Yeshiva University

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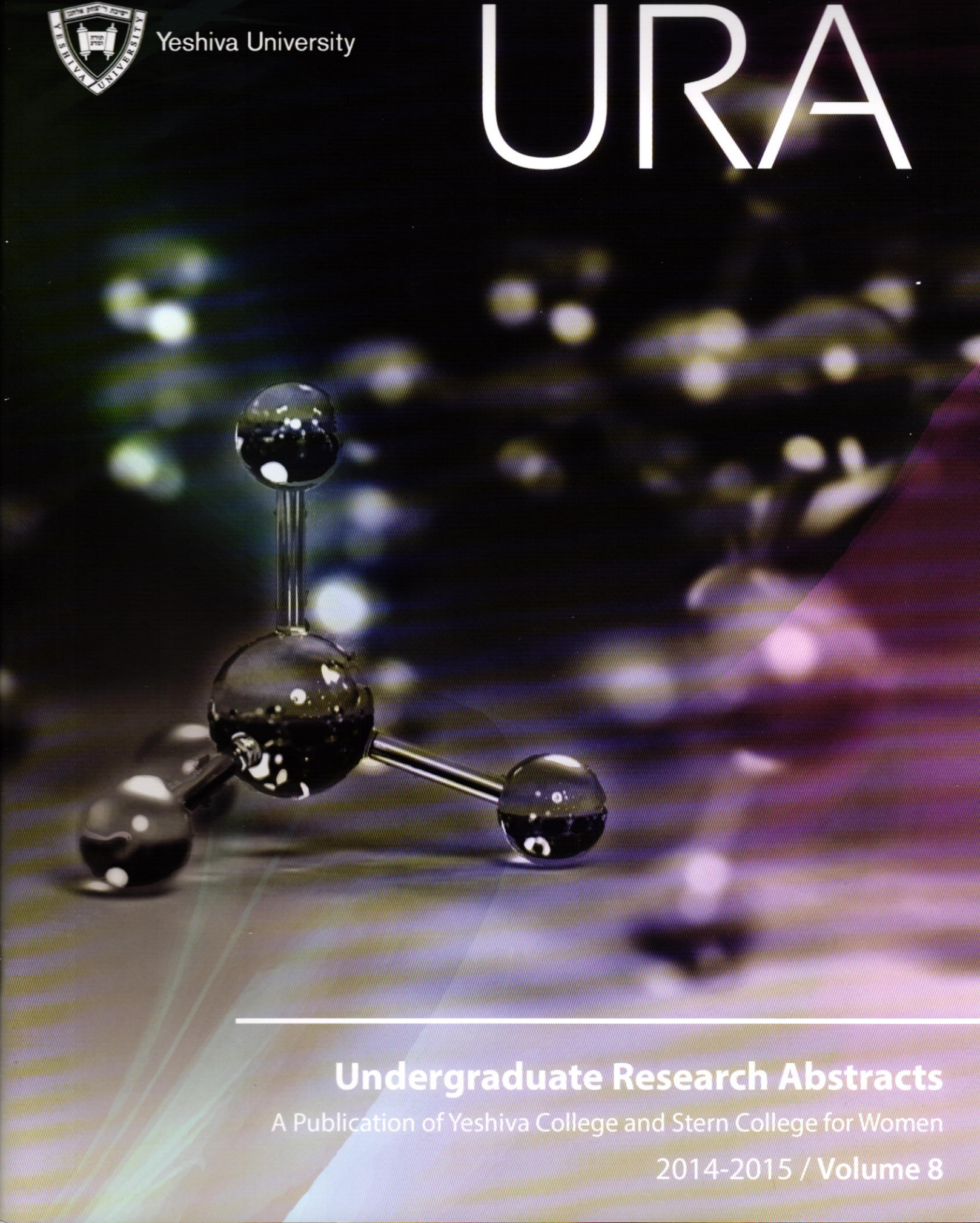
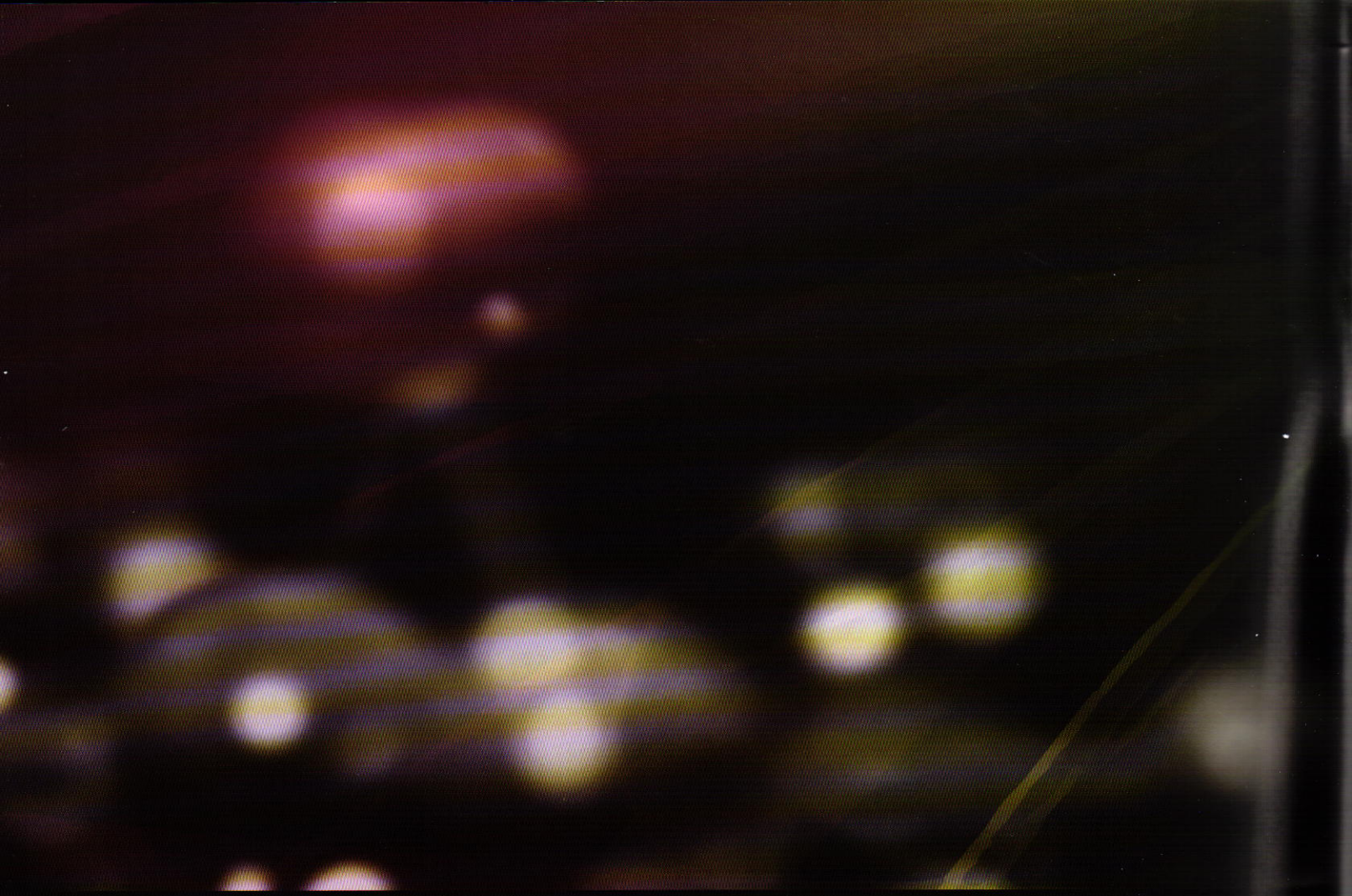


Undergraduate Research Abstracts

A Publication of Yeshiva College and Stern College for Women

2014-2015 / **Volume 8**



STAFF

Sincere gratitude is extended to the Yeshiva University Offices of the Provost and Admissions for their critical support and endorsement of this publication.

Undergraduate Research Abstracts Journal
A Publication of Yeshiva College and Stern College for Women
Volume 8: 2014-2015

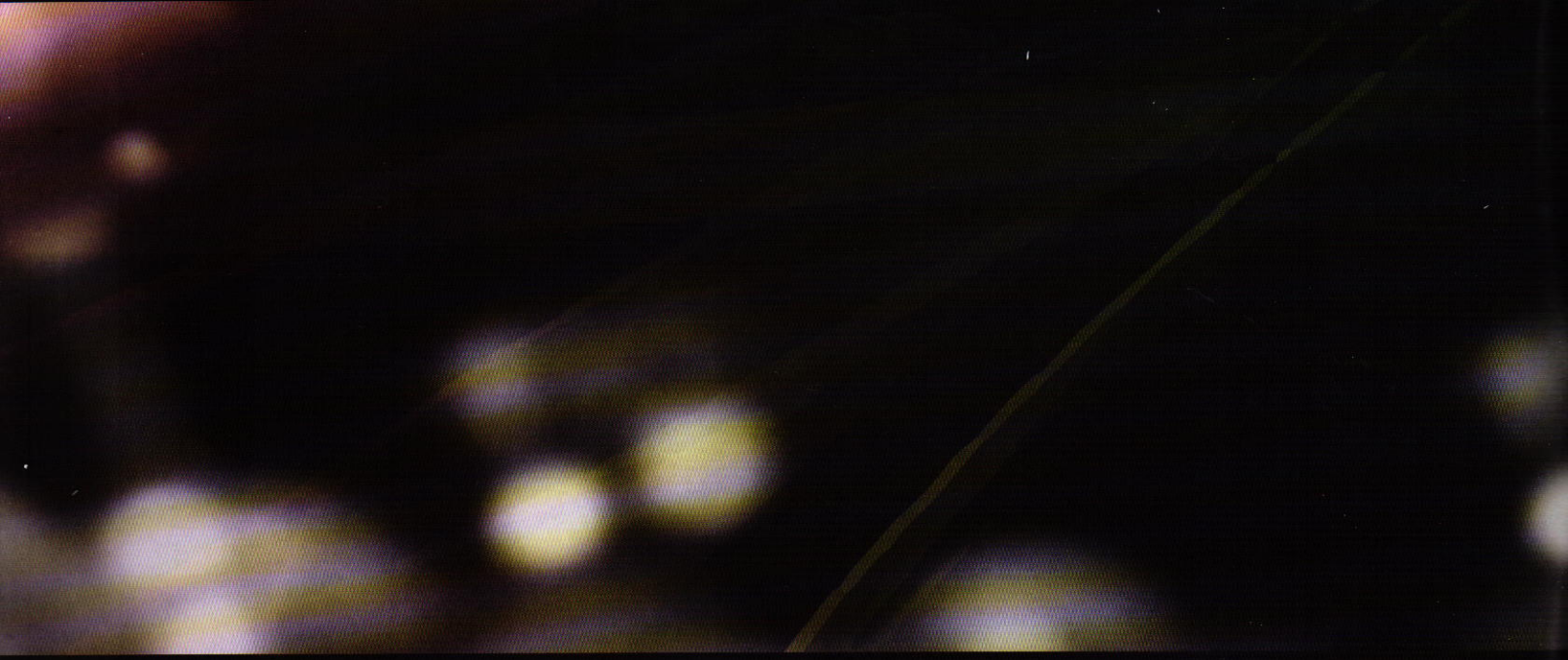
DEDICATION

In Tribute to our friends and mentors,

Eli Steinberger (USRP Co-President 2006-07)
&
Donny Ladell (USRP Co-President 2005-06)

Who founded many student research initiatives, including this journal, at Yeshiva College. May we continue to honor their memories through the exhibition of Yeshiva's ongoing undergraduate exploration of science.

Biology | Chemistry | Computer Science | Mathematics | Physics | Psychology



FOREWORD

This publication showcases the quality of research undertaken by Yeshiva University's undergraduates, and it highlights the superior quality of our student body. Congratulations to all of the students and their faculty mentors whose work we are honoring today!

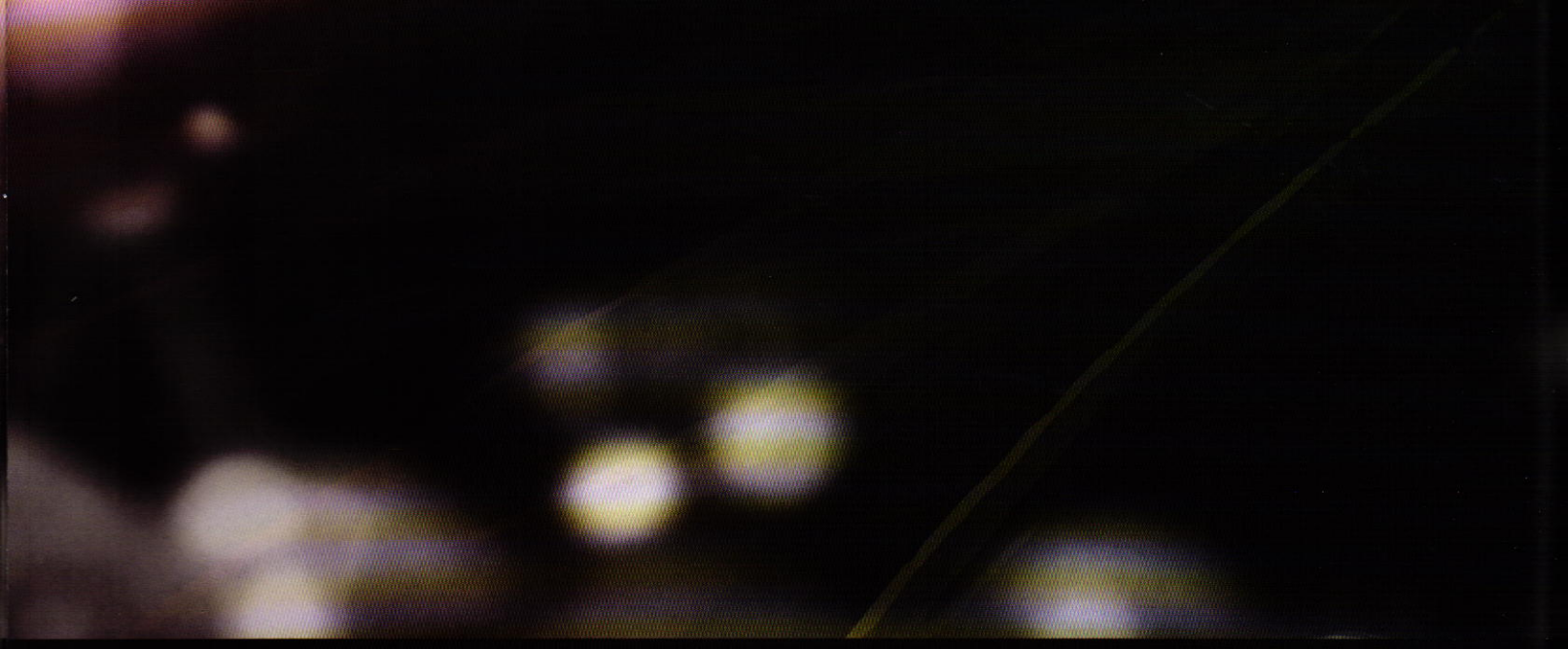
As academics, we know only too well the time and hard work that go into research. From my own inquiries into modern Egyptian history and politics, I know both the joys and disappointments of scholarship. I can recall many times during which I questioned the wisdom of embarking on a project, wondering if I would find sufficient information or if anyone would care about all of my efforts to unlock the mysteries of a certain period or series of events. However, I could never suppress my curiosity, my desire to know and to understand, and that propelled me forward. By the conclusion of the project, I was assured of the significance of historical investigation and the centrality of research in my life.

The research and creative endeavors that students have undertaken and that are published here will be some of the most important—even life-altering—experiences that they can have.

I celebrate their work and extend my heartfelt admiration to the researchers and their mentors for a job well done.

