Analisis Metilasi DNA Promotor dan Ekspresi mRNA Gen FN1 dan RAC1 sebagai Gen Adhesi Fokal pada Jaringan Endometrium Endometriosis = Analysis of Focal Adhesion Gene FN1 and RAC1 in Endometrial Endometriosis: Focus on Promoter DNA Methylation and mRNA Expression

Irwina Eka Deraya, author

Abstrak

Latar belakang: Telah dilaporkan bahwa terdapat perubahan pada ekspresi dari ribuan gen di jaringan endometrium endometriosis, termasuk diantaranya adalah gen FN1 dan RAC1. Perubahan ekspresi gen tersebut dapat disebabkan oleh mekanisme epigenetik seperti perubahan tingkat metilasi DNA pada gen.
Tujuan: Mengetahui tingkat metilasi DNA pada gen FN1 dan RAC1 serta ekspresi mRNAnya pada jaringan endometrium subjek endometriosis dan nir-endometriosis.
Metode: Penelitian ini merupakan cross sectional dengan jumlah sampel sebanyak 40 dari jaringan endometrium subjek endometriosis dan subjek nir-endometriosis. Sampel diambil dengan teknik mikrokuretase di RSUPN Ciptomangunkusumo dan RS Fatmawati Jakarta. Pada jaringan kemudian dilakukan isolasi DNA dan RNA. Pada isolat DNA dilakukan konversi bisulfit, MSP, elektroforesis dan analisis intensitas pita menggunakan software ImageJ untuk mendapatkan data persentase tingkat metilasi DNA. Pada isolat RNA dilakukan qRT-PCR untuk mendapatkan ekspresi relatif mRNA gen FN1 dan RAC1.
Hasil: Analisis persentase tingkat metilasi DNA promotor menunjukkan terdapat perbedaan bermakna (p=0,022) pada gen FN1 pada pasien endometriosis (37,95%) dibandingkan nir-endometriosis (59,22 %), sedangkan pada gen RAC1 tidak terdapat perbedaan bermakna (p=0,63) dengan tingkat metilasi subjek endometriosis (28.45%) dan subjek nir-endometriosis (26.11%). Penelitian ini juga melaporkan terjadinya peningkatan ekspresi relatif mRNA gen FN1 dan RAC1 dibandingkan dengan subjek nir-endometriosis, namun secara statistik tidak terdapat perbedaan bermakna (p>0,05). Tidak terdapat korelasi bermakna antara tingkat metilasi gen FN1 dan RAC1 dengan ekspresi mRNAnya.
Kesimpulan: Terjadi penurunan tingkat metilasi yang bermakna pada gen FN1 di jaringan endometrium endometriosis, namun tidak berkorelasi dengan peningkatan mRNA nya. Tidak terdapat perbedaan bermakna tingkat metilasi dan ekspresi mRNA pada gen RAC1 di jaringan endometrium subjek endometriosis dibandingkan dengan nir endometriosis.
<hr><i>It has been reported that there was a changes in the expression of thousands of genes in endometrial endometriosis tissues, including the FN1 and RAC1 genes. Changes in gene expression can be caused by epigenetic mechanisms such as DNA methylation in genes.
Objective: To determine the level of DNA methylation in FN1 and RAC1 genes and their mRNA expression in endometrial tissue of endometriosis and non-ndometriosis.
Method: This study was designed as cross sectional with a total sample of 40 of endometrial tissues in the subject of endometriosis and non-endometriosis. Samples were taken by microcuretase at Ciptomangunkusumo and Fatmawati Hospital, Jakarta. DNA and RNA was isolated. DNA isolates were converted by bisulfite procedure, MSP conversion, electrophoresis, analyzed intensity of the band which

appeared on gel electrophoresis using ImageJ software to obtain the percentage data of DNA methylation level. In RNA isolates, it was analyzed using qRT-PCR methode to obtain the relative mRNA expression level.
Results: Analysis of percentage of DNA methylation level showed significant differences (p=0.022) in the FN1 gene (37.95%) compared to non-endometriosis (59.22%), whereas in the RAC1 gene there was no significant difference (p=0,63) with methylation level of endometriosis subjects (28.45%) and non-endometriosis subjects (26.11%). For relative mRNA expression of FN1 and RAC1 genes showed no significant differences (p> 0.05). For correlation in endometrial endometriosis showed no significant between the rate of methylation of the FN1 and RAC1 genes with their mRNA expression.
Conclusion: There was a significant decrease in DNA methylation level of FN1 gene in endometrial endometriosis tissues, but it did not correlate with the increasing in its mRNA expression. There was no significant difference in DNA methylation level and mRNA expression of RAC1 gene in endometrial tissues of endometriosis subjects compared to non-endometriosis.</i>