Schizophrenia, characterized by hallucinations, delusions, inappropriate affects and bizarre or inappropriate behavior, is a chronic, disabling, and potentially life-threatening neuropsychiatric disorder which affects approximately 1% of the population. The etiology of schizophrenia remains unknown and involves both genetic and environmental factors. In this study we employed a label free quantitative mass spectrometry-based approach to analyze the metabolic and proteomic profiles of CSF and sera samples from first-onset, drug-naïve paranoid schizophrenia patients and healthy controls. Parallel least squares discriminant analysis showed a significant separation of first-onset, drug-naïve schizophrenia patients away from healthy controls in both metabolic and proteomic studies.

The results showed a significant separation of the two groups, with many of the identified metabolites and proteins being specific to the schizophrenia group. The metabolic profile showed a decrease in the levels of certain metabolic pathways, such as the tryptophan and tyrosine metabolism pathways, which are known to be disrupted in schizophrenia. The proteomic profile identified a number of proteins that are known to be associated with the disease, such as the complement factor C3, which is involved in the immune response, and apolipoprotein A-I, which is involved in lipid metabolism.

Partial least squares discriminant analysis showed a significant separation of the two groups. The results were confirmed by exact mass MS/MS, which confirmed the identity of the potential biomarkers. The metabolic and proteomic profiles were further analyzed using SIMCA-P, and the potential biomarkers were identified. The results showed a significant separation of the two groups, with many of the identified metabolites and proteins being specific to the schizophrenia group. The metabolic profile showed a decrease in the levels of certain metabolic pathways, such as the tryptophan and tyrosine metabolism pathways, which are known to be disrupted in schizophrenia. The proteomic profile identified a number of proteins that are known to be associated with the disease, such as the complement factor C3, which is involved in the immune response, and apolipoprotein A-I, which is involved in lipid metabolism.

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