

# THE IMPORTANCE OF THE VAGINAL MICROBIOME IN INTIMATE HEALTH: AN UPDATED OVERVIEW

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## INTRODUCTION

The vaginal microbiota (VM) plays a fundamental role in maintaining gynecological health, being dominated under ideal conditions by species of the genus *Lactobacillus*.

An imbalance of this microbiota (vaginal dysbiosis) is associated with infections such as bacterial vaginosis, candidiasis and mixed vaginitis, as well as impacts on fertility, pregnancy and risk of infection by other STIs.

In addition to assessing the presence of pathogens, the study of the VM allows understanding the overall composition of the flora, its diversity and degree of epithelial protection. Molecular techniques, such as real-time PCR, enable the simultaneous identification of multiple microorganisms, including commensals, enabling a more preventive and personalized approach.



## MATERIALS AND METHODS



A total of 903 female samples, age >18 years, cervicovaginal, collected in LBC (CellPreserv<sup>®</sup>, Kolplast<sup>®</sup>, São Paulo, Brazil) were analyzed. Samples were received between Feb–Jul 2025 at a private laboratory in São Paulo.



The assay uses quantitative real-time PCR – Femoflor Screen<sup>®</sup> (DNA-Technology Research & Production, LLC, Moscow, Russia<sup>®</sup>) to detect and quantify 13 relevant microorganisms.



The test indicates the degree of eubiosis or dysbiosis, and allows standardized clinical interpretation based on validated microbiological algorithms.



## RESULTS

Among the results, the following microorganisms were identified:

Table 1 – Frequency of identified microorganisms













Category / Biological agent	n (cases)	%	Category / Biological agent	n (cases)	%
 Normal flora – <i>Lactobacillus</i> spp.	807	89.3	 STI – <i>C. trachomatis</i>	7	0.8
 Conditional anaerobes – <i>G. vaginalis</i> , <i>P. bivia</i> , <i>Porphyromonas</i> spp.	523	57.9	 STI – <i>T. vaginalis</i>	5	0.6
 Fungi – <i>Candida</i> spp.	119	13.7	 STI – <i>N. gonorrhoeae</i>	3	0.4
 Mycoplasmas – <i>M. hominis</i>	69	7.6	 STI – <i>M. genitalium</i>	11	1.2
 <i>Ureaplasma urealyticum/parvum</i>	277	30.7	 Virus – HSV-1	1	0.1
			 Virus – HSV-2	2	0.2
			 Virus – CMV	19	2.1

Table 1: Results of the Femoflor Screen test, identified using data obtained at IPOGLab Laboratory, São Paulo.



## CONCLUSION



The incorporation of tests to identify components of the VM in gynecological practice contributes to more accurate diagnoses, avoids empirical treatments and improves the management of intimate health, especially in women with recurrent symptoms, infertility or pregnancy planning.



## ACKNOWLEDGEMENTS

The authors gratefully acknowledge IPOG Lab and its management for their valuable support and contributions to this study. We also thank Biomédica Equipamentos Médicos and DNA-Technology for their sponsorship and support.



## DISCLOSURE

The authors declare no conflicts of interest. This study was supported by Biomédica Equipamentos Médicos and DNA-Technology.



## REFERENCES

- Molina MA, et al.; Assessing the Cervicovaginal Microbiota in the Context of hrHPV Infections: Temporal Dynamics and Therapeutic Strategies. *mBio*. 2022 Oct 26;13(5)
- Linhares, IM, Giraldo, P.C., Baracat, E.C.; New findings about vaginal bacterial flora, *Rev. Assoc. Med. Bras.* 56 (3) • 2010
- Ravel J, et al. Vaginal microbiome of reproductive-age women. *PNAS*, 2011;108(Suppl 1):4680–4687.



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