

Development of a biomimetic spiral artery remodeling model

Sebastian Naranjo [1], Noo Li Jeon [2,3], Catherine Klapperich [1], Joyce Y. Wong [1]

[1] Department of Biomedical Engineering, Boston University [2] Department of Bioengineering, Seoul National University [3] Department of Mechanical Engineering, Seoul National University

Preeclampsia (PE) is the leading cause of maternal/fetal morbidity/mortality in the United States, accounting for more than 70,000 maternal and 500,000 fetal deaths every year. The leading mechanistic hypothesis for pathogenesis is the dysregulation of spiral artery remodeling (SAR)-where invasive placental cells (extravillous trophoblasts, EVT) remodel maternal vasculature to meet metabolic needs of the growing fetus in the 2 nd and 3 rd trimesters. Although there have been great efforts in developing a mechanistic understanding for PE, we have yet to define clinically translatable mechanisms for disease presentation and treatment. This is largely attributed to our inability to replicate the spatiotemporal microenvironmental intricacy required throughout SAR in current models. We conducted preliminary experiments to develop endometrial-specific vascular networks by differentially patterning compartments of our high-throughput microfluidic chip with fibrin/Coll-I, human endometrial microvascular endothelial cells (HEMEC), and normal human lung fibroblast (NHLF). Lumenized endometrial vascular networks were observed after 5 days of coculture. These studies will serve as the foundation for the development of a biomimetic spiral artery remodeling (SAR) model capable of hierarchically characterizing vascular tissue structure-functions during normal and PE-related SAR, particularly advancing our understanding of cell-cell and cell-ECM regulation of EVT-mediated remodeling.





Molly S. Kaissar[1], Elnaz Ghajar-Rahimi[2], Adalyn Meeks[2], Arden Shen[2], Yusheng Wu[1], Craig J. Goergen[2], Kyoko Yoshida[1]

[1] Department of Biomedical Engineering, University of Minnesota [2] Weldon School of Biomedical Engineering, Purdue University

The cardiovascular system adapts to meet rising physiological demands throughout pregnancy. Notably, the left ventricle grows to support an increased workload. While this pregnancy-induced hypertrophy has been historically characterized in rodents, there is a distinct lack of research exploring the postpartum period. After delivery, these cardiovascular adaptations are thought to reverse. However, whether the heart returns to its pre-pregnant size, shape, and function is unclear. Moreover, despite previous research showing that postpartum-specific conditions like lactation affect rodents' hemodynamics, the impact of lactation on left ventricular morphometry is still unknown. In this study, we investigate the impact of lactation on postpartum cardiac recovery. We monitored changes in left ventricular mass, volume, and function throughout pregnancy and postpartum using 4D cardiac ultrasound in mice allowed to nurse their pups for 21 days postpartum and in those whose pups were removed immediately after delivery. We analyzed the mechanisms driving the observed heart growth using an existing multiscale computational model of heart growth. Here, we observe that pregnancy-induced cardiac hypertrophy reverses by one week postpartum in non-lactating mice but continues increasing after delivery in lactating mice. Our computational analysis suggests that hemodynamic loading is a primary driver of postpartum growth. Further, animal-specific simulations indicate that individual hemodynamic changes contribute to the observed variability in experimental heart growth, particularly throughout lactation. Overall, this study provides a detailed timeline of cardiac hypertrophy during and after pregnancy, emphasizes the significance of lactation status on postpartum recovery, and highlights the importance of hemodynamics to this phenomenon.



Modeling the intrinsic viscoelastic behavior of the rhesus macaque cervix to study cervical remodeling

Camilo A. Duarte-Cordon [1], Shuyang Fang, Ivan M. Rosado-Mendez, Gerard Ateshian, Timothy J. Hall, Helen Feltovich, Kristin M. Myers

