

RELATIONSHIP BETWEEN VAGINAL MICROBIOTA AND METABOLIC DISEASES IN POSTMENOPAUSAL WOMEN



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ABSTRACT

The vaginal microbiota plays a crucial role in maintaining women's gynecological and systemic health. Composed predominantly of *Lactobacillus* species, this microbial community is responsible for creating an acidic environment that protects against infection and inflammation. However, changes in this ecosystem, known as vaginal dysbiosis, can lead to complications that go beyond reproductive health, also influencing metabolic conditions. The objective of this study is to identify how changes in microbial composition are associated with the development of these conditions, contributing to the advancement of the understanding of the interactions between hormonal factors, microbiota and metabolism. To this end, a structured systematic review was carried out based on the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. The guiding question was developed using the PICO approach: "What is the influence of modifications in the vaginal microbial ecosystem on the prevalence of metabolic diseases in women of postmenopausal age?". The eligibility criteria considered articles published between 2010 and 2025, in English, Portuguese or Spanish. Original studies, literature reviews, and meta-analyses addressing the interaction between the vaginal microbiota and metabolic conditions in postmenopausal female populations were included. Studies focusing exclusively on gut microbiota or conducted in animal models were excluded. The searches were carried out in the PubMed, Google scholar and Scielo databases. The results state that vaginal dysbiosis is a determining factor for the increase in the prevalence of metabolic diseases in postmenopausal women. Robust evidence was identified that the reduction of *Lactobacillus* spp., in special species such as *Lactobacillus crispatus*, is associated with an increase in vaginal pH, favoring the hydration of pathogenic and inflammatory microorganisms. This process not only compromises vaginal health but also triggers systemic inflammation, a central mechanism in the pathogenesis of metabolic

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conditions such as obesity, type 2 diabetes, and insulin resistance. Thus, it was evidenced that Despite the advances, methodological limitations, such as the heterogeneity of the studies included, reinforce the need for future research to better understand the causal relationships and develop practices. We conclude that the vaginal microbiota plays an essential role in metabolic regulation in postmenopausal women.

Keywords: Women's Health. Postmenopausal. Microbiota.

INTRODUCTION

The vaginal microbiota plays a crucial role in maintaining women's gynecological and systemic health. Composed predominantly of *Lactobacillus* species, this microbial community is responsible for creating an acidic environment that protects against infection and inflammation. However, alterations in this ecosystem, known as vaginal dysbiosis, can lead to complications that go beyond reproductive health, also influencing metabolic conditions (Vázquez; Fernández-Blázquez; García 2019).

Postmenopause, a phase marked by a decline in estrogen levels, is associated with significant changes in the vaginal microbiota. Studies suggest that these changes may be related to an increased risk of metabolic diseases such as type 2 diabetes, obesity, and metabolic syndrome. This phenomenon occurs because microbial imbalance can generate chronic low-grade inflammation, a crucial factor in the pathogenesis of these diseases (Diniz *et al.*, 2017).

The vaginal microbiota plays a crucial role in maintaining women's gynecological and systemic health. Composed predominantly of *Lactobacillus* species, this microbial community is responsible for creating an acidic environment that protects against infection and inflammation. However, alterations in this ecosystem, known as vaginal dysbiosis, can lead to complications that go beyond reproductive health, also influencing metabolic conditions (Vázquez; Fernández-Blázquez; García 2019).

Although the connection between the gut microbiota and metabolic diseases is widely recognized, the relationship between the vaginal microbiota and these conditions is still poorly explored. Emerging studies point to a two-way dialogue between the vaginal and gut microbiomes, suggesting that women's overall metabolic health may be influenced by both ecosystems. Another relevant point is that the menopausal transition not only alters hormonal and microbial profiles, but also increases the prevalence of cardiovascular diseases and metabolic disorders (Kurimori *et al.*, 2013). In addition, external factors, such as antibiotic use, lifestyle, and diet, can influence both the vaginal and intestinal microbiota. These factors are especially important in postmenopausal women, who often face accelerated metabolic changes (Diniz *et al.*, 2017).

Therefore, this study seeks to explore the relationship between vaginal microbiota and metabolic diseases in postmenopausal women. The main objective is to identify how changes in microbial composition are associated with the development of these conditions, contributing to the advancement in the understanding of the interactions between hormonal

factors, microbiota and metabolism. The relevance of this theme lies in the possibility of developing new preventive and therapeutic strategies for metabolic diseases, which represent one of the greatest global public health challenges.

