

P011 Differentially expressed microRNAs and their targets constitute molecular pathways associated with endometriosis
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Endometriosis is a common gynaecological disorder characterised by growth of endometriotic tissue outside the uterine cavity. MicroRNAs (miRNAs) are naturally occurring post-transcriptional regulatory molecules. For the first time, we have assessed miRNA expression with microarray analysis in paired ectopic and eutopic endometrial tissues and identified 14 up-regulated and 8 down-regulated miRNAs. The differential expression of 3 up- and 3 down-regulated miRNAs was confirmed with qRT-PCR. We determined the mRNA transcripts that are predicted targets of the 22 miRNAs *in silico*, and identified these targets among differentially expressed mRNAs in ectopic vs eutopic endometrial tissue, as determined by microarray. Functional analyses using Gene Ontology and Ingenuity Pathway Analysis showed that differentially expressed miRNA targets constitute molecular pathways associated with endometriosis and participate in biological processes characteristic of this disease. Endometriosis associated pathways therefore appear to be regulated at transcriptional level as well as by miRNAs post-transcriptionally. Pairs of differentially expressed transcription factors and miRNAs predicted to target common sets of genes were also identified *in silico*, suggesting fine-tuned regulation of endometriotic pathways. Our results suggest that miRNAs and their targets may contribute to the pathogenesis of endometriosis and that miRNAs potentially provide an alternative therapeutic path in the treatment of this debilitating disease.