Selma Botman

Provost and Vice President for Academic Affairs
Yeshiva University



PREFACE

The research experience usually begins with a meeting between the student and the research advisor. It is here the research advisor presents the overall research projects being pursued by the lab, along with their importance and significance to the respective research field. Finally, a research project is presented to student. It is here the student realizes that they have an opportunity to take advantage of a personal interest while being able to make a serious contribution to the sciences.

Although it sounds very generic and mundane, the paragraph above is very common. What it fails to explain, is that research is unlike any course a student may take in their undergraduate career. In research there is no syllabus, no midterm, and no final exam. Although a research project may have a final goal, everything in between is dictated by the nature of research, not by the student or the research advisor. This is what makes research such an important aspect of any undergraduate's career at Yeshiva College and Stern College for Women. The abstracts presented within give a glimpse into countless hours, level of dedication, and personal ownership many of these students have displayed in there research experiences. Through these research opportunities these students have not just learned to become more experienced researchers, but to be independent and analytical thinkers and scientists.

Daniel Lim
Assistant Professor of Chemistry
Yeshiva University

BIOLOGY

Drugged Wildlife: The Potential Impacts of Environmental Endocrine Disruptors on Reproductive Development

by

Melissa Y. Kramer, Nicole A. McNabb, Louis J. Guillette, Jr., and Satomi Kohno
Department of Marine Biomedicine and Environmental Sciences, Medical University of South Carolina, Charleston, SC

The growing use of oral contraceptives and hormone therapeutics gives rise to the concern that estrogenic and progestogenic compounds are present in wastewater at concentrations that may affect the reproductive health of aquatic species. This study showed that wastewater effluent produced by the Charleston Water System facility at Plum Island, when concentrated 100 times, contains endocrine active compounds at high enough concentrations to activate the human nuclear estrogen and progesterone receptors in an in vitro transactivation assay system. This may provide a mechanism for the alterations in secondary sex characteristics that have been reported in fish exposed to wastewater effluent from other locations. Some synthetic hormones have also been shown to bioaccumulate in teleost fishes. There is, therefore, potential for humans to be exposed to endocrine active compounds through consumption of these fish. The current study evaluated the effects of neonatal exposure to progestogens on the reproductive development of estradiol (E_2)-stimulated adults, using mice as a model. Quantitative PCR analysis of target genes from adult mice treated with the synthetic progesterone 17α-hydroxyprogesterone caproate (17PC) as neonates suggested that developmental exposure to progestogens might decrease sensitivity to E_2 at the uterine transcriptome level. The results showed patterns similar to microarray data that revealed that perinatal exposure to 17PC suppressed uterine E_2 sensitivity in the adult. These data indicate a need for further exploration of the long-term impacts of neonatal progestogen exposure on reproductive development.

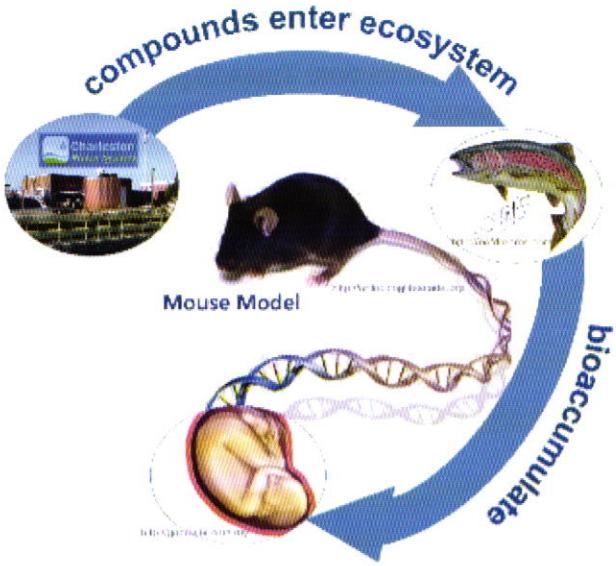


Figure 1. Hypothesized path of endocrine disrupting compounds through the environment, from wastewater to aquatic animals to humans. A mouse model was used to evaluate potential effects of neonatal endocrine disruption on adult reproductive development.

Student Researcher

Melissa Kramer is a senior at Stern College. She is currently majoring in Biology, but does not have any immediate plans for leaving Stern, so a minor in Chemistry remains a possibility. She plans to eventually pursue a PhD in a field related to marine biology.

The Effects of Peptide and Peptidomimetic Inhibitors on Enzyme Cathepsin-C and Their Role in Inhibition of Necrosis

by

Talia Felman, Shira Hirsch, and Amnon Albeck
Department of Chemistry, Bar Ilan University, Ramat Gan, Israel

The two most known forms of cell death are apoptosis and necrosis. Apoptosis is a controlled form of cell death, while necrosis was previously thought to be a more disorderly form of self-destruction. Recent research, however, suggests, that the process of necrosis is much more controlled than it has been understood to be. In fact, this systematic necrotic process plays a critical role in many harmful health conditions. For example, it is involved in the obstruction of blood vessels, neurodegenerative diseases, infection, inflammatory diseases, exposure to toxins, and cancer.

This study builds upon the research done by Dr. Natan at Ben-Gurion University and Dr. Amnon Albeck at Bar-Ilan University. Their research identified increased elastase-like proteolytic activity in cells exposed to necrosis inducers. In necrosis, proteolytic enzymes catalyze the hydrolysis of peptide bonds in proteins and peptides. It follows that the development of protease inhibitors may be important in the treatment of various disease states. This study focuses on the enzyme Cathepsin C, a cysteine protease.

Six inhibitors of the enzyme Cathepsin C were synthesized to be used in several experiments. The preliminary experiment tested if the compounds inhibited Cathepsin C's activity when the enzyme was isolated. Then, the compounds were tested in live cells. In the first live cell experiment, rat heart cells were incubated with the inhibitors in simulated hypoxic conditions. In the second live cell experiment, the compounds were incubated with PC-12 cells and necrosis was induced by toxic potassium cyanide (KCN), which is toxic to cells because it interferes with the activity of cytochrome c oxidase, thereby inhibiting oxidative phosphorylation and cellular respiration. The last experiment involved exploring how protective effects of the compounds vary depending on the compound concentration. These experiments shed light on the role of Cathepsin C and proteases in the controlled process of necrosis. Furthermore, identifying the cellular processes and key enzymes involved in necrotic cell death will provide insight into the mechanism of necrosis and will direct the development of drugs that prevent necrosis.

Student Researcher

Talia Felman is a student at Stern College majoring in Biology. When not studying in the library, Talia enjoys running, hiking, drawing, and spending time with her family. She hopes to one day pursue a career in medicine.

The Role of SIRT6 in Metabolism and Beta Oxidation

by

Sara Lis, Shoshana Naiman, and Haim Cohen

Department of Life Sciences, Bar Ilan University, Ramat Gan, Israel

Professcr Haim Cohen's lab analyzes the relationship between caloric restriction and metabolic diseases. SIRT6, an enzyme part of the sirtuin family, a group of NAD+-dependent deacetylases, has been shown to be involved in the metabolic pathway and is critical to the regulation of longevity.

In a past experiment, SIRT6 levels have increased in response to caloric restriction, indicating that SIRT6 may be a regulator of the metabolic response to caloric restriction. Mice deficient in SIRT6 were especially small, had metabolic deficiencies, and died prematurely, when compared to normal mice. Furthermore, male mice overexpressing SIRT6 were able to maintain normal homeostasis when fed a high-calorie diet and had an extended lifespan of about 15% compared to normal mice.

Since SIRT6 was found to be connected to metabolism, we investigated the role of SIRT6 in beta oxidation, the process of breaking down fatty acids during starvation. Both normal mice and mice overexpressing SIRT6 were treated with WY 14,643, a specific PPARA activator which activates beta oxidation. This treatment mimics starvation, possibly by activating SIRT6. We performed a genome-wide microarray analysis to measure over 30,000 genes in both normal and SIRT6 mice. An analysis of the data showed several beta oxidation genes were specifically altered in SIRT6 mice, confirming our initial hypothesis that SIRT6 regulates beta oxidation.

Another set of mice were starved in parallel to the WY treatment. These mice were placed in metabolic cages, which regularly measure various physiological patterns, such as food/drink intake, activity, RER (respiratory ratio) and temperature of each mouse. After the normal and starvation period, the data was analyzed to evaluate changes in mitochondrial activity. It was found that, during starvation, most energy comes from beta oxidation in the muscles as opposed to glycolysis; this positively correlates with the RER ratio. The data showed that the RER levels of the SIRT6 overexpressed mice were significantly higher than the levels in normal mice, indicating that SIRT6 may play a role in maintaining oxygen levels during caloric restriction. These preliminary results strongly indicate that SIRT6 positively regulates beta oxidation during starvation and possibly during high fat diets as well. These results and future results hold promise for the use of SIRT6 as a potential therapy for various metabolic diseases.

Student Researcher

Sara Lis is a senior at Stern College majoring in Biochemistry. When she is not exploring New York's exciting sites, Sara can be found on stage at any of Stern's multiple performances, including cabaret singing nights, dance shows, and musicals.

Clinical Trials Using Mobile Health Applications

by

Melissa A. LoPresti*[1], Mickey Abraham*[1], Geoff Appelboom[1], Olivier Bruyère[2], Justin Slomian[2], Jean-Yves Reginster[2], and E. Sander Connolly, Jr.[1]

[1] *Neuro & Digital Initiative at The Neurological Institute, Department of Neurosurgery, Columbia University Medical Center, New York, NY;*

[2] *Department of Public Health, Epidemiology and Health Economics, University of Liège, Liège, Belgium*

**Contributed equally to this work*

Background: Mobile health (mHealth) is a growing sector of technology used in clinical practice. With the ubiquity of this technology in today's society, the promise it holds for use in medicine is vast.

Purpose: To conduct a study examining the current research and clinical trials involving mobile health applications used by human participants worldwide.

Design: We searched the clinicaltrials.gov database for all original trials examining mobile health applications role and use internationally and in varying clinical settings.

Results: Fifty trials were included. Eighty-eight percent of included trials were initiated from 2012 to 2014, with only 20% of all included trials currently completed. The overwhelming majority of trials originated from the United States and other western or European countries. There was a broad distribution of the trials in regards to study focus and purpose, involving application in behavior change, treatment adherence, diagnosis, disease management, and patient-reported outcomes. Most included trials were performed in the setting of chronic diseases.

Conclusion: The use of mHealth is a growing field with broad implications and indications in clinical practice. This trend of increasing trials, studies, and pervasiveness of technology in health care is a more recent development. Evidence in support of this technology is unclear from the trials included in this study; however, the significance of mobile health applications, devices, and technology most assuredly has a role in chronic disease management and work to improve patient engagement.

Student Researcher

Mickey is a senior at Yeshiva University majoring in Biology. He spends time at the Cerebrovascular and Neurodigital Initiative Research Laboratory at New York Presbyterian Hospital studying the biotechnological impact on medicine, ethics, public health policy, and law. Mickey plans to pursue an MD and integrate a personalized medicine approach into clinical practice.

Smart Wearable Body Sensors for Patient Self-assessment and Monitoring

by

Geoff Appelboom[1], Elvis Camacho[1], Mickey E Abraham[1], Samuel S Bruce[2], Emmanuel LP Dumont[2], Brad E Zacharia[1], Randy D'Amico[3], Justin Slomian[4], Jean Yves Reginster[4], Olivier Bruyère[4], and E Sander Connolly, Jr[1]

[1]Neurodigital Initiative, Columbia University, Department of Neurological Surgery, New York, NY; [2]The Joan and Irwin Jacobs Technion-Cornell Innovation Institute, Cornell NYC Tech, New York, NY; [3]Bartoli Brain Tumor Research Laboratory, Columbia University Irving Cancer Research Center Columbia University Medical Center, New York, NY; [4]Department of Public Health, Epidemiology and Health Economics, University of Liège, Liège, Belgium and Support Unit in Epidemiology and Biostatistics, Department of Public Health Sciences, University of Liège, Liège, Belgium

Background: Innovations in mobile and electronic healthcare are revolutionizing the involvement of both doctors and patients in the modern healthcare system by extending the capabilities of physiological monitoring devices. Despite significant progress within the monitoring device industry, the widespread integration of this technology into medical practice remains limited. The purpose of this review is to summarize the developments and clinical utility of smart wearable body sensors.

Methods: We reviewed the literature for connected device, sensor, trackers, telemonitoring, wireless technology and real time home tracking devices and their application for clinicians.

Results: Smart wearable sensors are effective and reliable for preventative methods in many different facets of medicine such as, cardiopulmonary, vascular, endocrine, neurological function and rehabilitation medicine. These sensors have also been shown to be accurate and useful for perioperative monitoring and rehabilitation medicine.

Conclusion: Although these devices have been shown to be accurate and have clinical utility, they continue to be underutilized in the healthcare industry. Incorporating smart wearable sensors into routine care of patients could augment physician-patient relationships, increase the autonomy and involvement of patients in regards to their healthcare and will provide for novel remote monitoring techniques which will revolutionize healthcare management and spending.

Student Researcher

Mickey is a senior at Yeshiva University majoring in Biology. He spends time at the Cerebrovascular and Neurodigital Initiative Research Laboratory at New York Presbyterian Hospital studying the biotechnological impact on medicine, ethics, public health policy, and law. Mickey plans to pursue an MD and integrate a personalized medicine approach into clinical practice.

Anti-Cancer Activity of a p300 Inhibitor and Trimeric in Head and Neck Squamous Cell Carcinoma Cells

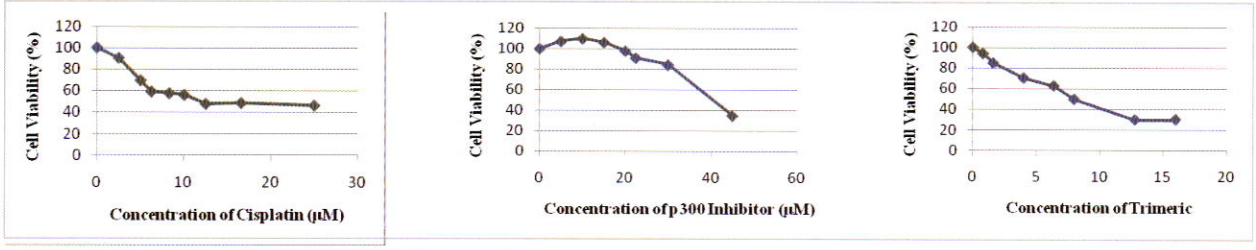
by

Emily Chase and Quintin Pan

Department of Otolaryngology-Head and Neck Surgery, The Ohio State University Wexner Medical Center, Columbus, OH

Head and neck squamous cell carcinoma (HNSCC) is the sixth most common cancer worldwide. In this study, we determined the anti-cancer activity of two novel drugs, p300 inhibitor and trimeric, in HNSCC cells. p300 is a transcriptional co-activator and plays a key role in integrating a cadre of signal transduction pathways. The p300 inhibitor used in this study blocks histone acetyltransferase activity of p300 to prevent p300-directed acetylation of target proteins. Trimeric is a novel formulation that combines the active anti-cancer components of three natural products. The goal of the study was to determine the efficacy of a p300 inhibitor and trimeric, as single-agent or in combination with cisplatin, a standard of care chemotherapeutic, to inhibit the viability of HNSCC.

In our experiment, HPV-negative CAL27 HNSCC cells were treated with vehicle or single-agent cisplatin, p300 inhibitor or trimeric. The MTS assay, an in vitro assay to quantitate the metabolic activity of cells, was performed to assess cell viability after drug treatment. Our results show that single-agent cisplatin, p300 inhibitor and trimeric reduced the viability of CAL27 cells compared to vehicle (Figure 1). In addition, we examined whether p300 inhibitor or trimeric will synergize with cisplatin to optimally ablate HNSCC cells. The combination regimen of the p300 inhibitor and cisplatin or trimeric and cisplatin resulted in lower cell viability than with cisplatin treatment alone (Figure 2). However, the addition of cisplatin did not show a conclusive advantage over the p300 inhibitor or trimeric monotherapy (Figure 2). Our work provides initial evidence that a p300 inhibitor and trimeric are active drugs to reduce the viability of HNSCC cells. The lack of synergy observed with the combination regimen suggests that a distinct cell population may be resistant to cisplatin, p300 inhibitor and trimeric.



