Monday, October 8, 2012

SCIENCE RESEARCH SYMPOSIUM

Student Presenter Research Abstracts

Rohan Bhandari
CC 2013
Physics

Rohan Bhandari is a senior studying physics. Currently he is a part of the ATLAS experiment at the European Organization for Nuclear Research (CERN). He is using data from the proton-proton collisions of the Large Hadron Collider (LHC) to search for Supersymmetry, a theory that predicts the existence of a "superparticle" for each of the existing fundamental particles. The evidence Rohan is looking for is photons that reach the detector slower than expected and also appear to have come from somewhere other than the collision point. Because of this, Rohan worked on calibrating and increasing the timing precision of the Liquid Argon Detector in order to differentiate between slow and normal photons. Aside from particle physics, Rohan has previously worked on studying the electronic properties of Graphene in a condensed matter physics laboratory. He is also the Co-Techincal Lead for the Uganda program of Columbia's chapter of Engineers Without Borders. In his free time, though, Rohan enjoys practicing with Columbia's Judo club, which he helped co-found.

Faculty Advisor: John Parsons

Increasing the Timing Precision of the Liquid Argon Calorimeter of the Large Hadron Collider

Even though the Liquid Argon Calorimeter has excellent timing precision, certain physics analyses, such as the search for evidence of supersymmetric models, require even greater resolution. Because of this, a timing calibration and resolution study using events with a Z particle decaying to two electrons was carried out to optimize the precision. The calibration required five corrections. The run number correction takes into account timing changes that occur between runs, such as those from seasonal changes and maintenance work. The front end board and channel offsets account for the discrepancies between the clocks of the different boards and sampling times, respectively. The timing can also be distorted if large amounts of energy are measured by a cell of the calorimeter. The energy-dependent correction adjusts for this. Lastly, there is a correction applied for cases in which the collision does not occur at the exact center of the detector. After all the corrections were applied, a timing resolution of ≈300 picoseconds is reached, given a cell with a large energy deposit.

Steven Castellano
CC 2013
Biophysics

Steven Castellano (CC'13) is a biophysics major who has been working in the Yang lab for the past three years. During his time in the Yang lab, he has predominantly been working on purifying and crystallizing intracellular regions of TRPM channels, though he has also worked on purifying and crystallizing intracellular domains of TRPC6 and the extracellular loop of

TRPML1. More recently, he has begun working on solving the crystals structures of nyctalopin and stathmin 2, proteins necessary for vision and growth cone formation, which bind to TRPM1 and TRPC5, respectively. Steven is also the Academic Affairs Representative to the Columbia College Student Council, the coordinator of Columbia Urban Experience, the Policy Chair of the Student Wellness Project, an Introductory Biology Teaching Assistant for Deborah Mowshowitz, and a volunteer tutor for middle school and high school students.

Faculty Advisor: Jian Yang

Identification of TRPC6 and TRPM8 Cytoplasmic Domains for Structural Studies by Fluorescence Detection Size-Exclusion Chromatography

TRPM8 channels are classes of TRP channels that play roles in depression cold sensation, yet the precise mechanisms by which they function are largely unknown. It is logical that the structure of the proteins in their N-terminus will help to understand these mechanisms. In this study, we attempt to identify the cytoplasmic domains that are suitable for structural studies by fluorescence. TRPM8 GFP-tagged constructs were made, and they were transformed into Rosetta II cells before protein expression was induced. When the proteins were then isolated and ran in a gel filtration column, only those that gave off the appropriate fluorescence spectrum for GFP were further studied, because such a spectrum indicated that those constructs produced well-folded, soluble protein. These proteins were then re-expressed and purified using six different methodologies until they were successfully isolated from Maltose Binding Protein. When the most stable isolated proteins were then concentrated and expressed in thousands of different environments, no crystals were found. Consequently, protease digestion, co-expression of the N and C termini, narrowing of the constructs, expression of the constructs in different vectors without MBP, and expression of the proteins from homologous regions on TRPM2, TRPM4, and TRPM5 were pursued, but the crystals obtained were either salt or not reproducible.

Monica Chen
CC 2014
Biochemistry

Monica Chen (CC'14) is a junior Biochemistry major. She has been working in Professor Donald Hood's visual science lab studying glaucoma progression. Monica is also the treasurer for the Columbia Undergraduate Science Journal (CUSJ) and the public relations chair for the Columbia Science Review (CSR).