[1] Columbia University, New York, NY, USA

The cervix is a collagenous tissue that plays a crucial mechanical role in pregnancy. During gestation, the cervix transforms from a rigid/closed structure that sustains the growing load of the fetus in the uterus to a soft/extensible structure that opens to allow birth at term. This function of the cervix is facilitated by extensive remodeling of its extracellular matrix (ECM), which gives rise to complex time-dependent mechanical properties of the cervix. Constitutive modeling and mechanical testing of ex vivo cervical tissues from humans and rodents have provided insights into cervical remodeling by analyzing changes in the equilibrium elastic modulus and viscoelasticity under compression. However, it remains unclear how the intrinsic or flow-independent viscoelasticity of the cervix is influenced by cervical remodeling. To better understand the role of the intrinsic viscoelasticity of the cervix, we formulated an anisotropic reactive viscoelastic model inspired by the solid components of the cervical ECM. To calibrate our model, we used force relaxation data from uniaxial tension tests on rhesus macaque cervical specimens chosen for their homology to humans and collected at four relevant gestational time points. We found that both the equilibrium and instantaneous elastic moduli significantly decreased from the non-pregnant to late pregnant stages. Additionally, cervical tissue from late 3rd-trimester rhesus macaques relaxed faster to equilibrium, potentially allowing efficient dissipation of tensile stresses during labor, preventing rupture. This work enhances the understanding of normal cervical remodeling, which is crucial for developing diagnostics and treatments for conditions such as spontaneous preterm birth.



Pregnancy-Induced Aortic Remodeling: Microscale Structural Adaptations and Macroscale Mechanical Responses

Ana I. Vargas [1], Mirza M. Junaid Baig [1], Turner Jennings [2], Rouzbeh Amini [1,2] Chiara Bellini [1]

[1] Department of Bioengineering, Northeastern University, Boston, MA, USA [2] Department of Mechanical and Industrial Engineering, Northeastern University, Boston, MA, USA

During pregnancy, the cardiovascular system undergoes profound adaptations to accommodate increased hemodynamic demands, yet the mechanisms driving remodeling in elastic arteries remain unknown. In this study, we investigated the microstructural and biomechanical changes in the aortic wall during pregnancy, focusing on collagen organization, nuclear morphology, and their roles in vascular remodeling.

Aortic segments were collected from pregnant and control C57BL/6 female mice and analyzed using multiphoton microscopy to visualize collagen, elastin, and cell nuclei across the aortic wall layers. Collagen fiber orientation and distribution were quantified using OrientationJ, while nuclear morphology was assessed by calculating the nuclear aspect ratio (NAR) of fibroblasts and smooth muscle cells. Computational methods, including Gaussian smoothing and Otsu's thresholding, were applied to segment cells and identify distinct cell types. Mechanical properties were derived from previous biaxial mechanical tests.

Pregnant samples demonstrated less collagen organization, indicated by lower κ values and a more rapid shift toward circumferential fiber orientation under physiological pressures. These changes correspond to increased circumferential stiffness, suggesting a remodeling process favoring an isotropic mechanical response. Despite these structural alterations, NAR distribution remained consistent across pressure ranges and between pregnant and control groups, indicating preserved nuclear configuration during pregnancy.

These findings highlight pregnancy-induced aortic remodeling, characterized by collagen reorientation and mechanical stiffening, alongside cellular adaptations that maintain nuclear homeostasis. This dual focus on microscale and macroscale responses provides new insights into the vascular adaptations of pregnancy, with implications for postpartum aortic function and maternal cardiovascular health.



Characterizing Microbial Biosensors in Whole Blood

Kaavya Akula [1], Luca Pungan [1], Maya Bartels [1], Miguel Jimenez [1]

[1] Department of Biomedical Engineering, Boston University, Boston, MA, USA

Fertility hormone testing provides vital information for women undergoing In Vitro Fertilization, ectopic pregnancies, miscarriages, and polycystic ovary syndrome. However, the current methods of testing pose many accessibility barriers to women around the world. At-home urine tests lack the sensitivity and specificity of blood tests that healthcare providers desire. However, blood tests require the patient to rely on testing centers. At these centers, extensive sample preparation is required, and results can take days. The goal of our research is thus to devise a test that can detect fertility hormones in whole blood in the comfort of the patient's home. To achieve this goal, genetically engineered microbial cells will be used as a robust sensing platform. However, the function of microbial cells in blood has not yet been well established. In order to test both the survival and sensing ability of engineered cells in blood, we synthesized four variants that would fluoresce in the presence of a model target molecule. Our experiments revealed successful designs of reporter action, with increased fluorescence in the presence of the target molecule. Now that these strains have been established, their behavior in whole blood may be explored. These results will inform the development of our fertility hormone sensors, and break down barriers to reproductive healthcare.



