**Association between the vaginal and uterine microbiota and the risk of early embryonic arrest**

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**Presenter:** Chia-Yu Tu                          **Date/Time:**2023/03/21, 15:10 -16:00

**Commentator:**Prof. Jenn-Wei Chen **Location:** Room 601, Med College Building

**Background:**

Early embryonic arrest, a common complication in early pregnancy, may result in adverse outcomes. Bacterial Vaginosis (BV) is directly linked to this phenomenon. In reproductive-age women, vaginal secretions are predominantly composed of *lactobacilli*, crucial for maintaining microbiota balance. Uterine microbiota, more diverse than the vaginal environment, includes *lactobacilli* like *L. iners*, *Prevotella spp.*, and *L. crispatus*. Imbalances in vaginal and uterine microbiota, associated with various diseases, can impact reproductive health and embryonic development. However, a lack of prospective and retrospective cohort studies hinders understanding these relationships, highlighting the need for research to comprehend specific microbiota changes and their potential impact on early embryonic arrest.

**Objective/Hypothesis:**To identify microbiota differences among women with early embryo arrest and abortion, to improve the microbiota markers related to early embryo arrest.

**Results:**

The study utilizing 16S rRNA gene sequencing analyzed 56 vaginal swab and intrauterine tissue samples to investigate the association between embryonic arrest and normal pregnancy. Vaginal swab samples from the embryonic arrest group exhibited significantly lower alpha diversity, determined by Chao1 index and PD whole-tree metrics, compared to the normal pregnancy group. Principal coordinate analysis revealed marked differences in bacterial composition between the two groups in vaginal samples, contrasting with no significant differences in uterine endometrial specimens. Abundance of *lactobacilli* was higher in the normal pregnancy group for vaginal samples, while *Bacteroides* and *Helicobacter* were more abundant in the embryonic arrest group. Linear discriminant analysis effect size analysis identified distinct microbial communities associated with each group, including a notable decrease in *L. iners* proportion in the embryonic arrest group. Receiver operating characteristic (ROC) curve analysis highlighted *Ensifer* and *Devosia* as having the highest predictive value for embryonic arrest diagnosis. In endometrial data, random forest analysis identified 18 differing genera, with *Eubacterium xylanophilum* exhibiting the highest predictive value according to ROC analysis for six significant markers.

**Conclusion:**

Examining uterine and vaginal microbiota in embryonic arrest versus normal pregnancy reveals key differences, signaling potential pathogenic mechanisms and predictive bacterial markers.