Proposal presentation

Title: Cellular composition and molecular phenotype of the endometrium in endometriosis and adenomyosis: A step toward understanding their pathological similarity or dissimilarity

Date: 13th February 2026

Time: 3 pm

Day: Friday

Mentor: Dr. Geetanjali Sachdeva

Endometriosis and adenomyosis are estrogen-dependent uterine disorders affecting approximately 10% and 1% women of reproductive age globally, respectively. Endometriosis is characterized by ectopic endometrial lesions located outside the uterus, whereas in adenomyosis the lesions develop within the uterine myometrium. Despite distinct lesion location, both disorders share similar clinical symptoms such as dysmenorrhea, and chronic pelvic pain. Notably, women with endometriosis often exhibit concurrent adenomyosis, with 6% prevalence among subfertile women. Substantial evidence indicates that eutopic endometrium in both disorders differs from healthy controls. In endometriosis, eutopic endometrium had higher natural killer T cells and upregulation of the PI3K and focal adhesion pathways. In contrast, adenomyosis is associated with higher macrophage and lymphocyte infiltration, altered inflammatory signaling, platelet aggregation, and elevated estradiol levels. A few studies have compared endometriosis and adenomyosis - one found KRAS mutations in the lesions of both disorders, another reported PI3K pathway enrichment in deep infiltrating endometriosis while RAS pathway in adenomyosis, although tissue source (eutopic or ectopic) was unspecified. The most recent study examining eutopic endometrium identified 115 shared genes altered in both the conditions as compared to the controls. However, no study has yet investigated etiopathogenesis, cellular heterogeneity and cell type and cell state specific transcriptional programmes in eutopic endometrium of endometriosis and adenomyosis using single-cell transcriptomics within the same experimental framework. Although two reviews have highlighted differences between endometriosis and adenomyosis, their findings may be confounded by varying menstrual cycle stages. We hypothesize that eutopic endometrium of adenomyosis, adenomyosis with endometriosis and endometriosis exhibits distinct cellular compositions and disease-specific transcriptional programmes compared to healthy controls.