2019
Summer Cancer Research Institute

“I worked with such an amazing mentor and research team. I wouldn’t want [SCRI] any other way”
– Brynna Izquierdo

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2019 Summer Cancer Research Institute

The Summer Cancer Research Institute (SCRI) is an 8-week intensive summer program supported by the National Cancer Institute U54 grants (CA221704 and CA221705; Contact PIs: Drs: Ma and Ogunwobi) to Temple University, Fox Chase Cancer Center and Hunter College. Trainees benefit from hands-on research training, mentorship from established investigators,and participation in cancer seminars and skill-building workshops.

Dr. Grace Ma speaking with SCRI trainees about the SPEECH partnership and related projects

SCRI trainees pose with Dr. Xavier Graña after a lecture on cancer biology

SCRI trainees learn about science communication strategies during an American Association for the Advancement of Science Workshop

Dr. Carolyn Fang discusses population health with SCRI trainees

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Gaitree Boojraj - Hunter College
Mentor: Nora Engel, PhD

Sex differences in transcription factor expression analysis in male and female mouse embryonic stem cells

Gaitree Boojraj[1], Daniel Deegan[2], Nora Engel[2]

[1] CUNY Hunter College
[2] Fels Institute for Cancer Research

Background: Studies of male and female sex differences have traditionally focused on the influence of sex hormones, however these do not account for all the differences at the molecular and epigenetic levels. There are many transcriptional variations between males and females in every tissue, even in essential organ such as the heart. Prdm14 (PR domain zinc finger protein 14) and Lef1 (Lymphoid enhancer-binding factor 1) are both transcription factors. Prdm14 plays a role of maintaining ES cell identity as well as regaining pluripotency in somatic cells. Lef1 is activated by the Wnt signaling pathway and targets specific genes for transcription. By analyzing the expression patterns of male and female mouse ES cells, we found that Prdm14 is more highly expressed in female cells and Lef1 is more highly expressed in male cells. To determine whether differences in expression levels of these TFs result in differences in their target gene activity or genomic occupancy in general, we will perform genetic engineering of the endogenous sites and genomic mapping by ChIP-seq. **Results:** Our previous studies revealed that many genes that are differentially expressed between male and female cells. By using weighted genome co-expression network analysis on male and female ES cell transcriptomes, the blue/violet network of genes is the one most highly correlated with the sex differences observed. *Prdm14* binding sites are top hit in the promoters of blue/violet module genes and is more highly expressed in female ES cells. Prdm14-responsive enhancer activity in male and female ES cells correlates with sex-specific *Prdm14* expression levels. We designed a system to tag the *Prdm14* and *Lef1* endogenous loci in order to perform genomic mapping. **Conclusion:** By tracing the dynamics of sex-biased gene expression in embryonic stem cells and across development, we show that a group of genes encoding transcription and epigenetic factors maintain their sex biases across the lifespan. Overall, our results support the existence of sexually dimorphic gene expression profiles. Future plans include studying how transcription factor differences affect their distribution across the genome and their target gene activities and tracing latent epigenetic marks across development to elucidate their connection to later developmental events.

"My mentor has surprised me by the amount of support she has for me as well as for her lab. It is inspirational. Dr. Engel is such a great [role] model to myself." – Gaitree Boojraj

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Safiyah Samad- Hunter College
Mentor: Kelly Whelan, PhD

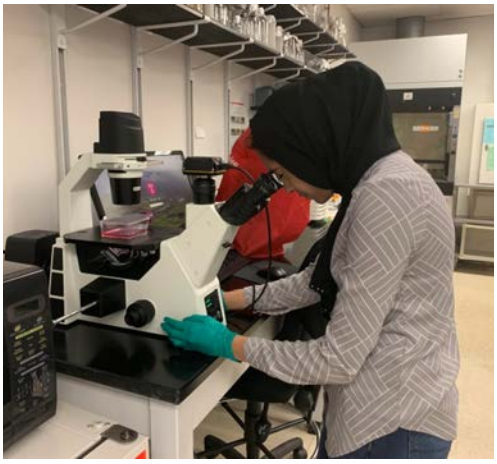
Effects of genetic and pharmacological autophagy inhibition on esophageal squamous cell carcinoma cell lines

