Identification of expressional pathways and specific cohort of genes associated with the pathogenesis of endometriosis

**Subject**

**Diagnosis**

Out Patient Departments
Pain clinics followed by Obstetrics and Gynecology

**Selection**

Pelvis Imaging: Ultrasound, MRI, Laparoscopy

**Tissue collection & staging**

Surgical laparoscopy: Staging (rASRM, 1997);
Paired eutopic(A) and ectopic(B) tissue collection

**Classification**

Sample classification based on clinical data:
Fertile with known severity stages and cycle phases

**Methodology**

Sample (A and B) processing

Tissue fixation, paraffin blocking, and histology

Total RNA extraction: Quality check and quantification

Whole genome microarray hybridization and image analysis (n=18, paired)

Cluster analysis to identify co-expressed genes and differential analysis of co-expressed (DC) genes

**Analysis**

Differential expression (DE) analysis:
Effects of tissue location, severity stage and cycle phase

*Post-hoc* functional analysis using gene ontology (GO) pathways & networks and gene set enrichment analysis (GSEA)

**Functional interpretation**

Expression cohort of marker genes

**Prediction analysis**

RT-PCR [28 genes] (n=8, paired)

array validation