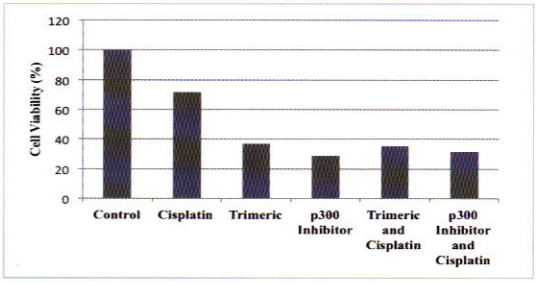


Figure 1 (above): Effect of cisplatin, p300 inhibitor, and trimeric on the viability of HNSCC cells.

Figure 2 (left): Effect of combination regimens on the viability of HNSCC cells

Student Researcher

Emily Chase is a junior at Stern College for Women majoring in Biochemistry. She hopes to one day find the answer to all of her questions, but for now she is ready to take it one step at a time.

Are More Frequent Early Follow-Up Mammogram Protocols Necessary After Breast Conserving Surgery and Radiation Therapy?

by

C. Kaufman, T. Fulop, S. Boolbol, D. Lucido, S. Naam, A. Gillego, and M. Chadha
Radiation Oncology, Beth Israel Medical Center, New York, NY

Background: In an era of choosing wisely in healthcare, there are many initiatives in radiology and oncology that are being evaluated for appropriateness of practice based on clinical evidence. More frequent follow-up mammogram protocols in the first 3 years after breast cancer treatment (BCT) are a widely accepted practice. However, such breast imaging schedules have no strong clinical evidence-base to support the added testing every 6 months, nor a rationale to justify patient anxiety and added unnecessary biopsy procedures. The goal of our study was to evaluate the frequency of BIRADS score 4 on short follow-up mammograms in a population of patients treated with breast conserving surgery and radiation therapy.

Methods: This is an IRB approved study. From 2001-2007, we identified 681 patients who underwent BCT and who also underwent follow up mammograms at our cancer center. We reviewed short follow-up mammograms defined as those obtained within the first 3 years after BCT. The BIRADS score was tabulated in all cases. Further, it was determined to study the frequency of BIRADS 4 score only, because this was deemed a clinically significant finding that routinely warranted additional evaluation.

Results: Median age of the study group was 51 years (range 31-80 years). Among the 681 patients, a total of 3648 follow-up mammogram sessions were obtained. The median number of follow-up mammogram sessions per patient during the observation period of 3 years was 6 (range 2-6 mammogram sessions). In 85% of patients followed, the mammogram scores were BIRADS 1 to 3. In 15% of the patients, the BIRADS score 4 was reported at least once. Among the BIRADS 4 category of patients, 56% had this score reported in the ipsilateral breast following BCT, and 44% had BIRADS 4 reported in the contralateral breast. Specifically in the ipsilateral breast, the frequency of BIRADS 4 was <10% and comparable between the treated ipsilateral breast and the normal contralateral breast. The pathology correlations showed a significantly lower yield of cancer in the BIRADS 4 subset of patients. In patients with BIRADS 3, we observed a very low yield of cancer from frequent follow-up protocol for the ipsilateral breast.

Conclusions: In promoting responsible medical care, it is important to establish appropriate follow-up guidelines and selection of schedules for groups of patients individualized by risk. Annual follow-up mammograms might be adequately frequent for the ipsilateral breast. This study warrants further evaluation and standardized protocols.

Student Researcher

Chavi Kaufman is a senior at Stern College majoring in Biology. When she is not studying or interning in the hospital, she spends much of her time coaching gymnastics and teaching dance. She plans to attend medical school and pursue a career in women's health.

Smad4 Loss Synergizes with TGFα Overexpression in Promoting Pancreatic Metaplasia, PanIN Development, and Fibrosis

by

Dario Garcia-Carracedo[1,2], Chih-Chieh Yu[1,2], Nathan Akhavan[2], Stuart A. Fine[2], Frank Schönleben[3], Naoki Maehara[4], Dillon C. Karg[2], Chuangao Xie[1,2], Wanglong Qiu[1,2], Robert L. Fine[5,6], Helen E. Remotti1[4], and Gloria H. Su1[2,6,7]

[1]Department of Pathology, Columbia University Medical Center, New York, NY; [2]Herbert Irving Comprehensive Cancer Center, Columbia University Medical Center, New York, NY; [3] Department of Vascular Surgery in the Hospital of the University of Munich, Grosshadern, Germany; [4]Department of Surgical Oncology and Regulation of Organ Function, Miyazaki University School of Medicine, Miyazaki, Japan; [5]Department of Medicine, Columbia University Medical Center, New York, NY; [6]Pancreas Center, Columbia University Medical Center, New York, NY; [7]Department of Otolaryngology and Head and Neck Surgery, Columbia University Medical Center, New York, NY

While overexpression of TGFα has been reported in human pancreatic ductal adenocarcinoma (PDAC), mice with overexpressed TGFα develop premalignant pancreatic acinar-ductal meta-plasia (ADM) but not PDAC. TGF-β signaling pathway is pivotal to the development of PDAC and tissue fibrosis. We sought to investigate the interplay between TGFα and TGF-β signaling in pancreatic tumorigenesis and fibrosis, namely via Smad4 inactivation. The MT-TGFα mouse was crossed with a new Smad4 conditional knock-out mouse (Smad4flox/flox;p48-Cre or S4) to generate Smad4flox/flox;MT-TGFα;p48-Cre (STP). After TGFα overexpression was induced with zinc sulfate water for eight months, the pancreata of the STP, MT-TGFα, and S4 mice were examined for tumor development and fibrotic responses.

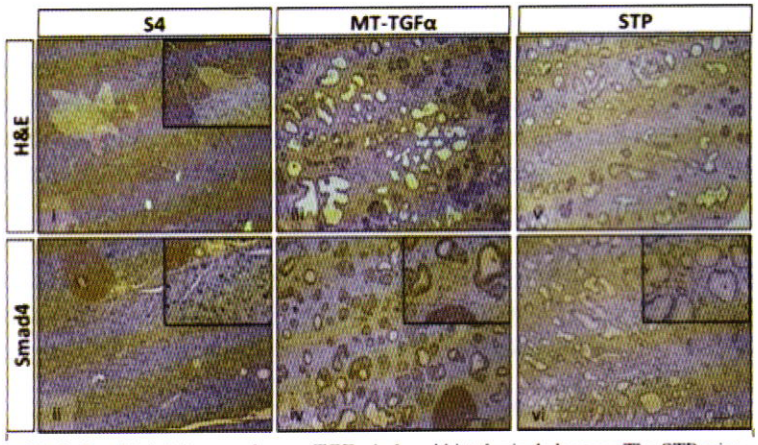


Fig 1. Smad4 deficiency enhances TGFα-induced histological changes. The STP mice displayed similar but more pronounced architectural changes in the pancreata than the MT-TGFα mice, while the no apparent change was detected in the pancreata of S4 mice. Histological sections from 8-months of zinc sulfate treated S4, MT-TGFα, and STP mice stained with H&E; with antibodies to Smad4.

Our STP mice exhibited advanced ADM, increased fibrosis, increased numbers of PanIN lesions, overexpression of chronic pancreatitis-related marker Muc6, and elevated expression of desmoplasia-associated marker Col1A1, compared to the MT-TGFα mice. The inactivation of Smad4 in the exocrine compartment was responsible for both the enhanced PanIN formation and fibrosis in the pancreas. The phenotype of the STP mice represents a transient state from ADMs to PanINs, closely mimicking the interface area seen in human chronic pancreatitis associated with PDAC. The STP mice could be a suitable animal model for interrogating the transition of chronic pancreatitis to pancreatic cancer.

Student Researcher

Nathan Akhavan is currently in his third year of undergraduate studies at Yeshiva College pursuing degrees in Biology, Chemistry, and Spanish. He enjoys sports and exploring New York City.

Sodium Iodide Symporter (NIS) Detection in Ovarian Cancer

by

Jonathan Aivazi[1], Andrea Reyna-Neyra[2], and Nancy Carrasco[2]
[1]*Department of Biology, Yeshiva College, Yeshiva University, New York, NY;*
[2]*Department of Cellular and Molecular Physiology, Yale School of Medicine, New Haven, CT*

The sodium iodide symporter Na^+/I^- (NIS) is a protein consisting of thirteen transmembrane segments, prominently featured in the thyroid where it is located at the plasma membrane, and is key for the production of T_3 and T_4 thyroid hormones by mediating active transport of Iodide. This uptake of iodide has led to successful radioiodine I^{131} treatments administered during thyroid cancer. In addition, NIS has been found in extra thyroidal tissues as well, and current research is exploring whether the NIS could serve as a target for radioiodine in tumoral tissue, in addition to the possibility that NIS could be used as a reporter gene or even implemented using gene therapy. With respect to ovarian cancer, we tested whether tumoral tissue cells (OV – 90) expressing human NIS (hNIS) that were injected in immunosuppressed mice, would retain their original human tumoral characteristics, and consequently if NIS would continue to be expressed post injection. OV and OV – 90 cancer cell lines, that had expressed hNIS, were injected in mice; the subsequent tumor samples were then obtained after three months post injection and subjected to a membrane preparation followed by a Western Blot that targeted the hNIS KELE, ETNL, and monoclonal peptide sequence. The resulting blot indicated broths and wide bands observable between 100 to 150 kDa, characteristic of hNIS and sharing similarity to the Wild Type hNIS positive control. These results suggest that the presence and expression of hNIS in ovarian cancer tissue is retained and could be a potential target for radioiodide treatment. Further research in hopes of clinical applications would investigate the level of NIS functionality and its ability to accumulate iodide in ovarian tissue and the precise subcellular localization of the NIS.

Student Researcher

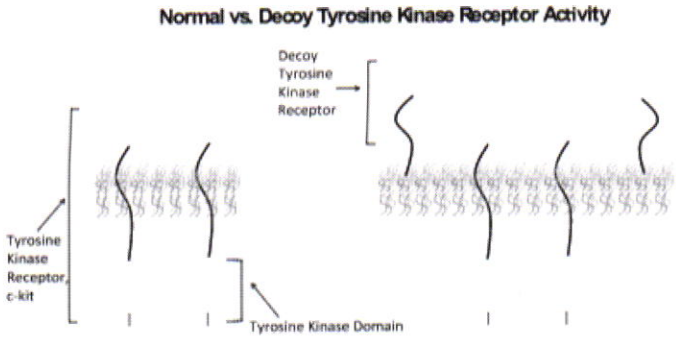
Jonathan Aivazi is currently in his second year of undergraduate studies at Yeshiva College. He is majoring in Biology, and aspires to attend medical school. When he isn't volunteering, doing research, or learning and studying, he enjoys playing basketball.

Identification of a Therapeutic Window for c-kit Inhibition to Extend Cardiac Regenerative Potential to Adolescence

by

Rebecca Garber[1], Rebecca Torres[2], Lin Tan[2], Nawazish Naqvi[2], and Ahsan Husain[2]
[1]*Department of Biology, Stern College for Women, Yeshiva University, New York, NY;*
[2]*Emory University School of Medicine, Atlanta, GA*

After birth, cardiomyocytes terminally differentiate and lose the ability to proliferate and fully heal after cardiac trauma. The stem cell factor receptor, c-kit, is responsible for activating terminal differentiation. In mice, c-kit is expressed instantly after birth and tapers off by day P10. Since fetal hearts lack c-kit, their undifferentiated cells are capable of division and repair. Therefore, inhibiting early postnatal c-kit may promote cardiomyocyte proliferation after injury. c-kit is essential to multiple cell types and organogenesis, thus, it was crucial to develop an inducible system that restricts c-kit inhibition solely to the heart. Using a transgenic mouse model (alpha-MHC:T660M-ckit-Tg), which contains an inducible decoy c-kit receptor and allows for the inhibition of a functional c-kit, our lab has shown that these cardiomyocytes never become terminally differentiated. The cardiomyocytes in the transgenic mouse accumulate a greater number of cells by adolescence compared to mice where c-kit is not inhibited during the early neonatal period. Our lab has also shown that mice with a greater number of cardiomyocytes have improved contractile heart function, suggesting that the transient inhibition of c-kit between birth and preadolescence will potentially allow adolescent hearts to regenerate after injury.



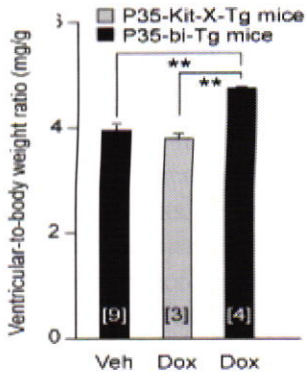


Figure 1 (left): Growth factors bind to cell receptors. Normally, growth factors will bind to the transmembrane tyrosine kinase receptor c-kit (left). However, decoy receptors (right) prevent growth factors from binding to the c-kit receptor. Since the decoy receptors are only on the extracellular membrane, they do not cause any changes inside of the cell.

Figure 2 (right): Doxycycline increases ventricular weight in bi-transgenic mice. The Kit-X and bi-transgenic mice were treated at the age of P1-P21 with either doxycycline (Dox) or vehicle (Veh). Ventricular-to-body weight ratio was determined at P35. There was a significant increase in ventricular-to-body weight ratio in the doxycycline treated bi-transgenic mice as compared to both doxycycline treated Kit-X mice and vehicle control mice. **P value <.05

Student Researcher

Rebecca Garber is a junior at Stern College for Women majoring in Biochemistry. All the way from Atlanta, GA, Rebecca is proud to say that she has nearly mastered the New York subway system and no longer looks like a tourist. After graduating, she hopes to pursue a career in the medical field and become a physician specializing in cardiology.

Hormone Extraction from Hair Samples

by

Dani Edelman, Yaeli Lev, Liat Arnon, Ruth Fishman, Devora Matas, and Lee Koren
The Mina and Everard Goodman Faculty of Life Sciences, Bar Ilan University, Ramat Gan, Israel

Until recently, levels of cortisol, a glucocorticoid stress hormone, and testosterone were measured in both humans and animals by analyzing blood, urine and saliva samples. There are several limitations with this methodology. Results only show the hormone levels at the moment of sample extraction without the ability to measure variations over time. Cortisol levels can be greatly affected by the acute stress resulting from the invasive procedure of taking the blood urine and saliva, thereby giving inaccurate readings. These samples are often difficult to obtain and need to be transported in specific conditions (i.e. frozen or cold). These methods also incur considerable risk of infection of the subject. Recently, new enzyme immunoassay (EIA) kits have been developed enabling hormone analysis from hair samples. As hair grows, hormones are deposited into the hair shaft. This acts as a biomarker indicating long-term activity of the hypothalamic-pituitary adrinocortical (HPA) axis. The hair samples can either be analyzed whole, giving average hormone levels secreted during the life of the sample, or segmented to analyze the hormone levels over a specific time period of hair growth. This method is also noninvasive and samples can be stored at room temperature. The application of these new EIA kits, however, has been limited due to their recent development. Because human hair grows approximately 1 centimeter per month, information about past events can be learned. Samples were analyzed using the new EIA kits for cortisol and testosterone levels. Similar experiments were conducted with hyraxes, Procavia capensis and nutrias, Myocastor coypus.

Student Researcher

Dani Edelman is currently a junior in Yeshiva College majoring in Biology and minoring in Chemistry. After YU, Dani is planning to pursue a career in the medical field.