Faculty Advisor: Professor Hood

The Transition Zone from Relatively Healthy to Severely Affected Retina in Glaucoma Patients

Purpose: To better understand the structural changes in the transition zone (TZ) from relatively healthy to severely affected regions in glaucoma patients using frequency domain optical coherence tomography (fdOCT).
Methods: High-quality fdOCT macular vertical line scans (3DOCT-2000; Topcon, Inc) were obtained from 12 eyes of 10 glaucoma patients (61.1 ± 7.7 yrs) with central defects and from 15 eyes of 15 healthy controls (55.1 ± 11.0 yrs). Using a previously validated [1] computer-aided manual segmentation procedure [2], retinal nerve fiber layer (RNFL) and retinal ganglion cell plus inner plexiform layer (RGC+) thicknesses were obtained and then normalized by subtracting the mean control thicknesses at each retinal point. These normalized thicknesses were plotted relative to the point *(tz_0)* they dropped below controls by 2 SD. A piecewise model was fitted to the plots of RNFL and RGC+ thickness versus retinal location relative to tz_0. According to the model, *T* (normalized thickness) = *0* when $x < x_1$ (healthy region), $T = m(x - x_1)$ when $x_1 \leq x \leq x_2$ (TZ region), and $T = r$when $x > x_2$ (severely affected region) where *x* is distance relative to tz_0 in mm, *m* is the rate of thickness change across the TZ in µm/mm, *r* is the residual thickness (µm) measured in the region severely affected by glaucoma, and *w* ($w = x_2 - x_1$) is the width of the TZ.
Results: The model provided a reasonable fit to the average RNFL ($R^2 = 0.99$) and RGC+ ($R^2 = 0.99$) data (model dashed, avg black, ±1 SE gray in Fig). The best fitting values (*m; r; w*) were -39 µm/mm; -25 µm; 0.64 mm for the RNFL and -53 µm/mm; -32 µm; 0.60 mm for the RGC+. For individual RNFL and RGC+ data, the range of best fitting values for TZ width *(w)* was 0.38 to 1.04 mm (RNFL) and 0.31 to 1.40 mm (RGC+). An abrupt model (dotted in Fig) did not fit as well [$R^2 = 0.78$ (RNFL), 0.80 (RGC+)].
Conclusions: There is a TZ between healthy and severely affected regions of glaucomatous field defects in the macula. While the TZ is relatively narrow, on average 2.2° (RNFL) and 2.1° (RGC+), it is broader than expected based on an abrupt model. It remains to be determined whether the RGC+ TZ represents "sick cells" or a mixture of healthy and lost cells. In any case, measurement of the TZ may provide a sensitive method for assessing progression.[1] Hood DC et al. OVS. 2011. [2] Hood DC, Lin CE et al. IOVS. 2009.

Woo Chang Chung
CC 2013
Physics

Woo Chang, CC' 13, is a physics and mathematics major from Allendale, NJ and originally from Seoul, South Korea. His primary interest is in condensed matter physics, a field that attempts to explain diverse complex phenomena in materials; it has been associated with the term "nanotechnology" over the last two decades and has rich potential for both new physics and applications. In the summer of 2012, Woo Chang studied the epitaxial growth of Bi2Se3 on hexagonal boron nitride substrates using atomic force microscopy (AFM) under the advice of Prof. Abhay Pasupathy in the Physics Department of Columbia University. Woo Chang is an I.I. Rabi Scholar and a board member of the Undergraduate Mathematics Society.

Faculty Advisor: Abhay Pasupathy

Characterization of the Epitaxial Growth of Bi2Se3 on h-BN

Topological insulator is a new state of matter that is of high interest to both theoretical and applied physicists. Topological insulators are insulating in the bulk domain but metallic on the surface, and they are predicted to have surprising electronic transport properties, such as locking of spin perpendicular to electron momentum and protection from scattering by time-reversal invariant disorder. Bi_2Se_3 is a three-dimensional topological insulator with a bulk band gap around 0.3 eV, which is larger than the thermodynamic energy scale of room temperature, making it a promising material for future applications such as in spintronics. An experimental problem with growing single-crystalline Bi_2Se_3 is the difficulty of obtaining an atomically sharp interface between the crystal and the substrate; hexagonal boron nitride (h-BN) is a nice candidate for the Bi_2Se_3 film substrate in this respect because of its amazing flatness. In the summer of 2012, I studied the epitaxial growth of Bi2Se3 films on h-BN, SiO2, and sapphire substrates by atomic force microscopy (AFM); film growth was done by collaborators at Rutgers University. AFM images of the film surfaces show that films grown on h-BN is superior to those on SiO2 in terms of flatness and crystallinity, and comparable to those on sapphire. It is of high interest how these growth characteristics translate to gated device performances, and future studies will involve fabricating a gated Bi2Se3 / BN device with Hall geometry and measuring its surface electron mobility and other transport properties.

