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Prevalence of anal infection by human papillomavirus in men who have sex with men and its associated clinical and epidemiological factors

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Sir,

We are writing to address findings from a recent study investigating the prevalence and incidence of multiple genotype anal Human Papillomavirus (HPV) infections among men who have sex with men (MSM) in our healthcare area concerning clinical and sociodemographic factors. HPV plays a crucial role in the etiopathogenesis of most anogenital neoplastic processes [1], making understanding its epidemiological variations essential. MSM have a significantly increased risk of developing anal cancer, particularly when HIV infection is also present [2].

Our retrospective descriptive study analyzed data from the initial HPV screening conducted between March and December 2023, focusing on rectal swabs from MSM patients attending our hospital's Infectious Diseases Unit. The method employed for HPV detection was the Anyplex™ II HPV 28 detection assay (Seegene, Republic of Korea). The electronic medical records were evaluated, and data on age, nationality, toxic habits, antibody detection, Mantoux test, anal cytology, and the detection of other sexually transmitted diseases (STDs) (Allplex™ STI Essential Assay, Seegene, Republic of Korea) in pharyngeal and rectal swabs and urine were recorded. The data were analyzed using Power BI (Microsoft) and SPSS. Chi-square values with $p < 0.05$ were considered significant.

Among the 214 MSM participants (average age: 40 ± 10.4 years), 63.1% were HIV positive (only 3% exhibited a viral load > 1000 copies/mL. In contrast, 76.3% had an undetectable viral load, while 20.7% showed a suppressed viral load), while the remainder were receiving pre-exposure prophylaxis (PrEP). A total of 43% had antibodies against *Treponema pallidum*, and 31.8% had a positive tuberculin skin test. The detection rates for other STDs via multiplex PCR in pharyngeal and rectal swabs and urine were 6.1%, 29.6% and 14%, respectively. No-

tably, only 11.3% of patients exhibited abnormal anal intraepithelial cytology (AIC).

A total of 169 (79%) tested positive for HPV. Among these, 45 (26.6%) had an infection with a single HPV genotype. The prevalence rates for High-Risk HPV (HR-HPV), High and Low-Risk HPV (HLR-HPV), and Low-Risk HPV (LR-HPV) were 31.3%, 56.2%, and 12.4%, respectively. The most common genotypes identified were types 53 (23%), 68 (21.3%), 42 (18.9%), 6 (18.3%), and 44 (18.3%). A total of 124 (73.4%) patients were co-infected with two or more different HPV genotypes. In this group, 45 (26.6%) patients had the presence of five or more genotypes, as shown in Table 1. Statistical analysis revealed that the probability of having an HPV infection was significantly higher in patients with antibodies against *Treponema pallidum* and hepatitis C virus. Additionally, the probability of infection with certain HPV genotypes was higher in those with coinfections with other STIs and in patients with abnormal AIC. *Treponema pallidum* antibodies and abnormal AIC were also found to be risk factors for oropharyngeal HPV infection in people living with HIV in our country [3].

This study's findings underscore the high prevalence (79%) of HPV infections and the substantial occurrence (73.3%) of multiple HPV genotypes, with a high prevalence of HLR-HPV genotypes detected. When comparing our results with various studies conducted in our country [4,5], two facts should be highlighted. Firstly, genotype 16 was notably absent from the top five genotypes identified in our cohort of MSM. Secondly, there was a higher proportion of HLR-HPV genotypes. When investigating these two findings, we realized that the most prevalent genotypes detected in our study were not included in the nonavalent vaccine. In our cohort, all patients aged 26 years or younger (7%) were vaccinated against HPV with the nonavalent vaccine, as they met the criteria established by the Murcian Health System for vaccine funding. Older patients (83%) were strongly encouraged to receive the vaccine; however, they had to purchase it independently. We do not have

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Table 1 Multiple HPV genotype distribution among the study population

Number of genotypes detected	N	%
1	45	26.6
2	32	18.9
3	32	18.9
4	45	8.9
5	16	9.5
6	12	7.1
7	6	3.6
8	3	1.8
9	4	2.4
10	3	1.8
11	1	0.6
Total	169	100

records of how many of these older patients were not vaccinated, but based on our results, this number is likely low [6].

Our study has several limitations. The molecular detection methods employed in other studies have demonstrated varying sensitivities and targeted different genotypes [7]. The affordability of the nonavalent vaccine could influence the genotype distribution, as demonstrated [6]. Finally, geographical and regional variations may influence the results of unicentric studies.

In conclusion, our study contributes valuable insights into the local epidemiology of anal HPV among MSM, supporting the optimization of clinical management strategies and the development of targeted prevention interventions to reduce the burden of HPV-related complications in this vulnerable population.

The authors state that this article is not under consideration for publication elsewhere, that its publication is approved by all authors, and that, if accepted, it will not be published elsewhere in the same form, in English or in any other language, including electronically without the written consent of the copyright-holder. This study was approved by the Ethical Committee of our institution.

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CONFLICT OF INTEREST

Authors declare no have conflict of interest.

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