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The art of onconeuroepitranscriptomics

Dito Anurogo*[1,2]

[1]International PhD Program for Cell Therapy and Regeneration Medicine (IPCTRM), College of Medicine, Taipei Medical University (TMU), Taiwan

[2]Faculty of Medicine and Health Sciences, Universitas Muhammadiyah Makassar, Indonesia

EDITORIAL

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***Corresponding author:**
dito.anurogo@med.unismuh.ac.id

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Onconeuroepitranscriptomics (ONE) discusses epitranscriptomics enriched with the paradigms of neuroscience, neurology, and oncology. The deep observation of RNA modifications, epitranscriptomics, has evolved into an in-depth study of the arrangement of gene interpretation.[1] Transformational modification of the RNA pathway has been identified in various brain physiology and various diseases, including cancers.[2] MicroRNAs (miRNAs) are non-coding RNAs that manage gene expression at the post-transcriptional level via translational repression and mRNA degradation.[3]

The biological function of some of the most basic mRNA modifications is unknown.[4] However, advanced technologies such as nanopore (Oxford Nanopore) and nanowell (SMRT) sequencing can be used for resolution-based detection.[5] Exact experimental design and replication, combined with inclusion control, are critical for achieving the highest level of confidence and avoiding false-positive results.[6]

According to the postulates of epigenetics, various views hold that histone modifications and DNA methylation are connected by the “writer” of enzymes, recruiting the “reader” of proteins, and are abolished by the “eraser” of enzymes.[7] The ONE viewpoint demonstrates that the elemental landscapes of RNA in epitranscriptomic alterations recommend that "erasers" and "readers" may not be essential to several modifications.[8] "Writer" enzymes have been demonstrated to be effective for assorted types of RNA modification.[9,10] The proteins m5C and m6A were designated as "reader" proteins. Some RNA modifications have a direct effect on RNA structure and/or base pairs and thus do not necessitate the use of a "reader" protein.[11] The process of modifying the RNA molecule has the potential to eliminate m6A.[12] Most of epitranscriptomic adjustment are not dynamic.[13] The methylation process of m6A RNA, which is a pioneer in neuroscience, can provide a multifaceted understanding of the improvement of the nervous system, neurological diseases and disorders.[14,15]

Several studies have confirmed that FTO (fat mass and obesity-associated, an m6A demethylase) is one of the major demethylases in m6A methylation, is plentiful in the brain and governs dopaminergic pathways and neurogenesis in adults.[16-18] The half-life of most eukaryotic RNAs is extremely short. Accordingly, convinced "erase" enzymes may enhance out-of-date, pricipally during epitranscriptomic modifications that can be comprehended through RNA molecule modification.[19] Because degenerating modifications are not advantageous to the cell, the process of epitranscriptomic modifications in various RNA molecules that are more stable, such as rRNAs, can be deficient in various "eraser" enzymes.[20-22] In cancer, especially in hepatocellular carcinoma, For miR-126, the prominence of m6A in miRNA advancement was first recommended.[23,24]

METTL3 is linked to hippocampal memory function. FTO performs a variety of pathophysiological functions in brain tissue.[25] Another valuable m6A RNA methyltransferase, METTL14, is involved in learning epitopes as well as transcriptional regulatory processes in the striatum.[26-27] m6A RNA methylation is

critical in cerebellar development.[28,29] Modification process of METTL14-dependent m6A is requisite for its refinement by the Microprocessor complex.[30] Adjustment of miR-126 by METTL-14 is very paramount to avert cell invasion.[31] In various malignancies, such as: colorectal, lung, bladder, gallbladder, and ovarian cancer advances the refinement of multioncomirs, i.e.: miR-143, miRNA-92, miR-1246, miR-221/222, and miR-126. They are targeting tumor suppressors. Moreover, the m6A-dependent accretion of miRNAs outcomes in tumor progression.[32,33] MiRNAs' ability to suppress target mRNA translation is reduced by m6A modification.[12] The m6A levels on let-7a-5p and miR-17-5p elevated in pancreatic and CRC tissues without affecting miRNA expression.[34]

RNA modifications are involved in a variety of neuronal mechanisms.[35] Different RNA modifications of tRNAs, small RNAs, and mRNAs are enforced for trivial biological mechanisms such as neuronal differentiation, brain development, and individual neuronal function.[36,37] Several modified RNA molecules and related complexes that regulate and "read" various RNA modifications are critical in controlling the function and development of multiorganism nervous systems.[38,39] Mutations in several human genes that modify transfer RNA are linked to neurological disorders, particularly intellectual disability (tRNA). In the absence of RNA modification, the stability of tRNA changes.[40] As a result, translational efficiency is reduced and tRNA fragments form, potentially impairing neuronal function.[41,42] As a presumed 2′-O-methyluridine methyltransferase, TRMT44 is estimated to methylate tRNASer residue 44.[43] Mutations in this gene were found to be the cause of incomplete epilepsy with pericentral spikes (PEPS), a new mendelian idiopathic epilepsy.[44]

PiRNA and siRNA are destabilized in the truancy of Hen1/Pimet, and sncRNA silencing activities are compromised.[45] Notably, under normal laboratory conditions, Hen1mutant flies do not show increased lethality or sterility, but do show increased memory delinquency, brain vacuolization, neurodegeneration, and an abridged generation.[46] This suggests that small RNA and Nm pathways may protect opposite to neurodegenerative occurences.[47] The union of RNA alterations with miscellaneous nervous system diseases and disorders proves the concern of this chemical for brain advancement and cognition.[48] The function of RNA modification in this process is not fully comprehended. The challenge is that scientists need to identify the class and existence of RNA that is directed by RNA-modifying enzymes and is the cause of neurological shortages.[49]

Neurons face different challenges about RNA localization to distal processes and local translation, most likely occurring in the brain, is the combined effect of RNA modification in each of the different RNA classes that represent the fundamental information layer that dynamically fine-tunes gene regulation.[50] Futuristic research has the opportunity to decipher this complex onconeuroepitransscriptomics code.

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