Age-dependent regulation of tumor-related microRNAs in the brain of the annual fish *Nothobranchius furzeri*.

Baumgart M, Groth M, Priebe S, Appelt J, Guthke R, Platzer M, Cellerino A (2012) Age-dependent regulation of tumor-related microRNAs in the brain of the annual fish *Nothobranchius furzeri*. *Mech Ageing Dev* 133(5), 226-233.

Details

PubMed

Abstract

MicroRNAs are regulators of gene expression. We used miRNA-seq by the Illumina platform to quantify and compare the temporal miRNA expression profiles in the brain of a short-lived (GRZ) and a longer-lived strain (MZM) of the annual fish Nothobranchius furzeri. We used fuzzy-c-means clustering to group miRNAs with similar profiles. In MZM, we found tumor suppressors with known negative interactions with MYC and/or positive interactions with TP53 among up-regulated miRNAs (e.g. miR-23a, miR-26a/b, miR-29a/b and miR-101a) in aged animals. Conversely, we found oncogenes which are MYC targets among down-regulated miRNAs (miR-7a, members of miR cluster 17~92). These latter were previously shown to be regulated in human replicative aging. In addition, three regulated miRNAs (miR-181c, miR-29a and miR-338) are known to be age-regulated and to globally contribute to regulation of their targets in the human brain. Therefore, there appears to be a degree of evolutionarily conservation in age-dependent miRNA expression between humans and N. furzeri. GRZ showed specific regulation of some miRNAs, notably a marked up-regulation of miR-124, a miRNA important for neuronal differentiation. The two strains

differ in their miRNA expression profiles already at sexual maturity. Short lifespan in GRZ could therefore be--at least partially--due to dysregulated miRNA expression.

Beteiligte Forschungseinheiten

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RNA-Seq Datenanalyse und Modellierung

Identifier

doi: 10.1016/j.mad.2012.03.015

PMID: 22487494