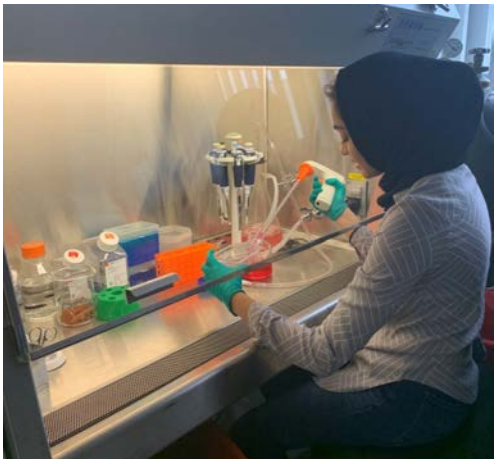
Safiyah Samad[1,2,3], Anbin Mu[3], Timothy M. Hall[3], Kelly A. Whelan PhD[3,4]

[1]*Hunter College, New York, NY*
[2]*John P. McNulty Scholars Program*
[3]*Fels Institute for Cancer Research & Molecular Biology*
[4]*Department of Pathology & Laboratory Medicine, Temple University*

Introduction: Esophageal squamous cell carcinoma is one of the most deadly cancers, exhibiting an extremely low survival rate associated with late-stage diagnosis, therapy resistance and early recurrence. A cellular process thought to contribute to therapy resistance in ESCC is autophagy. Autophagy is a homeostatic process activated in response to environmental stressors. Autophagy acts by degrading damaged organelles and protein. This function means that initially, autophagy constrains tumor formation in healthy tissue, but in tumors, autophagy serves as a cytoprotective mechanism that contributes to therapy resistance. **Methods:** To determine the role of autophagy in regulating the growth and sensitivity of ESCC cells to the chemotherapeutic agent 5-fluouracil (5-FU) we utilized MTT assays along with 5FU treatment alone or in combination with Chloroquine (CQ), a pharmacological inhibitor of autophagy. TE11 and AKR cells, human and murine ESCC cell lines, respectively were utilized. We further aimed to genetically inhibit autophagy using a lentiviral CRISPR/CAS9 construct targeting the autophagy-related gene *ATG7*. **Results and Conclusions:** Pharmacologically inhibiting autophagy failed to impact the efficacy of 5-FU. CQ alone, however, decreased viability in AKR cells. TE11 cells were successfully transduced with TCLV2 lentirvial ATG7 CRISPR/CAS9 as evidenced by puromycin resistance and doxycycline-induced GFR fluorescent reporter expression. Further studies are required to determine the dependence of ESCC tumor cells on autophagy and to understand how autophagy contributes to therapy resistance.

"SCRI has provided valuable research experience. Due to the various seminars, I have learned a lot about the disparities that exist within the medical field for different racial/ethnic communities."
- Safiyah Samad





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Melissa Driscoll & Jen Muse - Hunter College
Mentor: Carmen Sapienza, PhD

Race-associated methylation signatures and microbiome diversity: a pilot study to consider the impact of epigenetic influences on colorectal cancer incidence and mortality in African Americans

Melissa Driscoll[1], Jen Muse[1], Bryant Schultz[1], Carmen Sapienza[1]

