

# Age-Associated Molecular Patterns in the Elderly are Tissue-Specific

Vered Raz

Leiden University Medical Center, Netherlands

## 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 University Medical Centre, department of Human Genetics in The Netherlands. Her research is focused on molecular regulation of aging muscles and the role of RNA processing in aging.