Multiplexed isothermal assay for the detection of Plasmodium falciparum and Chlamydia trachomatis in urine

Joshua Dupaty [1], Clement Shihluli [2], Berit Schaus [1], Srinivasa Lolabattu [3], Jesse Gitaka [2], Catherine Klapperich [1]

[1] Biomedical Engineering Department, Boston University, Boston, USA [2] College of Graduate Studies and Research, Mount Kenya University, Thika, Kenya [3] Division of Research and Development, Jigsaw Bio Solutions, Bengaluru, India

Malaria in pregnancy (MIP) and sexually transmitted infections (STIs) are significant preventable causes of poor pregnancy outcomes. Plasmodium falciparum (Pf), the most virulent of the 5 human malaria species, is estimated to account for 10,000 maternal deaths, 100,000 newborn deaths and 200,000 infant deaths each year. Unlike other human malaria species, Pf can sequester within the placenta, making detection using standard microscopy and antigen point of care tests difficult due to low peripheral parasitemia. Thus, a diagnostic assay with a lower limit of detection (LOD) is required. Where malaria is prevalent, STI prevalence among pregnant people also leads to adverse outcomes such as stillbirths, low birth rates, and permanent infertility. In some regions, particularly Sub-Saharan Africa, this burden is notably high with Chlamydia trachomatis (CT) accounting for a large portion of comorbidities. Identifying and distinguishing these infections during prenatal visits will allow for immediate and appropriate treatment and could reduce poor pregnancy outcomes. Implementation of a user friendly, single sample, multiplexed point of care (POC) device using our novel isothermal molecular amplification technique to detect identical multi-repeat sequences (iso-IMRS) will allow for earlier and more sensitive detection of MIP and CT in prenatal populations in areas with endemic malaria. Here I characterize, optimize, and implement iso-IMRS, in urine as a working sample, to have sensitivity and specificity comparable to PCR (outclassing pre-existing isothermal methods such as LAMP and HDA). This workflow serves as a platform for the genome mining and analysis of other pathogens for POC screening.



Molecular Signatures of Mouse Ovarian Aging: Integrating Transcriptomic and Epigenetic Insights

Sharif Iqbal [1,2], Alexsander Tyshkovskiy [1,2], Maria Vina Lopez [1,2], Bohan Zhang [1,2], Ludger Goeminne [1],[2], Juan José Alba-Linares [1,2], Kejun Ying [1,2], Mahdi Moqri [1,2] and Vadim Gladyshev [1,2]*

[1] Division of Genetics, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA [2] Broad Institute of MIT and Harvard, Cambridge, MA, USA

Ovarian aging has profound implications for fertility, reproductive health, and overall longevity. Despite its significance, the molecular mechanisms driving ovarian aging remain largely unresolved. To address this, we established a mouse ovarian transcriptomic clock to accurately measure "transcriptomic age" and to monitor age-related molecular changes in ovarian tissue over time. By analyzing thousands of genes across different age groups, we uncovered novel molecular hallmarks of ovarian aging. Using module analyses, we further dissected the individual components that form the ovarian aging signature, identifying functional pathways enriched in pathways relevant to inflammation and tissue remodeling. We also performed cross-tissue comparisons, examining aging signatures in the brain and liver of the same mice. These analyses highlighted both shared features and tissue-specific distinctions in the aging process, reinforcing the notion that ovarian aging exhibits both parallels and unique regulatory mechanisms compared to other somatic tissues. Expanding upon transcriptomic data, we applied multi-omic approaches-integrating DNA methylation (DNAm) profiles with RNA sequencing (RNAseg) data-to capture the interplay between epigenetic age (eAge) and transcriptomic age (tAge). We identified top candidate genes with the strongest correlation to age, as well as key hypo- and hyper-methylation patterns that might contribute to ovarian aging. By integrating transcriptomic clocks, targeted module analyses, and epigenetic profiling, this work portrays a comprehensive picture of the molecular drivers behind mouse ovarian aging. Our findings shed light on critical pathways that may underlie the decline in ovarian function with advancing age. Understanding these processes provides a foundation for developing therapeutic strategies aimed at reproductive rejuvenation and extending the reproductive lifespan.



