JOURNAL OF THE Selva Andina Research Society
Official Journal of the Selva Andina Research Society.

Original Article

ISSN 2072-9294 (print edition)
JSARS
ISSN 2072-9308 (online edition)

Prevalence of high-risk HPV genotypes in Bolivian women: study in La Paz and Pando

Prevalencia de genotipos de HPV de alto riesgo en mujeres bolivianas: estudio en La Paz y Pando

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Article Date

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Keywords:

Human Papillomavirus (HR-HPV),
molecular genotyping,
cervical cancer.

J. Selva Andina Res. Soc.
2026; 17(1):70-81.
Article ID: 211/JSARS/2026

Article History

Received February 2026.
Returned May 2026.
Accepted June 2026.
Available online, August 2026.

Edited by:
Selva Andina Research Society

Palabras clave:

Virus Papiloma Humano de alto riesgo (HR-VPH),
genotipado molecular,
cáncer de cuello uterino,
prevalencia epidemiológica,
Bolivia.

Abstract

Cervical cancer is a priority public health problem in Bolivia, associated with the high-risk Human Papillomavirus (HPV-RA). Genotyping makes it possible to identify oncogenic variants and guide prevention and control strategies. A retrospective, cross-sectional study was carried out with 6445 cervical samples collected using endocervical brushes. After the purification, 6274 samples were analyzed. DNA extraction was automated, and detection/genotyping was performed by real-time PCR. Infection rates were calculated by department, municipality, age, and genotype. Statistical analysis included tests of association and linear trend. The overall prevalence of HPV-RA was 21.4 % (1320 cases). By departments, La Paz 21.84 % (95 % CI: 21.73-21.95), Pando 18.07 % (95 % CI: 17.88-18.26). In municipalities, the prevalence was higher in Nuestra Señora de La Paz, 24.11 % (95 % CI: 22.54-25.68), followed by El Alto 18.11 % (95 % CI: 16.41-19.81) and Cobija 18.39 % (95 % CI: 16.11-20.67). The most frequent genotypes were HPV 16 (13.97%), HPV 31 (12.19%), and HPV 51 (8.63%). The age group of 31-40 years concentrated 615 cases (46.6%) with a significant association ($p < 0.001$) and positive linear trend ($p < 0.001$). Monoinfections predominant by HPV 16 (15.8%) and multiple infections (5.3%) were observed, mainly combinations of HPV 16/31 and HPV 16/51. The high prevalence of HPV-RA in women from La Paz and Pando, together with the predominance of oncogenic genotypes, underscores the need to strengthen vaccination and molecular screening programs adapted to the Bolivian epidemiological profile.

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Resumen

El cáncer cervical es un problema prioritario de Salud Pública en Bolivia, asociado al Virus del Papiloma Humano de alto riesgo (HPV-AR). La genotipificación permite identificar variantes oncogénicas y orientar estrategias de prevención y control. Se realizo un estudio retrospectivo, transversal con 6445 muestras cervicales recolectadas mediante cepillos endocervicales. Tras la depuración, se analizaron 6274 muestras. Extracción de ADN fue automatizada, y la detección/genotipicación se efectuó mediante PCR en tiempo real. Se calcularon tasas de infección por departamento, municipio, edad y genotipo. El análisis estadístico incluyó pruebas de asociación y tendencia lineal. La prevalencia global de HPV-AR fue 21.4 % (1320 casos). Por departamentos, La Paz 21.84 % (IC 95 %:21.73-21.95), Pando 18.07 % (IC 95 %: 17.88-18.26). En municipios, la prevalencia fue mayor en de Nuestra Señora de La Paz, 24.11 % (IC 95 %:22.54-25.68), seguida de El Alto 18.11 % (IC 95 %:16.41-19.81) y Cobija 18.39 % (IC 95 %:16.11-20.67). Los genotipos más frecuentes fueron HPV 16 (13.97 %), HPV 31 (12.19 %) y HPV 51 (8.63 %). El grupo etario de 31-40 años, concentró 615 casos (46.6 %) con asociación significativa ($p < 0.001$) y tendencia lineal positiva ($p < 0.001$). Se observaron monoinfecciones predominantes por HPV 16 (15.8 %) y multiinfecciones (5.3 %), principalmente combinaciones HPV 16/31 y HPV 16/51. La elevada prevalencia de HPV-AR en mujeres de La Paz y Pando junto con la predominancia de genotipos oncogénicos, subraya la necesidad de fortalecer programas de vacunación y tamizaje molecular adaptados al perfil epidemiológico boliviano.

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Introduction

Cervical cancer is one of the main public health problems in women globally, with a disproportionately high burden in low- and middle-income countries (LMICs), accounting for about 90 % of cases and deaths. In contrast, in countries with a high human development index (HDI), incidence and mortality decreased significantly thanks to effective prevention programs, screening, and timely access to treatment[1-4].

According to the International Agency for Research on Cancer (IARC), Bolivia is the only country in the Americas that ranks first in both incidence and mortality of cervical cancer, with rates of approximately 22.4 and 18.8 %, respectively, reflecting a high local epidemiological burden. Globally, breast cancer is the most common cancer in women (23.8 % incidence), while cervical cancer is the fourth most common (6.9 %)[5,6].

The World Health Organization (WHO), in its Global Strategy for the Elimination of Cervical Cancer, set a goal of reducing the incidence to less than 4 cases per 100 000 women/year, with three objectives for 2030; vaccination of 90 % of girls under 15 years of age, screening of 70 % of women with high-precision tests and effective treatment of 90 % of precancerous lesions and invasive cancer detected[2,7,8].

