



Molecular Research in Bacterial Vaginosis

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Message from the Guest Editor

Bacterial vaginosis (BV) is a common and often recurrent disease. It is a polymicrobial disease, but the main causative agent is *Gardnerella vaginalis*. Molecular studies have shown genetic heterogeneity and taxonomic diversity within the genus *Gardnerella*. At least 13 distinct groups were found, and they were classified as separate species within the taxon formerly known as *G. vaginalis*. These *Gardnerella* species are closely related genetically; only some of them (pathogenic) can be associated with BV, and non-pathogenic species are found in healthy women. Thanks to the methods of PCR, hybridization and sequencing, it has become possible to quantitatively detect and accurately identify bacteria, including those associated with BV.

Combining the efforts of the scientific community in the search for genetic markers of recurrent forms of BV using molecular research methods will allow us to understand the frequent recurrence of BV as well as determine the composition of biofilms formed by *G. vaginalis* and BV-associated microorganisms. In this Special Issue, we want to demonstrate the huge potential of research in the field of molecular studies of BV.





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Message from the Editor-in-Chief

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