SESSION 6335 (SYMPOSIUM)

WHY DO AGE AND BIAS MATTER? HISTORICAL, SOCIAL, AND BIOLOGICAL IMPACTS ACROSS GENERATIONS OF LGBTQ OLDER ADULTS
Chair: Charles Emlet
Co-Chair: Karen Fredriksen Goldsen

We do not live in a stagnant world, politically, historically or socially - neither are the life experiences of lesbian, gay, bisexual, and transgender (LGBTQ) older adults. Their physical, psychological and social lives are impacted by their present and past historical contexts and generational identity, as well as the sociopolitical environment, social pressures, support and experiences of biases. This symposium draws upon data from Aging with Pride: National Health, Aging and Sexuality/Gender Study, the first longitudinal study of LGBTQ older adults in the United States, in order to examine how environmental, interpersonal and intrapersonal structures impact the lives of the three oldest generations of LGBTQ adults. Emlet and colleagues examine the generational and historical forces across the life course among 205 transgender older adults in order to illuminate how historical context and gender influences social life and physical health. Prasad and colleagues explore differences between various constructs of bias including lifetime discrimination, victimization, everyday discrimination and microaggressions on LGBTQ older adults and how those experiences impact depression, general health and quality of life. Lastly, Hoy-Ellis and colleagues explore how life course predictors including interpersonal violence, legal marriage, and identity management are associated with allostatic load (AL) in a sample of 317 LGBTQ older adults who range in age from 50-97. We will address the intersectionality of generational identity, experiences of bias and biomarkers, as well as the implications for policy and practice.

HISTORICAL AND GENERATIONAL FORCES AND GENDER DIFFERENCES IN THE IRIDESCENT LIFE COURSE OF TRANSGENDER OLDER ADULTS
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Shifting historical, political, and social times have impacted transgender older adults in experiences and development. Examining how gender identities interact with life events within a historical context elucidates differences by generations and gender. Using a transgender subsample (n=205) from the National Health, Aging, and Sexuality/Gender Study (N=2,450), logistic weighted regressions with sociodemographic adjustment were performed to examine generational differences and gender interaction in key life experiences in identity, work, kin, bias, community, and health/well-being. Silenced (born 1935-1949, 18%), than Pride (1950-1964, 79%), Generation disclosed identity later, is less visible, more likely to be retired and veteran, more likely for life-time opposite-sex marriage and divorce. Significant gender interactions exist in community engagement, kin relationships, and physical health. Despite small sample size, Invisible Generation (1914-1934, 3%) has unique differences. Findings show complexity of generational differences among transgender older adults, understanding of what helps better serve them as they age with their accumulated life experiences.

TYPES OF INTERPERSONAL BIAS: MEASUREMENT AND THEIR ASSOCIATION WITH HEALTH AMONG LGBTQ OLDER ADULTS
Anyah Prasad,¹ Karen Fredriksen Goldsen,² Hyun Kim,² and Hailey Jung,² 1. University of Massachusetts Boston, Boston, Massachusetts, United States, 2. University of Washington, Seattle, Washington, United States

Increasing diversity and rapidly evolving sociopolitical context is changing the face of bias experiences in contemporary America. Accordingly, literature has evolved into four unique ways of describing bias, namely lifetime discrimination and victimization, everyday discrimination, and microaggressions. However, there is less conceptual clarity on the way these constructs are operationized, measured, and their relationship to one another and health outcomes. In this paper, we discuss the measurement of these four constructs and report their prevalence among a national sample of LGBTQ older adults (N=2,450). The correlation between these constructs varied between 0.36 to 0.63, which shows that despite considerable overlap they are measuring distinct aspects of bias experiences. Each of the constructs had a significant association with depression, general health and quality of life. When the four constructs were entered into a regression model, everyday discrimination (due to sexual and gender identity and other factors) emerged as the strongest predictor.

LIFE COURSE PREDICTORS OF ALLOSTATIC LOAD AMONG LGBTQ OLDER ADULTS
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LGBTQ older adults are at significantly increased risk for poor mental and physical health, likely consequential to lifelong bias. Allostatic load (AL), the net effect of “wear and tear” on the body resulting from repeated, chronic over-activation of the psychophysiological stress response system. Utilizing the Health Equity Promotion Model, the aim of this study was to test potential life course predictors of AL, including interpersonal violence, legal marriage, and identity management in a sample of LGBTQ adults 50 to 97 years of age (n=317). Results from a series of hierarchical linear regression models showed that adult physical abuse and lifetime discrimination for those who had been in an opposite-sex marriage predicted higher AL in this sample of LGBTQ older adults, indicating need for increased research on bias over the life course as contributory to AL and biopsychosocial dysfunction among LGBTQ older adults.

