

The role of m6A RNA-methylation in linking histone-modifications and mRNA translation in brain disease and cognitive function

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An universal finding across species is that the formation of memories requires differential gene-expression in brain cells. The activation and inactivation of particular genes in response to specific stimuli is a tightly controlled process and its deregulation contributes to neurodegenerative and neuropsychiatric diseases. "Epigenetic processes" play a key role in the orchestration of these gene-expression dynamics and have been linked to brain diseases. One key epigenetic processes is linked to alterations that regulate the 3D structure of DNA and thereby define if a particular region of the genome is accessible for activation or not. However, to execute their cellular function, genes not only need to be transcribed but the corresponding messenger RNAs of coding genes have to be translated into proteins. So far, little is known if and how the regulation of these two processes of epigenetic gene-expression and protein translation are coupled. Based on preliminary data, the applicants hypothesize that another process, namely the methylation of messenger RNAs which is described as "epi-transcriptomics", may close this gap and provide a link between gene-expression dynamics and protein production in neurodegenerative diseases.

Projektbeteiligte

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