

1. ABSTRACT

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The study of bacterial microflora at patients with spontaneous early delivery

Diploma thesis

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Background: Premature delivery and premature rupture of membranes have been associated with maternal genital tract infections or with altered vaginal microflora during pregnancy. This work discusses knowledge about vaginal microbiome, premature delivery and analysis options of vaginal microbiome using next-generation sequencing. The aim of the work was to evaluate the composition of the bacterial microflora at patients with spontaneous preterm delivery and compared with each other of vaginal and cervical samples.

Methods: The study group consisted of 7 patients with diagnosed spontaneous preterm delivery. Samples were obtained on the basis of cooperation with the Department of Obstetrics and Gynecology of University Hospital Hradec Králové. The evaluation of the vaginal microbiome was performed by pyrosequencing method using Genome Sequencer FLX+.

Results: We have observed all typical patterns of the vaginal microflora in the samples tested. The most frequent species were *Lactobacillus crispatus/casei* and *L. iners*, which belong to the four most dominant lactobacilli in vagina. Several samples were characterized by dominance of *Gardnerella vaginalis*, typical for vaginal bacteriosis. *Ureaplasma urealyticum*, rarely *Ureaplasma parvum* and orders *Bifidobacteriales* and *Clostridiales* were present mainly in samples not dominated by lactobacilli.

Conclusion: *Lactobacillus crispatus/casei*, which is commonly found in healthy female genital microflora was the most occurred species, followed by *L. iners*, which represents rather transient but still healthy environment. The species *Gardnerella vaginalis*, associated with bacterial vaginosis, and *Ureaplasma urealyticum*, causing ureaplasmatic infections and also probably preterm delivery, were often found as dominant species. There were no major differences between vaginal and cervical fluid samples except for one cause.