Integrative transcriptomics approach for predicting endometrial receptivity using liquid biopsy

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Venue: Shanta Rao Auditorium

Successful embryo implantation depends on the precise temporal establishment of endometrial receptivity, a transient state defined by dynamic and tightly regulated transcriptional programs. Current clinical approaches for assessing endometrial receptivity rely on invasive endometrial biopsies, limiting their applicability for longitudinal monitoring and routine clinical decision-making. This constraint is particularly relevant for women experiencing recurrent implantation failure (RIF), where repeated, cycle-resolved assessment is often required. There is therefore a critical unmet need for a robust, non-invasive strategy to capture endometrial molecular states with clinical relevance.

This proposal aims to develop and validate cervicovaginal cell-free RNA (cfRNA) profiling as a non-invasive surrogate for endometrial transcriptional activity. Preliminary data demonstrate that endometrium-specific transcription factor RNAs are detectable in vaginal swabs, supporting the feasibility of this approach. We will systematically profile cfRNA obtained from cervical/vaginal lavages in proliferative, pre-receptive, receptive, and post-receptive phases to generate a phase to resolved molecular landscape of endometrial receptivity. High-throughput sequencing of mRNA, miRNA, lncRNA, and circular RNA will be employed to capture both coding and regulatory RNA layers.

By establishing cervicovaginal cfRNA profiling as, non-invasive diagnostic framework, we expect to provide mechanistic insight into implantation failure, enable improved patient stratification, and support personalized timing of embryo transfer. The outcomes have strong translational potential and directly address national priorities in women’s health, non-invasive diagnostics, and precision reproductive medicine.