

An Integrative Analysis of Kinomic and Proteomic Profiling in Chronic Mild Stress Mice

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Objectives: Major Depressive Disorder (MDD) is a severe mental health condition characterized by the DSM-5 as persistent feelings of sadness, hopelessness, and a lack of interest or pleasure in daily activities. In this study, we focus on modeling MDD in mice through Chronic Mild Stress (CMS), a well-established paradigm that mimics the chronic stressors contributing to the development and exacerbation of depressive symptoms. Kinomics, the study of protein kinases and their signaling pathways, and proteomics, the comprehensive analysis of proteins expressed in a biological system, offer a holistic perspective on the molecular alterations associated with MDD. By combining these two high-throughput techniques, we aim to unravel the intricate molecular landscape underlying depressive phenotypes induced by chronic stress.

Methods: We induced Chronic Mild Stress (CMS) in a mouse model to mimic Major Depressive Disorder (MDD) and collected brain tissue samples for analysis. Bioinformatic tools were employed to interpret the functional significance of differentially expressed proteins and identify kinase targets. The integrative analysis of kinomic and proteomic data unveiled intricate molecular changes associated with CMS-induced depressive phenotypes.

Results: Proteomic analysis revealed significant changes in protein expression patterns, indicating a broad impact on cellular processes in response to the experimental conditions. Kinomic profiling identified alterations in kinase activity, suggesting potential modulation of signaling pathways. Integrative analysis and the observed overlap between proteomic and kinomic changes hinted at complex regulatory networks affected by the experimental manipulations.

Conclusions: In summary, our study employing a mouse model subjected to Chronic Mild Stress (CMS) successfully illuminated significant alterations in protein expression and kinase activity, providing valuable insights into the molecular landscape associated with Major Depressive Disorder (MDD). The integrative analysis of kinomic and proteomic data unveiled intricate regulatory networks, underscoring the complexity of molecular changes induced by chronic stress and offering potential avenues for understanding and addressing depressive phenotypes.