Sialidase enzymes derived from bacterial vaginosis associated bacteria may impair sperm function by remodeling the sperm glycocalyx

Sarah Dohadwala [1], Purna M Shah [1], Maura K Farrell [1], Joseph A Politch [2], Kevin Whaley [3], Deborah J Anderson [1],[2], Catherine E Costello [1]

[1] Boston University, Boston, MA, USA [2] Boston University Medical School, Boston, MA, USA [3] ZabBio Inc., San Diego, CA, USA

Bacterial vaginosis (BV), a dysbiosis of the vaginal microbiome, affects approximately 23 to 29 percent of women worldwide and is associated with several adverse health outcomes including preterm birth, subfertility, and sexually transmitted infections (STI). BV-associated bacteria, such as Gardnerella vaginalis, are known to cause epithelial damage and degradation of the vaginal mucosa through the activity of sialidase enzymes that remodel the epithelial glycocalyx and metabolize mucin glycoproteins. This damage to the vaginal glycocalyx creates an inflammatory environment which likely contributes to adverse health outcomes. However, whether BV-associated glycolytic enzymes can also damage sperm during their transit in the reproductive tract has not yet been determined. Here, we show that sialidase-mediated glycocalyx remodeling of human sperm increases sperm susceptibility to innate immune damage within the female reproductive tract. In particular, we report that upon exposure to physiologically relevant amounts of sialidase enzymes, desialylated human sperm demonstrate increased susceptibility to complement lysis (~2.5-fold) and agglutination (~2-fold). Our results demonstrate a potential mechanism by which BV glycolytic enzymes may affect sperm survival and function and thereby contribute to adverse reproductive outcomes such as subfertility.



Fallopian Tube-on-a-Chip to Investigate Sex Steroid Hormone Impact on Neisseria gonorrhoeae Infection-Induced Tubal Factor Infertility

Emily Schwartz [1], Joyce Y. Wong [1]

[1] Department of Biomedical Engineering, Boston University

Fallopian tubes are essential for fertility, but the genesis of tubal disorders is not well understood. When sexually transmitted infections (STIs) such as Neisseria gonorrhoeae (NG) infect the fallopian tubes, they may trigger an inflammatory response leading to tissue damage, scarring, tubal blockage, and tubal factor infertility. Currently there is no way to reverse tubal damage caused by NG infection, and the only available treatment is in vitro fertilization (IVF). The severity of NG infections may be influenced by hormonal changes during the menstrual cycle. Using a fallopian tube-on-a-chip model, we are studying how sex steroid hormones impact NG infection severity to better understand the mechanisms underlying tubal infertility.



High Content Stimulated Raman scattering imaging of breast cancer Chinmayee Prabhu Dessai [1], Hongli Ni [2], Haonan Lin [1], Wei Wang [3], Shaoxiong Chen [4], Ji-Xin Cheng[1,2]

[1] Department of Biomedical Engineering, Boston University [2] Department of Electrical and Computer Engineering, Boston University [3] Hologic Inc [4] Indiana University School of Medicine

One of the most diagnosed cancers in women is breast cancer. The current conventional method of diagnosis is histopathology which includes Hematoxylin and Eosin staining and immune-histochemistry to detect to cancer grade and cancer biomarker. Both are cumbersome, time-consuming, and subject to inter and intra laboratory variations. Here we present a technique of Stimulated Raman Scattering (SRS) histology imaging using hyperspectral SRS and decomposition of the image using spectral unmixing into biochemical maps of lipids, protein, saturated fat, and collagen that help to differentiate between cancerous and healthy breast tissue. Our technique can be promising for a quicker breast cancer diagnosis without laborious staining and is highly sensitive.





Elizabeth. E. Marr [1], Mariana Alonso-Riquelme [1], Manavi Vajhallya [1], Manek Khedia [1], Mollie A. O'Brien [2], Peter R. Movilla [2], Juan S. Gnecco [1]

[1] Department of Biomedical Engineering, Tufts University, Medford, MA 02155 [2] Newton Wellesley Hospital, Newton, MA, 02462

Endometriosis is a debilitating gynecologic disease which impacts 190 million people globally and is associated with up to half of infertility cases. Leukemia inhibitory factor (LIF) is an immunomodulatory cytokine involved in fertility and altered LIF signaling has been associated with patients with endometriosis. Here, we hypothesize that exposure to inflammatory signals temporally regulates LIF signaling and subsequent endometrial cell function. To test this, we aimed to identify the mechanism by which pro-inflammatory challenges impact spatial and temporal LIF/ LIFR expression using endometrial organoids and stroma from patients with and without endometriosis.