[1]Fels Institute for Cancer Research and Molecular Biology

Introduction: Colorectal cancer ranks as the fourth most common cancer in the United States, representing 8.3% of all cancer diagnoses each year. While mortality rates continue to decline year over year, the rates of incidence and mortality remain significantly higher amongst the African American population. Epidemiological and experimental evidence demonstrates that the increased risk in African Americans may be correlated with race-associated aberrant DNA methylation patterns and alterations in their microbiome. **Methods:** To examine the theory, this pilot project has been divided into two aims. First, to determine the existence of race-associated methylation signatures for cancer patients and healthy controls, DNA methylation profiles were analyzed for 850,000 CpG sites in the normal colon mucosa of 138 subjects, with each group evenly representing African Americans and Caucasians. Those CpG sites with significant differences in methylation patterns will be assessed, examining the corresponding genotypes and related single nucleotide polymorphisms (SNPs) in *cis* to explore whether these differences should be attributed to the genome or epigenome. Secondly, the gut microbiome will be classified for the 138 candidates, with trends in the specific microflora compared to the cancer- and race-related methylation signatures or genome variations. **Results:** Initial patterns in the methylation assay data indicate that significant differences exist in the methylation of CpG sites, with African Americans showcasing a more disrupted epigenome, with high incidence of hypomethylation. However, when comparing healthy controls of either race to matched cancer patients, similar methylation patterns are apparent, indicating the existence of key "cancer-signature" sites. **Future Research:** Trends in the methylation data will continue to be assessed and compared to population based mutational variations to determine whether race-associated differences can be attributed to genomic or epigenomic influences. Further, this information will be correlated with the results of the microbiome sequencing data.

"…I feel like there's been a huge jump in my confidence from the beginning of the program…" – Jen Muse

"I was able to accomplish far more than I expected. My biggest success was being able to go from very little lab experience to creating a barcoded pilot library of 24 bacterial DNA samples as well as complete the first round of PCR for the rest of the 138 samples" – Melissa Driscoll

Melissa Driscoll

Jen Muse

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Yu Qing Xu - Hunter College
Mentor: Xavier Graña, PhD

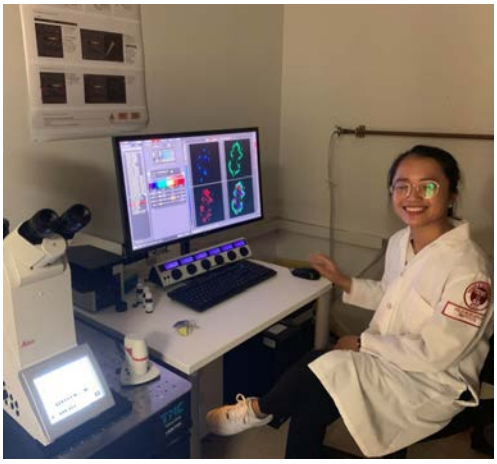
Characterization of PP2A/B55α in prostate epithelial and cancer cells

Yu Qing Xu[1,2], Ziran Zhao[2], Morgan Pantuck[2], Xavier Graña[2]

1: Chemistry Department, City University of New York, Hunter College
2: Fels Institute for Cancer Research and Molecular Biology, Temple University Lewis Katz School of Medicine, Philadelphia