Allelic Diversity of IFNAR-1 in African Patients with Malaria

by

Jacqueline Benayoun[1], Lucas R. Cusumano[2], Seungjin Ryu[2], Catherine Manix Feintuch[2], Daouda Ndiaye[3], Esther Gondwe[3], Karl Seydel[3], Terrie Taylor[3], Yousin Suh[2], and Johanna P. Daily[2]

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[2]*Department of Microbiology and Immunology, Albert Einstein College of Medicine, Bronx, NY;*
[3] *Blantyre Malaria Project, Blantyre, Malawi*

Malaria is a serious and sometimes fatal disease that caused 207 million clinical episodes and 627,000 deaths in 2012 alone (World Health Organization). Genetic predispositions can modulate the risk for severe malaria. Prior studies have found the association of mutations within the Type I Interferon Receptor (IFNAR1) and disease outcomes in *Plasmodium falciparum* malaria. To further explore the role of mutations in IFNAR1 we carried out an in-depth Single Nucleotide Polymorphism (n=21 SNPs) analysis at the IFNAR1 locus. We examined genomic DNA from children with cerebral malaria from Malawi and tested associations with disease outcomes. In addition we examined the IFNAR1 allelic diversity between West Africa (Senegal) and East Africa (Malawi).

Type I IFNs are involved in host response to malaria. Type I IFNs prime macrophage pro-inflammatory responses, enhance intracellular killing, dendritic cell maturation and T helper 1 cell responses; and promote lymphocyte activity. Type 1 IFN has been associated with modulating malaria infection outcomes in the animal model of cerebral malaria and in human malarial disease. Type I IFN receptor (IFNAR1) polymorphisms are associated with disease outcomes in malaria. This will be tested through an association study of IFNAR1 alleles in patients with mild versus severe malaria.

Genomic DNA was extracted from dry blood spots of African Patients using a DNeasy extraction kit. The samples were quantified by nanodrop and amplified using PCR. Gel electrophoresis was run to confirm the presence of the DNA. Then, Iplex mass- spectrophotometry was performed to determine the alleles present in the African cohorts in 21 SNPs. Finally, a Typer program was used to generate the patient spectra and allele call rate.

After testing 21 SNPs, a 94% call rate from 20 SNPs was achieved. Out of the 20 primers that worked, 7 primers were monomorphic. From the remaining 13 primers, 4 primers showed no significant differences between the acute and mild cohorts, and 3 were statistically significant. Significant differences are present in the IFNAR1 locus between severe and mild malaria cohort. Further studies should be repeated using a mild malaria cohort from Malawi to match population background. Additionally, the functional significance of this allelic diversity must be defined and linked to additional disease outcome (such as anemia and survival rate).

Student Researcher

Jacqueline Benayoun is a graduating senior at Stern College majoring in Biochemistry. She spent her time on campus writing for the Observer, tutoring at Norman Thomas High School, and volunteering at Morgan Stanley Children Children's Hospital with the pediatric patients. She is most grateful to Yeshiva University and the Summer Undergraduate Research Program at Albert Einstein College of Medicine for supporting the research that she performed and promoting biomedical research.

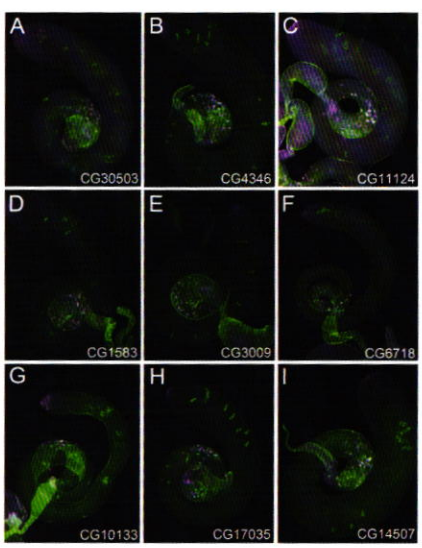
Phospholipid-Derived Signaling Molecules in Spermatogenesis

by

Yosef Frenkel, Geulah Ben-David, Eli Miller, and Josefa Steinhauer
Department of Biology, Yeshiva College, Yeshiva University, New York, NY

In many well-studied cell communication pathways, extracellular proteins act as messengers between cells, but certain lipids also can act as communication mediators. Fatty acids, which are precursors for potent lipid signaling molecules, are stored in membrane phospholipids and are released by phospholipases A_2 (PLA_2s). Lysophospholipid acyltransferases (ATs) oppose PLA_2 activity, re-esterifying fatty acids into phospholipids, in a biochemical pathway known as the Lands Cycle. Following release from phospholipids, fatty acids are metabolized into signaling lipids such as prostaglandins, which play key roles in mammalian immunity and fertility. We are investigating the function of the Lands Cycle and phospholipid-derived signals in *Drosophila.* BLAST analysis reveals ten predicted PLA_2 genes in the *Drosophila* genome. RNAi –mediated knockdown indicates that some PLA_2s are essential for viability, while others are not. We are investigating the cause(s) of lethality for the essential PLA_2 genes. We also are testing for redundancy amongst the PLA_2s. We have shown that *Drosophila* Lands Cycle ATs Oys and Nes are required for spermatid individualization, suggesting an evolutionarily conserved role for this pathway in male fertility. RT-PCR shows that seven PLA_2 genes are expressed in the testis. We are using RNAi, overexpression, and in situ hybridization to investigate PLA_2 function there. Furthermore, we have found that mutants for the *Drosophila* cyclooxygenase Pxt, which creates prostaglandins from fatty acids, also show spermatid individualization defects. Our results suggest that specific lipid signals, whose abundance is regulated by the Lands Cycle, are important regulators of spermatogenesis.

Hairpin RNA Targeting Each PLA2 Gene Expressed in the Testis with *bam-GAL4-VP16, babP-GAL4*, and *UAS-Dcr2.*



Student Researcher

Yosef Frenkel is a junior in Yeshiva College majoring in Biology with a minor in Speech and Drama. When Yosef is not working in the lab, he can be found in the theater working on YCDS's next production or in the gym covering basketball games for the Macslive broadcasting network. Yosef also enjoys being an EMT for the Hatzalah Volunteer Ambulance Corps and will be applying to MD programs this summer.

Survey on Funding and Access to Genetic Testing

by

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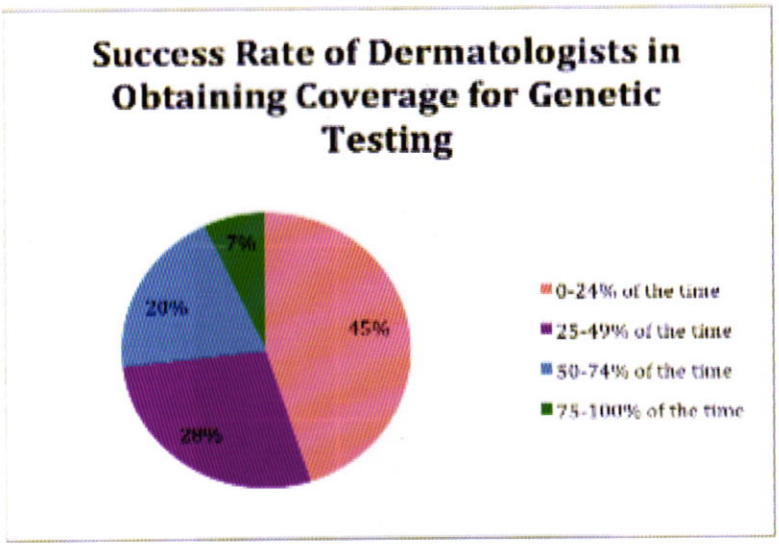
Advances in molecular genetics have made genetic testing a useful and necessary tool in many fields of medicine. Dermatologists have experienced an increasing need to use genetic tests for their patients in order to provide the most accurate diagnosis and determine the best plan of care. The most significant barrier that many physicians face with regards to genetic testing is cost. The aim of our study was to gain an understanding of the obstacles dermatologists face in obtaining the funding for genetic tests and their experiences trying to procure the testing they seek to use. To accomplish this, we sent a survey to 480 dermatologists and received 145 responses. We found that of the 66.4% of dermatologists who have gone through the effort of explaining the need for testing to reluctant insurance companies, half were only successful in obtaining payment coverage from insurances less than 25% of the time. Only 7% of the physicians surveyed reported that they succeeded in obtaining coverage 75-100% of the time. The more often a dermatologist wanted to order a test, the more time they spent dealing with insurance companies to obtain coverage (χ^2 (4)=12.76, p <.01). Additionally, the dermatologists who devoted more time to pursuing coverage had more success in obtaining it (χ^2 (4)=51.05, p<.001). To improve the access to genetic testing, societies such as the American Academy of Dermatology should create guidelines for genetic testing that make clear the necessity for coverage. Additionally, methods to reduce the cost of testing should be improved and utilized. Lastly, it is important that a detailed system be established that aids providers in determining the appropriate genetic test to use for diagnostic purposes in each individual patient case.



Student Researcher

Maddie Tavin Zimilover is a senior in Stern College for Women majoring in Political Science and minoring in Biology. She hopes to attend medical school and become a pediatrician. Maddie is the president of the Stern Social Justice Society and has been involved in Model UN for six years.

Standardization of Trypan Blue Viability Assay for Cryopreserved-Thawed Hematopoietic Progenitor Cell Products

by

Hadassa Holzapfel[1], Carlo Palesi[2], Domenica Imperato[2], Anesa Mirza[2], and Ljiljana V. Vasovic[2,3]

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Hematopoietic progenitor cells (HPCs) can differentiate to various specialized blood cells and form the basis of cellular therapies for patients with cancers and other disorders of the blood and immune systems. The cellular therapy product (CTP) containing HPCs can be obtained directly from the bone marrow or can be collected by an apheresis procedure after HPCs are mobilized into circulating blood. Cryopreservation then allows CTP to be stored at -80°C to -196°C until the transplant is medically indicated but this reduces cell viability. Laboratory determination of CTP viability is a measure of product quality and is traditionally based on a Trypan Blue (TB) assay for total nuclear cell (TNC) viability. The method is well standardized and optimized for the staining of fresh cells. However, viability determination of post-thaw CTP is a challenging and difficult procedure to standardize with high technologist inter-observer variability. The traditional cryoprotectant containing DMSO is cytotoxic in a time-related manner. DMSO also interferes with viability determination. The standard TB assay procedure usually requires a 10 to 100 times dilution of the CTP sample since TB has a greater affinity for serum proteins than for cellular proteins, rendering suboptimal dead cell color intensity. The cryopreserved cells post-thaw are very fragile and sensitive to an osmotic shock introduced by sample dilution by saline, therefore we modified our TB staining procedure to perform stepwise dilution of cryopreserved post-thaw sample with Dextran 40. Fresh HPC, apheresis CTPs collected from peripheral blood were processed immediately. A sample was taken after addition of a cryopreservative containing 10% DMSO. Frozen CTP bags were thawed and split into two aliquots: 1. Unmanipulated, undiluted CTP and 2. 10% Dextran 40 solution in saline gently diluted 1:2. Cell viability was counted by trypan blue neat or by first diluting each sample 1:10 with either saline or Dextran 40, and then staining with trypan blue 1:2. The cell viability of a fresh, pre-manipulation CTP was not affected by sample dilution method. The viability of the fresh cells decreased after the addition of DMSO-cryopreservative. The sample dilution with saline decreased viability of the cells more than the dilution with Dextran 40. The cell viability of thawed products was most preserved when first diluting the sample with Dextran 40, then trypan blue 1:2. Furthermore, thawed, undiluted CTP samples had lower viabilities than samples diluted 1:2 with Dextran 40.

In conclusion, the viability of fresh, unmanipulated cells can be accurately determined using a standard trypan blue staining protocol. Saline dilution significantly decreases viability results while Dextran 40 dilution maintains accuracy of the assay. The viability of cryopreserved, thawed CTP is significantly decreased upon dilution in trypan blue neat or saline. Dextran 40 dilution maintains high viability of cells for an extended period of time.

Student Researcher

Hadassa Holzapfel is a senior at Stern College majoring in Biochemistry. She plans to attend medical school and pursue a career in oncology.

Mathematical Model for Natural Killer Cell Development in the Liver

by

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The Mina and Everard Goodman Faculty of Life Sciences, Bar Ilan University, Ramat Gan, Israel

A Natural Killer (NK) cell is a type of lymphocyte that is part of the innate immune system—the "first line of defense" for when a pathogen enters the body. The innate immune system is non-specific to certain types of pathogens. Therefore, NK cells target bacteria and viruses based on general patterns on their outer surfaces; they also target cells in the body that have irregular MHC class-I on their membranes. NK cells are especially important in the liver, since the liver cleans the blood, including nutrient-carrying blood from the digestive system which might contain pathogens.

There are four stages in the development of NK cells, and these stages are defined in mice based on whether or not the cell has one, both, or neither of the following receptors on its membrane: $CD27^{-}CD11b^{-} \rightarrow CD27^{+}CD11b^{-} \rightarrow CD27^{+}CD11b^{+} \rightarrow CD27^{-}CD11b^{+}$. Humans have different receptors marking the development of their NK cells, including CD56, which also have different levels of expression ($CD56^{bright}$ and $CD56^{dim}$).

The experiment conducted analyzed the dynamics of NK cell development in the liver. Through mathematical modeling, we found the rate at which NK cells at each of the four stages of development enter the liver, proliferate, transition to the next developmental stage, exit the liver, and die. Furthermore, we also found the carrying capacity for each population in the liver.

Based on the results from the modeling, we concluded that Stage 4 cells have the highest residence time, carrying capacity, and influx into the liver. This is most likely due to the fact that the liver needs the mature NK cells in order to efficiently kill microbes without causing inflammation.

Student Researcher
Tamar Wasserman is a senior at Stern College majoring in Biology.

Regulation of Immune Repose to Influenza A Following Treatment with Favipiravir

by

Jonathan Willner, Miguel Fribourg, and Stuart Sealfon

Department of Neurology and Center for Translational Systems Biology, Icahn School Of Medicine at Mount Sinai, New York, NY

Favipiravir (T-705) is an antiviral drug that blocks viral RNA production by selectively inhibiting RNA-dependent RNA polymerase which has been shown to thwart influenza replication and has been associated with better clinical outcomes. While favipiravir's antiviral effects are well documented, little is known about the effects of the drug on the early immune response to the viral infection. Interferon beta (IFNβ) is a crucial component of the early antiviral immune response and induction of IFNβ mRNA can be detected and quantified starting at two hours post infection. We hypothesized that favipiravir will alter the levels of IFNβ expression, specifically the levels of mRNA observed between the first four to eight hours after infection. To address this question we measured IFNβ mRNA in monocyte-derived dendritic cells by RT-PCR and single-cell single-molecule measurement of mRNA in situ, a technique that allows for the quantification of the precise number of IFNβ and viral mRNA molecules within each cell. We believe that the determination of the effect of favipiravir on the early immune response will provide a greater understanding as to how this drug modulates the immune response to viral infections.

Student Researcher

Jonathan Willner is currently in his third year at Yeshiva University majoring in Chemistry and Biology. He aspires to attend medical school following graduation. He is involved in the Undergraduate Student Research Society, Physiology Club, and Student Government.

The Innate Antiviral response of HEK 293 Cells to Varicella Zoster Virus

by

Jennifer Grossman, Odeya Marciano, and Ron S. Goldstein
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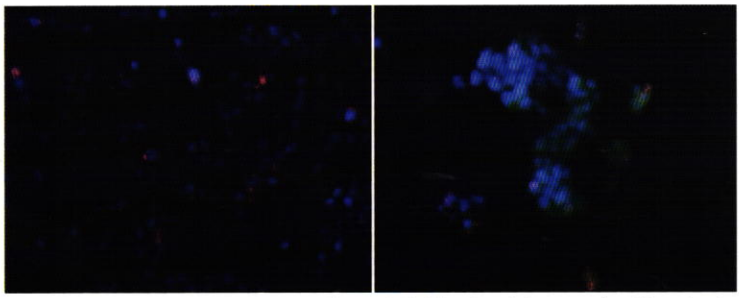
When homo sapiens inhale the varicella-zoster virus (VZV), VZV infects lymphocytes, primarily in the tonsils, that carry it to the skin, where it causes a productive infection in the form of lesions (chickenpox). The virus also infects sensory and sympathetic ganglion neurons, either via transport from the skin lesions or via infected lymphocytes. VZV remains latent in these peripheral neurons for many years. Often stress causes the virus to reactivate, resulting in a lytic infection in the form of shingles.