Endometrial epithelial organoids (EEOs) were embedded in a multi-arm PEG-based hydrogel to generate epithelial luminal and glandular structures in vitro, then co-cultured with and without endometrial stromal cells. Epithelial phenotypes of the lumenal (LE) surface and gland (GE) structures were characterized via FOXA2 and SOX9 antibody staining. Cells were treated with sex hormones to mimic the menstrual phases and exposed to inflammatory cytokine IL-1b to mimic the endometriotic phenotype. LIF/LIFR expression was measured in cells across 15 days using immunofluorescent imaging and ELISA assays.

Structurally, EEOs seeded in PEG hydrogels demonstrated LE and GE compartmentalization of the native endometrium. Distinct LIF/LIFR expression patterns in the GE/LE in response to progesterone stimulation was observed in co-cultures compared to monocultures. LIF secretion demonstrated a biphasic response to acute IL-1b stimulation. These results suggest that both stromal-epithelial crosstalk and inflammatory cues are regulators of physiological LIF signaling in the endometrium.



Capillary morphogenesis gene 2/anthrax toxin receptor 2 (CMG2/ANTXR2) in endometriosis

Jane B. Maoga [1] and Michael S. Rogers [1]

[1] Department of Surgery, Vascular Biology Program, Children's Hospital Boston, Harvard

Medical School, Boston, MA, USA

Endometriosis, a gynecological condition characterized by the occurrence of endometrial tissue outside the uterus is mainly associated with chronic pelvic pain. dysmenorrhea and infertility. It affects about 10% of women in the reproductive age. Capillary morphogenesis gene 2 or anthrax toxin receptor 2 (CMG2/ANTXR2) is a transmembrane extracellular matrix receptor that also functions as the primary anthrax toxin receptor. It is dysregulated in endometriosis lesions, and its targeting reduces cell migration, adhesion and tube formation in primary stromal cells. However, this is not known in immortalized endometriotic epithelial (12Z) and ectopic stromal (iEC-ESCs) cells. In endothelial cells CMG2 activity can be inhibited with penta-O-galloyl-β-D-glucose (PGG), a plant-derived polyphenol with antitumor and anticancer properties. The aim of this study was to determine the anti-endometriotic activities of CMG2 targeting using PGG on endometriotic cell growth, migration and chemotaxis. The effects of PGG on cell viability, growth and migration of endometriotic cells were analyzed using the cell counting kit-8, colony formation, wound healing and chemotaxis assays respectively. PGG at concentrations of 3 µM and above reduced endometriotic epithelial cell viability after 48 hours. At non-toxic concentrations, PGG reduced the number of colonies formed by these cells. Furthermore, it decreased the random movement of the cells (chemokinesis) and their ability to move towards a concentration gradient (chemotaxis). Together, these results suggest that CMG2 and PGG may be a promising target and possible potent anti-endometriotic agent. respectively. Further studies on the mechanisms involved are necessary.





Profiling the expression of Specialized Pro-resolving inflammatory Mediators (SPMs) across human endometrial health.

Mariana Alonso-Riquelme [1], Elizabeth E. Marr [1], Mollie A. O'Brien [2], Peter R. Movilla [2], and Juan S. Gnecco [1]

[1] Tufts University, Department of Biomedical Engineering, Medford, MA, 02155[2] Newton Wellesley Hospital, Newton, MA, 02462

Endometriosis is a chronic inflammatory disease affecting over 190 million individuals worldwide. Dysregulation of inflammation plays an essential role in ectopic endometrial tissue growth. Further, specialized pro-resolving mediators (SPMs) are lipid-derived molecules that play a key role in resolving inflammation and restoring homeostasis. However, whether SPMs play a role in endometrial health remains largely unexplored.

