Transcriptomic analysis of dorsal and ventral subiculum regions in Wistar rat

B. B. Aoyama[1],G.G Zanetti[1], E.V. Dias[1], A. S. Vieira[1]

[1]Department of Structural and Functional Biology, Institute of Biology; University of Campinas (UNICAMP); and the Brazilian Institute of Neuroscience and Neurotechnology (BRAINN), Campinas, SP, BRAZIL.

Introduction: The subiculum connects the hippocampus (CA1) to the entorhinal cortex (EC), it allows high amplification of neuronal response, short-term memory, and spatial memory codification. The subiculum region is anatomically divided into dorsal (dSub) and ventral (vSub) regions, which have different characteristics associated with its functions and morphology. The dorsal subiculum processes information of space, movement, and declarative memory, and its neurons project outputs to the mammillary nucleus and presubiculum, receiving projection from dorsal CA1 neurons and layer III dorsolateral entorhinal cortex neurons. The ventral subiculum is associated with stress modulation through inhibitory projections for the hypothalamic limbic system. Its neurons project outputs to the medial hypothalamus, amygdaloid complex, and parasubiculum, receiving inputs from the ventral CA1 and the entorhinal cortex layer III neurons. The aim of this study is to investigate the transcription profile and molecular mechanisms in the dorsal (dSub) and ventral (vSub) subiculum.

Methodology: The brains from *Wistar* rats (CEUA 3850-1 protocol) were submitted to laser-microdissection (LCM), and the dorsal (dSub) and ventral (vSub) subiculum regions were isolated. The dSub and vSub samples were submitted to RNA-sequencing in a Hiseq 4000 platform. The alignment was performed by STAR package and the statistical analysis was performed by DESEq2 package to estimate gene expression in both regions.

Results: We identified 4670 differentially expressed genes in dSub compared to vSub, 2496 genes were upregulated and 2172 genes were downregulated. The gene ontology was performed by clusterProfiler package and our analysis identified a total of 128 enriched pathways, in which 42 enriched pathways were found considering down-regulated genes and 86 enriched pathways considering up-regulated genes.

Conclusion: Our results suggest an extensive difference in the molecular profile of the dorsal and ventral subiculum in rats.