Small noncoding RNAs as marker for age-associated memory decline

Aging is associated with a declining cognitive function but the underlying mechanisms are not well understood. So far, most studies were analyzed age-associated memory function in a cross-sectional experimental setting, comparing for example 3 to 18 month old mice. The aim of this project was to identify age-related microRNAs (miRNAs) and to assay age-associated memory function in mice using a longitudinal approach.

To this end we investigated blood miRNAome of mice at 12, 13.5 and 15 months of age. Another group of animals were subjected to the Morris water maze training. Together with blood miRNA profiling in these animals (at the same time points), spatial memory at 13.5 and 15 month of age was analyzed as well. We could detect many miRNAs with changed transcripts levels along with aging, and also several miRNAs in animals with cognitive decline. Placing mice in enriched environment did not result in improved spatial memory, possibly because of age of animals at the start point of experiment. Nevertheless, we observed some miRNAs uniquely deregulated in mice from enriched environment. Based on our data we hypothesize that age-associated memory decline is mechanistically linked to altered expression of microRNAs and that such changes are – at least in part – also reflected in blood. Further analysis of miRNAome from blood and short-and long-term memory related brain subregions in mouse at later age would help to elucidate the link between the levels of miRNAs and age-related cognitive functions.

Keywords topic: small noncoding RNAs, aging, memory, and biomarkers