In this study, we test the hypothesis that progesterone regulates SPM biosynthesis in the endometrium, leading to inflammation resolution. Using a PEG-based hydrogel and patient-derived endometrial organoid in vitro models, we characterized the expression of SPM-associated lipoxygenase (ALOX) enzymes, receptors, and metabolites across the menstrual cycle via transcriptomic, imaging, and lipidomic approaches. Temporal and spatial expression patterns were observed differentially across immune, endometrial epithelial, and stromal cell populations.

We identified that in stromal cells, progesterone impacted the activation of ALOX5, 15-1, and 12, as noted by the perinuclear translocation of ALOX15-1 coinciding with increased production of 5, 15, and 12-HETE intermediates. Interestingly, the SPM pathway products, lipoxins, were not observed in monocultures. Contrastingly, LXB4 was measured when co-cultured with epithelial organoids, highlighting the importance of trans-cellular crosstalk in SPM biosynthesis.

Additionally, IL-1β challenges disrupted the localization of SPM receptors FPR2 and GPR18. Finally, exogenous lipoxins attenuated inflammatory responses and influenced progesterone responsiveness, emphasizing their role in endometrial health.

These findings reveal progesterone's impact on modulating SPM pathways in the endometrium and their role in inflammation resolution. Targeting these pathways offers a promising therapeutic approach for managing chronic inflammatory diseases like endometriosis, where homeostasis is disrupted.





Exploring the dual hormonal and anti-fibrotic role of Relaxin-2 in Uterine Fibroids Zoe Garman [1]

[1] Department of Biomedical Engineering, Boston University, MA, USA

Uterine fibroids (UFs) are one of the most common non-malignant disorders, affecting up to 70% of women. There are no approved curative pharmacotherapies for UFs, only surgical intervention to remove the leiomyomas or parts of the uterus. Relaxin-2 (RLX) is a peptide hormone involved in the endogenous hormone cycle and has been used as an anti-fibrotic due to its extracellular matrix (ECM) remodeling properties. Primary human uterine smooth muscle cells (SMCs) and primary uterine fibroblasts (UFbs) were cultured on tissue culture plates and treated with transforming growth factor beta 1 (TGF-1) to induce a fibrotic state. These cells are then treated with RLX and analyzed via Western blot and qPCR for fibrosis markers type I collagen and alpha smooth muscle actin (SMA). Cells were embedded into type I collagen gels crosslinked with varying amounts of ribose and treated with TGF- β 1 and RLX for 48 hours. Indentation mechanical testing was performed after 11 days to determine the changes in stiffness due to the treatments.



Symptomatic Uterine Fibroids at Boston Medical Center

Kendra Lujan BS [1,2] , Julia C. Bond, PhD [3] , MPH, Ezinnem Ugoji MD [3] , Nyia L. Noel, MD, MPH [3]

[1] Boston University Chobanian & Avedisian School of Medicine, Boston, MA, USA [2] Boston University School of Public Health, Boston, MA, USA [3] Department of Obstetrics & Gynecology, Boston Medical Center, Boston, MA, USA

We aimed to identify and characterize factors associated with repeat emergency department (ED) visits for symptomatic uterine leiomyomas (fibroids).

We performed a retrospective chart review of individuals aged 18-89 years presenting

to the Boston Medical Center (BMC) ED for uterine fibroids between 2014 and 2020. ED visits were identified by primary ICD-10 diagnosis, and the presence of pre-identified fibroid-related symptoms. We used generalized linear models to estimate prevalence ratios (PR) and 95% confidence intervals (CI) for the association between patient and visit characteristics at initial ED visit and repeat ED visit prevalence.

A total of 873 participants contributed 1036 ED visits. Subjects were grouped number of ED visits: 1 (n = 750) and >1 visit (n = 123, 14%) Anemia diagnosis and iron transfusion therapy at the initial ED visit were positively associated with a repeat visit (PR 2.58, 95% CI 1.65, 4.27; PR 2.92, 95% CI 1.72, 4.40). Neither receiving an outpatient gynecology referral at initial visit, nor seeing a gynecologist for follow up within 2 weeks of initial visit, were appreciably associated with the prevalence of a repeat visit.

Our analysis revealed that anemia status and the need for blood transfusion during an initial ED visit for fibroid was the strongest predictor of a repeat ED visit for fibroids.Providers should be aware of anemia as a particularly salient feature for patients presenting with uterine fibroids to the ED.



