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Investigation of the microRNA expression dynamics in the retina of rats during aging and the development of retinopathy similar to age-related macular degeneration

Shklyar A.[1]*, Kozhevnikova O.[2]

[1] *Novosibirsk State University, Novosibirsk, Russia*

[2] *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

** Shklyaraa@bionet.nsc.ru*

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Motivation and Aim: Age-related macular degeneration (AMD) is a leading cause of blindness worldwide affecting individuals over the age of 50. MicroRNAs are a class of single-stranded, non-coding RNAs, about 22 nucleotides in length, which negatively regulate gene expression at the post-transcriptional level. MicroRNAs are dysregulated in AMD and may facilitate the early detection of the disease and monitoring disease progression. However there is practically no information about the patterns of microRNA expression in the retina at different stages of AMD development. The confirmed AMD model is OXYS rats, which develop retinopathy, corresponding to AMD in clinical, morphological and ultrastructural manifestations. The aim of the study was to evaluate the microRNA level dynamics (miR-9a, miR-16, miR-27, miR-34a, miR-146, miR-155, miR-320) in the retina of Wistar rats (control) with age and OXYS rats during the development of AMD- like retinopathy at preclinical (20 days), early (6 months), and advanced (12 and 18 months) stages of disease.

Methods: The data for analysis were obtained from retina samples using the method of microRNA reverse transcription and Taqman qPCR (Applied Biosystems). Relative fold gene expression changes were calculated by the $2^{-\Delta\Delta Ct}$ method.

Results: We showed that the expression of miR-27a was elevated with age in the OXYS rats. The levels of miR-27 at the age of 12 and 18 months were considerably higher than at the age of 21 days ($p = 0{,}0007$ and $p = 0{,}007$ accordingly). No significant associations with age or strain were found with miR-9, miR-34a, miR-146a, miR-155a and miR-320a. Given that miR-27a could promote choroidal neovascularization and activate WNT signaling pathway, our data suggest a possible contribution of miR-27 to the development of retinopathy in OXYS rats.

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