Background: The human microbiota has emerged as an unexpected modulator of the immune system. The placenta, long thought to be sterile, harbors a unique microbiome and variations in their composition could be related to prevent pregnancy disorders.

Objective and hypotheses: To profile the placental microbiota (microorganisms) and microbiome (group of microbial genomes in an environment) in women with gestational diabetes (GDM) and study their relation to maternal metabolism and placental expression of anti-inflammatory cytokines.

Methods: Placental microbiota and microbiome and expression of anti-inflammatory cytokines (IL10, TIMP3, ITGAX and MRC1MR) were analysed in placenta from women with GDM (n=11) and from control women (n=11; all samples were obtained under sterile conditions). Fasting insulin, pre- and post-load glucose, lipids and white blood cell counts were assessed at 2nd and 3rd trimester of pregnancy.

Results: Bacteria belonging to the Acinetobacter genus and Pseudomonadales order showed lower relative abundance in women with GDM compared to control (p<0.05). In GDM women, lower abundance of placental Acinetobacter was associated with a more adverse metabolic (higher post-load glucose) and inflammatory phenotype (lower blood eosinophil count and lower placental expression of IL10 and TIMP3) (p<0.05 to p=0.001). In GDM women, placental microbiome showed increased expression of genes involved in calcium signalling (PC1, PC2 and PC3).

Conclusion: Placental microbiota and placental gene expression profiles were different in pregnant women with GDM compared to controls. Pregnant women with GDM showed lower abundance of Acinetobacter and decreased expression of IL-10. GDM could constitute a state of placental microbiota-driven altered immunologic tolerance, making placental microbiota a new target for therapy in GDM.