The exact method of the establishment of latency in neuronal cells remains elusive. However, Dr. Goldstein's lab at Bar-Ilan has found that when human embryonic kidney (HEK) 293 cells are infected with VZV, the virus enters but does not elicit a productive infection and its genome remains resident, which may serve as a model for latency in an easily grown and genetically modified cell line. Promylelocytic leukemia protein nuclear bodies (PML bodies) are structures in cells, including neurons, which have been proposed to play a role in innate immunity, by capturing VZV in cages in an attempt to prevent their replication. Therefore, we examined whether PML bodies might be involved in the prevention of productive infection in HEK 293 cells.

The normal distribution of PML bodies present in HEK 293 cells as wells as in adult retinal pigment epithelial (ARPE) cells, a cell line in which VZV produces a productive infection, was established using immunofluorescence. Both cell lines were subsequently infected with VZV. Immunofluorescence was used to analyze the PML bodies of these cells 24 hours post infection. The VZV-infected HEK 293 cells displayed a very similar pattern of PML bodies to that of uninfected HEK 293. By contrast, VZV infection dramatically changed the pattern of PML body pattern in infected ARPE cells: after infection, almost no PML bodies were observed.



Left: Uninfected HEK 293 cell nuclei (blue) with PML bodies (red). **Right:** HEK 293 cell nuclei 24 hours post VZV infection (green), showing PML bodies (red).

These findings suggest that this intrinsic immune response is not successful in preventing replication of the VZV virus in cells in which VZV elicits a productive infection. In contrast, the presence of PML bodies in VZV infected HEK 293 cells suggests that PML bodies could be involved in the inability of HEK 293 cells to undergo productive infection.

Student Researcher

Jennifer Grossman is a senior in the Honors Program at Stern College for Women, Yeshiva University majoring in Biology with a concentration in Molecular and Cellular Biology.

Production of Bioethanol from the Green Algal Species, *Ulva lactuca*: The Role of Ulvan-Degrading Enzymes in a Synthetic Operon

by

A. Wakschlag, M. Klyman, M. Kopel, E. Foran, G. Yerushalmi, and E. Banin
Institute of Nanotechnology and Advanced Materials, The Mina and Everard Goodman Faculty of Life Sciences, Bar Ilan University, Ramat Gan, Israel

Ulva lactuca is a species of green seaweed favorable from many standpoints for the production of ethanol fuel via the conversion of its polysaccharides - namely, ulvan, comprised of rhamnose, glucuronic acid, xylose, and glucose - into ethanol. As part of an attempt to bioengineer a microorganism that will carry out this entire conversion process, five genes coding for ulvan-degrading enzymes of native ulvan-degrading bacteria were isolated, genetically sequenced, and quantitatively characterized as collectively efficient in ulvan sacchrification. (Names of genes, enzymes, and bacterial strains are not disclosed at this time due to patent concerns.) In this research effort, the first of several ulvan-degrading enzymes was constructed into what will be a synthetic operon that will facilitate the sacchrification of ulvan. The subsequent ulvan monomers are to be fermented into ethanol through modified metabolic pathways of the same organism, *Escherichia coli* KO11.

In order to carry out the most efficient sacchrification of ulvan, we have employed a synthetic operon system developed by the laboratory of Ron Milo at the Weizmann Institute of Science in Rehovot, Israel. This project aims to create a library of synthetic operon permutations, consisting of six different ribosome binding sites (RBSs A-F) and five separate genes for specific ulvan-degrading enzymes necessary for complete ulvan degradation. The purpose of the utilization of varied RBSs is to fine-tune the synthetic operon by pinpointing the appropriate expression levels of each enzyme. Each RBS demonstrates unique affinity to the ribosome, corresponding to the distinct level of the subsequent gene's expression. At the end of the synthesis process, the operon with the combination of RBSs that yields the most effective ulvan-degradation will be selected.

During the initial assembly of the synthetic operon, the resistance cassette for the antibiotic, chloramphenicol, (Cm^R) is sewn onto the genetic inserts and ligated to six temporary host plasmids pNIV A-F (each pNIV accommodating a unique RBS) in order to allow for selection of plasmids containing the genes of interest. pNIV plasmids and genes with Cm^R are restricted and ligated to one another, one gene at a time, until all five are incorporated into a single insert. The end result is a library of 6^5 (7,776) combinations of the complete operon. The synthetic operon in its numerous forms is then transferred out of the pNIV plasmids and into pTAC, a plasmid that demonstrates better gene expression than pNIV. Subsequent biochemical assays will determine the most efficient ulvan-degrading operon permutation, and the plasmid containing that sequence will be transformed into the final organism, *E. coli* KO11. The current research effort has successfully integrated the first gene of the operon into pNIV A-F plasmids, setting the stage for further synthesis of the operon.

Student Researcher

Adina Wakschlag is a Molecular and Cellular Biology major at Stern College. She has conducted research in several microbiology laboratories and has co-authored publications in *The Journal of Biological Chemistry* and *Antimicrobial Agents and Chemotherapy*, among other journals.

BRAF-V600E Detection from Stained Cytology Smears in Thyroid Carcinoma Fine Needle Aspirations Utilizing Clamp qPCR Technology

by

Laleh Hakima[1], Elie Flatow[2], Evan Pieri[2], Samer Khader[1], Antonio Cajigas[1], Mark Suhrland[1], Maja Oktay[1], and Sumanta Goswami[2]

[1]Department of Pathology, Montefiore Medical Center, Bronx, NY;
[2]Department of Biology Yeshiva University, New York, NY

Mutational analyses are increasingly important for guiding treatment decisions. This is particularly important for surgical management of thyroid nodules with indeterminate cytological diagnoses. Thyroid lesions are frequently diagnosed using fine needle aspiration (FNA) cytology as they are highly vascular and a more aggressive method of tissue collection may result in hemorrhage. Molecular diagnostic tests of cytologic samples are commonly performed using paraffin embedded tissue (PET); however, insufficient cellularity presents an obstacle. Several studies reported successful molecular diagnostic tests performed from Diff Quik-stained cytology smears. This approach ensures that material sent for molecular testing is representative of the lesion and is associated with a rapid turnaround time. We successfully determined the presence of the BRAF-V600E mutation in papillary thyroid carcinomas (PTC) and follicular thyroid carcinomas (FTC) using clamp qPCR technology on direct cytology smears. Clamp qPCR is highly sensitive detecting mutant DNA in as few as 50 cells with a 2% mutation detection level, compared to the reference lab threshold of 400 cells and10% detection level.

FNA smears from 24 cases of PTC and 2 cases of FTC with corresponding PET were collected. Areas of interest were marked on the Papanicolaou and Diff Quik-stained smears and DNA was extracted. BRAF-V600E mutant DNA was selectively amplified and detected using clamp qPCR method. Corresponding PET was tested in parallel to assess concordance. Two cases of PTC, one positive and one negative, were sent for reference laboratory testing which validated our method.

Of 22 PTC cases (14 classic, 7 follicular variant, 1 micropapillary) with unknown mutation status, 17 (77%) tested positive for BRAF-V600E and 5 tested negative on both direct cytology smears and PET. Of two FTC cases, both tested negative on cytology smears and PET. There was 100% concordance between direct cytology smears and PET.

Molecular testing of FNA smears reliably detects DNA mutations in thyroid cancers and shows 100% concordance with PET. The percentage of BRAF-V600E (77%) in this study is higher than the percentage reported in literature (50%). These 2 observations suggest that molecular testing of cytology smears utilizing clamp qPCR technology has increased sensitivity to molecular testing using PET and may improve quality of patient care because FNA is minimally invasive and offers a quick turnaround time.

Student Researcher

Elie Flatow is currently in his third year of studies at Yeshiva University. Majoring in Biology and minoring in Spanish, he enjoys spending time with children in the pediatric ward of New York Presbyterian Hospital. He also is an avid fan of sports and culture.

BRE1's Effect on PSG Formation

by

Joshua Azar, Lee Peters, Ofri Karmon, and Shay Ben-Arroya

Department of Molecular Biology, Bar Ilan University, Givat Shmuel, Israel

Protein homeostasis, or proteostasis, is essential for the maintenance of regular bodily functions. Misfolded proteins cause the protein to lose its functionality or to become toxic which can damage other proteins that operate in the near vicinity. Many neurodegenerative diseases, including Alzheimer's and Parkinson's have been linked to misfolded proteins and aggregates. Cells, therefore, have evolved to rely on a number of different protein quality control (PQC) pathways to prevent protein aggregation and target terminally misfolded proteins for degradation. In eukaryotes, the ubiquitin proteasome system (UPS) plays a major role in PQC by selectively marking and targeting proteins for degradation.

The UPS regulates proteins through a pathway known as ubiquitination. Ubiquitination consists of labeling a protein with polyubiquitin chains which marks that specific protein for degradation in the proteasome. The 26S proteasome is a multisubunit protease that is highly enriched in the nucleus and is responsible for degrading a large number of potentially harmful proteins. The proteasome consists of a 20S core particle and two 19S regulatory particles. Ubiquitinated proteins are unfolded as they are fed down the 19S shaft and then translocated to the 20S core particle where the protease activity breaks down the protein into short peptide molecules.

A recent study showed that, upon carbon source deletion, proteasomes are stored in Proteasome Storage Granules (PSGs), where they can be quickly and efficiently prepared for use when needed. Proteasome activity has never been seen within these PSGs and it is unclear whether they are functional and if they are not functional what exactly keeps them inactive. Much of the current research in the lab is focused on understanding the mechanics and role of these PSGs.

BRE1, an E3 ligase, has been recently implicated in the lab as a factor in the relocalization of the proteasomes into PSGs. BRE1 is known to ubiquitinate lysine at the 123rd position on the histone H2B [k123] and without BRE1proteasomes will not go into PSGs. However, it is unclear whether the ubiquitination of H2B k123 is a factor in the formation of PSGs or perhaps BRE1 causes the formation of PSGs through a passage not involving H2B ubiquitination. Using baker yeast Saccharomyces Cerevisiae as a model system to determine BRE1's effect on PSGs we created 3 different strains. One WT strain which has RPN5, a proteasome subunit marked with GFP. In this strain the proteasome should go to PSGs when carbon levels are low. A second strain consisted of RPN5-GFP but with a deletion of BRE1 preventing the formation of PSGs. A third strain contained RPN5-GFP and mutated k123 in H2B to observe whether PSGs will form when there is a valid copy of BRE1 but without lysine which is ubiquitinated on H2B-(k123). As of this printing, the strains have been created and we hope to run the experiments soon.

Student Researcher

Joshua Azar is a senior in Yeshiva College majoring in Biology with plans to attend dental school next year.

Creation of Double Mutant Cells for Nek3 and Nek5 Kinases by CRISPR/Cas9 Method and the Identification of Nek5 in the Brain and Lung

by

Michal Schechter[1], Sivan Cohen[2], and Benny Motro[2]

[1]*Department of Biology, Stern College for Women, Yeshiva University, New York, NY;*

[2]*Department of Life Sciences, Bar Ilan University, Ramat Gan, Israel*

Transition from one cell cycle phase to another occurs in an orderly fashion and is regulated by multiple evolutionary conserved proteins. In our lab, we researched the Nek kinase family, which is known to be involved in the transitions between the cell cycle phases. The mammalian NIMA-related kinases (NRK's) genes, which are designated as Nek1-11, encode for evolutionarily conserved serine/threonine kinases, structurally related to the fungal mitotic regulator, NIMA. In conditional absence of NIMA activity, fungal cells arrest in G2, exhibiting interphase microtubules and uncondensed chromosomes.

Several mammalian Nek kinases have shown to be critical for the cell cycle and the centrosome cycle. However, the functions of the other mammalian Nek kinases are less obvious. The catalytic domains of Nek1, Nek3, Nek5 and are highly homologous. Due to the possibility that Nek3 had compensated for the absence of Nek5 in the mutant mice, the first goal of my project was to create a double mutant for Nek3 and Nek5 in cells. We attempted to create this double mutant by using the CRISPR/Cas9 system, which is a new method which is based on the Cas9 system in bacteria and is usually used for targeted gene editing. We planned and constructed unique genomic sequences for Nek3 and Nek5, which possessed recognition sites for endonuclease Cas9. Based on the phenotype of Nek1, we expect to see an abnormal phenotype in the cell cycle or in the DNA damage response of the double mutants for Nek3 and Nek5. Since the mice mutant for Nek5 did not have an obvious abnormal phenotype, our lab also checked to see in which specific organs Nek5 is expressed. Based on previous Northern blotting analysis, we concluded that Nek5 is mainly concentrated in the brain and lung. LacZ was inserted downstream of the endogenous Nek5 promoter, thus lacZ staining was expected in areas where Nek5 is expressed. We were able to demonstrate that lacZ staining (and thereby Nek5) is specific to the arterioles in the lung, while no expression could be seen in the alveoli or other structures in the lung. As the arterioles are ciliated, it may be speculated that Nek5 is involved in cilia genesis.

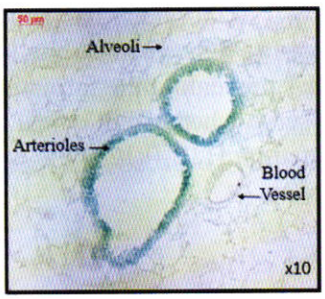


Figure 1. Beta-galactosidase staining of a lung tissue from a heterozygote Nek5 mouse (x10).

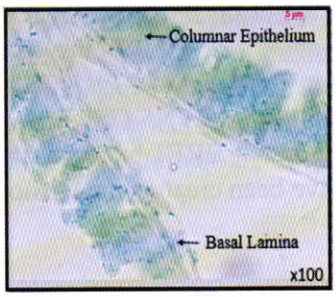


Figure 2. Beta-galactosidase staining of a lung tissue from a heterozygote Nek5 mouse (x100).

Student Researcher

Michal Schechter is a senior at Stern College for Women majoring in Biology with a concentration in Political Science.

Platelet-Activating Factor Clustering: Relevance for Excitotoxicity and Epilepsy

by

Aitan Magence[1,2,3], Nathan Herrmann[1,2], Graham Mazereeuw[1,2,3], Myuri Ruthirakuhan[1,2], Hongbin Xu[4], Steffany AL Bennett[4], and Krista L Lanctôt[1,2]

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[2]*Department of Pharmacology and Toxicology, University of Toronto, Toronto, Ontario, Canada;*
[3]*CIHR Training Program in Neurodegenerative Lipidomics, Ottawa, Ontario, Canada;*
[4]*University of Ottawa, Ottawa, Ontario, Canada*

Platelet activating factor (PAFs) are a family of potent phospholipid mediators that promote inflammation and oxidative stress, and cause neurotoxicity through excitotoxic and apoptotic pathways in the brain. Pre-clinical work suggests that PAFs may demonstrate different effects on target cells based on carbon chain (CC) identity. Therefore, we hypothesized that certain PAFs in plasma would correlate with other PAFs of similar CC length in coronary artery disease (CAD) patients, a population with a wide range of PAF concentrations suitable for investigation of PAF-PAF relationships ("clusters").CAD patients participated in a12-week (wk) exercise-intervention. Fasting blood plasma was collected at wks 0 and 12. PAFs were sampled from plasma using electrospray ionization mass spectrometry and abundance was log transformed to achieve normality. Correlations between PAFs were assessed cross-sectionally using linear regression andthen explored at *a priori*to clarify relationships among highly correlated PAFs. Distinct clusters were generated when the PAF species were significantly related to other PAFs within the same cluster.

23 CAD patients were included in this study (mean age 59.9, 69.6% male, 43.5% history (Hx) of coronary artery bypass graft, 56.5% Hx of percutaneous transluminal coronary angioplasty, 43.5% Hx of myocardial infraction). 26 PAFs were detected. Several PAFs were significantly correlated with the plasma abundance of other PAFs. At the $p \leq .05$ and $p \leq .01$ levels of significance many PAF-PAF correlations were identified, however, they did not distinguish clusters of PAFs. The $p \leq 0.005$ level of significance was the threshold where distinct PAF clusters could be observed (Figure 1). Four distinct clusters were revealed at wk 0. Over 12 wks, only one distinct PAF cluster was evident for the change score values at $p \leq .005$, but several PAFs clustered together both cross-sectionally and over 12 wks of exercise. All PAF-PAF correlations were positive.This study has shown that PAFs will cluster based on similarities in their CC identities, suggesting mechanistic associations.

