

EP12.19 *Amniotic fluid Proteomic alterations in Recipient twins with Twin-Twin Transfusion Syndrome.*

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Introduction

Twin-to-twin transfusion syndrome (TTTS) is a severe complication of monochorionic twin pregnancies caused by unbalanced placental vascular anastomoses. However, the molecular mechanisms underlying its pathophysiology remain incompletely understood. This study aimed to characterize proteomic alterations in the amniotic fluid of recipient twins with TTTS.

Methods

Amniotic fluid samples were obtained from recipient twins with TTTS at 16–18 weeks of gestation during fetoscopic laser surgery. Amniotic fluid from singleton pregnancies undergoing amniocentesis for fetal karyotyping served as controls. Proteomic profiling was performed using liquid chromatography–tandem mass spectrometry (LC–MS/MS), and differential protein expression between groups was analysed.

Results

Amniotic fluid samples from five recipient twins with TTTS and six singleton controls were analyzed. A total of 1,747 proteins were identified.

Among these, 51 proteins were upregulated more than 16-fold in TTTS recipient twins compared with controls, whereas 140 proteins were downregulated to less than one-sixteenth of control levels. Thrombospondin-4 (TSP-4) showed the most prominent increase in expression, while calcium and integrin-binding protein 1 (CIB1) demonstrated markedly decreased expression. These proteins are associated with extracellular matrix regulation and angiogenic signalling pathways.

Conclusion

Altered expression of proteins involved in extracellular matrix remodelling and vascular signalling may reflect underlying vascular and placental pathophysiology in TTTS. Comprehensive proteomic profiling of amniotic fluid may therefore provide novel insights into disease mechanisms and facilitate the identification of candidate biomarkers for TTTS.