Samuel Grunblatt
CC 2013
Astrophysics

Samuel Grunblatt is a member of the Columbia College class of 2013 studying Astrophysics. His past research has included study of gravitational wave signatures, photometry of cataclysmic variable stars, and spectroscopy of high-energy astrophysical phenomena. His current project was a comparative spectroscopic study of gamma ray burst afterglows in the optical and infrared. Outside of his studies, Sam is the Music Director of the Columbia Kingsmen, Columbia's original a cappella group, and is also a member of the Columbia Ski and Snowboard Club and the CU Jazz Performance Program.

Faculty Advisor: Professor Joe Patterson

Color-Color Plotting of Gamma Ray Burst Afterglows in Seven Filters

Gamma ray bursts are the most powerful phenomena we know of in our Universe. Although the bursts themselves last only a few seconds and appear in the gamma ray spectrum, the afterglow from these bursts may persist for up to weeks afterwards, visible in many other parts of the spectrum. Currently, the best way to find these afterglows are to observe possible candidates for weeks at a time to see if they follow the typical progression of gamma ray burs afterglows. Here the GROND telescope in La Silla, Chile has been used to observe multiple afterglows in the optical and infrared spectrum, through g, r, i, z, J, H, and K filters

simultaneously. These images have then been reduced, and the colors of all objects in the field have been found for g-r, r-i, i-z, z-J, J-H, H-K, J-K, and r-K. The afterglow has then been identified and corrected for extinction. Synthetic stars have also been added for clarity. I find that the afterglows deviate from the main sequence, and can be grouped in a redder region, although results vary depending on the colors used. These data will help us to better identify gamma ray bursts as quickly as possible, as it does not require the use of a time progression.

Mytra Haerizadeh
CC 2013
Premedical Sciences/Hispanic Studies

Mytra Haerizadeh is a Columbia College senior majoring in Hispanic Studies and Premedical Sciences. She is very interested in public health issues, and this led her to the Nicotine Research Lab at the Columbia Medical Center. She is currently a research intern investigating the effects of pioglitazone on nicotine abuse and addiction. Outside of the lab, she is a Campus Coordinator for Health Leads, a national non-profit dedicated to breaking the link between poverty and poor health. She is also the Co-President of the Columbia Iranian Students Association and a member of the Undergraduate Recruitment Committee.

Faculty Advisor: Dr. Adam Bisaga, M.D.

Effects of Pioglitazone on the Abuse Liability of Nicotine

Nicotine dependence is an important public health problem that contributes to significant morbidity and mortality in our society. Treatment efforts are hampered by high relapse rates, despite the development of somewhat effective treatment modalities such as the Nicotine Replacement Treatment (NRT). The goal of this research is to improve the effectiveness of treatment for nicotine dependence by testing a new pharmacological strategy. Pioglitazone, a peroxisome proliferator-activated gamma receptor agonist, is being tested in combination with agonist-based nicotine treatment. If pioglitazone is proven to reduce nicotine craving and relapse, then our society would have a novel way of combating addiction to cigarettes and other substances.

Veronica Jove
CC 2014
Biological Sciences

Veronica Jove is in her junior year in Columbia College, studying Biological Sciences and Hispanic Studies. Veronica began her research in Dr. Manley's lab after her freshman year and, through the support of an Amgen Scholar grant, she was able to continue this past summer. The Manley lab focuses on the regulation and mechanisms of gene expression and

Veronica's project studies mutations in the multi-functional TLS/FUS protein that misregulates expression in motor neurons and causes Amyotrophic Lateral Sclerosis (Lou Gehrig's Disease). After graduation, Veronica intends to pursue a Ph.D. in Molecular Biology. Outside of the lab, Veronica discusses her cell cultures and clones as if they were her children. She is also a board member of the Columbia University Triathlon Club and Relay for Life Committee. Veronica enjoys learning *una mica de* Catalan and plans to study abroad in Barcelona this spring.

