Molecular profile of suicide: an bioinformatic approach

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Introduction: Although suicide is a major and emergent public health problem, its pathophysiology is not yet well elucidated. Leveraging advanced bioinformatics tools alongside omics approaches offers novel insights into understanding the pathophysiology of this phenomenon. This study aimed to identify biological processes and pathways associated with suicide using a combination of proteomic and bioinformatics approaches. **Methods:** A systematic review was conducted following the PRISMA Statement 2020 protocol (PROSPERO registration CRD42023397405), utilizing the Embase, PubMed, and Web of Science databases. The review included proteomic studies on brain samples from individuals who died by suicide, published up to March 2023. Bioinformatic analysis of the proteomic data from the selected articles was performed, considering differentially expressed proteins (DEP) as those with FDR ? 0.4 and |LogFC| > 0.06. Each DEP was mapped to its corresponding gene, and the analysis of biological processes and pathways was carried out using the ClueGO plugin (v.2.5.10) of the Cytoscape software. **Results:** The initial search yielded 461 articles. After removing duplicates and analyzing abstracts and full texts, three studies met the eligibility criteria. A total of 442 DEPs were identified, with 410 present in the prefrontal cortex (PFC) and 20 in the amygdala. In the amygdala, biological processes such as structural constituents of the cytoskeleton, protein folding, and processes involving intermediate filaments were prominent. The main biological processes identified in the PFC included anterograde axonal transport, cellular detoxification, pyruvate metabolic processes, negative regulation of metabolic processes, and the generation of precursor metabolites and energy. For the most associated pathways in each tissue, L1CAM interactions, autophagy, and pathways involving Prefoldin and TriC/CCT were observed in the amygdala. In the PFC, pathways related to metabolism, synaptic transmission via chemical synapses, the citric acid cycle, respiratory electron transport, and hemostasis were identified. **Conclusion:** This study highlights the importance of cellular energy systems and effective transport through synapses in the molecular profile of suicide, indicating potential biological processes and pathways that may be underlying suicide phatophysiology. This finding may provide insights to identify suicide ideation and possibly further development of preventive treatments. However, validation of these results in future studies with larger samples is crucial to consolidate the clinical significance of these discoveries and advance suicide prevention strategies.

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