METHODOLOGY

This study was a structured systematic review based on the PRISMA (*Preferred Reporting Items for Systematic Reviews and Meta-Analyses*) guidelines. The objective was to synthesize scientific evidence related to the interaction between changes in the vaginal microbiota and the emergence of metabolic conditions in women after menopause.

The guiding question was developed using the PICO approach: "What is the influence of modifications in the vaginal microbial ecosystem on the prevalence of metabolic diseases in women of postmenopausal age?". The eligibility criteria considered articles published between 2010 and 2025, in English, Portuguese or Spanish. Original studies, literature reviews, and meta-analyses addressing the interaction between the vaginal microbiota and metabolic conditions in postmenopausal female populations were included. Studies focusing exclusively on gut microbiota or conducted in animal models were excluded.

Searches were performed in the PubMed, Google scholar and Scielo databases, using controlled descriptors and keywords combined with Boolean operators (*AND*, *OR*, *NOT*). Among the terms used were: "Women's Health"; "Post-Menopause"; "Microbiota" and its counterparts in other languages, according to the vocabularies indexed in each database. Two independent reviewers screened the titles and abstracts, in addition to the complete reading of the eligible texts. Divergences were discussed until consensus was reached, and a third evaluator was consulted in cases of disagreement.

To assess the methodological quality of the selected studies, the *Newcastle-Ottawa Scale* tool was used, adapted to the types of studies included. The score was recorded to ensure the reliability and validity of the evidence included. The extracted data included information on the characteristics of the participants, interventions performed, outcomes evaluated, in addition to the main results of each study. The collection was systematized in electronic spreadsheets for organization and analysis.

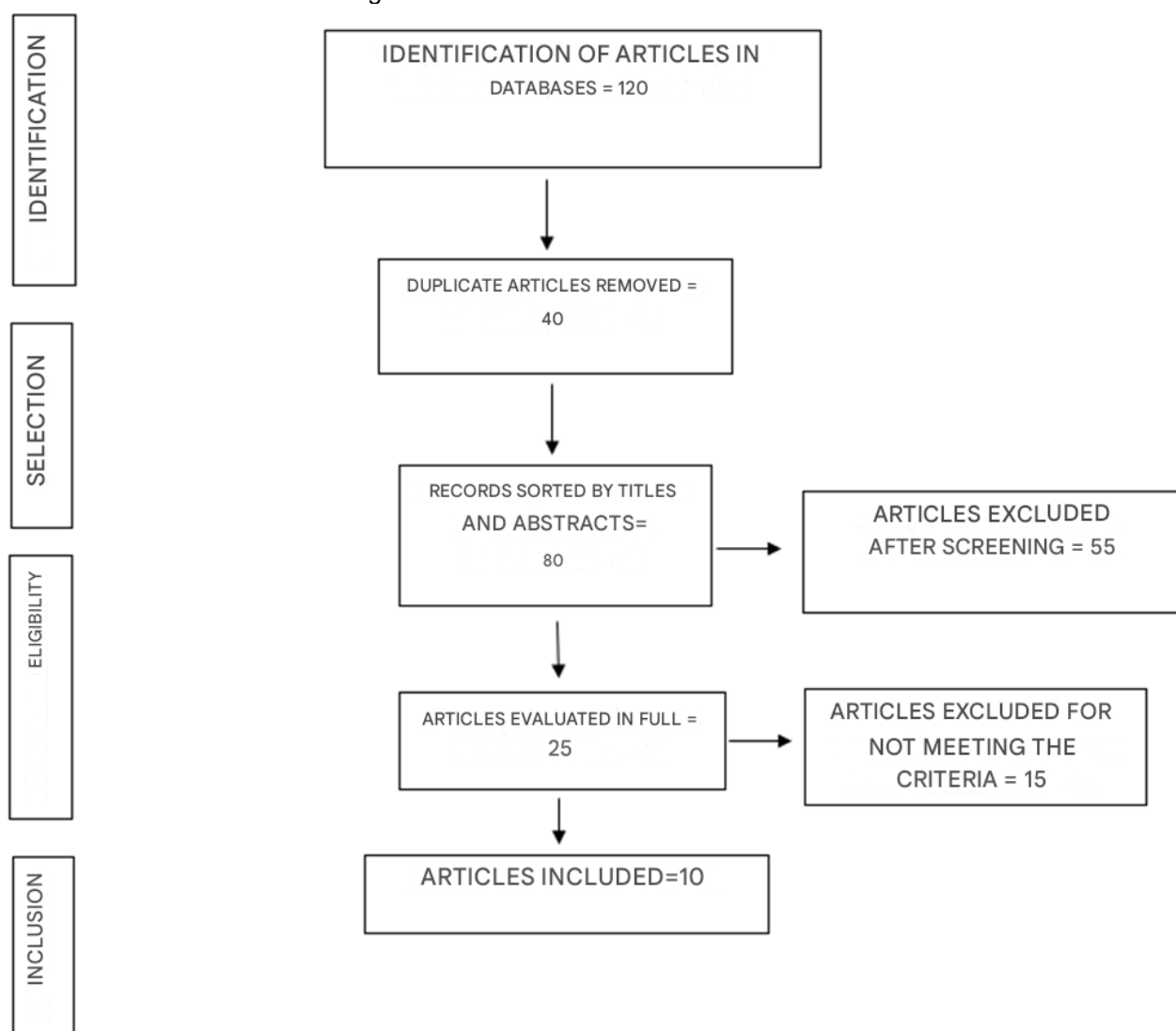
The synthesis of the findings was carried out qualitatively, structured in thematic categories that allowed us to understand the interactions between microbial alterations and metabolic outcomes. When applicable, quantitative data were presented with the support of