Faculty Advisor: Dr. James Manley

Mutations in TLS/FUS Alter Expression of MECP2 in Amytrophic Lateral Sclerosis

TLS/FUS (translocated in liposarcoma/fused in sarcoma) is a heterogeneous ribonucleoprotein that regulates fundamental gene expression processes, most notably transcription and splicing. Our lab has recently identified several target genes of wild-type TLS/FUS, including MECP2 (methyl CpG binding protein 2), which is known to be crucial for proper motor neuron functioning. Normally, wild-type TLS/FUS is primarily localized in the nucleus, where it can bind to specific cis-regulatory elements called TLS-binding motifs (also known as TREs) in the promoter region of MECP2 and positively regulate its transcription. In Amyotrophic Lateral Sclerosis (ALS) patients, ALS-specific point mutations in the TLS/FUS protein have been linked to mislocalization and aggregation of mutant TLS/FUS in the cytoplasm. It is unknown how these mutations and their resulting mislocalization contribute to neurodegeneration at the molecular level. We hypothesize that mutant TLS/FUS improperly regulates MECP2 expression at multiple levels such as splicing and translation. The alternatively spliced isoform of MECP2 has been shown to restore proper neuronal functioning in Rett's-syndrome model mice and our lab has shown that over-expression of mutant TLS/FUS protein in cell culture increases detected mRNA levels of the alternatively spliced isoform, yet there is an overall decrease in its protein levels. To understand the interaction between the TLS/FUS mutant and cis-regulatory elements in the wild-type MECP2 gene, we are cloning recombinant human MECP2 mini-genes and sub-domain deletions of the TLS/FUS protein. Understanding the mechanism of how mutant TLS/FUS misregulates the expression of MECP2 may lead to the development of new therapeutics to treat ALS.

Sara Lavenhar
CC 2014
Environmental Science

Sara Lavenhar is a junior in the class of 2014 at Columbia majoring in Environmental Science with a Special Concentration in Sustainable Development. Currently, Sara is working in the Biology Department at Barnard College with Dr. Krista McGuire and Dr. Angela Kong from the Center for Climate Systems Research studying microbial diversity in rooftop farming systems. Prior to the summer of 2012, Sara had never done work in microbiology, but an internship through the Lamont-Doherty Earth Observatory (LDEO) opened the door to

amazing research opportunities in areas she hadn't ever considered. The current project she is working on is a unique study investigating microbial community responses to different nutrient inputs in an effort to understand nitrogen cycling in rooftop farming systems. The study aims to expand our understanding of the potential impact of rooftop farms on greenhouse gas emissions and urban food security and provide a basis for future research into rooftop farming. This project is a continuation of the summer 2012 internship at LDEO and has not yet reached completion. Sara is also a member of the Columbia Women's Varsity Archery Team, and an active member of Morningside Monthly Meeting of the Religious Society of Friends (Quakers). After graduating, she intends to go to graduate school to study sustainable agriculture.

Faculty Advisor: Dr. Krista McGuire & Dr. Angela Kong

Assessing Ammonia-Oxidizing and Denitrifying Bacterial Abundance in Urban Rooftop Farming Systems Receiving Varied Fertilizer Amendments

With the rise in popularity of green roof technology, there has also been growing interest in employing rooftops to expand urban farming systems to help address urban food insecurity. Agricultural practices, particularly those involving synthetic fertilizer additions, can be sources of greenhouse gas emissions, such as nitrous oxide (N_2O). The potential contribution of rooftop farms to urban greenhouse gas emissions is currently not well understood. The goal of this study is to characterize the microbial community that plays a role in nitrogen (N) cycling and potentially generating N_2O and nitric oxide (NO) emissions and relate this to N processes (e.g., loss and crop uptake) in rooftop farming systems. Using real-time quantitative polymerase chain reaction (qPCR) assays of functional genes, this project will assess the abundance of ammonia-oxidizing bacteria (AOB) and denitrifying bacteria in rooftop farm media amended with different fertilizers across the 8-week growing season of Swiss chard (*Beta vulgaris*) in a greenhouse. We will investigate rooftop media amended with the following: Scott's Osmocote® fertilizer, NYC Dept. of Sanitation municipal green compost, Lower East Side Ecology Center vermicompost, and Stone Barns Agricultural Center composted chicken manure. Results of this study will be coupled with analyses of crop productivity, crop N uptake, and N loss via leaching associated with each amendment. Environmental parameters, e.g., pH, electrical conductivity, and soil moisture, will also be measured. Preliminary results midway through the experiment (three out of five sampling events) indicate that concentrations of DNA extracted from the media amended with Stone Barns compost (4.11×10^3 ng DNA g^{-1} dry soil, averaged across three sampling events) are higher than in the control and Osmocote® treatment (2.31×10^3 and 2.62×10^3 ng DNA g^{-1} dry soil, average across three sampling events, respectively). Mean pH values ranged from 7.39 – 7.868 across all sampling times and soil amendments. pH values were generally lower in the Osmocote® treatment, but few differences were found among the other treatments at the 2nd and 3rd sampling events. In addition, all treatments showed similar chard biomass at the 2nd and 3rd sampling date. This project will continue through 2013.

