# miRNA expression and functional pathways in tubal ectopic implantation

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## Abstract

Expression of 800 miRNAs were compared in embryonic/trophoblast rich tubal tissue sampled from four Fallopian tubes bearing ectopic pregnancy versus tubal mucosal, smooth muscle and serosal layers of four non-pregnant healthy Fallopian tubes in a pilot study involving eight volunteer participants who required laparoscopic surgical management at Royal Hospital for Women, Randwick, Sydney, NSW in. 2013-2016

## Objectives

Clustering of elucidated miRNA transcription factors by function with arranged ranked lists of gene networks was analysed in attempt to elucidate which pathways/physiological processes in the context of tubal ectopic pregnancy might be important in the following scenarios:
1. Non-pregnant intact Fallopian tube (extracellular matrix factors) versus pregnant Fallopian tube (nuclear transcription factor regulation),
2. Maternal tubal mucosal and muscle substrate (blood vessel development) versus fetal (neuronal differentiation) tissue

## Methods

A computational analysis to identify the statistically significant signaling pathways which might be modulated by the key differentially expressed miRNAs in two study groups was performed. DIANA-mirPath v.3 software was used to analyse which gene targets and pathways of the differentially expressed miRNAs found in ectopic tubal samples might be altered. Both 'Pathway analysis' Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology 'GO analysis' were performed in the standard enrichment computation method. The ontology domain of biological process was analysed, and Fisher's exact test was applied. The P-value($P<0.05$) denotes the significance of GO terms enrichment in the DE genes. The lower the P-value ($P<0.05$), the more significant the GO Term. The top-20 Enrichment Score value of the significant enrichment terms were reviewed.

## Results

A number of potentially affected pathways with different genes targeted by the miRNAs was identified, suggesting that the altered expression profile of these miRNAs in ectopic tubal pregnancy may affect biological processes related to cell cycle/tissue proliferation, immunological and inflammatory response. Interestingly, statistically significant KEGG pathways found in group 1 were the allograft rejection and cell adhesion molecules pathways.
Using in silico approach, the main pathways that could be altered in tubal implantation site (group2) were analysed. Among these pathways the ECM-receptor-interaction pathway, the mucin type O-Glycan biosynthesis and signaling pathways regulating pluripotency of stem cells were statistically significant

## Conclusion

Mechanisms driving microRNAome of pregnancy include multitude of factors aggravated by compounding developmental complexity. Altered variations of miRNA expression in ectopic tubal pregnancy modulate signalling pathways during early embryo-maternal crosstalk.

## References

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