MOLECULAR GENETIC DETECTION OF BACTERIAL VAGINOSIS AT KAZAKH WOMEN

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Background: The incidence of sexually transmitted infections (STIs) has sharply increased. A steady rise in STIs is observed among young individuals and women of reproductive age, often leading to complications such as disability, infertility, and prenatal infections that contribute to fetal and neonatal diseases. The aim of our study was to analyze the molecular genetic detection of bacterial vaginosis (BV) in women of reproductive age using noninvasive methods.

Objective: To assess the microflora of the endometrial mucosa in 96 women of reproductive age.

Materials and Methods: Total DNA was extracted from vaginal samples of 96 women aged 15 to 45 years who provided informed consent. The analysis of PCR amplification products was performed using real-time PCR.

Results: It was found that in cases of bacterial vaginosis, the presence of three infectious agents was observed less frequently compared to one or two (18.5±3.5%, 38.9±6.3%, and 42.6±6.5%, respectively; $p<0.05$).

Conclusion: Our study demonstrates that using a DNA panel and real-time PCR enables the identification of BV patients through minimally invasive techniques.We demonstrated an association between the increased severity of BV and a higher future risk of contracting an STI. Although the scoring systems used in this study may not be practical for routine hospital use, our findings are valuable for patient counseling, as severe cases of BV put patients at an increased risk of acquiring future STIs.

Keywords: Bacterial vaginosis (BV), real-time polymerase chain reaction (PCR-RT), sexually transmitted infections (STIs), pelvic inflammatory diseases (PID), morbidity, mortality.