

International conference on

HUMAN PAPILLOMAVIRUS

October 20-21, 2016 Chicago, USA

Heterogeneity of the cervical microbial communities within HPV-induced carcinogenesis

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Introduction & Aim: Human papillomavirus is a key agent in the development of cervical cancer. However, it has been suggested that HPV infection alone may not be sufficient to promote cervical carcinogenesis and that other cofactors could be involved. The purpose of the present study was the evaluation of the existence of an association between cervicovaginal infection and precancerous lesion of the uterine cervix. The study material was cervix microbiota from healthy women and HPV positive women with L-SIL and H-SIL.

Methods: We determined cervicovaginal microbiota by high throughput sequencing of 16S rDNA amplicons and classified it in community state types of healthy women, patients with low-grade squamous intra-epithelial lesions (LSIL) and high-grade squamous intra-epithelial lesions (HSIL).

Results: Clustering analysis of the bacteria classes has indicated that in healthy women and patients with L-SIL, flora is composed predominantly of Bacilli class bacteria. Moreover, in patients with H-SIL, Gammaproteobacteria class is also detectable. Species of bacteria of Actinobacterium class, forming clusters distinct from other species are *Gardnerella vaginalis* and *Propionibacterium acnes* for healthy women, *Gardnerella vaginalis* and *Actinomyces turicensis* for group with L-SIL diagnosis; *Gardnerella vaginalis*, *Corynebacterium glaucum*, *Corynebacterium matruchotii*, *Propionibacterium acnes* and *Propionibacterium humerusii* for patients with H-SIL diagnosis. Bacteria species of Bacilli class forming distinct clusters from other species are *Lactobacillus crispatus*, *Lactobacillus iners* and *Lactobacillus taiwanensis* for healthy women, *Lactobacillus iners* and *Lactobacillus acidophilus* for patients diagnosed with L-SIL; *Lactobacillus iners*, *Lactobacillus acidophilus* and *Lactobacillus crispatus* for women with H-SIL diagnosis.

Conclusion: Our findings suggest that the presence and prevalence of specific cervicovaginal microbiome CSTs may be involved in the pathogenesis of cervical cancer. CST for healthy women cervical smear is dominated by *Lactobacillus crispatus*, *Lactobacillus iners* and *Lactobacillus taiwanensis* and depleted by *Gardnerella vaginalis* and *Lactobacillus acidophilus*. CST for L-SIL patients is dominated by *Lactobacillus acidophilus* and *Lactobacillus iners* and depleted by *Lactobacillus crispatus*. CST for H-SIL women is dominated by *Gardnerella vaginalis*, *Lactobacillus acidophilus* and depleted by *Lactobacillus taiwanensis*, *Lactobacillus iners* and *Lactobacillus crispatus*. Noteworthy, the concentration of *Lactobacillus acidophilus* in cervical smears from women diagnosed with L-SIL as well as with H-SIL are similar. Our results suggest that HPV-induced cancerogenesis is associated with increasing cervicovaginal microbiota heterogeneity and may be involved in regulating viral persistence and disease progression.

Biography

Wojciech Kwasniewski is currently working in the Department of Gynecologic Oncology and Gynecology at Medical University Lublin, Poland.

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