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Proteomics in plasma of ovariectomized rats and those exposed to estradiol valerate

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?Context?The menopausal period, an inevitable physiological process for women, is frequently associated with physiological and psychological dysfunction attributable to substantial fluctuation and gradual decrease in female hormones induced by ovarian failure, leading to corresponding symptoms and diseases that impact multiple systems in the body to varying degrees.
?Object?To approach menopausal disease incidence risk and pathogenesis through systemic plasma proteomics analysis.
?Methods?Female Sprague-Dawley rats were randomly divided into sham, ovariectomized, and estrogen treatment after ovariectomy group. Tandem Mass Tag quantitative proteomics analysis of their plasma identified over 900 proteins by MS.
?Results?Between group fold change of >1.2 and $p < 0.05$ (Student's t test) identified 121 (including 36 up-regulated and 85 down-regulated), 117 (69 up-regulated and 48 down-regulated), and 109 (41 up-regulated and 68 down-regulated) differentially expressed proteins between groups, respectively. Of these, 5(GHR, LIFR, apoA IV, RTN, and Lin28b) were verified by parallel reaction monitoring to be reliable. Further application of optimized screening criteria and performance of a series of bioinformatics analyses allowed the selection of 35 optimal differentially expressed proteins.
?Main Outcome Measures?Gene ontology annotation results suggested that the differentially expressed proteins are mainly annotated as protein binding, cell, and single organism process in terms of molecular function, cell composition, and biological process, respectively. KEGG pathway analysis indicated that the PI3-Akt pathway has the highest aggregation degree of differentially expressed proteins. Protein-protein interaction analysis noted GLUT4 as an important node protein.
?Conclusion?This research is the first to comprehensively analyze plasma protein changes, together with estrogen efficacy, in ovariectomized rats. The findings facilitate our understanding of the molecular mechanism of systemic menopausal changes and provide valuable clues for developing diagnostic biomarkers for menopausal dysfunctions and selecting clinical therapeutic strategies.

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