Dylan Marshall
CC 2013
Biology

Dylan Marshall (CC '13) is from Ardsley, New York and is majoring in Biology with a concentration in Hispanic Studies. He is Pre-Med and hopes to matriculate into medical school in Fall 2013. He is also the President of the Shotokan Karate club, a Health Advocate with Health Leads, a volunteer with the Child Life Program at St. Luke's Hospital, and is a brother in the Pi Kappa Alpha Fraternity. He worked under the supervision of Dr. Herbert Terrace at the New York State Psychiatric Institute from August 2010 to June 2012 examining the cognitive abilities of the Rhesus Macaque (*Macaca mulatta*) non-human primates. Specifically, Dylan began to illuminate that the Rhesus Macaque is capable of prospective metacognition. In conjunction with other research conducted in the Terrace Lab, these findings would call for a re-evaluation of the way that we understand cognition in humans.

Faculty Advisor: Dr. Herbert Terrace

Prospective Metacognition in the Rhesus Macaque

Metacognition allows one to make confidence judgments about knowledge and ability through introspection. Until recently, metacognition has been denoted as only a human characteristic due to the highly developed prefrontal cortex (PFC). While several studies show that the rhesus macaque is capable of retrospective metacognition, this study aimed to show that the macaque is capable of prospective metacognition as well through the use of a gambling paradigm. If the non-human primate subjects were capable of prospective metacognition, then the current information processing model established for humans must be reassessed.

Frank Pavia
CC 2014
Earth Science

Frankie Pavia, Class of 2014, is a third-year Earth Science major and chemistry concentrator. He conducts research in organic geochemistry at Columbia's Lamont-Doherty Earth Observatory to determine how carbon storage in Alaskan peatlands is affected by changing climate, vegetation, and hydrology. A rabid sports fan hailing from Seattle, Frankie also works as a sports economics research assistant at the Columbia Business School and is an active member of the Columbia Sports Business Society.

Faculty Advisor: Jonathan Nichols & Dorothy Peteet

Reconstructing Paleoclimate and Carbon Storage of Alaskan Peatlands During the Holocene

We examined the rate of carbon storage and its relationship to changing climate and vegetation in a transect of Alaskan peatlands spanning 12 degrees of latitude. These peatlands can act both as sources and sinks for atmospheric carbon, and their status is highly sensitive both to climatic shifts and to vegetation assemblage. It is unknown whether future warming in the Arctic will stimulate productivity, thereby increasing organic accumulation and carbon storage, or initiate higher decay rates and trigger the release of stored carbon. We reconstructed carbon flux, effective moisture, and vegetation assemblage using loss on ignition and AMS carbon-14 dating of plant macrofossils; hydrogen isotope ratios of specific organic biomarkers; and biomarker distributions and macrofossil counts. By reconstructing both carbon flux and paleoclimate of peatlands within in the same samples, we observe how climate and peatland carbon storage are interconnected. We find that times when peatlands are under more evaporative stress, sedge communities take over the peatland, and less carbon is stored. *Sphagnum*, the most effective taxa for sequestering carbon, is more abundant during times when effective moisture is higher in peatlands. Further, we find that moisture balance at our Alaskan peatland sites is controlled by the interplay between atmospheric conditions over the Arctic and north Pacific Oceans, a dynamic highly sensitive to anthropogenic warming.

Ethan Perets
CC 2014
Biochemistry

Ethan Perets is a junior in Columbia College majoring in biochemistry and philosophy. In his years at Columbia, Ethan has been involved as a group member in the Dalibor Sames laboratory in the Chemistry Department, and most recently as a researcher in the laboratory of Julio M. Fernandez in the Department of Biological Sciences. Ethan's' work has ranged from studying the effects of small molecules on neuronal differentiation pathways, to computational evolutionary biology. More recently, Ethan was awarded the Summer Undergraduate Research Fellowship at Columbia University, where he studied the emerging method of Ancestral Sequence Reconstruction under Julio M. Fernandez, and was employed as a TA in the Chemistry Department. Outside of his scientific studies, Ethan is also a member of WKCR, the undergraduate-run University radio station, where he headed the New Music Department for over a year.

