding. VWF also plays a major role in stroke and myocardial infarction, which we hope to study and quantify using our MT system.

POSTER SESSION 4

Balcony, Easel 115

4:15 PM to 5:45 PM

Movement of Salmon Carcasses from Streams into Riparian Areas by Brown Bears (*Ursus arctos*)

Brendan Smith, Junior, Biology (Ecology, Evolution & Conservation)
Mentor: Thomas Quinn, Aquatic & Fishery Sciences
Mentor: Morgan Bond, Aquatic and Fishery Sciences

Each summer, millions of Pacific salmon (*Oncorhynchus spp.*) leave the ocean to return to the streams and lakes where they were born several years earlier. These fish provide a rich resource of nutrients (e.g. eggs, carcasses) to a wide variety of consumers in their spawning watersheds; from insects to fishes, birds and apex consumers like the coastal brown bear (*Ursus arctos*). While most fish are consumed by bears in the spawning areas of streams, some proportion of the total population of fish is moved into adjacent riparian zones by the bears for later consumption. Although the importance of this subsidy is well documented, few studies have attempted to measure the population level impact of bear consumption on spawning salmon. We quantified the extent and geographic range of bear consumption and carcass movement in a small stream in Bristol Bay, Alaska by conducting daily surveys on the riparian trails used by bears and counting carcasses found there. Our surveys built upon nearly 50 years of in-stream salmon counts where the daily number of dead and alive fish, as well as the degree of consumption of each fish has been measured. We found that 31% of the total fish population was moved into riparian zones during the 2012 season. The mean distance moved was 3.68 meters and the maximum distance recorded was 30 meters. We found no significant differences in the distance moved between sexes of salmon, or in carcass consumption as a function of distance moved. The large quantity of salmon removed from the stream by bears indicates that salmon abundance estimates obtained through manual stream surveys in 2012 significantly undercounted the returning population of salmon. We suggest that riparian carcass removal be factored into future stream surveys for salmon abundance estimation, and present potential methods for further quantifying this effect.