SESSION 6500 (SYMPOSIUM)

THE FUTURE OF AGING RESEARCH
Chair: Stephen Helfand
Co-Chair: Jackson Taylor

We are at a particularly propitious time in the history of the biology of aging and the science of health and humanity.
It is a time for us to “Honor the Past, Enrich the Future”. Not long ago the study of the biology of aging was exclusively one of description of what happened with age—how do organisms, including humans, change with age at the level of proteins, cells, tissues and physiology. The identification of major genetic factors that substantially increase lifespan in model organisms ushered in the advent of a highly exploratory period focusing on the molecular, cellular and genetics mechanisms of aging. The convergence of many different streams of basic and clinical research have brought us to today, where we stand on the cusp of new environmental, molecular genetic and pharmaceutical breakthroughs in the biology of aging that presage new interventions that promise a healthier lifespan. The presentations in this Presidential Symposium will be from four Early Career Investigators presenting their own pioneering research in some of the most important areas of research in the biology of aging.

MECHANISMS OF LIFESPAN EXTENSION BY SIRT6 IN DROSOPHILA MELANOGASTER
Jackson Taylor, Jason Wood, Matthew Finn, Julianna Liu, Evan Mizerak, Sarah Gordon, Corinne Hutfilz, and Stephen Helfand, Brown University, Providence, Rhode Island, United States

Sirt6 is a multifunctional enzyme that regulates numerous cellular processes connected to longevity. Overexpressing Sirt6 extends lifespan in mice, but the underlying cellular mechanisms are unclear. Here, we used the powerful genetic tools and short lifespan of Drosophila melanogaster to better understand the precise mechanisms by which Sirt6 regulates longevity. Sirt6 OE in flies produces robust extension of median lifespan in both sexes. Molecular and biochemical analyses reveal that Sirt6 OE reduces expression of genes involved in protein synthesis, including many Myc target genes, via epigenetic regulation. We will further discuss our findings on the connection between Sirt6, Myc, and the molecular regulation of protein synthesis and lifespan, as well as additional Sirt6 longevity mechanisms we identified, including autophagy and silencing of transposable elements.

NEW COMPUTATIONAL APPROACHES TO AGING RESEARCH
Morgan E. Levine, Yale University School of Medicine, New Haven, Connecticut, United States

Aging is associated with numerous changes at all levels of biological organization. Harnessing this information to develop measures that accurately and reliably quantify the biological aging process will require systems biology approaches. This talk will illustrate how epigenetic data can be integrated with cellular, physiological, proteomic, and clinical data to model age-related changes that propagate up the levels—finally manifesting as age-related disease or death. I will also describe how network modeling and machine learning approaches (linear and non-linear) can be used to identify causal features in aging from which to generate novel biomarkers. Given the complexity of the biological aging process, modeling of systems dynamics over time will both lead to the development of better biomarkers of aging, and also inform our conceptualization of how alterations at the molecular level propagate up levels of organization to eventually influence morbidity and mortality risk.

EPIGENETICS, HEREDITY, AND AGING
Eric Greer, Boston Children’s Hospital/Harvard Medical School, Boston, Massachusetts, United States

Longevity has long been shown to be regulated by genetic and environmental factors. We recently showed that longevity in the nematode Caenorhabditis elegans can also be regulated by the transmission of epigenetic information. We have shown that several chromatin modifying enzymes have a transgenerational non-Mendelian effect in worms on the longevity of their descendants. I will discuss some of our recent work attempting to decipher how epigenetic modifications can regulate complex phenotypes, including longevity, and how this non-genetic information can be transmitted across generations.

SEX-DIMORPHISM IN AGING GENE REGULATION: ARE WE MISSING HALF OF THE PICTURE?
Bérénice Benayoun, Ryan Lu, Nirmal Sampathkumaran, and Min Hoo Kim, University of Southern California, Los Angeles, California, United States

The existence of human supercentenarians reveals a surprising predictor for exceptional longevity: being female. Not only are 33 out of 34 living supercentenarians women, women are also more resistant to most diseases responsible for age-related morbidity in the US. However, because most molecular aging studies generally opt to use only one sex, sex-driven differences in aging remain poorly understood. A key compartment that can actively respond to sex-specific inputs throughout life is the immune system. Indeed, the majority of age-related diseases share common inflammatory mechanisms, a phenomenon described as “inflamm-aging”. Macrophages play an important role in the inflammatory response throughout life, and are considered major mediators of this phenomenon. Thus, to unbiasedly dissect sex differences in immune aging, we generated ‘omics’ data from 4 and 20 months old female and male mice. Intriguingly, we found that transcriptional aging in primary macrophage populations varies strongly between sexes, with up to 20-fold more aging changes in female vs. male cells. Pathways specifically downregulated in females with aging included lysosome, inflammation and phagolysosome. We confirmed experimentally that metabolic preferences of macrophages are indeed directly modulated in this context (e.g. glycolytic preference for male-derived cells). Our results support the notion that there are functional differences in aging trajectories in the immune system of female vs. male mice. Our research could provide new insights into the molecular underpinnings of sex-dimorphism in aging and disease.

SESSION 6505 (SYMPOSIUM)

METABOLISM AND AGING: NEW APPROACHES TO NUTRITION AND DIET IN AGING
Chair: Blanka Rogina

Aging is associated with a functional decline in metabolic, physiological, proliferative, and tissue homeostasis...