Prostate cancer (PCa) is the most common cancer diagnosed in men, accounting for 20% of estimated new cases and 10% of estimated deaths in males[1]. The *PPP2R2A* gene, which encodes for an isoform of the B regulatory subunit of protein phosphatase 2A (B55α), is often hemizygously deleted in prostate adenocarcinomas.Protein phosphatase 2A (PP2A) is a major serine/threonine phosphatase involved in many critical cellular functions such as the cell cycle, apoptosis and the DNA damage response. PP2A is composed of scaffold (A), catalytic (C) and one of many isoforms of B regulatory subunits to form the functional heterotrimeric holoenzyme. Inactivation of PP2A is a key step required for transformation of the normal human cells in vitro. However, because there are several PP2A trimeric complexes in cells it is unclear which of these complexes mediate the tumor suppressive function of PP2A. Here we aim to 1) determine if reactivation of B55α/PP2A inhibits invasiveness of PC-3 prostate cancer cells in 3D culture by either inducible B55α expression or treatment with pharmacological small molecules of PP2A activator (SMAP)[2]; 2) determine if loss of PP2A/B55α deregulates cell growth and proliferation in normal prostate epithelial cells. 3D culture provides advantages in reconstructing tumor microenvironment and drug screening because it mimics physiological *in vivo* conditions. PC3 prostate cancer cells, RWPE-1 and primary human prostate epithelial cells (HuPrEC) were cultured in Matrigel and the formed three-dimensional organoids were characterized with immunofluorescent staining for cell adhesion and invasion markers. In our experiments, PC3 prostate cancer cells can form spheroids with invasive filopodia in Matrigel after 9-14 days. Induction of B55α expression at Day 6 retains round PC3 spheroids with a smooth basement membrane, preventing PC3 spheroids from displaying an invasive phenotype, while activation of PP2A with SMAP treatment induces apoptosis. In the context of RWPE-1 prostate epithelial cells immortalized with HPV-18, we characterize the function of PP2A/B55α by knockout with CRISPR/Cas9. RWPE-1 B55α knockout clones reduce proliferation in both 2D and 3D cell culture. In 3D culture, RWPE-1 B55α knockout clone formed smaller spheroids with less cell-cell adhesion compared to wild type RWPE-1. In clonogenic assay in 2D culture, B55α knockout in RWPE-1 cells limits colony size though increases the number of colonies. In the ongoing and future directions, we further plan to knockout B55α in HuPrEC once we immortalize the cells with human Telomerase (hTERT) and the co-inactivation of the *CDKN2A* locus, which encodes the senescence inducing proteins p16 and p14. Expression level of p16 has been examined in HuPrEC and will be tested in the selected HuPrEC clones immortalized with lentiCRISPR-*CDKN2A* and hTERT lentivirus.

"My SCRI experience helped me develop my critical and scientific thinking skills, which will help me in the future as a physician-scientist" – Yu Qing Xu



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Timmy Lin - Temple University
Mentor: Grace Ma, PhD

Preventing cervical cancer using HPV self-sampling: A culturally tailored intervention among low-income Asian American women

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Background: Human papillomavirus (HPV) screening rates are low among Asian American women, especially among first-generation immigrant women and those with low socioeconomic status. These health disparities suggest that innovative methods are urgently needed to promote screening uptake among underserved, hard-to-reach women. Self-sampling for HPV is a convenient and cost-effective way to increase screening. This study aims to assess the impact of a culturally-tailored intervention to promote HPV self-sampling among low-income Asian American women. **Methods:** We used the community-based participatory research (CBPR) approach to design and implement a culturally-tailored intervention to improve HPV self-sampling among low-income Asian American women. Between 2014 and 2015, we recruited 156 female participants from three ethnic groups, Chinese (56), Korean (50), and Vietnamese (50) from community-based organizations (CBOs) such as churches and community centers in the greater Philadelphia metropolitan area. All participants received educations on HPV symptoms, transmissions, and screening, through workshops and group discussions at the CBOs. The workshops included handouts, lectures, and a demonstration on conducting a self-sampling HPV test in Chinese, Korean, and Vietnamese languages. Participants were also given self-sampling kits and were contacted 30 days post intervention (booster contact). **Results:** Most of the sample was Asian American women with low annual household income (62.3% earned less than $20,000) and low educational attainment (61.3% without a college degree). We used paired sample t-tests to assess the differences between baseline and post-intervention for knowledge, social support, self-efficacy, and comfortability conducting a HPV self-sample test. We found significant increase in participants' knowledge on HPV (baseline: 2.83, post: 4.89, $p < 0.001$), social support (baseline: 3.91, post: 4.09, $p < 0.001$), self-efficacy (baseline: 3.05, post: 3.59, $p < 0.001$), and comfortability conducting a HPV self-sample test (baseline: 3.62, post: 4.06, $p < 0.001$). Within 6 months post intervention, all (100%) participants completed the HPV self-sampling test and returned the kits, which were then sent to the lab for analysis. **Conclusion:** Our findings showed that culturally tailored messages and hands-on demonstrations of the self-sampling kits were highly effective in empowering low-income Asian immigrant women to conduct HPV self-sampling tests. More efforts are needed to disseminate the intervention to the broader Asian American communities. Future research is also needed to examine this CBPR approach in different underserved populations. **Keywords:** HPV self-sampling test; cervical cancer prevention; women's health

