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TRANSCRIPTOMIC ANALYSIS OF THE SUBICULUM REGION OF THE HIPPOCAMPUS IN ANIMALS WITH TEMPORAL LOBE EPILEPSY (ELTM) INDUCED BY PILOCARPINE

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Abstract

Mesial temporal lobe epilepsy (MTLE) is the most frequent type of epilepsy in adults and it is usually refractory to clinical treatments. In most patients with MTLE a characteristic histopathological lesion is observed, including hippocampal sclerosis (HS). The subiculum is an important area which connects the hippocampus with the enthorrinal cortex. In this study aims to understand the molecular role of the subiculum in MTLE in the classical model of pilocarpine using RNA-seq (RNA sequencing).

Key words:
Epilepsy, Subiculum, Transcriptomic

Introduction

Epilepsy is a neurological disorder characterized predominantly by spontaneous and recurrent seizures.
In the histopathological aspect the most frequent feature is hippocampal sclerosis (HS), which basically is characterized by the loss of pyramidal neurons in CA1 and CA3 regions [1]. The hippocampus is a structure localized in the mesial temporal lobe and its function is related with memory formation and emotional control. The subiculum forms the transition that connects the hippocampus with the enthorrinal cortex [2], which allows for high amplification and modulation of the neuronal response, and it is involved in the recovered short-term memory [3] and spatial memory codification [4]. In this study we used molecular biology technique, RNA-seq, to understand the molecular role in epileptogenic process of Mesial temporal lobe epilepsy (MTLE) though differential expressed genes in dorsal subiculum region.

Results and Discussion

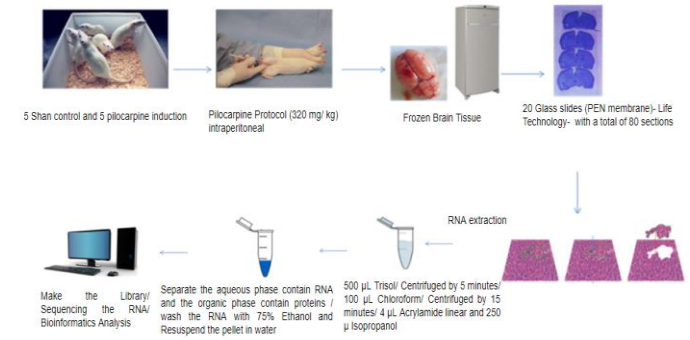

Image1. Methodology.

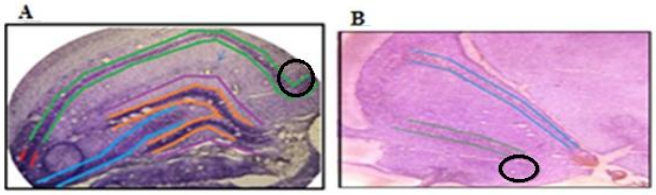

Image2. A Hippocampus from control Sham. Green coloring indicates sub-region CA1, red coloring indicates sub region CA2, blue coloring indicates sub region CA3, orange coloring indicates the granular layer of the dentate gyrus and purple indicates the molecular layer of the dentate gyrus. Circulated areas in black indicates the dorsal subiculum region. B Control sham hippocampus marked to the same colors, and circulated in black is the ventral subiculum region.

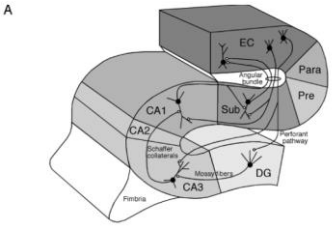

Image3. Figure adapted from The Hippocampus Book (Andersen et al., 2006). A, circuits of hippocampal formation. The neurons from layer II of entorhinall cortex project to dentate gyrus and then from dentate gyrus to CA3. Neurons in layer III of entorhinal cortex project to CA1 and then from CA1 to subiculum. The granule cells of dentate gyrus project to CA3, the pyramidal cells of CA3 project to CA1, the pyramidal cells of CA1 project to subiculum and neurons of subiculum project back to entorhinal cortex.

Pathways Enrichment	Altered genes	FDR	Genes expression
Ubiquinone Metabolism	NDUFA2, NDUFA4, NDUFA5, NDUFA8, NDUFB3, NDUFB5, NDUFC2, NDUFS2, NDUFS3, NDUFS8, NDUFV2	6,077e-12	Downregulated
Translation Initiation	Eif-6, NOLA-3, LAMR1, RP40, RPL24, RPL27, RPL37-A, RPL4, RPL41, RPLP1, RPS11, RPS15, RPS21, RPS25, RPS29, RPS3, RPS7	2,520e-11	Downregulated
Ubiquitin Proteolysis	HSP70, PSMA2, PSMA7, PSMB1, PSMB2, PSMB4, PSMB6, UEV1A	5,801e-3	Downregulated

Tab1. Dorsal subiculum pathways enrichment, altered genes, FDR for each pathway enrichment and genes expression.

Conclusions

This study allows observing differential expression pathways from control and pilocarpine samples in dorsal subiculum region, showing possible risk genes in protein metabolism pathways. Therefore, through this present study, we are able to understand the role of subiculum in epileptogenic process.

Acknowledgement

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