Background

- Placenta accreta spectrum (PAS) is associated with severe obstetric morbidity with an increasing incidence of 1 in 300 in the United States.
- The cellular heterogeneity and function at the maternal-fetal interface of PAS is unknown.

Objective

- To utilize advances in single-cell RNA-sequencing to characterize the transcriptomic signature of PAS.

Study Design

- UCLA IRB #13-001254-CR-00008
- Comparison of 3 groups: site of placental invasion (AI) vs. site of normal placentation (AO) in PAS placentas vs. controls (C)
- Chromium 10x genomics 3’ Single Cell Gene Platform with Illumina NovaSeq S2
- R package Seurat (v 3.1.2) for analysis
- Enrichment analysis using gene ontology

Results

- Analysis of 31,406 cells identified trophoblasts, stromal (endothelial and fibroblasts), myeloid, and lymphoid cell populations across 8 samples from AI (3), AO (2), and C (3).
- DLK1, EGFL6, and COL3A1 were differentially expressed in AI compared to AO and C.
- Stromal cells demonstrated specific upregulation of DLK1, EGFL6, APOLD1, and AGTR1.
- Pathways upregulated in AI included Syndecan 1 (syncytiotrophoblasts) and PI3K-Akt (stromal and extra villous trophoblasts).

Conclusion

- Transcriptomic analysis of PAS identified differential expression of genes involved in endothelial signaling, extracellular matrix, and inflammation.
- Stromal cells likely contribute to a post-cesarean environment permissive for future accreta.

Questions?

Take a picture of this QR code to access the UCLA MFM website or email Dr. Yin at oyin@mednet.ucla.edu