Faculty Advisor: Julio M. Fernandez

Resurrection of a Highly Thermostable a-amylase by Ancestral Sequence Reconstruction

Alpha-amylases comprise a diverse group of enzymes responsible for the degradation of complex poly-saccharides into mono and disaccharides with fermentable reducing ends. These enzymes have been found in every domain of life, and function in organisms as an efficient means for capturing energy from their surrounding environments. Moreover, a-amylases have found widespread and varied use in biotechnological applications, thus motivating the search for a highly active and thermostable form. Due to recent advances in genomics and computational power, ancestral sequence reconstruction (ASR) has become a powerful method

for investigating the biochemical properties of ancient proteins. The study presented here reports the reconstruction and expression of a 3.1 billion year-old-a-amylase inferred to have belonged to the last bacterial common ancestor. This enzyme is expected to show increased stability and activity at X C higher than a-amylases isolated from any known extant thermophilic bacterium. It is shown that ASR offers a highly directed method for the determination of thermostable sequences.

Katharina Shaw
CC 2013
Biology

Katharina Shaw is currently a Columbia Senior studying biology. Although she spent more than two years in the laboratory of Dr. Scott Snyder pursuing the total synthesis of natural product derivatives of resveratrol (the "longevity" factor in red wine), this past summer she worked on Hepatitis C Virus at The Rockefeller University. In addition to basic science research, Katharina also participates in clinical HIV/AIDS vaccine research at Columbia Medical Center and is a Teaching Assistant (TA) for immunology and biology classes at Columbia.

Faculty Advisor: Dr. Charles Rice & Dr. Robert Darnell

Interchanging the miRNA dependence of Hepatitis C Virus

Introduction: Liver-specific Micro-RNA (miRNA) 122 facilitates hepatitis C virus (HCV) replication by recruiting a RISC-like complex containing Argonaute 2 to the 5' end of the HCV genome. This requires basepairing between the miR-122 seed site and two sequences in the 5'
UTR of the HCV RNA.1 A consequence of HCV replication in hepatocytes is the functional de-repression of host miR-122 targets, or the so-called "miR-122 sponge effect." To determine whether HCV's utilization of miR-122 during replication specifically mediates this sponge effect, we sought to exchange the miRNA dependence of HCV.
Method: Overlap PCR methods were utilized to generate HCV mutants capable of binding alternative miRNAs – their replication competency was determined after transfection of three different cell types through luciferase assays and real time quantitative PCR.
Result: The M15 mutant, designed to bind miR-15 in place of miR-122, replicates in Huh7.5 cells. Additionally, M15 replication is boosted in the presence of miR-15 mimic and is insensitive to LNA-122, making M15 a promising candidate for a miR-122 independent virus.
Conclusion: Further inhibition studies are necessary to prove M15 is miR-15 dependent. If M15's miRNA dependence proves to have been swapped, M15 provides an avenue by which to study the "miR-122 sponge effect" and its specific role during viral replication.

Cristina Sorrento
CC 2014
Biochemistry

Cristina Sorrento is a Biochemistry major in Columbia College, Class of 2014. Her research interests include neuroscience, biochemistry, and structural biology. Since her first year at Columbia, she has worked as a research assistant under the direction of Stephen Rayport at the NYS Psychiatric Institute searching for small molecule inhibitors of the enzyme glutaminase for the pharmacotherapy of schizophrenia. She has also worked with Seth Darst at Rockefeller University studying the structures of bacterial RNA polymerases. On campus, she is an editor of the Columbia Undergraduate Science Journal, a member of Columbia's pre-medical chapter of AMSA, a coach for the non-profit organization Girls On the Run, and a member of the Columbia Catholic Undergraduates.

Faculty Advisor: Seth Darst

Expression and Purification of the Mycobacterium bovis RNA Polymerase Holoenzyme

The bacterial RNAP holoenzyme is composed of a core with four distinct subunits and an essential transcription factor, the σ factor. High resolution crystal structures of the RNAP holoenzyme in *Taq* and *E. coli* have been obtained. The purpose of this study was to optimize the expression and purification of the *M. bovis* RNAP holoenzyme for structural studies. *M. bovis* core RNAP and σ^A were expressed in *E. coli* in a T7 expression system. RNAP was purified with a series of five different purification steps (a combination of affinity, anion exchange , and size exclusion chromatography, as well as precipitation), while σ^A was purified in four steps. The catalytic activity of incubated holoenzyme was assessed with a transcription assay. Pure active holoenzyme was obtained from the expression and purification. A long induction period leads to optimal expression and purification of active RNAP holoenzyme. Screens will be set up in order to find optimal conditions for protein crystallization.

