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Convergent Transcriptomic Signatures: Identifying ASD Genetic Pathways Through Integrated Blood and Neural Developmental Analysis

Autism Spectrum Disorder (ASD) affects 1 in 54 children in the United States, with substantial evidence supporting a genetic basis; however, connecting developmental genetic alterations with persistent peripheral biomarkers remains a significant challenge. Our research employs a dual-platform approach combining RNA sequencing of peripheral blood samples from ASD individuals and neurotypical controls and meta-analysis of published iPSC-derived and peripheral blood transcriptomics. For biomarker discovery, we implement high-throughput RNA sequencing followed by qPCR validation in independent cohorts, while our developmental transcriptomic analysis utilizes a bioinformatics pipeline with stringent quality control measures including FASTQC/MultiQC assessment, STAR alignment, and feature Counts quantification. Published data indicate significant dysregulation in several gene categories: synaptic function genes (SYN1, PSD95, SYP, NR2B) affecting neurotransmission; cell adhesion molecules (PCDHA1, PCDHHA6, CNTN3) disrupting neural connectivity; ion channels and receptors (CACNA2D3, SCN9A, GRIK2) altering neuronal excitability; and neural development genes (ERBB4, NTNG1, TSHZ3) influencing critical neurodevelopmental processes. By pairing "big data" analytic approaches with ongoing clinical programs, our research program has potential to advance our understanding of molecular pathways associated with developmental alterations, which may facilitate earlier ASD diagnosis and reveal novel therapeutic targets.