Abstract

Endometriosis is a systemic gynecological disorder characterized by the growth and establishment of endometrial-like tissue outside the uterus. It affects 5-10% among women of reproductive age and commonly associated with chronic pelvic pain and infertility issue. An impaired immune system has been observed as the main facilitator of ectopic lesion survival and growth following retrograde menstruation cell seeding and hormonal imbalance stimulation. Presentation of endometriosis is highly heterogenous, introducing a complexity to understand the disease pathophysiology and further identify potential therapeutic targets. Here, we use single-cell RNA sequencing (scRNA-seq) approach to delineate immune cell landscape in normal endometrium and endometriosis of human biopsies. Through projection of basic cell markers and differentially expressed genes, cytotoxic CD8+ T cells, tissue-resident NK cells, classical monocytes, and non-classical monocytes clusters were observed in a very high cell numbers in endometriosis compared to normal. They also expressed unique cell phenotypes which mainly function as anti-apoptotic and cell exhaustion responses. Comparing them with the immune cell phenotypes from normal endometrium, these differentially expressed genes may serve as the preliminary study for immunopathophysiology of endometriosis.

*Keywords: endometriosis, immunological dysfunction, single-cell RNA sequencing, differentially expressed genes.*