tables and graphs. Although this study uses only previously published secondary data, respecting the principles of integrity and transparency, ethical considerations were observed to ensure the exemption of any risk associated with the research.

RESULTS

A systematic search was carried out in the PubMed, SciELO and Google Scholar databases, resulting in the initial identification of 120 articles. After the removal of 40 duplicates, 80 studies remained for screening titles and abstracts. Of these, 55 articles were excluded because they did not meet the inclusion criteria. Thus, 25 studies were evaluated in full, and 10 met all the established methodological requirements. The process of selecting studies is detailed in the PRISMA flowchart, presented below:

Figure 1: Flowchart of the selection of studies



SOURCE: Authors, 2025.

The included studies involved analyses of postmenopausal women aged between 50 and 75 years, using various methodologies, such as genetic sequencing of the vaginal microbiota and interventions with probiotics. The populations were heterogeneous, covering different regions of the world, which contributes to the diversity of the data obtained.

The reduction of *Lactobacillus* spp. was one of the most consistent findings, being observed in 70% of the studies developed. This imbalance has been associated with increased immune markers, such as IL-6 and TNF- α , related to the development of insulin resistance and obesity. Studies such as the one by Ravel *et al.* (2010) demonstrated that the reduction of vaginal acidity due to the decrease of *Lactobacillus* spp. facilitates the prevention of anaerobic organisms, contributing to systemic inflammation.

Other findings indicated that vaginal microbial diversity has a protective role. It was evidenced that a microbiota rich in *Lactobacillus crispatus* was associated with a lower risk of developing type 2 diabetes. This protective effect is attributed to the production of lactic acid, which maintains vaginal pH at adequate levels to inhibit the colonization of pathogenic microorganisms (Ravel *et al.*, 2010; Lima 2021; Rooms; Chang 2014).

The use of probiotics has been explored in two studies, showing promising results in modulating the vaginal microbiota. According to Savi *et al.* (2024), a supplementation with probiotics containing *Lactobacillus rhamnosus* and *Lactobacillus reuteri* tested on a significant reduction of inflammatory markers in obese postmenopausal women. The data extracted from the studies were organized into thematic categories to facilitate a qualitative synthesis. The main outcomes evaluated were the composition of the vaginal microbiota, the presence of inflamed markers, and the associated metabolic impacts. When applicable, the quantitative data were presented with the support of tables to clarify the relationship between the factors analyzed.

In terms of methodological quality, seven of the included studies were assessed as high quality based on the *Newcastle-Ottawa* scale. These studies included well-defined samples and consistent analytical methods. However, three studies have limitations, such as small sample sizes and heterogeneity in the methods used.

