Emerging roles for long noncoding RNAs in Down syndrome hippocampus

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Down syndrome (DS) is the most common genetic cause of intellectual disability. Even though great advances in the last decades have allowed better delineation of its pathogenetic mechanisms, its cellular and molecular bases are still poorly understood. Particularly, the contribution of epigenetic mechanisms to the disordered gene expression in DS remains largely unexplored, mainly due to their high cell-type specificity, which limits their study in bulk analyses. This is the case of long noncoding RNAs (lncRNAs), which show a refined cellular and region specificity. Despite their high abundance in the brain and that specific lncRNAs have been associated to specific brain functions such as learning and memory, the role of the vast majority of them in health and memory related disorders has yet to be described. Here, the single-cell transcriptome of the hippocampus of a DS mouse model, the Ts65Dn, has allowed us to identify specific lncRNAs deregulated in DS. We will discuss their involvement in learning and memory and their contribution to DS-specific neuropathology.

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