Marek Svoboda
CC 2014
Neuroscience and Behavior

My name is Marek Svoboda and I am an international student from Zlín, Czech Republic. I graduated from the Czech high school Open Gate, boarding school in Babice, Prague in 2010 and I have been studying at Columbia College (CC'14) ever since. I major in Behavioral Neuroscience and I am also a pre-med student. In the spring semester 2011 I started to work in professor Peter Balsam's lab in NYSPI under kind supervision of Kathleen Taylor, where I have worked on several research projects, the last of which is focusing on the neuroscience of habit, which I was working on during this summer's SURF program. This is the project I would like to present at the Research Symposium.

Faculty Advisor: Kathleen Taylor

Neuroscience of Habit

It has been suggested in previous studies that habit plays significant role in drug addiction. As behavior shifts from goal-directed to habit-driven, subjects may become more stereotypical in their behavior. For example, the presence of various external cues (such as drug paraphernalia or the environment) associated with the process of taking drugs over many repeated instances can elicit craving for the substance, which further promotes repetitive drug intake. As this positive feedback loop of habitual behavior is created, it becomes much harder for addicts to quit drug abuse. If we succeeded in tracing the physiological basis of habit acquirement, we might be able to help prevent or treat undesired habits from being further behaviorally expressed. While some brain areas, such as dorsal striatum, amygdala, and prefrontal cortex, have been known to be involved in habit formation, the exact "habit-formation pathway" is still yet to be discovered. We previously found that during the process of habit acquirement, changes on the level of genetic expression take place in dorsal striatum. In our current study, we used Golgi staining in order to analyze changes in neuron morphology in dorsal striatum during habit acquirement that would reveal more specifically how changes in genetic expression can be traced on the physiological level, since this has not been done before. We expect to find changes in the number and neurophysiological properties of dendritic spines in dorsomedial and dorsolateral striatum in habit-driven rats when compared to goal-directed subjects. This result would show that actual morphological changes in neurons take place during habit acquirement, while previous studies have been only able to show the role of these two anatomically distinct structures in control of goal-directed or habit-driven behavior via lesions. It would also provide new possibilities for further research detailing potential habit-formation pathway.

Bryan Terrazas
CC 2013
Astrophysics

Bryan is a senior in Columbia College from Springfield, Virginia, just outside of the nation's capital. He is majoring in astrophysics and after he graduates he plans on receiving his PhD and going on to pursue research. He will work this year with Greg Bryan on the formation of the first stars in the universe. This past summer, he went to Kitt Peak National Observatory and used the MDM telescopes to observe cataclysmic variable stars for a week of intensive research. For the rest of the summer, he worked at the Harvard-Smithsonian Center for Astrophysics for the Smithsonian Astrophysical Observatory REU which was funded by the National Science Foundation. He worked under Dr. Paul Nulsen on relativistic jets spewed from supermassive black holes at the center of the most massive galaxies in the universe. These jets could provide a direct link between the black hole and the large scale structure of the cluster. In the past, he has worked with Professor of Astronomy Jacqueline van Gorkom on looking at extended HI regions of galaxies in the cluster Abell 963. Analysis of HI extended disks could reveal whether the environment plays an important role in galaxy evolution and how this changes throughout the history of the universe. Last summer he did research at the

European Organization for Nuclear Research (CERN) in Geneva, Switzerland where he teamed up with a former Columbia graduate student and current CERN Fellow, Heather Gray, to analyze the data from the ATLAS experiment. This experiment is only one of the five currently being performed at the Large Hadron Collider (LHC), a particle accelerator which holds the title of the most powerful and technologically sophisticated machine ever built. The LHC hopes to provide scientists with answers to the most compelling questions in physics today. Bryan has also worked with Professor of Physics and Dean of Science Amber Miller's experimental cosmology group where he created Frequency Selective Surface filters which will be used in an experiment to detect the radiation from when the universe was only a fraction of one percent of its current age. Both of these summer opportunities have been funded by the CUSP Summer Enhancement Fellowship. Along with astrophysics, Bryan is a clarinetist and takes lessons with Jessica Phillips, the acting principal clarinetist of the Metropolitan Opera Orchestra. Previously he has studied with Wayne Titerence, former principal clarinetist of the Air Force Band, and Steve Williamson, former principal clarinetist at the Metropolitan Opera Orchestra and newly appointed principal clarinetist of the Chicago Symphony Orchestra. He participates in the Columbia University Orchestra, Society of Emerging Artists, Columbia Classical Performers, and the Columbia Music Performance Program.

