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THE VAGINAL MICROBIOME AND BACTERIAL VAGINOSIS

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Abstract: Bacterial vaginosis (BV) is a state of dysbiosis characterised by a decrease in the number of Lactobacillus and an increase in the anaerobic polymicrobial community; its aetiology remains unclear and is unlikely to be attributable to a single pathogen [2;3;14;19]. The topic is of global importance, as BV is widespread in Europe, Asia, North America, Africa and other regions and is associated with adverse reproductive and infectious outcomes [1;7;11;15].

Key words: vaginal microbiome, dysbiosis, bacterial vaginosis

Introduction

The vaginal microbiome (VM) in women of reproductive age is most commonly described as a system comprising **five CST types**, four of which are typically dominated by *Lactobacillus* (*L. crispatus, L. gasseri, L. iners, L. jensenii*), whilst the fifth is characterised by a deficiency of lactobacilli and a predominance of anaerobes [6;8;13;16]. This lactobacillus-dominated state is usually associated with a low pH, low species diversity and barrier protection of the mucosa through the production of lactic acid and other antimicrobial factors [3;4;5;6;8;9;13;17].
Bacterial vaginosis (BV) is a state of dysbiosis in which the number *of Lactobacillus* decreases whilst the anaerobic polymicrobial community increases; however, the aetiology remains unclear and is unlikely to be attributable to a single pathogen [2;3;14;19]. This topic is of global significance, as BV is widespread in Europe, Asia, North America, Africa and other regions and is associated with adverse reproductive and infectious outcomes [1;7;11;15].

Materials and methods

This article is presented as **a narrative review** in the IMRAD format, based on 20 published studies, including molecular studies of the microbiome, reviews, systematic reviews, meta-analyses and clinical guidelines [7;11;15;20]. The analysis included data on the composition of the vaginal microbiota, diagnostic criteria for bacterial vaginosis, regional differences and the clinical consequences of dysbiosis [2;5;9;19].

Results

In various studies, the normal vaginal microbiome is similarly described as
a **low-diversity** community with a high proportion of lactobacilli; however, the composition within this category is heterogeneous, and functional properties depend on the species and even the strain

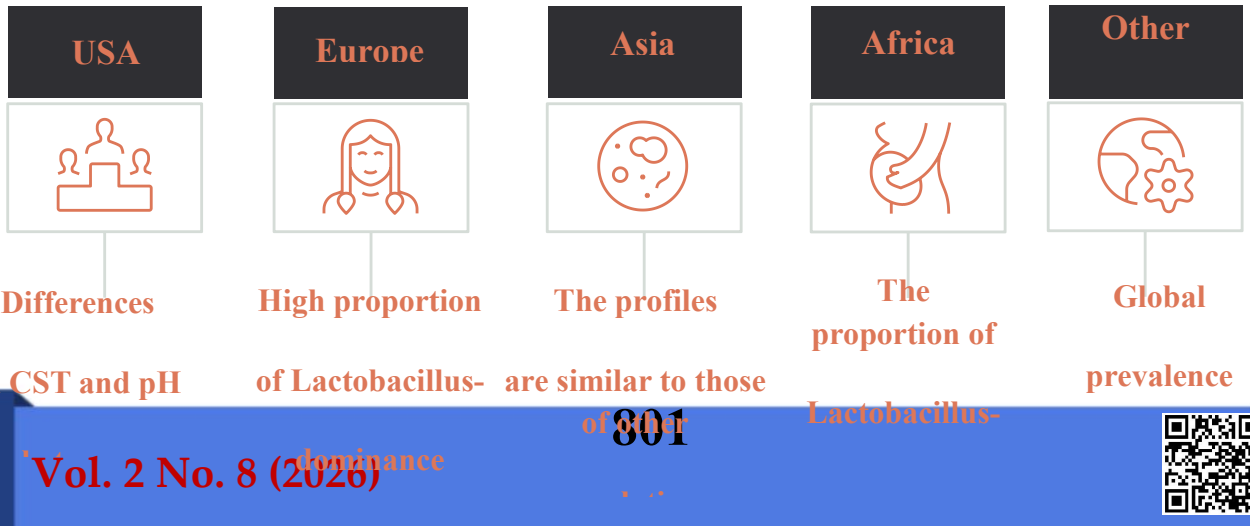
[8;9;12;17]. An *L.* crispatus-dominant microbiome is generally considered to represent a particularly stable protective state, whereas *L.* iners dominance appears less stable and closer to transitional or dysbiotic states [4;5;9;19].
In BV, there is a shift towards **CST IV** or similar polymicrobial configurations, in which the proportion of *Gardnerella, Atopobium, Prevotella, Mobiluncus, Sneathia* and other anaerobes increases [4;5;8;9;13;14;20]. *Gardnerella vaginalis* is often a key component of BV and the polymicrobial biofilm, which, according to reviews and clinical studies, hinders the long-term eradication of the dysbiotic community [3;4;20].

