Introduction/Background: Mechanisms by which microbiota exert their influences on human health are not well-defined, but under certain circumstances certain bacterial communities can become altered, thereby disrupting normal homeostasis and resulting in human disease. While disruption of the vaginal microbiome may potentially promote gynecologic carcinogenesis (i.e. cervical cancer), the exact role of the microbiome in endometrial cancer still remains unclear. The aim of the present study was to identify selected species of microorganisms in women with endometrial cancer, and endometrial precancerous lesions.

Methodology: 48 women with endometrial cancer, endometrial atypical hyperplasia and benign gynecological conditions were included in this study. In each case, two swabs were taken: vaginal and endocervical. Each patient signed an informed consent form. Real-Time PCR was used to identify bacterial species. Differences between vaginal and endocervical microbiota were examined.

Results: Samples from the vagina in terms of isolated microbial species were more diverse than samples from endocervical canal. Mobiluncus curtisi and Fusobacterium nucleatum were the most frequent species detected in vaginal sample, whereas Gardnerella vaginalis i Atopobium vaginae were the most frequently detected in endocervical canal samples. Patients with endometrial cancer have more abundant vaginal microbiota than those with other gynecological diagnoses. Women from control group have a comparable number of isolated microorganisms statistically decreased in cancer patients compared to controls.

Conclusion: Microbiome of patients with endometrial cancer shows clear quantitative and qualitative differences when compared to control groups. The results of our study raise the possibility of a microbiome role in the manifestation and/or etiology of endometrial cancer that should be further investigated.