Faculty Advisor: Paul Nulsen

Blowing Bubbles in the Intracluster Medium: The Growth and Evolution of Radio Lobes from Active Galactic Nuclei

Observations from Chandra have allowed detailed analyses of cavities created by radio lobes in the X-ray emission of galaxy clusters. These lobes are thought to heat galaxy clusters and provide a solution to the cooling flow problem but their impacts integrated over time are not known. We provide a simple model for the evolution of a radio lobe in a cluster atmosphere. The motion of a lobe is determined by its pressure and the pressure and density of the surrounding atmosphere. The model assumes the lobe is made up of three components: electrons, a magnetic field, and non-radiating particles. These three components evolve due to inputs from the jet, changing external pressure, and radiative losses. The synchrotron spectrum of the lobe is computed from the electron distribution and magnetic field strength. We chose to model the sources 2A 0335+096, A2052, A2199, A478, and A4059 with data from Birzan et al. (2008). Our simple model is able to match observed radio fluxes at frequencies 327, 1400, 4500, and 8500 MHz. Although the simple model works well, the number of free parameters and the lack of data limits how well we can constrain the properties of these systems. Using lower frequency radio data and a more complete physical model will enable better measurements of the impacts of distant radio galaxies on their cluster hosts in the future.

Samuel Zeng
CC 2015
Biochemistry

I am currently a sophomore in Columbia College and intend to major in biochemistry. Recently, I have begun working as a research assistant at Columbia Medical Center, under Dr. Megan Sykes. My project centers on investigating the viability of incorporating porcine cells into mice with humanized immune systems without triggering immune rejection. We hope this could open the door to the clinical possibility of xenotransplantations to resolve the current transplantation organ shortage. For the past summer, I worked at Harvard as a summer intern, under Professor Qiao Zhou in the Department of Stem Cell and Regenerative Biology. As my poster will elaborate, we have found some exciting data pertaining to curing Type 1 Diabetes. I also participated in lab research as a high school student, part of the City of Hope Summer Research Academy, working under Dr. Wendong Huang in the Department of Gene Regulation and Drug Discovery. At that time, we observed miR-194, a form of microRNA, could reduce liver cancer growth and metastasis. That exciting data has been published in *Hepatology* (2010; 52(6): 2148-57).

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Induced B-Cells Require Maturation Period Prior to Full Functionality

Afflicting over 25 million Americans, Type 1 diabetes involves the autoimmune destruction of β-cells, leading to an inability to regulated glycemia. A crucial step in curing this disease, therefore, is replenishing the depleted β-cell population. One approach has been to try and differentiate stems cells into functional β cells as replacements. But of late, there have been attempts to directly reprogram one adult cell form into another. The appeal of this approach is a potentially shorter production time, as well as greater *in vivo* potentials. In 2008, Zhou etc al demonstrated the first successful reprogramming of pancreatic exocrine cells into β-cell* . These induced β-cells were shown to be morphologically indistinguishable from endogenous β-cells, and were capable of ameliorating hyperglycemia in streptozotocin treated mice. However, the glycemic conditions of these experimental mice were worse off than wild types. This current study looks into greater depth at the maturation process and epigenetic changes of cellular reprogramming of the exocrine cells in hopes of ultimately discovering methods of optimizing the transdifferentiation process.

The reprogramming of pancreatic exocrine cells, specifically acinar cells, into induced β-cells relies on a combination of three virally delivered transcription factors, Ngn3, MafA, and Pdx1. We have discovered these cells must undergo a crucial developmental period prior to achieving equivalent functionality to that of endogenous β-cells. On day 10, these cells first express insulin; day 30, they respond to glucose but cannot effectively regulate glycemia; day 60, they effectively regulate glycemia. A microarray assay of gene expressions has revealed differences in expressions in each of these stages. As could be seen, the passage of time leads the percentage of genes enriched in both induced and endogenous β-cells to increase, reflecting the maturation process. Consistent patterns of gene expression we have identified include genes

that are only transiently upregulated, as well as those continually upregulated or downregulated with maturation. Additionally, a number of genes were found to be transiently downregulated. We will look into the specific genes belonging to said patterns in hopes of identifying a key pathway or mechanism driving the transdifferentation process.