Gene expression in the endocannabinoid system in the endometrium of women with and without endometriosis

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Introduction – Endocannabinoids (AEA and 2-AG) are endogenous lipid-based ligands found in many organs including the female reproductive system and can influence cellular function. Aberrant expression of the endocannabinoid system has been implicated in the pathogenesis of endometriosis, a disease that affects 10-15% of women of reproductive age impacting on their quality of life with direct and indirect cost for patients and the health economy.

Methods – Endometrial biopsy was taken from women who underwent surgery for suspected endometriosis. Statistical comparison of gene expression of the endocannabinoid system were made between women with and without endometriosis.

Results – The majority of the differences between the two groups involved the synthesising and catabolising enzymes and occurred during the early secretory phase. There was an upregulation of NAPE-PLD, the major synthesising enzyme of AEA, and a downregulation of FAAH, the main degrading enzyme of AEA. There were upregulations of other enzymes involved in AEA synthesis including PLA2, PLD and GDE4 during the secretory phase. Furthermore, there was an upregulation of CB1 receptor in the mid secretory phase.

Discussion – Our results suggest increased synthesis and decreased degradation of AEA as well as increased expression of CB1 during the secretory phase in the endometrium of women with endometriosis compared to controls. This may play a role in the pathogenesis of endometriosis by stimulating endometrial cell migration and proliferation through activation of CB1 receptors. In addition, increased production and decreased degradation of AEA in the early secretory stage may result in excessive production of arachidonic acid which is known to promote inflammation and may explain the pain symptoms experienced by women with endometriosis prior to the onset of menstruation.