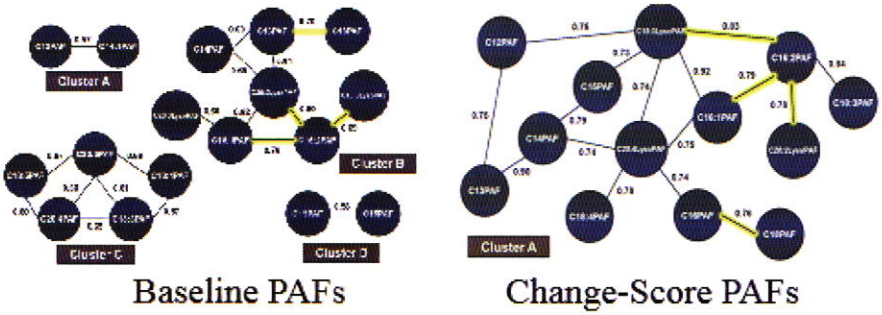


Figure 1. Baseline and change-score PAF clusters. PAF relationships highlighted in yellow demonstrate a significant relationship, both cross-sectionally and longitudinally. Pearson correlation values ($p \leq .005$) are indicated above the line.

Student Researcher

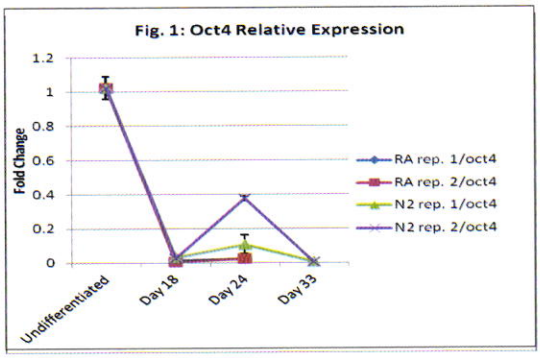
Aitan Magence is a senior at Yeshiva College majoring in Biology. In his spare time, he volunteers at New York-Presbyterian Hospital and tutors fellow students in the sciences. He plans to pursue an MD degree in the coming years.

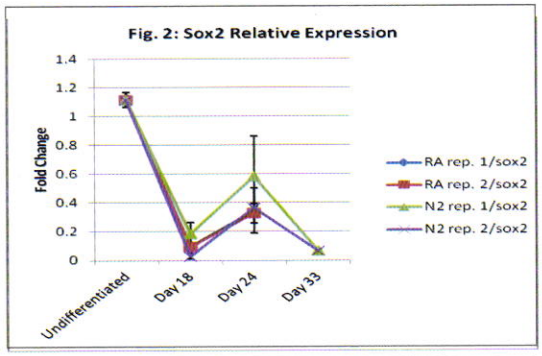
Relative Quantification of Induced Pluripotent Stem Cell and Neuronal Markers Along Neuronal Differentiation

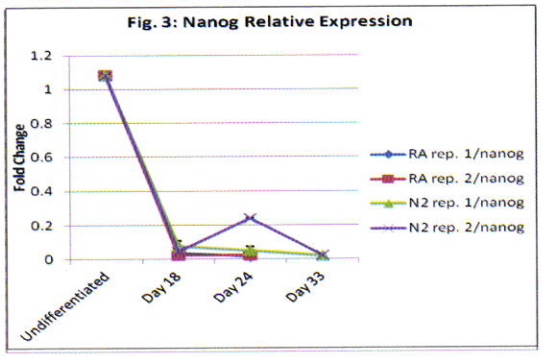
by

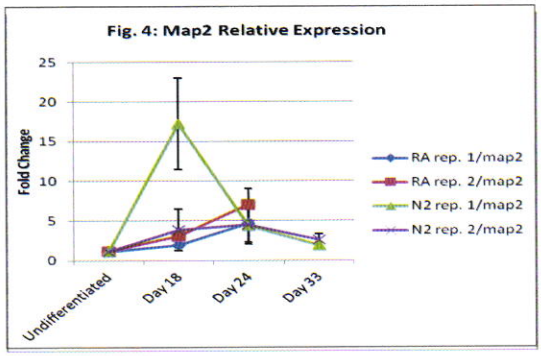
Alita Teitz and Gilli Moshitzky
Department of Biological Chemistry, The Hebrew University of Jerusalem, Jerusalem, Israel

Human embryonic stem cells can be differentiated into neurons by growing the cells in culture with retinoic acid or N2 media. The progressive stages of differentiation can be monitored by the presence of cell markers which are indicators of cellular activity. As such, in our research we followed the progression of neuronal differentiation by using RNA from stem cells at three separate time points post-treatment for quantifying the levels of known stem cell and neuronal markers. We used Nanog and Oct4 as stem cell markers, and for neural markers we employed the progenitor marker Sox2, and the neuronal markers Tuj1, Map2 and Nestin. The process began with extracting RNA from cells treated with RA or N2 to induce their differentiation. We then produced cDNA from this RNA and tested it in RT-PCR with the cell markers. By comparing the resultant Cq values with control genes, we found reduced concentrations of stem cell markers in differentiated compared to undifferentiated stem cells, and likewise, the neuronal markers showed higher concentrations in differentiated compared to undifferentiated stem cells. The quantification of the Cq values using the $2^{-\Delta\Delta CT}$ (Livak) method also showed differences in the cellular expression levels of the marker genes at the three time points. The stem cell and neuronal markers showed a decrease in expression over time, and the neuronal markers showed an increase (Figures 1-4), which indicates that cells were differentiated successfully.









Figures 1 – 4: Relative expression of Oct4, Sox2, Nanog and Map2 (respectively) in cells in N2 and RA media

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Student Researcher

Alita Teitz is a junior in Stern College majoring in Molecular and Cellular Biology. She enjoys frequent visits to Israel and hopes to move there in the near future.

Subcloning of Sodium Channel Voltage-Sensing Domains for Structural Toxin-Binding Studies

by

Sébastien F. Poget, Mohammed H. Bhuiyan, and Isaac A. Snyder

Department of Chemistry, College of Staten Island-CUNY, Staten Island, NY

The human genome contains genes for 9 voltage-gated sodium channels that are involved in different excitatory tissues and physiological roles. $Na_V1.7$ is encoded by the SCN9A gene, mutations of which cause congenital insensitivity to pain, thus making the channel an important target for pain treatment by selectively blocking the $Na_V1.7$ channel without the side effects of current treatments and the unnecessary strain on the heart that is associated with painkillers. $Na_V1.1$, encoded by the SCN1A gene, is associated with various seizure disorders. NaV1.2, encoded by the SCN2A gene, has been linked to autism and infantile spasms. $Na_V1.5$ is encoded by the SCN5A gene; mutations of which can cause fatal cardiac arrhythmias through Brugada Syndrome and Long QT3, due to an increased or decreased repolarization of the heart, respectively. Given these important physiological roles, sodium channels are promising drug targets. Each channel has 4 voltage sensing domains (VSD1-4), which are known to be the binding site for a number of animal peptide toxins. In order to better understand this toxin binding and use the structural information in drug design, we need to recombinantly express and purify the VSDs. The first step in this process is the generation of an expression construct. In order to insert a 500bp DNA insert into a 5000bp plasmid, we replicated the VSD gene using Polymerase Chain Reaction (PCR), then digested both the DNA and the plasmid, which in this case is Pet28b+ with 3 histidines added to the polyhistidine purification tag via site-directed mutagenesis, with the same set of restriction enzymes. The plasmid and insert were then ligated and transformed into *E. coli*. The plasmid was purified from overnight cultures of the resulting colonies, and the presence of the insert was checked by performing small-scale digestion on the purified plasmid, followed by agarose gel electrophoresis. Four VSDs were successfully cloned (Figure 1). Expression and purification of these VSDs is currently ongoing for future structural studies.

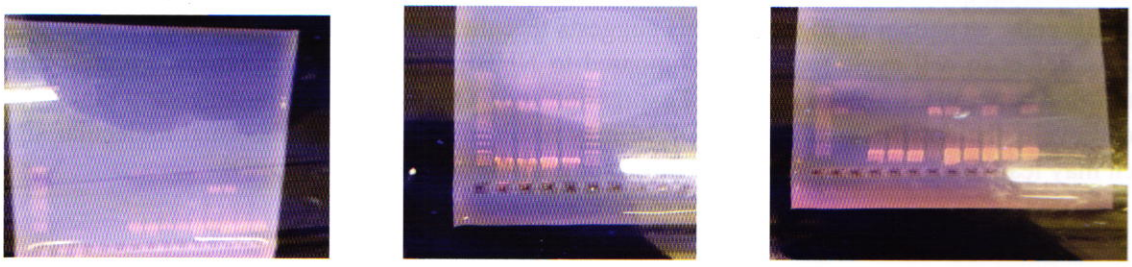


Figure 1: Successful cloning is shown by the presence of an insert fragment of about 500 bp (indicated by an arrow) for the following constructs: Left - 1.5D2 & 1.1D2, Middle - 1.1D4, Right - 1.2D2.

Student Researcher

Isaac Snyder is a junior at Yeshiva College majoring in Biology with a strong interest in researching inflammatory bowel disease (IBD). During his free time he can be found reading IBD papers, cooking or running TEACH modules.

Understanding of the Role of CDK14 in Tobacco-Related Diseases

by

Allison Tawil, Rachel Yarmush, Yuxuan Xiao, and Margarita Vigodner
Department of Biology, Stern College, Yeshiva University, New York, NY

Chronic obstructive pulmonary disease (COPD) is the third leading cause of death in the United States, and is most commonly caused by tobacco smoke. One of the pathological changes that can cause COPD onset is the degradation of the lung tissue separating alveoli. Due to this phenomenon, many alveoli of the lungs merge into one, large alveolus, decreasing the surface area for gas exchange, leading to a reduction of oxygen intake, causing the feeling of impaired breathing. Other symptoms of COPD include wheezing, shortness of breath, and chest tightness.

Cyclin-dependent kinase 14 (CDK14) is a new member of cdc2 related cell cycle regulators. It is a gene that helps a cell progress normally through the cell cycle and is also involved in molecular signaling in lung epithelial cells. Previous research has found that tobacco smoke caused down-regulation of CDK14 in different tissues and cell lines including primary human bronchial-derived cell lines.

Since the lungs are the first organs affected by tobacco smoke, this study sought to compare the difference in CDK14 expression in lung tissue of people with COPD and those without. Two cell lines were used to mimic the tissue of diseased and non-diseased lungs. Normal human bronchial epithelial cells (NHBE) were used to mimic normal lungs and were isolated from the epithelial lining of airways in the lungs of normal humans. Diseased human bronchial epithelial cells (DHBE) were used to mimic lungs affected by COPD and were isolated from the epithelial lining of airways in the lungs of humans with COPD. Real-time polymerase chain reaction (qPCR) was used to detect differences in cdk14 expression in the two cell lines.

The results of the qPCR showed that the expression of CDK14 was down-regulated in DHBE cells compared to NHBE cells, as shown in Figure 1. This suggests that the DHBE cells have less CDK14, indicating a possible defect in cell cycle regulation compared to NHBE cells. These results also suggest a putative relationship between the change in CDK14 expression and COPD. Since Cyclin-dependent kinases regulate the cell cycle, the down-regulation of CDK14 may result in cell death or abnormal molecular signaling, which may lead to tissue degradation and cause some of the symptoms of COPD.

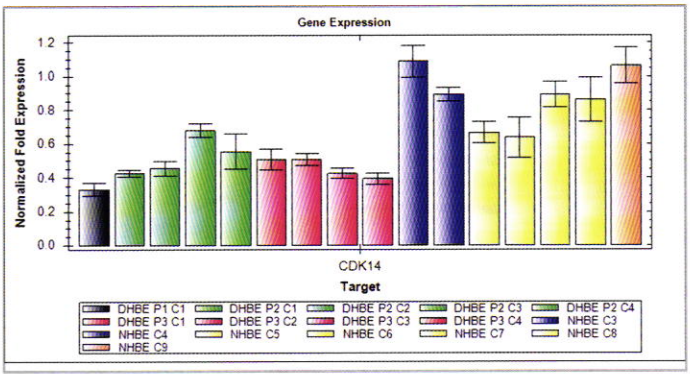


Figure 1: This graph illustrates the decrease of CFK14 production in DHBE cells as compared to NHBE. Different cell passages and time points were analyzed.

Student Researchers

Allison Tawil is a student at Stern College and is majoring with Biochemistry and minoring in Mathematics. Rachel Yarmush is currently a junior at Stern College majoring in Biology with a minor in Psychology.

Assessing Pattern Completion in Spatial Navigation

by

Tamar Golubtchik and Eitan Okun

[2]*Department of Brain Science Research, Bar Ilan University, Ramat Gan, Israel*

Spatial learning is the process by which animals encode information about the environment in order to facilitate navigation through space and recall locations of motivationally relevant stimuli. Pattern completion refers to the ability to recall a previously learned location in space based on degraded or missing visual cues. Computational models of the hippocampus suggest that the CA3 sub region of the hippocampus can perform pattern completion. The Morris Water Maze (MWM) is a common behavioral task that assesses hippocampus-dependent spatial learning in rodents. In this task, mice are given three consecutive 90 second trials to find a hidden platform within a circular water pool. Latency to reach the platform as well as path efficiency are measured to determine performance of the mice in this task. We have utilized the MWM in order to test spatial pattern completion in healthy mice. The mice were kept in a completely dark room, lit only with an infrared (IR) light to enable video tracking using an IR-sensitive camera. Four screens on each wall in the room provided visual cues for the mice.

Initially, a visible platform stage was performed to assess the motivation of the mice as well as any visual or motor impairments that could potentially disqualify mice from this experiment. Following training of the mice using the hidden platform, during which optimal latency to reach the platform was obtained (Figure 1), mice were tested in the probe stage. During the probe stage, the platform was removed and the mice were divided into five groups, each with nine mice. Each group was tested and exposed to 4, 3, 2, 1 or 0 cues respectively. It was hypothesized that the groups of mice given more cues (4 or 3) would spend more time in the quadrant of the pool that contained the platform compared to mice exposed to fewer visual cues.

During the probe test, as hypothesized, the mice spent the most time in the platform quadrant with either four or three available cues (figure 2). When there were only 2, 1 or no cues available, the mice spent relatively equal amounts of time in each of the quadrants (Figure 2). These findings are consistent with our assumption and suggest that mice use the mechanism of pattern completion during the MWM task.

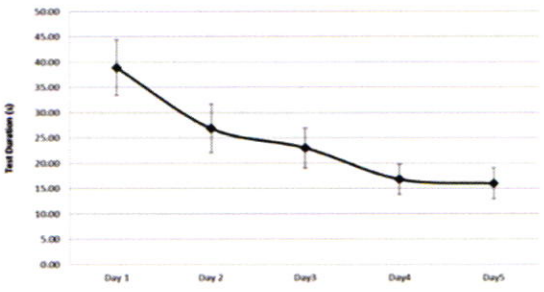


Figure 1: Plot of average test duration during the hidden platform stage with a 12cm x 12cm platform.

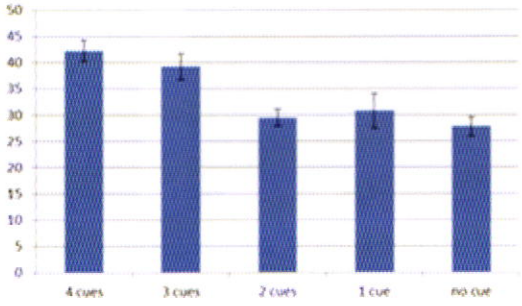


Figure 2: Graph of average time spent in lower right quadrant during probe test, based on how many visual cues were illuminated.

