PERBANDINGAN PROFIL MIKROBIOTA VAGINA PADA PASIEN ENDOMETRIOSIS DAN TANPA ENDOMETRIOSIS

TESIS

OLEH :

dr. SEF ZANI MERIA

2150305207

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ABSTRAK

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Sef Zani Meria[1], Haviz Yuad[2], Andani Eka Putra[3]

[1]Departemen Obstetri dan Ginekologi, Fakultas Kedokteran Universitas Andalas/ RSUP Dr. M.Djamil, Padang
[2]Subbagian Fertilitas dan Endokrinologi, Departemen Obstetri dan Ginekologi, Fakultas Kedokteran Universitas Andalas/ RSUP Dr. M.Djamil, Padang
[3] Laboratorium Pusat Diagnostik dan Riset Penyakit Infeksi, Fakultas Kedokteran Universitas Andalas

Pendahuluan: Endometriosis merupakan penyakit ginekologis kompleks dan heterogen yang menyerang sekitar 10 % wanita usia reproduksi, melibatkan peradangan dan disregulasi imun. Mikrobiota vagina dengan keanekaragamannya merupakan bagian integral dari mikroekologi vagina yang berinteraksi dengan anatomi vagina, sistem endokrin dan imunitas lokal vagina. Ketidakseimbangan dalam mikroekologi yang dikenal sebagai disbiosis diketahui memicu berbagai penyakit inflamasi. Hubungan antara disbiosis vagina dan endometriosis masih kontroversial

Tujuan: Mengetahui perbandingan profil mikrobiota vagina pada pasien endometriosis dan tanpa endometriosis

Metode: Penelitian menggunakan desain studi *case control* pada pasien yang didiagnosis endometriosis di RSUP Dr. M. Djamil. Penelitian dilakukan pada Desember 2023 hingga Juni 2024 di Poliklinik RSUP Dr. M. Djamil dan Laboratorium Pusat Diagnostik dan Riset Penyakit Infeksi (PDRPI). Diagnosis endometriosis ditegakkan melalui ultrasonografi dan histologis. Pengukuran mikrobiota dilakukan dengan miSeq Illumina Next Generation Sequencing. Perbandingan profil mikrobiota dilakukan dengan uji Mann Whitney. Perbandingan kejadian disbiosis dilakukan dengan uji Chi square.

Hasil: Terdapat 40 responden yang terdiri dari kelompok endometriosis (n=20) dan kelompok tanpa endometriosis (n=20). Pada tingkat filum, profil mikrobiota vagina kelompok endometriosis didominasi oleh *Firmicutes, Proteobacteria, Actinobacteria,* dan *Bacteroidetes.* Sedangkan pada kelompok tanpa endometriosis meliputi *Firmicutes, Actinobacteria, Bacteroidetes,* dan *Proteobacteria.* Pada tingkat genus, kelompok endometriosis didominasi oleh *Lactobacillus* sp., *Desulfovibrio* sp., *Flavobacterium* sp., *Gardnerella* sp, sedangkan pada kelompok tanpa endometriosis didominasi oleh *Lactobacillus* sp., *Prevotella* sp., *Desulfovibrio* sp., *Bifidobacterium* sp. Tidak ada perbedaan signifikan dari jumlah kelimpahan mikrobiota ($p>0,05$) dan kejadian disbiosis ($p>0,05$) antara kelompok endometriosis dan tanpa endometriosis di tingkat genus dan filum.

Kesimpulan: Tidak terdapat perbedaan jumlah kelimpahan mikrobiota antara kelompok endometriosis dan tanpa endometriosis. Namun terdapat perbedaan urutan dominasi mikrobiota vagina setelah *Firmicutes* pada tingkat filum dan *Lactobacillus* pada tingkat genus antara kedua grup.

Kata kunci: Endometriosis, disbiosis, mikrobiota vagina, Lactobacillus, Flavobacterium, Firmicutes, Proteobacteria

ABSTRACT

COMPARISON OF VAGINAL MICROBIOTA PROFILES IN PATIENTS WITH ENDOMETRIOSIS AND WITHOUT ENDOMETRIOSIS

Sef Zani Meria[1], Haviz Yuad[2], Andani Eka Putra[3]

[1]Department of Obstetrics and Gynecology, Faculty of Medicine, Andalas University/ Dr. M. Djamil Hospital, Padang
[2]Division of Fertility and Endocrinology, Department of Obstetrics and Gynecology, Faculty of Medicine, Andalas University/ Dr. M. Djamil, Hospital, Padang
[3]Center for Infectious Disease Diagmostic and Research Laboratory, Faculty of Medicine, Andalas University

Introduction: Endometriosis is a complex and heterogeneous gynecological disease that affect approximately 10% of women in reproductive age, involving inflammation and immune regulation. The vaginal microbiota with its diversity is an integral part of vaginal microecology that interacts with vaginal anatomy, the endocrine system and local vaginal immunity. The disruption in microecology, known as dysbiosis is known to trigger a variety of inflammatory diseases. The relationship between vaginal dysbiosis and endometriosis remains controversial

Objective: To determine the comparison of vaginal microbiota profiles in patients with endometriosis and without endometriosis

Method: The study was using the case control design on patients diagnosed with endometriosis at Dr. M. Djamil Hospital. The study was conducted on December 2023 to June 2024 at the Polyclinic of Dr. M. Djamil Hospital and the Center for Infectious Disease Diagnostic and Research Laboratory. The diagnosis of endometriosis was confirmed via ultrasonography and histology. Microbiota were measured with miSeq Illumina Next Generation Sequencing. Comparison of microbiota profiles was carried out using the Mann Whitney test. Comparison of dysbiosis was carried out using the Chi square test.

Results: There were 40 respondents divided into endometriosis group (n=20) and without endometriosis group (n=20). At the phylum level, the vaginal microbiota profile in endometriosis group were dominated with *Firmicutes, Proteobacteria, Actinobacteria*, and *Bacteroidetes*, while in without endometriosis group consist of *Firmicutes, Actinobacteria, Bacteroidetes*, and *Proteobacteria*. At the genus level, endometriosis group were dominated with *Lactobacillus* sp., *Desulfovibrio* sp., *Flavobacterium* sp., and *Gardnerella* sp., while in without endometriosis group were *Lactobacillus* sp., *Prevotella* sp., *Desulfovibrio* sp., and *Bifidobacterium* sp. There was no difference in the abundance of microbiota ($p>0.05$) or the incidence of dysbiosis ($p>0.05$) between endometriosis group and without endometriosis group at the genus and phylum levels.

Conclusion: There was no difference in the abundance of microbiota between endometriosis group and without endometriosis group. However, there were differences in the order of dominance of the vaginal microbiota after *Firmicutes* at the phylum level and *Lactobacillus* at the genus level between both groups.

Keywords: Endometriosis, dysbiosis, vaginal microbiota, Lactobacillus, Flavobacterium, Firmicutes, Proteobacteria