Implementation of a Shared Decision-Making Tool for Uterine Fibroid Care Kenya Mathieu [1]

[1] Department of Obstetrics & Gynecology, Boston Medical Center

Uterine fibroids (UF) affect 26 million people with uteruses in the U.S., disproportionately impacting Black patients and contributing to significant healthcare inequities. Our mixed methods study aims to improve patient-provider communication, increase patient self-efficacy, mitigate provider bias, and reduce racial inequities in fibroid outcomes by incorporating a shared decision-making (SDM) tool into fibroid care. To date, preliminary analysis of patient and provider interviews (n=23) and patient surveys (n=61) shows high potential for long-term feasibility of the tool with positive overall impressions of the tool.

More patients who used the SDM tool during their clinic visit gave the visit the highest possible patient-centeredness rating (52%) compared to patients who did not use the tool (31%). One patient said "I felt the tool to be incredibly helpful. And I'm still referring back to it to this day as I'm...trying to...process everything and finally make a final decision for my next appointment." Patients and providers both shared detailed suggestions for updating the tool, including feedback on illustrations, layout and design, educational content, plain-language accessibility, and implications for sustainability using paper versus digital modalities. Many interviewees commented that translating the tool into multiple languages would significantly increase accessibility. Future directions for this project include continuing recruitment until qualitative thematic saturation is reached and 100 patient surveys are collected. We anticipate refining the SDM tool based on the feedback obtained from this pilot study and translating the tool into Haitian Creole and Spanish for future research and use in clinical care.



Spatially Mapping the Mechanical and Structural Properties of the Seedling Uterine Fibroid-Myometrium Interface

Daniella Fodera [1], Alara Sutcu [2], Arielle Joasil [1], Aiden Therien [1], Johanna L.L. Jackson [1], Shuyang Fang [1], Arnold Advincula [2], Joy Vink [2], Xiaowei Chen [2], Christine Hendon [1], Tal Korem [2], Michelle Oyen [3], Kristin Myers [1]

[1] Columbia University, New York, NY, USA [2] Columbia University Irving Medical Center, New York, NY,USA [3] Washington University in St. Louis, St. Louis, MO, USA

Uterine fibroids (leiomyomas) are highly-prevalent, noncancerous tumors that form within the uterus and are characterized as stiff, collagen-dense, heterogeneous masses of tissue. Limited diagnostic and treatment options for this disease are underpinned by poor mechanistic understanding of fibroid pathophysiology. Using a multi-faceted, discovery-driven approach, this study seeks to spatially map the mechanical, structural, and compositional properties of the fibroid-myometrium interface ex vivo with microscale resolution. In accordance with IRB approval, human uterine tissues embedded with mm-sized fibroids (n = 39) were collected from nonpregnant women (N = 12) undergoing hysterectomies for noncancerous indications. Tissues were subsequently characterized with nanoindentation, histological, second harmonic generation imaging, and guantitative biochemical approaches. Statistical significance was determined with a linear mixed model (p<0.05). Relative to patient-matched myometrial tissues, seedling uterine fibroids exhibited increased stiffness, decreased permeability, increased diffusivity, no change in viscoelasticity, decreased hydration, increased collagen content, and distinct collagen organization. At the fibroid-myometrium interface, a band of aligned myometrial fibers immediately adjacent to the fibroid was observed, and multiple transition patterns in material properties were identified. Ultimately, this study establishes foundational knowledge on the mechanics and structure of seedling uterine fibroids and will facilitate future developments of clinically translatable detection tools.



Strain Dependent Impacts of Sex Hormones on Female Tendon Extracellular Matrix Remodeling

Caitlin Colicchio [1], Brianne Connizzo [1]

[1] Department of Biomedical Engineering, Boston University, MA, USA

Remodeling of the extracellular matrix (ECM) is required for the proper healing, strengthening, and maintenance of tendon tissue. Sex and hormones have been investigated as factors which alter this remodeling process, however the individual effects of sex, hormones, and mechanical strain have yet to be decoupled. Therefore, the objective of this study was to investigate the influence of estrogen and progesterone, the two main female sex hormones, on tendon remodeling under various static and cyclic tensile strain conditions. We hypothesized that both estrogen and progesterone would exhibit strain-dependent impacts on tendon ECM remodeling. Flexor digitorum longus tendon explants from female mice were cultured in no hormone, estrogen-supplemented, progesterone-supplemented, or dual hormone medium and subjected to various strain conditions. Biochemical assays which assess ECM protein content, DNA content, metabolism, and synthesis of the tendon were completed to evaluate changes in ECM remodeling. Both estrogen and progesterone exhibited complex, strain-dependent impacts on tendon health, biosynthesis, and ECM content with lower levels of strain representing a homeostatic level of mechanical stimulation for female tendons. Further, these results suggest that estrogen has a role in regulating sGAG turnover while progesterone is more influential in the maintenance of collagen, regardless of applied tensile strain.





