AGING

Filling in the slate with transcriptomes for mice across ages

The Tabulua Muris Consortium *Nature* **583**, 590—595 (2020)
Schaum, N. et al. *Nature* **583**, 596—602 (2020)

In 2018, an international consortium of researchers began filling in the 'blank slate' that was the mouse transcriptome with the *Tabula Muris*, or Mouse Cell Atlas. Using two different methods for separating cells—fluorescence-activated cell sorting (FACS) and microfluidic droplets—the researchers isolated and sequenced the transcriptomes of 100,605 individual cells, taken from 20 different organs from four male and three female C57BL/6JN mice. The data revealed novel cell types, as well as cellular commonalities and differences between those different organs.

It was a massive snapshot of murine cell types and gene expression, but one that captured a single moment in time: the seven mice were all healthy young adults, each about 3 months old. But life is not static—animals age, with notable impacts on their health. New work from the *Tabula Muris* Consortium adds that element of aging to their transcriptomic resource.

The *Tabula Muris Senis*, or Mouse Ageing Cell Atlas, compiles single-cell RNA sequencing data from of a total of 356,213 individual cells isolated from 23 organs and tissues. This time, those cells were sampled from 19 male and 11 female C57BL/6JN mice across 6 different ages, between 1 month and 30 months old. The effects of age were apparent in those single-cell data and in additional data from Nicholas Schaum et al. that were compiled with a bulk sequencing approach across tissues. The latter datasets contain additional transcriptome and plasma proteome data measured from 17 organs from C57BL/6JN mice of 10 different ages, from which the researchers analyzed broader trajectories of gene expression over time.

Just as different organs can express different subsets of cell types, those populations can shift over time—the number and composition of cells differ with age, as does gene expression levels in those cells. Timing varies organ-to-organ but similar change trajectories were observed in the bulk dataset, while the published analysis of the single-cell sequences notes signs of senescence as well as the effects of aging on genome stability and the immune system.

"The cell atlas provides a deep characterization of phenotype and physiology and serves as a reference for understanding many aspects of the changes in cell biology that occur in mammals during their lifespan," the Consortium concludes. The teams' full analyses can be found in their respective publications, and the underlying data for genes, tissues, and ages of interest can be explored online.

The writing on the slate is clear: aging is a dynamic process, with notable molecular and cellular hallmarks to be further explored.

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