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Impact of Environmental Enrichment and Repeated Mixing on the Porcine Brain Transcriptome

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Environmental factors significantly impact livestock welfare, behaviour, and productivity. Enriched environments can reduce stress and potentially enhance cognitive functions in animals, while repeated mixing can cause chronic stress and alter physiological responses. However, the molecular mechanisms underlying these effects, particularly in the brain, remain largely unexplored. We therefore, investigated the transcriptomic adaptations of key brain regions (hypothalamus, prefrontal cortex, and hippocampus) in pigs subjected to environmental enrichment and different levels of allostatic load induced by repeated mixing. Using bulk RNA sequencing, we analysed brain transcriptomes across 48 pigs assigned to enriched or barren environments with either repeated or minimal mixing. We applied differential expression analysis and Weighted Gene Co-expression Network Analysis (WGCNA) to identify hub genes and pathways within each tissue. Our result show that, while environmental enrichment had limited impact on brain transcriptomes, repeated mixing influenced gene expression in the hippocampus, revealing 38 differentially expressed genes linked to neuronal function, hormone regulation, and immune responses. WGCNA identified distinct co-expression modules across different brain regions, with the hippocampus showing the strongest response to allostatic load. Our findings provide novel insights into the molecular mechanisms by which environmental enrichment and allostatic load influence the brain transcriptome in pigs. Understanding these transcriptomic changes is crucial for improving livestock welfare in farming systems.