Student Researcher

Tamar Golubtchik is a junior at Stern College majoring in biology. She did research under Dr. Eitan Okun in Bar Ilan University during the summer of 2014 and hopes to pursue a career in medicine.

Computerized Cognitive Testing of Individuals with Down Syndrome and Alzheimer Disease

by

Michael Gutman, Ethan Moskovic, and Joseph Jeret
Mercy Medical Center, Rockville Centre, NY

Background: Alzheimer disease (AD) neuropathology typically begins at age 35-40 years in Down syndrome (DS), with lifetime risk approaching 100%. Cognitive evaluation of these individuals is challenging and time consuming.

Objective: The National Task Force on Intellectual Disabilities and Dementia Practices Consensus Guidelines (Mayo Clin. Proc. 2013; 88:831-840) acknowledged the absence of an accepted standard for cognitive assessment. We evaluated the reliability and reproducibility of an easy-to-use computerized cognitive test to serially quantify function in this population.

Methods: 14 adults (10 females) with DS and mean age of 52 years were diagnosed with AD using ICD-10 criteria. Baseline MMSE scores were 8 to 26. All subjects were treated with a cholinesterase inhibitor (donepezil, 13, rivastigmine, 1), and 8 also received memantine. Subjects were evaluated with the NeuroTrax Moderate to Severe Impairment Assessment Battery (Mindstreams, Newark, NJ). Memory, executive function, verbal function, and visual spatial were evaluated. The test was administered 4 times at 6 month intervals.

Results: Scaled scores from the first and last tests were compared. Memory (42.3, 45.5), executive function (63.2, 59.5), verbal (69.5, 73.4), visual spatial (80.1, 74.4.), and global scores (59.2, 55.9) did not significantly change. There was no significant depression on the Geriatric Depression Scale or anxiety on the Zung Self-Rating Anxiety Scale.

Conclusions: The precision, reproducibility, and ease of computerized cognitive testing make it a valuable tool in the evaluation of this particularly difficult-to-assess population. Small case studies have suggested efficacy of treatment with cholinesterase inhibitors and possibly memantine. The stability demonstrated by our cohort during the 18-month testing period could suggest therapeutic response to therapy. Randomized trials addressing this question are required.

Student Researcher

Michael Gutman is currently in his senior year at Yeshiva University majoring in Biology. He is involved in the Literacy program, local soup kitchens, and the Country and Traditional Music Appreciation Club. He aspires to attend medical school following graduation.

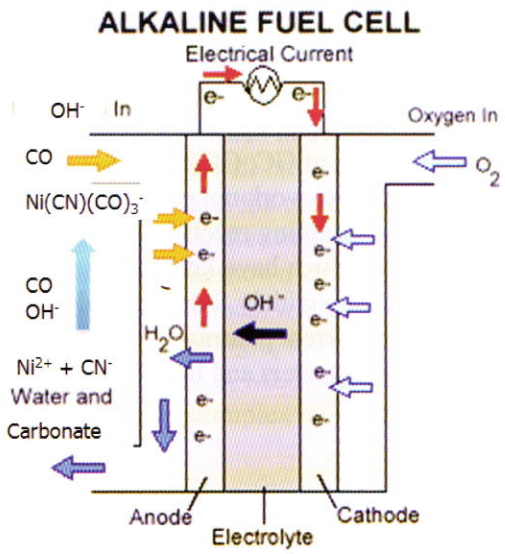
Oxidation of Carbon Monoxide in Basic Solution Catalyzed by Nickel Cyano Carbonyls Under Ambient Conditions and the Prototype of a CO-Powered Alkaline Fuel Cell

by

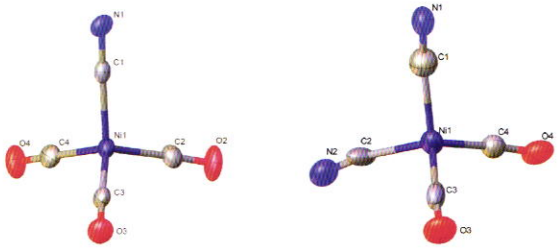
Wenfeng Lo, Chunhua Hu, Tyler Berenson, Nathaniel Tracer, Daniel Shlian, Michael Khaloo, Avraham Benhaim and Jianfeng Jiang

Department of Chemistry, Yeshiva College, Yeshiva University, New York, NY

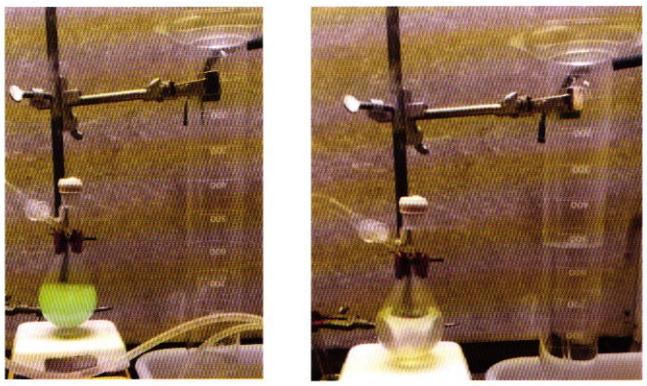
CO reduces nickel(2+) cyanides in basic solution to form tetrahedral $Ni^0(CN)(CO)_3^-$ or $Ni^0(CN)_2(CO)_2^{2-}$. Both nickel(0) complexes can be oxidized back to nickel(2+) cyanide/ hydroxide so that they behave as CO oxidation catalysts in basic solution. An initial kinetics study of carbon monoxide oxidation by oxygen gas was performed and the rate law suggested that the catalyzed carbon monoxide oxidation was first order and depended on oxygen partial pressure. A primitive fuel cell was constructed to demonstrate the feasibility of a CO-powered fuel cell.



Simple diagram of CO-powered fuel cell.



ORTEP (crystal structure) drawing of Ni0(CN)(CO)3- and Ni0(CN)2(CO)22- at 50% probability level.



The reaction setup of nickel chloride, sodium cyanide, and excess hydroxide in aqueous solution under 1 atmospheric CO at the beginning (left) and end (right) of the reaction. A graduated cylinder was used to measure gas volume change.

Student Researcher

Avraham BenHaim is an undergraduate at Yeshiva University, studying Psychology and Chemistry. He has been conducting research under Professor Jiang since 2013, and hopes to pursue a career in medicine.

Daniel Shlian is a second-year student at Yeshiva College majoring in Chemistry and Jewish Studies. He has been researching with Professor Jiang since Summer 2014 and hopes to pursue a career in chemistry research.

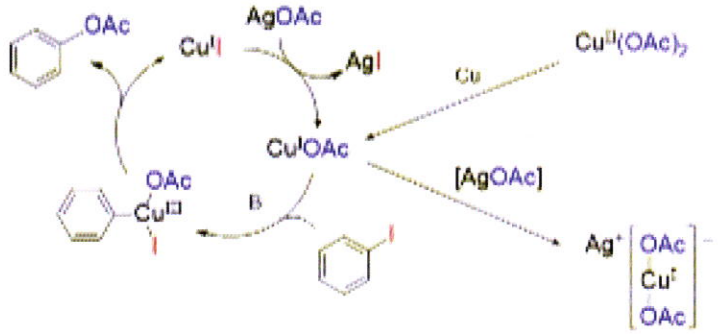
Copper-Promoted Aromatic Acyloxylation: Expanding the Scope

by

David Drory, Benyamin Ben-Tzvi, and Fabiola Barrios-Landeros

Department of Chemistry, Yeshiva College, Yeshiva University, New York, NY

Cross-coupling reactions catalyzed by transition metals have revolutionized the field of organic synthesis. Aryl halides can be coupled with multiple nucleophiles promoted by metals, commonly copper or palladium, and can form various types of C—C and C—heteroatom bonds. Carboxylic acids, however, have rarely been used as coupling partners and the synthesis of esters has received little attention. The metal-promoted acyloxylation currently being explored by the lab will offer new synthesis options that circumvent the drawbacks of traditional methods. Previous research developed a successful method for copper promoted acyloxylation using phenyl iodide or bromide as the substrate and copper (I) acetate as the catalyst and acetate source. We are currently exploring ways to expand the scope of this reaction by applying it to more diverse and complex substrates and by using more accessible and stable copper salts. For substrate trials, specific attention was given to understanding the effect of steric and electronic properties of the aryl ring on the yield of reductive elimination of aryl acetate. Larger molecules, substituted rings, and oxygen or nitrogen containing compounds were all examined as potential reaction partners. During the reaction, the copper is believed to fluctuate between its first and third oxidation states, beginning the reaction with copper I, an unstable form that oxidizes when exposed to air. Attempts have been made to start the reaction using copper II and alternative carboxylate sources, which are also less expensive and more available. Efforts will be made to facilitate redox chemistry during the reaction to enable starting with Copper II salts that can become reduced to the catalytically active form. The research involves advanced separation techniques for analysis of the desired aryl carboxylate products and relies heavily on the use of GC, GC/MS, IR, TLC, and distillation to isolate and analyze products of unknown properties. The current work not only helps answer questions about the structure and reactivity of copper complexes in cross-coupling reactions, but will also aid in developing new and efficient ways of synthesizing aromatic esters, which have known valuable applications. Moieties with aromatic esters like coumarin and its derivatives are widely found as biologically active natural products, and have found use in marketed drugs as well as in current pharmaceutical research. Additionally, the new catalytic system can help synthesize new modified polyesters and liquid crystal polymers that have desirable qualities.



Proposed Reaction Mechanism of Copper-Promoted Acyloxylation

Student Researcher

David Drory is a senior in Yeshiva College majoring in Biology with a minor in Political Science. In addition to academics, David is a resident advisor and leader of the YU chapter of Music VS., a volunteer organization. David is graduating in May and will be applying to MD programs this summer.

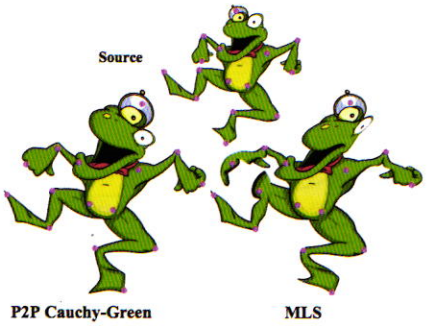
The Deformation of 3D Images Using Moving Least Squares and the Complex P2P Cauchy-Green Method

by

Michelle Levine and Ofir Weber
Department of Engineering, Bar Ilan University, Ramat Gan, Israel

The goal of this research is to create an efficient algorithm to deform images while maintaining a realistic picture. An image can be transformed by setting a mathematical path for each vertex from its original position to the new deformed location. Simple transformations include translation, scaling, and rotation in 2D and 3D polygons. Translation is when the image is shifted, but all points, angles, and lines remain the same relative to each other. Scaling entails enlarging or shrinking an image, and rotation provides a specific map in which everything in the image moves around a designated axis or point. Here, we are trying to find an effective way to transform an image by moving a vertex and mapping corresponding paths for the surrounding vertices. One method that has been developed is to deform images using Moving Least Squares (MLS). In this technique, the paths of the vertices are determined by continuous functions, which are calculated by a weighted least squares quantity. The points surrounding the chosen vertex are more greatly affected than those farther away from the focus. Three classes of linear functions used in MLS deformations are affine, similarity, and rigid transformations.

The issue with these methods of deformation is that the weighted MLS calculation determines the affect on other points based on proximity to the requested point, without taking into account the borders of the image. This causes issues when there are two vertices in close proximity with each other but separated by a border. The second vertex will have a larger deformation than intended, causing an unrealistic and warped result. Professor Weber and his colleagues came up with the P2P Cauchy-Green method in which the borders of the image are calculated and the points are then weighted within those boundaries. The difference between the two methods is shown clearly in the left image below, in which the MLS deformation causes a warped result in the frog's knee, while the P2P method effectively separates the vertices based on the image border. In the image on the right, the border restricts the coordinates of the point and the effects on the surrounding region in P2P, but in MLS, the effect spills over into the nearby knee. The ongoing research focuses on potentially using complex numbers in order to weigh the proximity of the surrounding vertices.



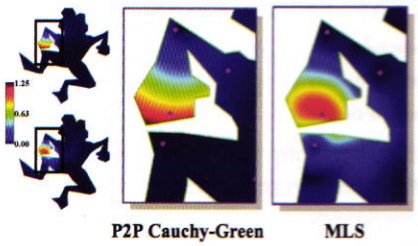


Figure 13: *Absolute value of the P2P and MLS coordinates of the point on the left hand. The MLS coordinate "spills" into the leg near it, whereas the P2P coordinate does not.*

Student Researcher

Michelle Levine is a senior at Stern College majoring in Physical Sciences with a concentration in Computer Science. In addition to getting involved on campus and running the Stern Computer Science Club, she enjoys playing tennis, volleyball, running outside and decorating cakes. She will be pursuing a Masters degree in Computer Engineering at Columbia University next year.

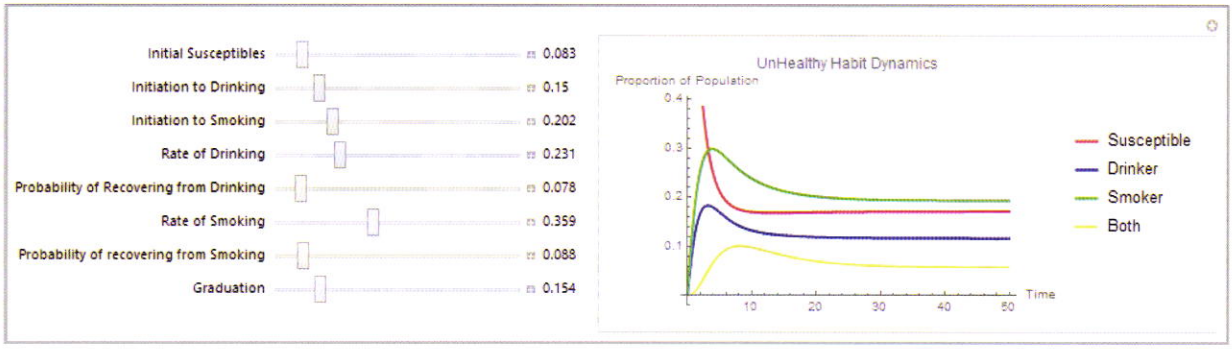
Differential Equations Models for Social Transmission of Unhealthy Habits

by

Miriam Herman and Marian Gidea

Department of Mathematical Sciences, Stern College for Women, Yeshiva University, New York, NY

This research is devoted to mathematical modeling of the spreading of unhealthy behaviors in a population of college age students. The underlying premise is that health risk behaviors spread interpersonally through complex social interactions and influences, through direct peer interactions, or through indirectly observing others engaging in risky behaviors. We adapt an existing model from epidemiology, the susceptible-infected-susceptible model (SIS), which regards a certain population as a static network, in which interacting individuals become infected, changing their health status from susceptible to infected through various channels. They can also recover from an infection, reverting their status back to susceptible. In our work we focus on two negative habits: smoking cigarettes and drinking alcohol, as well as the spreading of these habits among students through the college years. We describe the dynamics through a system of differential equations that tracks the change in time of the number of students with some distinctive behaviors. The variables of our system are: the number of susceptible who are neither drinkers nor smokers, the number of drinkers, the number of smokers, and the number of those who are both smokers and drinkers. The evolution laws of these variables are expressed via differential equations that depend on several parameters, such the likelihood of individuals beginning to adopt from one another one or both of these unhealthy habits, the likelihood of adopting an unhealthy behavior due to euphoria, the likelihood of recovering from these habits (e.g., due to campus interventions), the enrollment rate, and the graduation rate. As a case study, we considered the population of college students at Northeastern Illinois University (NEIU). The parameters of our models have been estimated from surveys done at NEIU, as well as from national data, assessing how many students are likely to begin university with the aforementioned negative habits, how many will pick them up, and also the efficacy of various types of interventions to recover from negative habits. Using the software Mathematica, we simulated the evolution in time of the number of individuals in each category (smokers, drinkers, smokers and drinkers, neither) and studied the dependence of the dynamics on the system parameters. These simulations show that the number of individuals in each category approaches an equilibrium state, and that by adjusting the parameters of the model we can maximize the number of individuals who do not have any of the two unhealthy habits.



