# Researchers reveal aging signatures across diverse tissue cells in mice

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Researchers have identified molecular signatures of the aging process in mice, publishing their results today in the open-access *eLife* journal.

Their analyses provide one of the most comprehensive characterisations of the molecular signatures of aging across diverse types of cells from different tissues in a mammal, and will aid future studies on aging and related topics.

Aging leads to the decline of major organs and is the main risk factor for many diseases, including cancer, cardiovascular and neurodegenerative diseases. While previous studies have highlighted different hallmarks of the aging process, the underlying molecular and cellular mechanisms remain unclear.

To gain a better understanding of these mechanisms, the Tabula Muris Consortium created the single-cell transcriptomic dataset, called Tabula Muris Senis (TMS). The TMS contains over 300,000 annotated cells from 23 tissues and organs of male and female mice. "These cells were collected from mice of diverse ages, making the data a tremendous opportunity to study the genetic basis of aging across different tissues and cell types ," says first author Martin Jinye Zhang, Postdoctoral Researcher in the Department of Epidemiology, Harvard University, Boston, US.

The original TMS study mainly explored the cell-centric effects of aging, aiming to characterize changes in the composition of cell types within different tissues. In the current gene-centric study, Zhang and colleagues focused on changes in gene expression that occur during the aging process across different cell types.

Using the TMS data, they identified aging-dependent genes in 76 cell types from 23 tissues. They then characterized the aging behaviors of these genes that were both shared among all cell types ('globally') and specific to different tissue cells.

"We found that the cell-centric and gene-centric perspectives of the previous and current studies are complementary, as gene expression can change within the same cell type during aging, even if the composition of cells in the tissue does not vary over time," explains co-senior author Angela Oliveira Pisco, Associate Director of Bioinformatics at the Chan Zuckerberg Biohub, San Francisco, US. "The identification of many shared aging genes suggests that there is a coordinated global aging behavior in mice."

The team then used this coordinated activity to develop a single-cell aging score based on the global aging genes. This new high-resolution aging score revealed that different tissue-cell types in the same animal can have a different aging status, shedding light on the diverse aging process across different types of cells.

"Taken together, our results provide a characterisation of aging genes across a wide range of tissue-cell types in the mouse," concludes senior author James Zou, Assistant Professor of

Biomedical Data Science at Stanford University, Stanford, US, and a Chan Zuckerberg Biohub Investigator. "In addition to providing new biological insights on the aging process, this work serves as a comprehensive reference for researchers working in related fields."

**More information:** Martin Jinye Zhang et al, Mouse aging cell atlas analysis reveals global and cell type specific aging signatures, *eLife* (2021). DOI: 10.7554/eLife.62293

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