Amniotic fluid metabolomic profile in cases of twin-to-twin transfusion syndrome

University Hospital La Paz, Madrid, Spain

Objective

TTTS is associated with significant fetal and perinatal short and long-term adverse outcomes. We apply high-throughput amniotic fluid (AF) metabolomics analysis for better understanding of the pathophysiology of TTTS and aim to provide meaningful information about new potential biomarkers.

Methods

AF samples were collected from pregnant women with (n = 12) or without TTTS (n = 4). Detailed clinical information on each pregnancy was obtained from obstetrical and neonatal medical examination. Liquid chromatography/mass spectrometry (LC-QTOF-MS; Agilent 6550), followed by data alignment and filtration were performed. Univariate and multivariate statistical analysis were used to analyse the data. Identification of metabolites was performed by searching for possible identity of accurate masses in several databases including CEU Mass Mediator database and by final confirmation according to LC-MS/MS analysis.

Results

Multivariate analysis showed clear separation of the control and TTTS group with good quality of the variance explained and variance predicted. Statistically significant differences were found in 8 masses in positive and 5 in negative ionization mode between women with and without TTTS. The compounds identified included vitamin B6, uric acid, oxaloacetic acid, dihydroxy-pregnane glucuronide, lysoglycerophosphocepholipids sphingosine, and amides.

Conclusion

High-throughput LC/MS based metabolomics fingerprinting of AF enables in-depth study of molecular changes, altered metabolic pathways and gives a unique opportunity to identify potential new biomarkers in TTTS.