Association Between Reproductive History and Cognition in Post-Menopausal Latinas from the Boston Latino Aging Study

Avery Giudicessi [1]

[1] Department of Psychological and Brain Sciences, Boston University, MA, USA

Sex disparities in Alzheimer's disease (AD) risk are significant, with nearly twothirds of AD cases occurring in females. While research has begun exploring connections between women's endocrine history and cognitive aging, studies often neglect to investigate reproductive events' influence on cognition, particularly among Latino populations who experience a disproportionate AD burden. This study investigates potential relations between

reproductive history and cognitive function in Latinas after age 55.

Sixty-one Spanish-speaking Latinas from the Boston Latino Aging Study (BLAST) participated (mean age=66.8, SD=11.0; education=11.0, SD=5.0). Reproductive factors were assessed via health history questionnaire. Cognitive function was measured using the Preclinical Alzheimer's Cognitive Composite-5 (PACC5), adapted for Spanish-speakers. Regression models adjusted for age and education examined associations between reproductive factors and cognition.

Mean MMSE score was 25.9 (SD=3.3). Reproductive span averaged 33.6 years (SD=8.0), with 3.6 average pregnancies (SD=1.8). Greater number of pregnancies associated with worse PACC-5 composite score (β =-0.09, 95% CI: -0.19 to -0.01, p<0.05) and DSST scores (β =-0.16, 95% CI: -0.28 to -0.04, p<0.01). No significant relations emerged between cognitive scores and other reproductive factors.

Results reveal a significant negative relationship between number of pregnancies and cognitive function in Latina females. Further research with larger samples and longitudinal designs is needed to explore these associations and potential interventions.



Cervical Cancer Brachytherapy Survivor Interviews Illuminate Critical Unmet Needs in Informed Consent, Treatment Experience, Pain Management Protocol and Outcomes

Eve McDavid, BJ, Missouri-Columbia School of Journalism, Cervical Cancer Survivor, CEO and Co-Founder of Mission-Driven Tech, Onyinye Balogun [2], MD, MSc, WeillCornell Medicine/ New York Presbyterian, Assistant Professor of Radiation Oncology,Co-Founder of Mission-Driven Tech, Areion Allmond,BS, Weill Cornell Medicine, ResearchPartner

Gynecologic Brachytherapy is vital for cervical cancer treatment and significant increases 5-year survival rates. However, procedure discomfort, anxiety, and distress leadup to 40% of patients from dropping out from treatment prematurely. Limited research

highlights how current practices impact survivors' physical, mental, and sexual health. Despite being documented in medical research, these issues have not yet influenced brachytherapy protocols. Knowledge gaps and inconsistent procedures leave patients unprepared and in extreme pain with debilitating long-term side effects. Improving compliance and quality of life requires standardized pain management, comprehensive education, and innovative technologies. This study aims to: 1) raise awareness of unmet needs in gynecologic brachytherapy; 2) assess the impact of current practices on survivorship; and 3) identify necessary communication tools to enhance quality of life.

Eighteen cervical cancer survivors who underwent brachytherapy were interviewed in-person and via virtual meetings. Semi-structured interviews documented patient experiences and identified challenges faced by patients and provider. Participants were recruited through US and international advocacy networks.

Thematic analysis revealed five critical unmet needs: 1) comfort and safety concern regarding medical devices; 2) establishment of standardized pain management protocols; 3) education for staff and patients on treatment side effects; 4) mental and sexual health support referrals; and 5) provider training on gender sensitivity and empathy.

The findings indicate significant room for improvement in the gynecologic brachytherapy experience. Further research is essential to ensure cervical cancer survivors receive standardized, high-quality care that enhances their post-treatment quality of life.