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Methods, Compositions, and Kits for Assessing Endometrial Transformation

Researchers at Stanford and the Chan Zuckerberg Biohub have developed a transcriptomic characterization of human endometrium and identified specific gene signatures for use in evaluating endometrial samples for one or more menstrual cycle events.

In a human menstrual cycle, the endometrium undergoes remodeling, shedding and regeneration, all of which are driven by substantial gene expression changes. Traditionally, a cycle can be divided into two major phases by the event of ovulation: the proliferative (preovulatory) and the secretory (postovulatory). During the secretory phase, the endometrium enters a narrow window of implantation (WOI) that is both structurally and biochemically ideal for embryo implantation. Remarkably, and given its relevance to human fertility and regenerative biology, our molecular understanding of endometrial transformation has been rudimentary.

Stage of Research
The inventors present a high-resolution molecular and cellular characterization of human endometrial transformation across the natural human menstrual cycle. The authors use single-cell RNA sequencing to study both the static and dynamic aspects of endometrial tissue to provide single-cell transcriptomic delineation of endometrial transformation. Cell-type-specific gene expression analysis, including a previously uncharacterized ciliated epithelial cell type, identified biomarkers that can be used to evaluate, assess, or otherwise probe endometrial samples from a subject to detect one or more menstrual cycle events, such as the WOI.

Stage of Development
Research – in vitro

Applications

- Transcriptomic assessment of various endometrial cells throughout the menstrual cycle
- Practical or clinical application of the identified gene signature panels to detect a particular menstrual cycle event of a subject (e.g., follicular phase, ovulation, luteal phase, or WOI), such as treatment and/or management of patients, including those in need of assisted reproduction

Advantages

- Biological samples can contain multiple endometrial cell types, or cells can be separated before gene signature analysis
- Transcriptomic analysis and biomarker identification was performed in human subjects with no influence from exogenous hormones or gynecologic pathology

Publications

- Wang, W et al. Single-cell transcriptomic atlas of the human endometrium during the menstrual cycle. Nature Medicine 2020.

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