48. Transcriptomic analysis of cumulus cells shows altered pathways in patients with

minimal and mild endometriosis

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Abstract

Endometriosis is a chronic inflammatory disorder that is highly associated with infertility.

This association seems to be related to oocyte impairment, mainly in the initial stages of

endometriosis (minimal and mild), where no distortions or adhesions are present.

Nonetheless, invasive oocyte analyses are not routinely feasible; thus, indirect assessment of

oocyte quality is highly desirable, and, in this context, cumulus cells (CCs) may be more

suitable targets of analysis. CCs are crucial in oocyte development and could be used as an

index of oocyte quality. Therefore, this prospective case-control study aimed to shed light on

the infertility mechanisms of endometriosis I/II by analyzing the CCs' mRNA transcription

profile (women with endometriosis I/II, n = 9) compared to controls (women with tubal

abnormalities or male factor, n = 9). The transcriptomic analyses of CCs from patients with

minimal and mild endometriosis revealed 26 differentially expressed genes compared to the

controls. The enrichment analysis evidenced some altered molecular processes: Cytokinecytokine

receptor interactions, Chemokine signaling, TNF signaling, NOD-like receptor

signaling, NF-kappa B signaling, and inflammatory response. With the exception of

CXCL12, all enriched genes were downregulated in CCs from patients with endometriosis.

These findings provide a significant achievement in the field of reproductive biology,

directing future studies to discover biomarkers of oocyte quality in endometriosis.