

Gas Chromatography-Mass Spectrometry (GC-MS) Metabolites Analysis in Endometriosis Patients: A Prospective Observational Translational Study.

Autori: Angioni S, Congiu F, Vitale SG, D'Alterio MN, Noto A, Monni G, Santoru ML, Fanos V, Murgia F, Atzori L

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ABSTRACT

BACKGROUND: Endometriosis affects women of reproductive age, and its pathogenesis is still unclear. Typically, it overlaps other similar medical and surgical conditions, determining a delay in early diagnosis. Metabolomics allows studying metabolic changes in different physiological or pathological states to discover new potential biomarkers. We used the gas chromatography-mass spectrometer (GC-MS) to explore metabolic alterations in endometriosis to better understand its pathophysiology and find new biomarkers.

METHODS: Twenty-two serum samples of patients with symptomatic endometriosis and ten without it were collected and subjected to GC-MS analysis. Multivariate and univariate statistical analyses were performed, followed by pathway analysis.

RESULTS: Partial least squares discriminant analysis was performed to determine the differences between the two groups ($p = 0.003$). Threonic acid, 3-hydroxybutyric acid, and proline increased significantly in endometriosis patients, while alanine and valine decreased. ROC curves were built to test the diagnostic power of metabolites. The pathway analysis identified the synthesis and degradation of ketone bodies and the biosynthesis of phenylalanine, tyrosine, and tryptophan as the most altered pathways.

CONCLUSIONS: The metabolomic approach identifies metabolic alterations in women with endometriosis. These findings may improve our understanding of the pathophysiological mechanisms of disease and the discovery of new biomarkers.