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Derajat metilasi dna dan tingkat ekspresi mrna gen reseptor progesteron-b pr-b pada jaringan endometriosis peritoneum, endometrioma, endometrium dan darah menstruasi pasien endometriosis = Dna methylation and mrna expression level of progesterone receptor b pr-b gene in peritoneal endometriosis, endometrioma, endometrium and menstrual blood of endometriosis patients

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Abstrak

Latar belakang: Resistensi progesteron akibat gangguan ekspresi reseptor progesteron pada jaringan endometriosis telah diketahui menjadi faktor yang memperberat kondisi klinis pasien endometriosis. Tujuan penelitian ini adalah untuk menganalisis tingkat metilasi DNA pada promoter gen PR-B pada berbagai jaringan endometriosis seperti eutopik endometrium, lesi ektopik peritoneum, endometrioma dan darah menstruasi serta pengaruhnya terhadap ekspresi mRNAnya dibandingkan dengan kontrol endometrium normal; untuk mengetahui patomekanisme endometriosis pada berbagai lokasi terkait dengan resistensi progesteron.
Metode: Penelitian ini menggunakan desain potong lintang yang melibatkan 20 sampel untuk masing-masing kelompok kasus dan kontrol. Tingkat metilasi DNA dari gen PR-B diukur menggunakan metode Methylated Specific PCR MSP lalu intensitas pita di dalam gel agarose dihitung dengan software ImageJ. Presentase intensitas pita pada sampel dibandingkan dengan kontrol positif disebut dengan tingkat metilasi DNA. Pengukuran ekspresi relatif mRNA PR-B menggunakan qRT-PCR dua tahap dan analisis dilakukan dengan metode Livak.
Hasil: Dari penelitian ini didapatkan perbedaan bermakna antara tingkat metilasi DNA gen PR-B pada jaringan endometriosis ektopik peritoneum 72,4 termetilasi , endometrioma 85 termetilasi dan eutopik endometrium 72,21 termetilasi dibandingan dengan kontrol p
<hr />Background: Progesterone resistance, due to alteration of progesterone receptor PR expression in endometriosis, was known as a disrupt factor in response to progesterone. The aim of this study is to analyze DNA methylation level on PR B promoter in various tissues include eutopic endometrium, ectopic peritoneal, endometrioma and menstrual blood from endometriosis patient as well as the implication on it's mRNA relatif expression compare with normal endometrium control to know the patomechanisms of endometriosis in various lession in term of progesterone resistance.
Methods: It was a cross sectional study, involved 20 sample for both patient and control. DNA isolate from each sample were converted by bisulfite conversion. DNA methylation level of PR B gene was analysis by Methylated Specific PCR MSP method, then band intensity in gel agarose was measured by ImageJ software. Percentage of band intensity in sample compared with positive control was determined as DNA methylaton level. Quantitative real time PCR was conducted to assess expression of mRNA PR B for each sample and Livak method was used to analysis it's relatif expression compare with control.
Result: There were significant different of methylation level of PR B gene in ectopic peritoneal endometriosis 72,40 methylated , endometrioma 85 methylated and eutopic endometrium 72,21 methylated compared with control p