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Testing Life Course Models Whereby Juvenile and Adult Adversity Combine to Influence

Speed of Biological Aging

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ONLINE SUPPLEMENT ON MEASURES OF AGING

The epigenetic measures of Horvath (2013) and Hannum et al. (2013) are probably the most widely accepted measures of biological aging. They correlate much more strongly with chronological age ($r > .90$) than any of their competitors and they have been shown to predict all-cause mortality in 13 cohorts (Chen et al. 2016). Further, accelerated aging using these measures has been linked to frailty, some types of cancer, cardiovascular disease, and both Alzheimer's and Parkinson's disease (Jylhava et al. 2017). However, these indices are unrelated to many types of cancer, their relation with cardiovascular disease is weak, and they are not associated with disease risk factors such as smoking, diabetes, hypertension, lipoproteins, insulin, glucose, triglycerides, or C-reactive protein (Horvath et al. 2016). In addition, it is unclear whether the Horvath and Hannum epigenetic clocks are a cause, consequence, or correlate of aging (Jyhava et al. 2017). Finally, it is now a challenge to obtain the methylation data necessary to construct either Horvath's or Hannum's epigenetic measures. Their indices were originally formed using the Illumina 450 Beadchip. Illumina has replaced the 450 beadchip with the new EPIC 850 Beadchip. This new platform has the advantage of providing data on 850,000 methylation sites compared to the previous approach that assayed only 450,000 sites; but, much to the dismay of biomedical researchers, it also omits several of the sites included in both the Horvath and Hannum epigenetic indices.

For much of the new millennium, leucocyte telomere length has been a popular measure of aging. Telomere length correlates roughly .50 with chronological age and several studies have reported that this measure is associated with increased risk of mortality (Jylhava et al. 2017). Meta-analyses also report that telomere length is related to cardiovascular risk (Haycock et al. 2014), and some cancers (Wentzensen et al. 2011). Unfortunately, however, research on

telomeres has often been plagued by inconsistent findings. Even meta-analytic efforts often produce limited conclusions (Gardner et al. 2013; Jylhava et al. 2017). Further, some established findings obtaining with the measure are rather puzzling. Several studies, for example, have failed to find an association between socioeconomic status and telomere length (e.g., Carroll et al. 2013; Steptoe et al. 2011), or between age and telomere length among black Americans (Needham et al. 2013). Further, there is research indicating that telomere length is longer among black Americans than white Americans of the same age (Needham et al. 2013; Rewak et al. 2014), a paradoxical finding given the high rates of adversity, morbidity, and mortality suffered by blacks compared to other ethnic groups living in the United States (Williams 2012). Importantly, DNA extraction methods used to assess telomere length have been shown to have a pronounced influence on telomere length values and this variability likely contributes to spurious or lost associations in epidemiological studies (Raschenberger et al. 2016). Finally, like the epigenetic clocks of Horvath and Hannum, it is not clear whether telomere length is a cause or a consequence of aging (Jylhava et al. 2017). Although the epigenetic clock and telomere studies have furthered our understanding of aging, it is clear that both of these approaches present limitations as measures of biological aging. Indeed, most studies find that the correlation between the epigenetic clocks and telomere length are either very low or non-significant (Jylhava et al. 2017).

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