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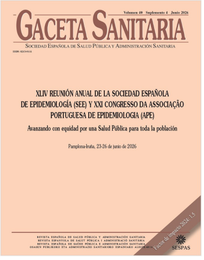

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SESPAS

322 - DETERMINANTS OF THE VAGINAL MICROBIOTA IN SOCIALLY DIVERSE MIDDLE-AGED WOMEN

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Resumen

Background/Objectives: The vaginal microbiota plays a key role in women's health by ensuring their protection against genital and sexually transmitted infections. While the vaginal microbiota has been more studied during the reproductive years, evidence on factors that may alter its composition in middle-aged women remains limited. Indeed, during the menopausal transition, the vagina becomes more vulnerable to colonization by harmful microorganisms. We aimed to examine the vaginal microbiota's composition and its determinants in middle-aged women.

Methods: We conducted a cross-sectional study on 381 women (age range 37-64 years) from the INMA-Valencia and PAPILONG cohorts (recruitment: 2019-2023), representing a broad socioeconomic spectrum, from middle-to-upper class to socially disadvantaged women. Vaginal microbiota composition was assessed using 16S rRNA amplicon sequencing and classified into community state types (CSTs), which were grouped into four categories for analysis: CST I-II-V, CST III (both Lactobacillus-dominated), CST IVA-IVB, and CST IVC (both with a more diversified and less protective microbiota). Data on sociodemographic, sexual and reproductive health, lifestyle and clinical domains was gathered using questionnaires. For statistical analyses, we applied generalized multinomial linear models using a two-step selection procedure.

Results: The prevalence of vaginal microbiota profiles was respectively 37.8%, 28.9%, 17.6% and 15.7% for CST I-II-V, CST III, CST IVA-IVB and CST IVC. Regarding the possible determinants of vaginal microbiota composition (compared to CST I-II-V): i) CST III was inversely associated with post-menopause (OR [95%]: 0.53 [0.27-1.04]; p-value: 0.066), Spanish-origin by birth (0.53 [0.29-1.00]; 0.049) and oral medication intake (0.50 [0.26-0.99]; 0.046); ii) CST IVA-IVB were inversely associated with being in a stable relationship (0.55 [0.28-1.05]; 0.069) and Spanish-origin (0.33 [0.16-0.65]; 0.001); iii) CST IV-C was positively associated with post-menopause 7.29 [3.50-15.16]; < 0.001), stable relationship (2.52 [1.10-5.80]; 0.029) and chronic disease history (2.82 [1.06-7.50]; 0.038).

Conclusions/Recommendations: Sociodemographic, clinical and lifestyle factors emerged as key determinants of vaginal microbiota composition, highlighting the relevance of these findings for understanding vaginal health in midlife and guiding future research.

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