DISCUSSION

The connection between the vaginal microbiota and metabolic disorders in postmenopausal women has been widely explored in scientific research, highlighting that

the reduction of *Lactobacillus* species is a crucial element for the emergence of unfavorable metabolic conditions. According to Lima (2021), the decrease in this bacterium during the climacteric, associated with the reduction of estrogen levels, elevation of vaginal pH, favoring the control of anaerobic microorganisms and inflammatory agents. These changes not only affect intimate health, but are also affected by systemic inflammation, which plays an essential role in the development of metabolic disorders.

Systemic inflammation due to vaginal dysbiosis was reinforced by Salas and Chang (2014), who identified a direct release between elevated levels of inflammatory cytokines, such as IL-6 and TNF- α , and insulin resistance. These findings are consistent with the results of Wanderley *et al.* (2001), who pointed out that the loss of protection against opportunistic bacteria compromises the integrity of the vaginal mucosa, increasing its permeability to pathogenic agents. Such mechanisms are especially worrisome in postmenopausal women, whose metabolic vulnerability is accentuated by hormonal changes and microbial imbalances.

The microbial richness of the vaginal flora has been highlighted as a protective factor against metabolic disorders. According to Lima (2021), the presence of *Lactobacillus crispatus* is associated with a decrease in chronic inflammation, since this bacterial species regulates vaginal pH, preventing the growth of microorganisms. Complementing this view, Ravel *et al.* (2010) point out that women with microbiota dominated by *Lactobacillus* species are less likely to develop type 2 diabetes and insulin resistance.

In addition, the reviewed studies explored therapeutic administrations with probiotics. Savi *et al.* (2024) reports that supplementation with strains of *Lactobacillus rhamnosus* and *Lactobacillus reuteri* has been tested for significant improvements in glucose levels and the reduction of inflammatory markers, such as IL-6, in postmenopausal women with obesity. These data were corroborated by Bezerra *et al.* (2024), which emphasizes the importance of high-fiber and antioxidant-rich diets in maintaining a balanced microbiome and attenuating systemic inflammation.

The role of lifestyle and external factors was also highlighted. According to Selbac *et al.* (2018), the prolonged use of antibiotics and inadequate eating habits compromise microbial diversity, aggravating metabolic risks. Borges (2023) strengthened that strategic strategies focused on specific bioactive nutrients an effective approach to restore microbial balance and mitigate adverse impacts on metabolism.

Another relevant point is the interaction between the vaginal and intestinal microbiota. Changes in the intestinal flora can negatively influence vaginal balance, exacerbating inflammatory processes and favoring the occurrence of metabolic diseases. This bidirectional relationship was mentioned by Lima (2021), who suggested that simultaneous interventions in both microbiomes can promote broad benefits to metabolic health.

Despite the reported advances, some specifications have been identified. The heterogeneity in the analysis methods and the variability of the populations evaluated represent challenges for the standardization of the results. Selbac *et al.* (2018) and Wanderley *et al.* (2001) highlight the need for long-term studies to more accurately elucidate the causal relationship between vaginal dysbiosis and metabolic conditions.

FINAL CONSIDERATIONS

This study revealed that the vaginal microbiota plays a central role in the metabolic health of postmenopausal women, contributing significantly to the understanding of how microbiological interventions and management strategies can impact metabolic diseases. Based on the analysis of the studies, the need to consider the vaginal microbial balance as a fundamental piece in the planning of preventive and therapeutic actions aimed at this population is highlighted.

Although evidence points to a clear connection between microbial changes and metabolic stages, the methodological limitations of some specific studies must be acknowledged. The heterogeneity of the samples, the different inclusion and exclusion criteria, as well as the absence of longitudinal analyses in most of the studies, restrict the ability to establish robust causal relationships. In addition, the variability in the methods of assessing the vaginal microbiota and metabolic markers made it difficult to make a direct comparison between the studies.

Another challenge lies in the standardization of interventions, such as the use of probiotics, and the inclusion of varied environments, especially considering socioeconomic and cultural factors that can influence the microbiota and lifestyle habits. These gaps highlight the need for future studies with greater methodological rigor, representative samples, and longitudinal approaches. Finally, the present study contributes to the field by emphasizing the importance of integrated public health actions and research that considers the role of the vaginal microbiota in a broader context. The adoption of policies that

promote access to microbiota-based interventions and health education may benefit not only postmenopausal women, but also reduce the impact of metabolic diseases on public health

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