"The biggest success through this experience was submitting an abstract to the upcoming American Association for Cancer Research [Health Disparities] conference in San Francisco." - Timmy Lin

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Oluwatoyin Odumuwagun - Hunter College
Mentor: Camille Ragin, PhD

Investigation of infiltrating Immune cells patterns in prostate cancer tissues from black and white men

Oluwatoyin Odumuwagun[1,2], Devarajan Karthik[1], Andrew Gachii[3], Jasvir Khruana, Adam Reese[4], Olorunseun Ogunwobi[2], Geou-Yarh Liou[5], Camille Ragin[1]

[1]Fox Chase Cancer Center - Temple University Health
[2]Hunter College
[3]Tara Labs, Nairobi Kenya
[4]Temple University Hospital
[5]CCRTD, Clark Atlanta University

African ancestry has been implicated as a relevant risk factor in the pathogenesis of Prostate cancer, underlining it as a health disparity issue. The immune system plays an important role in the coordinated body response to cancer cell growth in the prostate gland by producing various types of immune cells. We aim to identify if specific patterns of infiltration of these immune cells (T-cells, B-cells, Tissue associated macrophages (TAM), and Neutrophils) do exist in prostate cancer tissues among Black American (AB), Kenya Blacks (KB)and White American (AW) men. Immunohistochemistry affords us the use of specific standardized cell surface-associated biomarkers to detect the presence and quantify each type of immune cell and their locations in the cancer tissues. The respective quantities of each cells were counted for the Cancer, Benign and Prostatic Intraepithelial Neoplasia (PIN) region of each specimen, and analysis of variance was carried out by fitting linear models of the data obtained while adjusting for Age and Gleason score. The median ages at time of prostatectomy for AB, KB, and AW are 61, 74, and 61.5 years, respectively. The average Gleason score for KB population is 8.4 (±0.81), AW population is 7.7 (±0.82), and AB population is 6.9 (±0.99). The median B-cells count for KB (2085) is significantly higher than for other racial groups); 124 for AB (p-value= 0.000137) and 303 for AW (p-value= 0.00715). The cell number per unit area (density) also follow a similar trend with highest median count in Kenya black population. These data provide evidence that suggests higher B-cell infiltration in prostate cancer tissues of Kenya black than American blacks and Whites.

"I have been able to learn about the researcher's culture, how they think, the underlying protocols generally utilized in conceiving a research idea and designing an experiment.....I have gained better clarification on how to navigate future career endeavors through SCRI" – Oluwatoyin Odumuwagun

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Daniel Wiese - Temple University
Mentors: Kevin Henry, PhD & Shannon Lynch, PhD

Comparing Geographic Distribution Patterns of Advanced Prostate Cancer Defined by Stage and/or Gleason Grade: Implications for Screening Interventions in Pennsylvania

Daniel Wiese[1], Angel Ortiz[2], Kevin A. Henry[1,2], Adam Reese[2], Camille Ragin[2], Carolyn Fang[2], Mary Daly[2], Shannon M. Lynch[2]

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[2]Fox Chase Cancer Center, Philadelphia, PA, USA