Regional differences

Regional data show that BV is prevalent worldwide, but its prevalence varies: in a meta-analysis, the prevalence in the general population was **23 per cent** in Europe and Central Asia, **24 per cent** in East Asia and the Pacific, **27 per cent** in North America and **29 per cent** in South Asia [15]. A systematic review of global epidemiology also demonstrated that rates vary significantly not only between regions but also between ethnic groups within countries in Europe, Asia, North and South America, and the Middle East [11].

In the USA, the microbiome and the prevalence of BV vary between ethnic groups: in a North American cohort, the distribution of CST differed statistically between white, Black, Latin American and Asian women, whilst pH was higher among Black and Latin American participants [16]. This is consistent with a meta-analysis in which a higher prevalence of BV was observed in Black and Latin American women in North America compared with white and Asian women [15].
European and Asian data also show heterogeneity. In a Belgian population of 3,345 women, *Lactobacillus* dominated in **78 per cent** of samples, and the composition of the microbiome was associated with age, childbirth and the phase of the menstrual cycle [13]. Among Japanese women, the types of vaginal communities were generally similar to those found in women of other racial groups, whilst Asian populations as a whole have been described as exhibiting marked intra-group variability [11;16].

Data from Africa highlight that definitions of ‘normal’ are not always universal. In a large postpartum cohort of **1,107 women** from rural Malawi, a Lactobacillus-deficient, often Gardnerella-dominated profile predominated, demonstrating the limitations of universal Western models of the normal microbiome [5].



Marked ethnic	In Belgium, 78 percent of the samples were Lactobacillus-dominant	Cross-country differences persist	In Malawi, a consistent Gardnerella-dominant profile following	Across all macro-regions, the estimates ranged from 23–29 per cent

Table 1: Comparison of vaginal microbiome characteristics and bacterial vaginosis by region

Pathogenesis diagram

The transition from eubiosis to BV is usually described as a decrease in the proportion of lactobacilli, an increase in anaerobes, biofilm formation and an increased risk of inflammatory and infectious complications [6;9;10;18].

