Conserved and distinct signatures of transcriptional aging across tissues in rhesus macaques.

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While all animals age, aging processes vary within populations. Some of this variation is between individuals, but rates and patterns of aging can also differ across cells and tissues within individuals. Little is known about intra-individual variation in aging in primates, in part because most studies have only been able to measure one tissue: blood. To address this gap, we characterized patterns of transcriptional aging in a cross-sectional sample of free-ranging rhesus macaques from the island of Cayo Santiago. Using RNA-seq, we measured gene expression in liver, spleen, and skeletal muscle samples from 237 rhesus macaques ranging in age from infancy to late life. We identified over 2,000 age-associated genes (AAGs) in each tissue (local false sign rate; lfsr < 0.1) Interestingly, only 9% (n=594) of these genes differed by age in all three tissues (lfsr < 0.1), suggesting that aging patterns are highly tissue-specific. Additionally, AAGs showed lower levels of tissue-specific function and higher inflammatory signaling in older individuals (adjusted $p < 0.1$), likely driven by tissue-specific cell composition changes (e.g., reduction of hepatocytes in the liver of older animals; adjusted $p < 0.05$). To test the hypothesis that tissue specificity declines with age, we evaluated whether genes that were lower with age were more likely to be tissue-specific and found evidence for this in the liver and spleen. Our results provide insight into variation in aging between organs and are suggestive of age-associated patterns of higher inflammation and lower tissue-specific functioning in older individuals.