Background: Prostate cancer (PC) is one of the most commonly diagnosed cancers among Pennsylvania men. While the survival rate is relatively high, Black men compared to White men are more likely to be diagnosed with advanced PC and to die of the disease. Identifying areas or neighborhoods where men are more likely to be diagnosed with advanced PC would aid in intervention planning; however, different definitions of advanced PC are often used. Spatial scientists often define advanced PC by tumor stage, whereas clinicians prefer Gleason Grade alone or in combination with stage. This is the first study to compare cluster detection results by different definitions of advanced PC in order to inform PC screening interventions. **Methods:** The study population included all male cases of PC diagnosed between 2005 and 2015 in the State of Pennsylvania. Cases were geocoded to the census tract of residency at time of diagnoses. Three definitions of advanced PC were used in this study: 1) late-stage (defined as Regional and Distant, i.e. Stage 3 and 4 cases (n=15,001); 2) Clinically significant Gleason grade (i.e. grade>7 or Gleason grade groups (GGG) 2-5 (n=54,792); 3) late-stage AND high grade cases (n=12,060). We applied Poisson models of the spatial scan statistic (SaTScan) to calculate relative risk and detect clusters ($p<0.05$) of census tracts with higher rates than expected of advanced PC. All models were adjusted for diagnosis year, age and race. Then, we calculated and compared socio-demographic characteristics of the detected clusters (proportions of race groups, poverty) **Results:** Identified clusters varied by PC definition (five significant clusters were identified with the stage only variable vs nine in the GGG only definition vs six based on combined variable). Of the 3217 census tracts in PA, 506 were identified as being located in a high-risk cluster across all three definitions. **Conclusion:** Definition used for advanced PC has a major impact on cluster identification and subsequent intervention planning. Definition of advanced PC using both stage and Gleason grade is most similar to the clinical practice criteria used to determine treatment and screening approaches in men at risk for or diagnosed with PC. Its application resulted in the selection of least number of cases while detecting more target areas than using stage only, and included the most number of overlapping census tracts. Thus, moving forward, this definition of advanced PC should be considered in geospatial analyses and may be more valuable for epidemiologists, practitioners and policy makers.

"My participation in the SCRI was an outstanding opportunity to learn more about different fields in cancer research, meet other scientists and experts as well as to participate in a highly interesting and impactful project" – Daniel Wiese

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Anna O'Neil - Hunter College
Mentor: Teh Lin, PhD

Quality Assurance of Four-Dimensional Computed Tomography (4dct) Scan in Lung Cancer Patients

Anna O'Neil, Teh Lin

Department of Radiation Oncology, Fox Chase Cancer Center, 333 Cottman Ave, Philadelphia, PA 19111

Background: Four-dimensional computed tomography (4DCT) combines patients' respiratory signal with 3D CT images for thoracic and abdominal tumors such that a patient specific organ excursion range can be obtained. External respiratory monitor systems are used during 4DCT as the tools for breathing signal collection. In Fox Chase Cancer Center, Siemens' ANZAI belt Respiratory Gating System and RPM (Varian's Real-Time Position Management) systems are used as the respiratory surrogates for Siemens Somatoform Definition AS 4DCT imaging. The stability of these systems is essential to assure the imaging quality. In this study, we aimed to propose a quality assurance (QA) procedure for the monitoring systems as an addendum to our current CT QA protocol. To quantify the response linearity of the ANZAI pressure sensor to the exerted force, a number of coins and copper plates were placed on top of the senor and the corresponding pressure reading was measured using the ANZAI AZ733V software. For the RPM, a number of cassettes were used to change the location of the infrared marker box on the couch and the corresponding displacements were measured by the RPM camera readout system. To evaluate the reliability of the respiratory monitoring system with different conditions during 4DCT scans, a phantom with a movable disk at two different oscillation speeds was used for 4DCT scans with different couch moving speed and X-ray source rotation speed. The Maximum-intensity-projection (MIP) and Average-intensity-projection (AIP) images were then generated from the CT acquisition workstation. The volume of the three ball markers that reside inside the phantom were measured and compared among different 4DCT scans and phantom oscillation speeds. A helical scan was also taken for the phantom with different oscillation speeds. **Results:** The pressure reading of the ANZAI sensors (Deep or Standard cell) was found to be linear with the mass of the materials (coins and coppers) put on the sensor. The linearity was confirmed for the RPM displacement reading versus the physical location of the infrared marker at different couch positions (zero, +50cm, -50cm and -57cm). The volumes of the ball markers measured from MIP, AIP and helical scans were found to be consistent with different 4DCT acquisition conditions (scan setting for 6 or 12 respirations/minute, phantom oscillation speed at 10 or 15 cycles/minute), showing high reliability of the ANZAI belt monitoring system used for 4DCT. **Conclusion:** The response linearity of both ANZAI and RPM systems to the measured physical metrics are investigated and satisfies the criteria for clinical implementation. The 4DCT images acquired in different conditions using the ANZAI system are in agreement with different phantom motion speeds, showing high performance reliability of this respiratory monitoring system. The measurement methods proposed in this study may be used to establish an individualized QA procedure for the ANZAI belt and RPM systems as part of QA procedure for CT scanner.