Student Researcher

Miriam Herman graduated in May 2014 from Yeshiva University with a major in Mathematics and a playful curiosity for computer science, poetry and quantum mechanics. She now works as a software engineer.

Relaxation and Thermalization of Isolated Many-Body Quantum Systems

by

E. J. Torres-Herrera, Davida Kollmar, and Lea F. Santos

Department of Physics, Stern College for Women, Yeshiva University, New York, NY

An active area of research, relevant to experimental studies with optical lattices, is the evolution of quantum many-body systems. We studied the evolution of such systems after a quench, which is when an isolated system undergoes a perturbation that instantaneously changes its Hamiltonian.

The first question we studied was the speed of evolution of these systems. The local density of states (LDOS) is the weighted energy distribution of the initial state, and can be used to calculate the fidelity, which is the overlap between two states such as the initial state and an evolved state. When the LDOS is single-peaked, the fastest decay occurs for full random matrices: $[J_1(2\sigma_{ini}\, t_R)]^2 / (\sigma_{ini}^2\, t_R^2) = 3/D$ (Figure 1, top). However, this type of model is unphysical. For a realistic system, the LDOS is Gaussian, and the fidelity decay time gives $t_R = \sqrt{(\ln(IPR_{ini}))}/\sigma_{ini}$ (Figure 1, bottom). We next studied the size of the time fluctuations of observables after relaxation. We found that for both chaotic and integrable systems, time fluctuations decreased exponentially with system size, as long as there were no degeneracies. Each type of observable has a different fluctuation size. For the fidelity, the standard deviation is $\sigma_F = \sqrt{(IPR_{ini}^{-2} - \sum_\alpha |\, C_\alpha^{ini}\, |^8)}$ (Figure 2). The final question we studied was the viability of thermalization of these isolated systems after relaxation. A system is thermalized if its infinite time average is the same as its thermal average. For systems with two-body interactions we found that for both local and global quenches in space, the systems approached thermalization as the energy of their initial state moved towards the center of the spectrum and the perturbation grew stronger. In this scenario, the eigenstates grew more chaotic and eigenstate expectation values of an observable became similar for eigenstates close in energy.

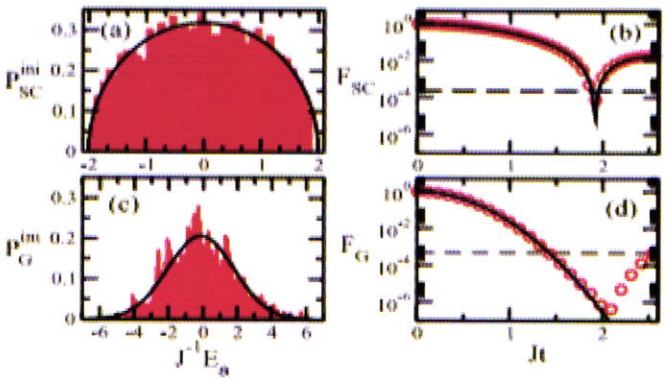


Figure 1: LDOS (right) and fidelity decay (left). Top: Initial state from full-random matrix, D=12 870. Bottom: Néel state, with Gaussian LDOS.

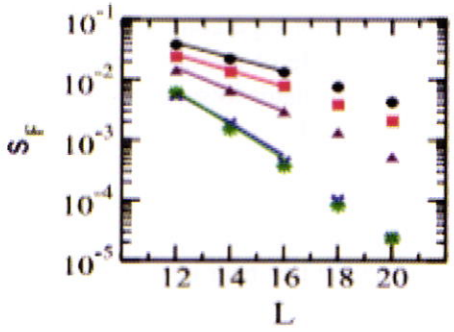


Figure 2: Log plot of standard deviation of time fluctuations of fidelity vs. system size for Néel state. Solid curve represents analytic results. Different lines represent different Hamiltonian parameters.

Student Researcher

Davida Kollmar is a second-year student in GPATS, Stern's Master's Program in Biblical and Talmudic Interpretation. She graduated from Stern College in 2013 with a degree in physics, and completed an Honors thesis on "Using Entropy to Detect Quantum Phase Transitions."

Superconductors, Disorder, and the Proximity Effect

by

Aviad Frydman and Chaim Metzger

Department of Physics, Bar Ilan University, Ramat Gan, Israel

When certain elements are sufficiently cooled they can become superconductors, meaning the material exhibits zero resistance. At temperatures approaching absolute zero (-273C), a quantum freeway for electrons and energy to flow without resistance is formed. It has been experimentally proven that a given element's ability to become a superconductor depends upon the level of disorder in its structure, or structural disorder. A material capable of superconductivity will not be able to superconduct if it is sufficiently disordered.

Even when a potential superconductor's structure is sufficiently disordered, it can still become more ordered again by being in the vicinity of another conductor through the "Proximity Effect." The "Proximity Effect" is when you couple another metal or conductor to a superconducting material and the conductive properties of one material bleed onto the other. Interestingly, the coupled conductor does not need to be able to be superconducting itself in order to turn the disordered potential superconductor into a proper superconductor.

Our challenge is getting indium oxide to turn from an insulator or limited conductor to a superconductor through evaporation of ultra-thin (nanoscale) gold layers which by themselves are not superconductors. An example of a sample of indium oxide transitioning from insulator to superconductor is shown in Figure 1.

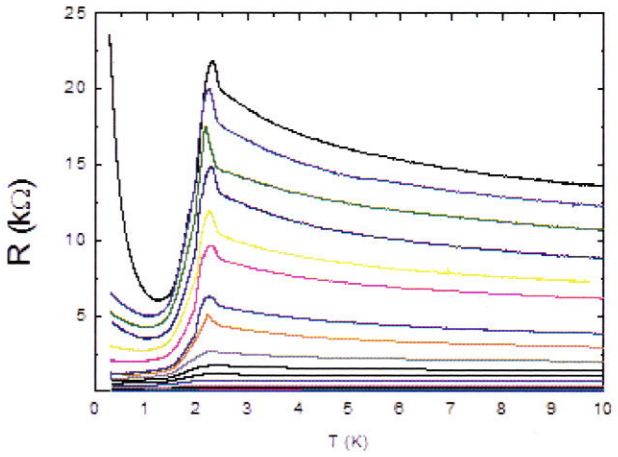


Figure 1: Resistance v. Temperature for Indium Oxide Covered by Gold Nanolayers

For this result, we used a special technique called quench condensation for evaporating gold at temperatures near absolute zero (0-12K). By heating the gold, we can liquefy and evaporate part of it despite the local temperature being near absolute zero. Beginning with the black line you can see how with each successive nanolayer of gold coating the indium oxide the film crosses over from an insulator to a superconductor. The black line (before gold evaporation) shows the resistance increasing as the temperature decreases towards absolute zero (0K). With each subsequent line representing another application of gold we see that the indium oxide reaches superconductivity represented by the orange line.

Student Researcher

Chaim Metzger is a senior at Yeshiva University majoring in Physics and Mathematics while pursuing Semikha at RIETS. Chaim serves as Vice President of Yeshiva University's Honors Student Council, a member of the Shabbos Enhancement Committee of both the Wilf and Beren campuses, a starting member of the YU Maccabees Wrestling Team, and as a member of the Student Athletes Committee. Chaim hopes to pursue a PhD in physics.

Faces in the Face of Death: Effects of Mortality Salience on Electrophysiological Perception of Facial Expressions

by

Shoshana Schneider and David Anaki

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The focus of our experiment was to systematically examine the influence of facial expressions on neuronal activity in the context of mortality salience, measured using ERP (Event-Related Potential). In the framework of the Terror Management Theory, anxiety was associated with an existential threat caused by facial expressions and recognition when presented with mortality salience conditions. However, there are contradictions in the literature about the nature of this relationship, which may be due to the various stages of awareness of death such as proximal versus distal. In this study, participants were proximally presented with mortality salience.

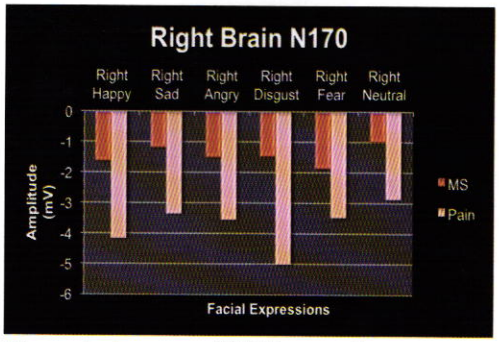

Figure 1: Average of N170 recordings in the right brain

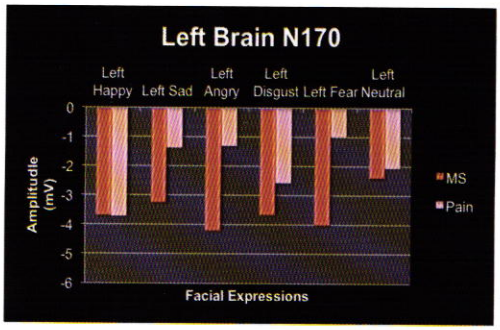

Figure 2: Average of N170 recordings in the left brain

We measured electrophysiological components activated in response to threatening (fear / anger), negative (sadness / disgust), positive (happy), and neutral faces. Participants were given either the pain condition, which entailed writing about a painful visit to the dentist, while seeing the word *pain* flashed between each facial expression, or the death condition, where participants had to write about what they expect their own death to be like, while the word *death* flashed between each facial expression.

In the results (Figures 1 & 2) we found significant differences in the P1 and N170 components between the mortality salience condition and the pain condition. In the P1 component, which measures arousal, there is a significant difference between the pain and mortality salience conditions. Participants in the mortality salience condition showed higher arousal to the various facial expressions. Additionally, we discovered a strong incongruence in the N170 (the facial recognition component) between the right and left sides of the brain. For the pain condition, there was a much higher electrophysiological response on the right side of the brain. This finding is congruent with previous research that demonstrated higher arousal in the right side of the brain in the context of facial expressions and emotions. Fascinatingly, in the death salience condition, recognition in the left side of the brain increased tremendously, while it deteriorated in the right side. This experiment suggests that the amplitude of the N170 will be higher in the left side of the brain when presented with facial expressions in the context of mortality salience.

Student Researcher

Shoshana is a senior at Stern College for Women. She is majoring in psychology with an interest in neuropsychology. After graduating this spring, she will pursue a career in neuropsychology and is applying to PhD programs in the fall. She is currently involved in research looking at biomarkers for depression and treatment.

Power, Stability, and Behavioral Approach

by

Daniel Elias Atwood and Jenny L. Isaacs

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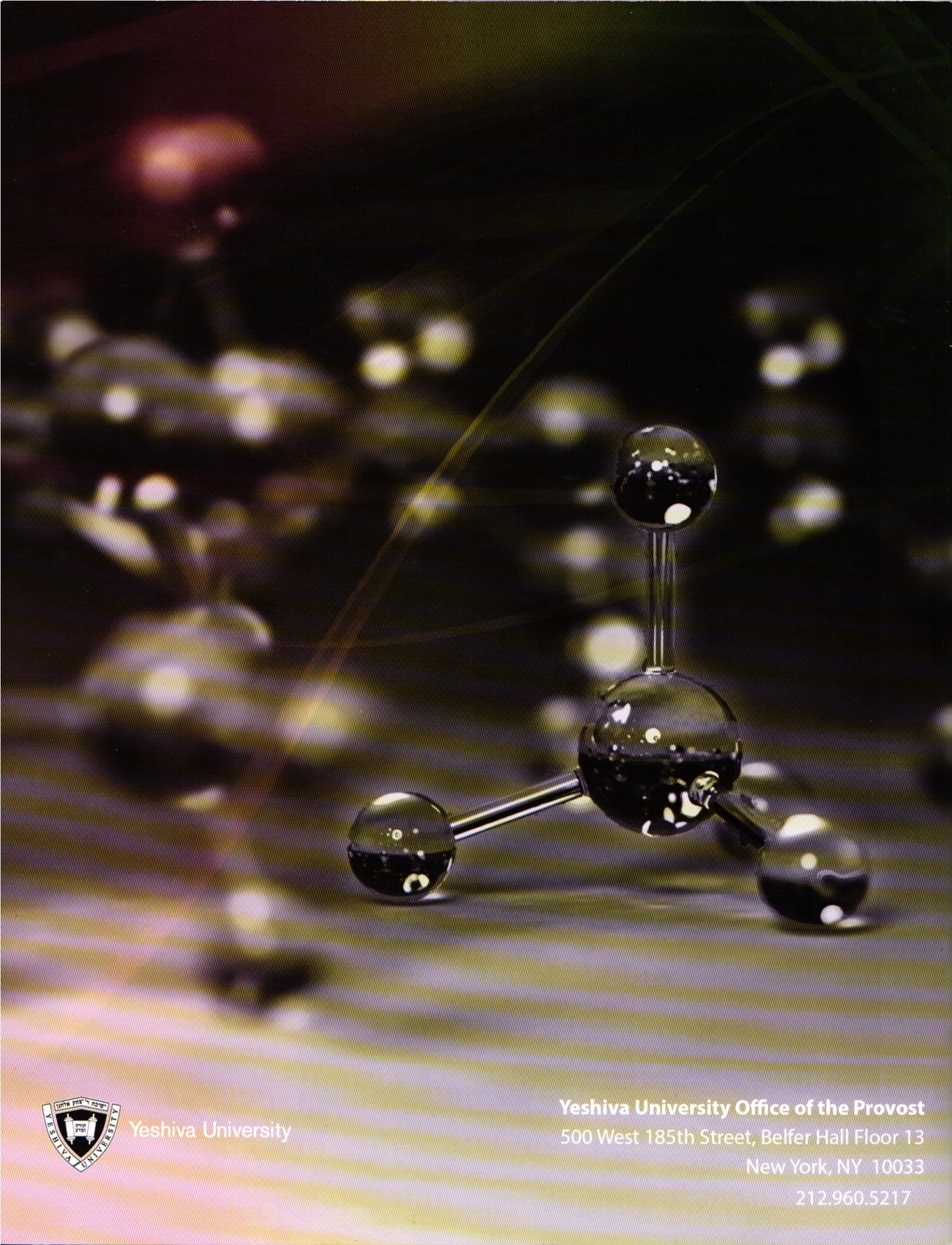
Social power is often defined as the ability to control both your own resources and the resources of others. Keltner, Anderson, & Gruenfeld (2003) provided a theory about social power and behavioral approach. Those high in power tend to engage in more behavioral approach, including risk taking, aggression, action behaviors, and positive affect, while those with low power tend to display more behavioral inhibition. Many boundary conditions have been placed on this theory of power and approach, such as the legitimacy of power. One possible boundary condition is power stability. It is possible that when the power structure is unstable that the powerful will act more inhibited than when the power structure is stable. We examined the interaction between power and stability at work in predicting approach behaviors. Power predicted risk taking, aggression, and positive affect at high levels of stability. However, when stability was low, power's effects on these variables subsided. This study provides correlational support to the theory that power only leads to behavioral approach when that power is stable. When power is unstable, however, power is no longer associated with behavioral approach. We suggest that attention to rewards and threats are the mechanism behind this theory. The stable powerful are looking to gain, and will thus seek out rewards. The unstable powerful, however, are attentive to perceived threats, and thus will be more inhibited in order to prevent loss.

Student Researcher

Daniel Elias Atwood is a senior in the Honor's Program at Yeshiva College, majoring in Psychology and Jewish Studies. In May 2014 he received the distinguished Kressel Fellowship for his research in psychology. In addition to his studies, Daniel is the Senior Opinions Editor and Managing Editor of *The Commentator,* Yeshiva College's official undergraduate newspaper. Daniel will be pursuing his rabbinical ordination at Yeshivat Chovevei Torah Rabbinical School beginning Fall 2015.



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