

Age-associated molecular patterns in the elderly are tissue-specific

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Abstract

RNA landscape has dynamically changed with age and substantial changes are associated with aging. Age-associated trends of RNA expression profiles could provide an objective description of physiological aging process and molecular signatures of aging could be extracted. Unravelling patterns of age-associated changes could help understanding the process of aging. A new statistical method has been developed to extract age-associated patterns from RNA expression profiles of cross sectional studies. With this method technical differences between studies can be overcome, and thus tolerating an age-associated comparison between tissues and different biological groups. The age-associated molecular patterns were found to be different between tissues and tissues may age at different rates. Some tissues may be more resistant for age-associated changes compared with other tissues. In some tissues, like blood and kidney cortex, major molecular changes are restrained around mid-seventies, whereas in other tissues, like skeletal muscles and brain cortex, major changes occur first at midlife and secondary during mid-seventies of age. Incorporating this data into a health care program could be beneficial to improve healthy aging and decisions for clinical acts in the elderly.

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Biography

Vered Raz has been graduated from The Weizmann Institute of Science in Israel as a molecular biologist. She followed up post-doc positions at the University of Pennsylvania, USA, and Wageningen University, The NL. Presently she is having a Lecturer position at Leiden

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