Characterization of Overexpressed Neural-Related Genes Based on Single-Cell mRNA Sequencing Data in Regenerated Intestines of Sea Cucumbers Holothuria glaberrima

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Nervous system disorders, including Alzheimer's and Parkinson's diseases, affected 43% of the global population in 2021 and are rapidly escalating. Projections indicate that by the year 2050, approximately 4.9 billion individuals will be diagnosed with a neurodegenerative disease. This trend results from an evolutionary trade-off in which the development of specialized neural functions came at the expense of regenerative capacity, now limited to just 0.2% in the brain. This study explores the genetic mechanisms underlying gut regeneration in Holothuria glaberrima, a species with exceptional regenerative capabilities. Using data from single-cell mRNA sequencing by Medina et al. (2024), 59 nerve-related genes were identified through FASTA and BLASTp tools, and categorized into 14 functional groups including neurotransmission, cell signaling, and differentiation. The highest level of overexpression was observed in neuroepithelial cells, highlighting their role in regeneration. Sequence alignments between species H. glaberrima and H. sapiens through Uniprot Multi-sequencing alignment techniques revealed up to 76.7% homology, suggesting evolutionary conservation and functional similarities of neuronal-related sequences. Analysis through the UCSC Cell Browser revealed that H. glaberrima’s differential gene expressions (DGEs) share the most remarkable similarity with intermediate neurons in the human intestinal tract, further supporting previous research that emphasizes these neurons as important in the regeneration of this species. These findings confirm that not only pluripotency is needed but also high cellular plasticity, supported by genetic evidence of cellular reprogramming and the expression of genes associated with plasticity.

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