Posttraumatic stress disorder (PTSD) is twice as prevalent in women as in men, and is an established risk factor for chronic disease, but few studies have comprehensively assessed lifetime PTSD in middle-aged and older civilian women. We surveyed 33,328 women aged 54-74 from the Nurses' Health Study II from August 2018 to January 2020 to understand trauma exposure, PTSD based on the Diagnostic and Statistical Manual of Mental Disorders Version 5, and trauma-related treatment use. The majority (82.2%) of women reported one or more lifetime traumas. 10.5% of those with trauma had lifetime PTSD and 1.5% had past-month PTSD. The most common trauma types were sudden or unexpected death of a loved one (44.9%) and interpersonal or sexual violence (43.5%). Almost 30% experienced occupational (nursing-related) trauma. Interpersonal or sexual violence event types explained the largest proportion of PTSD cases (33.6%) out of seven categories of events assessed. Only 25% of women with trauma ever accessed trauma-related treatment, but this proportion was higher (66.4%) among those with diagnosable PTSD, and among those with current depression (35.9%). Treatment was most common among women who experienced interpersonal/sexual violence and lowest among those with occupational trauma, but treatment satisfaction did not vary by worst trauma type. Psychotherapy was the most common type of treatment. These results demonstrate that trauma is nearly universal in middle-aged to older women, which has important implications for their long-term health and well-being—particularly in the era of COVID-19 which is likely to produce additional trauma in this population.

Session 3600 (Symposium)

Models to Study Aging

UNIVERSAL DNA METHYLATION AGE ACROSS MAMMALIAN TISSUES

Chair: Viviana Perez Ake Lu,[1] Zhe Fei,[2] Ken Raj,[3] and Steve Horvath,[2] *1. UCLA, Los Angeles, California, United States, 2. UCLA, Los Angeles, California, United States, 3. Centre for Radiation, Chemical and Environmental Hazards, Public Health England, Chitlon, England, United Kingdom*

Aging is often perceived as a degenerative process caused by random accrual of cellular damage over time. In spite of this, age can be accurately estimated by epigenetic clocks based on DNA methylation profiles from almost any tissue of the body. Since such pan-tissue epigenetic clocks have been successfully developed for several different species, it is difficult to ignore the likelihood that a defined and shared mechanism instead, underlies the aging process. To address this, we generated over 10,000 methylation arrays, each profiling up to 37,000 cytosines in highly-conserved stretches of DNA, from over 59 tissue-types derived from 128 mammalian species. From these, we identified and characterized specific cytosines, whose methylation levels change with age across mammalian species. Genes associated with these cytosines are greatly enriched in mammalian developmental processes and implicated in age-associated diseases. From the methylation profiles of these age-related cytosines, we successfully constructed three highly accurate universal mammalian clocks for eutherians, and one universal clock for marsupials. The universal clocks for eutherians are similarly accurate for estimating ages (r>0.96) of any mammalian species and tissue with a single mathematical formula. Collectively, these new observations support the notion that aging is indeed evolutionarily conserved and coupled to developmental processes across all mammalian species - a notion that was long-debated without the benefit of this new and compelling evidence.

THE COMMON MARMOSET: A HIGHLY TRANSLATABLE SMALL NONHUMAN PRIMATE MODEL OF AGING

Ricki Colman, *University of Wisconsin, Madison*

BATS: SECRETS OF EXTENDED HEALTHSPAN

Emma Teeling, *University College Dublin, Ireland, Ireland*

Of all mammals, bat possess the most unique and peculiar adaptations that render them as excellent models to investigate the mechanisms of extended longevity and potentially halted senescence. Indeed, they are the longest-lived mammals relative to their body size, with the oldest bat caught being >41 years old, living approx. 8 times longer than expected. Bats defy the 'rate-of-living' theories that propose a positive correlation between body size and longevity as they use twice the energy as other species of considerable size, but live far longer. The mechanisms that bats use to avoid the negative physiological effects of their heightened metabolism and deal with an increased production of deleterious Reactive Oxygen Species (ROS) is not known, however it is suggested that they either prevent or repair ROS damage. Bats also appear to have resistance to many viral diseases such as rabies, SARS and Ebola and are the suspected reservoir species for a huge diversity of newly discovered viruses, including Sars-CoV-2 This suggests that their innate immunity is different to other mammals, perhaps playing a role in their unexpected longevity. Here the potential genomic basis for their rare immunity and exceptional longevity is explored across multiple bat genomes and divergent ageing and immune related markers (e.g. microbiome, telomeres, mitochondria, cellular dynamics, cytokine response) studied in wild bat populations. These findings provide a deeper understanding of the causal mechanisms of ageing and tolerant immunity, potentially uncovering the key molecular pathways that could be utilised to benefit society.

Session 3605 (Paper)

Nursing Homes

A CROSS-SECTIONAL STUDY COMPARING YOUNGER AND OLDER NURSING HOME RESIDENTS IN WESTERN CANADA

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