"The whole experience of being a part of SCRI at Fox Chase Cancer Center was surprising - starting from the lab that chose to have me, lab members I work with, people I meet at weekly meetings and knowledge and skills I gain from being a part of this amazing team trying to cure cancer." –Anna O'Neil

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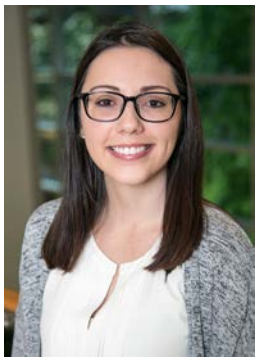
Brynna Izquierdo - Temple University
Mentor: Jennifer Reese, PhD

Understanding the Quality of Life among Men with Prostate Cancer who Experience Biochemical Recurrence

Brynna C. Izquierdo, BS,[1] Lauren A. Zimmaro, PhD,[1] Daniel M. Geynisman, MD,[1] Marijo Bilusic, MD, PhD[2], Jennifer B. Reese, PhD[1]

[1]Fox Chase Cancer Center, Philadelphia, PA, USA; [2]National Institutes of Health, Rockville, MD, USA

Objectives: Biochemical recurrence (BCR) of prostate cancer occurs when a prostate-specific antigen (PSA) rises following localized treatment without evidence of disease on conventional imaging (PSA at least 0.2 ng/mL if the patient had radical prostatectomy and Phoenix criteria = 2.0 + PSA nadir if patient had radiation therapy). Little is known about the quality of life (QOL) among men experiencing BCR. Therefore, we first aimed to characterize QOL among a sample of men with BCR to compare their QOL to normative data of the general U.S. adult population and adult patients with cancer. Second, we aimed to examine whether demographic variables (age and body mass index [BMI]) correlated with overall QOL and its subdomains (physical, social/family, emotional, functional, prostate-specific). **Methods:** 19 male adults (M age = 65.2, SD = 5.7) were recruited as part of a larger ongoing prospective clinical trial. All men had hormone-sensitive prostate cancer, experienced BCR after primary therapy and had a BMI > 25. Participants completed a self-report health-related QOL questionnaire at baseline (Functional Assessment of Cancer Therapy – Prostate [FACT-P]). T-tests and correlations were used to compare mean patient scores with normative data and assess demographic associations, respectively. Descriptive statistics and within-sample one-way ANOVA with Bonferroni post-hoc tests were used to characterize the FACT-P scores. Pearson correlation and Kendall's tau were used to examine correlations with demographic variables. Descriptive statistics and correlations were used for item-level exploratory analyses. **Results:** The study sample reported high scores on the FACT-P with higher score indicating higher QOL (total range = 0-156, M = 139.4; physical: range = 0-28, M = 27.4, SD = 1.2; social/family: range = 0-28, M = 24.9, SD = 4.1; emotional: range = 0-24, M = 19.4, SD = 2.6; functional: range = 0-28, M = 25.9, SD = 2.4; prostate-specific: range = 0-48, M = 40.6, SD = 5.3). Compared to both normative data from general adult and cancer samples, this sample endorsed significantly higher levels of physical, social/family, functional, and general well-being (p's < 0.05), but comparative levels of emotional well-being (p's > 0.05). Within subjects, there were significant differences between mean item-scores of the five subdomains, $F(4,56) = 8.95$, $p < 0.001$. Specifically, emotional well-being was significantly lower than physical, functional, and social well-being (p's < 0.01), and prostate-specific well-being was significantly lower than physical well-being ($p < 0.004$). Age and BMI were not associated with overall QOL or subdomains. In item-level analyses, the most highly endorsed item was "I am able to work" (M = 4.00); the least endorsed item was "I am able to have and maintain an erection" (M = 1.46). Age was inversely correlated with nervousness and worry about dying, such that younger age was associated with more nervousness ($\tau = -0.69$, $p = 0.02$) and worry about dying ($\tau = -0.83$, $p = 0.003$). **Conclusions/Implications:** Overall, the sample endorsed high QOL relative to normative samples of both U.S. adults and patients with cancer. In interpreting this finding, it is important to note that the men in this sample had completed their prostate cancer treatment, had no physical evidence of disease, and were participating in a clinical trial for which they were screened for significant medical and psychiatric comorbidities. In short, the men in the sample were overall in very good health. It is thus possible that the sample completed their QOL survey with "rose-colored glasses" in contrast with the reduced QOL they may have experienced during active treatment. In addition, the normative cancer sample used as a comparison group consisted of only 8% prostate cancer, whereas colorectal, lung, and head and neck cancers were more commonly represented, and survivors of these cancers might report different levels of QOL from prostate cancer survivors. Relative to the other domains of QOL, however, patients in this study reported lower emotional well-being. They also reported continued problems with sexual function, suggesting that these problems may linger after completing treatment even for healthy survivors. Study limitations included the small sample size, which may have decreased the variability of QOL scores, as well as a small number of demographic and medical variables (i.e., age, BMI) analyzed in relation to QOL. Future studies should examine a greater number of predictors of QOL among a larger sample of men with BCR who span a wider range in age and physical and mental health status. **Keywords:** biochemical recurrence, prostate cancer, quality of life



