Is Inflammation the Major Driver of Polycystic Ovary Syndrome (PCOS)? A Proteomic Approach to Understanding PCOS in Adolescents and the Search for Novel Non-Invasive Biomarkers

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INTRODUCTION + AIM

PCOS is common and associated with significant comorbidity. However, its pathogenesis is complex and poorly understood, particularly during adolescence. We have developed new methods for deep phenotyping discovery proteomic profiling of urine in PCOS in adolescents.

METHOD

We present the baseline proteomic data from a subset of n=15 samples from our prospective, longitudinal PCOS study (total cohort n=232). We undertook proteomic analysis (nanoLC-MS/MS).

RESULTS

We performed multivariate SIMCA® analyses on all proteins to identify cohort-level differences in the proteomes. OPLS-DA analysis showed distinct clustering within, and separation between all cohorts (fig. 3), indicating quantifiable differences between the proteome of all three cohorts (PCOS vs. controls, IR), but similarities within them.

Gene Ontology Analysis

• Gene ontology (GO) is the study of the function of genes and their proteins. We undertook GO analysis of all consensual DEPs to better understand their function in PCOS and wider biological processes.

• These 66 consensual proteins are involved in the processes shown below in figure 4. A significant number of these proteins were identified as mediators of inflammatory and immune pathways.

BIBLIOGRAPHY


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