

microRNA dysregulation in neurodegenerative diseases: A systematic review

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While the root causes for individual neurodegenerative diseases are distinct, many shared pathological features and mechanisms contribute to neurodegeneration across diseases.

Altered levels of microRNAs, small non-coding RNAs involved in post transcriptional regulation of gene expression, are reported for numerous neurodegenerative diseases.

Yet, comparison between diseases to uncover commonly dysregulated microRNAs during neurodegeneration in general is lagging. We performed a systematic review of peer-reviewed publications describing differential microRNA expression in neurodegenerative diseases and related animal models.

We compiled the results from studies covering the prevalent neurodegenerative diseases in the literature: Alzheimer's disease, amyotrophic lateral sclerosis, age-related macular degeneration, ataxia, dementia, myotonic dystrophy, epilepsy, glaucoma, Huntington's disease, multiple sclerosis, Parkinson's disease, and prion disorders. MicroRNAs which were dysregulated most often in these diseases and their models included miR-9-5p, miR-21-5p, the miR-29 family, miR-132-3p, miR-124-3p, miR-146a-5p, miR-155-5p, and miR-223-3p. Common pathways targeted by these predominant miRNAs were identified and revealed great functional overlap across diseases.

We also identified a strong role for each microRNA in both the neural and immune components of diseases. microRNAs regulate broad networks of genes and identifying microRNAs commonly dysregulated across

neurodegenerative diseases could cultivate novel hypotheses related to common molecular mechanisms underlying neurodegeneration.

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