"I'm really proud of my poster and the fact that I was able to carry out a research study from start to finish. The entire process has been a success and I have learned so much along the way." – Brynna Izquierdo

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At the completion of the SCRI program, trainees had the opportunity to present their projects to mentors and fellow trainees from Hunter College, Temple University and Fox Chase Cancer Center.

SCRI trainees pose with their certificates of achievement

Yu Qing Xu, Daniel Wiese and Safiyah Samad cheer on fellow SCRI trainees

Brynna Izquierdo presents her work at the SCRI mini-symposium

Carolyn Fang, PhD welcomes the audience to the first SCRI mini-symposium

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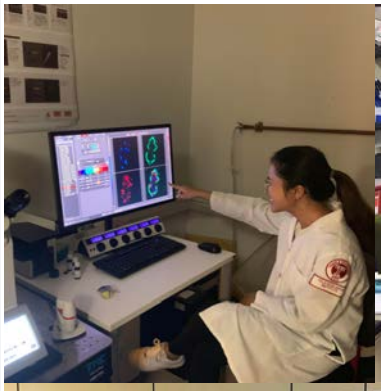

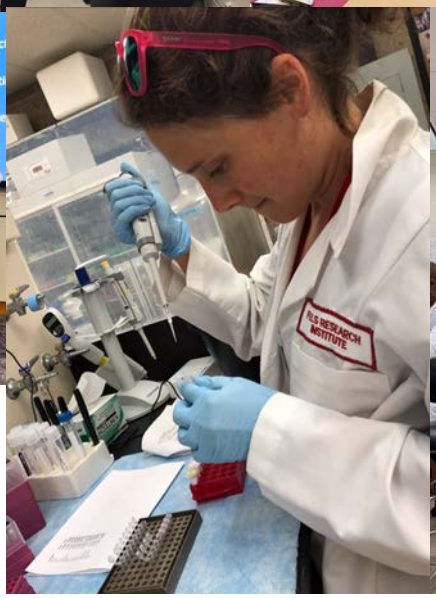

"I am very grateful and appreciative of this program and what it has given me. I have an endless amount of knowledge that I did not have beforehand. This was a great and fun experience" – Gaitree Boojraj

Research Education Core Leaders:
Carolyn Fang, PhD - Fox Chase Cancer Center
Olorunseun Ogunwobi, MD, PhD - Hunter College

For questions regarding the Research Education Core and any upcoming events, please contact one of our research coordinators:
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TUFCCC_HC Research Education Core

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