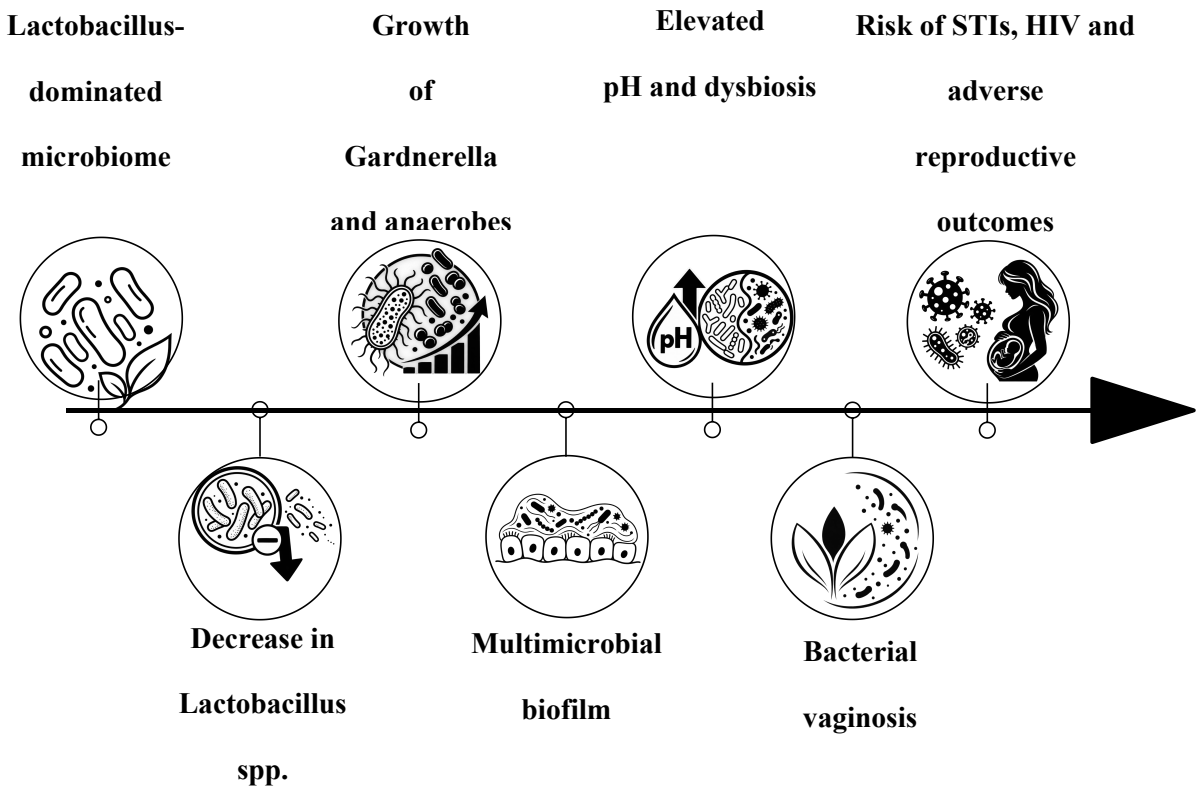


Figure 1: Diagram of the transition from vaginal eubiosis to bacterial vaginosis

Discussion

Current evidence supports the view of BV as a **syndrome** of **polymicrobial dysbiosis** rather than a disease caused by a single pathogen [2;14]. This explains why standard clinical criteria are useful but do not fully reflect the molecular diversity of BV and do not always predict the course of the disease [2;9;19].

The clinical significance of BV is determined not only by its symptoms but also by its association with HIV and adverse pregnancy outcomes. A meta-analysis of 23 studies involving 30,739 women showed an increased risk of HIV acquisition, with a relative risk of **1.6** (95% CI **1.2–2.1**) [1]. A systematic review and a network

meta-analytic model also showed that a low-lactobacilli microbiome is associated with a higher risk of preterm birth compared with *L.* crispatus dominance, with an OR **of 1.69** and a 95% CI of **1.15–2.49** [7].

Treatment studies generally show **short-term efficacy** of antibiotics and frequent relapses. Clinical reviews and guidelines indicate that metronidazole or clindamycin are generally effective in the short term, but recurrence remains common [2;4;9;18]. A pilot randomised trial of recurrence following **a 7-day course of oral metronidazole** also evaluated intermittent probiotic therapy; all interventions were safe, and the incidence of BV was **10.18** cases per person-year in the control group, compared with **1.41** per person-year among metronidazole users and **3.58** in the Ecologic Femi+ group [19]. These results appear encouraging, but the effects disappeared shortly after the intervention ended, and inter-individual variability was high [19].

Conclusion

VAG and BV are best described as a dynamic system in which a reduction in the proportion of lactobacilli—particularly the loss of stable protective configurations—is associated with a transition to a polymicrobial anaerobic state and an increase in clinical risks. **A licensed clinician** is required to make individual decisions regarding diagnosis or treatment; the research to date primarily supports the conclusion that BV has a high global prevalence, regional variability and that standard therapy has limited long-term efficacy.

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