The main cause of cervical cancer is persistent infection with high-risk (HR) types of the Human Papillomavirus (HPV), transmitted mainly sexually[2,9,10]. More than 200 HPV genotypes have been identified, of which 14 are considered oncogenic, with types 16 and 18 responsible for about 70 % of cases[2,11,12]. Recently, the International HPV Reference Centre (IHRC) recognised six new types (HPV 226-231), redefining the total number of HPV types[13].

The identification of circulating genotypes is essential to guide vaccination and screening programs. Since the population efficacy of vaccines depends on their agreement with the predominant types. Likewise, molecular surveillance makes it possible to monitor changes in genotypic distribution, evaluate the effectiveness of interventions and strengthen strategic planning towards the elimination goals proposed by the WHO.

In Bolivia, the Unified Health System (SUS) guarantees free cervical cancer screening in women between 30 and 65 years of age, and exceptionally in women under 30 with risk factors, according to medical criteria. However, epidemiological data on the prevalence of HPV-HR genotypes in the national population are scarce[14-16], which limits the comprehensive understanding of the molecular behavior of the virus and hinders decision-making based on local evidence.

Faced with this gap, the National Institute of Health Laboratories (INLASA), through the Center for Molecular Genetics Research (CIGMO), in 2023 continued with the detection and genotyping program of the 14 HPV-HR genotypes using multiplex PCR techniques implemented since 2020.

Based on the above, the objective was to determine the prevalence of the 14 HPV-HR genotypes in samples analyzed at CIGMO during the 2023 management (January-December), providing updated epidemiological evidence that strengthens cervical cancer prevention, vaccination, and control strategies in Bo-

livia.

Material and methods

Study design. The present study was retrospective, observational and cross-sectional, whose objective was to identify the prevalence of the 14 HPV-HR genotypes in the samples analyzed at CIGMO during the 2023 management (January to December).

Study population. During the 2023 management, CIGMO processed 6445 samples, for HPV-HR detection by real-time PCR. Each sample was collected after completing a form that included informed consent, guaranteeing and respecting the bioethical principles of the Declaration of Helsinki. A total of 171 samples were excluded because they did not meet inclusion criteria (spilled samples, incomplete data, absence of verifiable consent in children under 18 years of age, origin from other departments). Finally, 6274 samples of women between 18 and 79 years old were evaluated: 4935 (78.65 %) from the department of La Paz and 1339 (21.34 %) from Pando.

Geographical distribution. INLASA, as a national reference, received samples from first, second and third level health facilities. In La Paz, 4935 samples from seven provinces were analyzed: Aroma (Patacamaya), Camacho (Mocomoco), Ingavi (Viacha), Los Andes (Pucarani), Murillo (Nuestra Señora de La Paz, El Alto), Omasuyos (Achacachi) and Sud Yungas (Palos Blancos). In Pando, 1339 samples from four provinces (Abuna, Madre de Dios, Manuripi and Nicolás Suárez) were processed, distributed in municipalities such as Cobija (17.7 %), Puerto Gonzalo Moreno (1.7 %), among others.

Sample collection. CIGMO has provided all Health Facilities with the means of viral transport (disposable tube for collecting viral samples, manufactured by Shenzhen Huaree Technology CO., LTD) and endocervical brushes (Cervical Brush // Cyto - Brush produced by MA. Shanghai Channelmed Import & Export CO., LTD. China). Before collecting samples, training was carried out on the technique for taking endocervical samples and previous conditions necessary for patients. The samples were collected in the offices of the First, Second and Third Level Health Centers by medical professionals, including gynecologists, family doctor, SAFCI doctor, Medico Mi Salud and General Practitioner duly trained, following the practice protocols currently accepted and replicated in the trainings. Subsequently, the samples were sent to CIGMO for molecular diagnosis.

Sample. In a volume of 3 mL containing a solution for the preservation of cells and genetic material. It was stored at a temperature of 4° C for a period of up to 5 days before shipping. Subsequently, all samples were sent to the CIGMO Laboratory in a triple packaging, designed to ensure their integrity and safety during transport, considering their biological nature.

Extraction of genetic material. DNA extraction was performed using an automated system with magnetic beads (MD-NAE 32, MagHT ™ Nucleic Acid Isolation Kit, E-diagnosis), from 400 µL of sample, with a final elution of 80 µL.

Real-time PCR detection and amplification. For detection and genotyping, the Anyplex™ II HPV HR Detection PCR kit (Seegene, Korea) was used, which allows the simultaneous detection of 14 genotypes (16, 18, 45, 31, 33, 35, 39, 51, 52, 56, 58, 59, 66 and 68) using DPO™ and TOCE™ technologies. Each reaction included 15 µL of Master Mix and 5 µL of DNA with positive and negative controls.

Amplification was performed on a CFX96 (Bio-Rad) system, and the results were interpreted with Seegene Viewer, manually confirmed. The detection limit was 50 copies/reaction.

Statistical analysis.

Overall prevalence. The overall prevalence was calculated by dividing the number of positive samples

by the total analyzed, with 95 % confidence intervals (95 % CI).

Infection rates were estimated by department and capital municipalities (Nuestra Señora de La Paz, El Alto and Cobija). The distribution of the 14 HPV-HR genotypes and their relative frequency were analyzed. Prevalence was stratified by age groups (≤ 20, 21-30, 31-40, 41-50, 51-60 and ≥ 61 years), with 95 % CI for each category. The association between age and infection was evaluated using contingency tables and Chi-square test, considering statistical significance at $p < 0.05$. All analyses were performed using IBM SPSS Statistics v25.0 and Microsoft Excel 2021.

Results

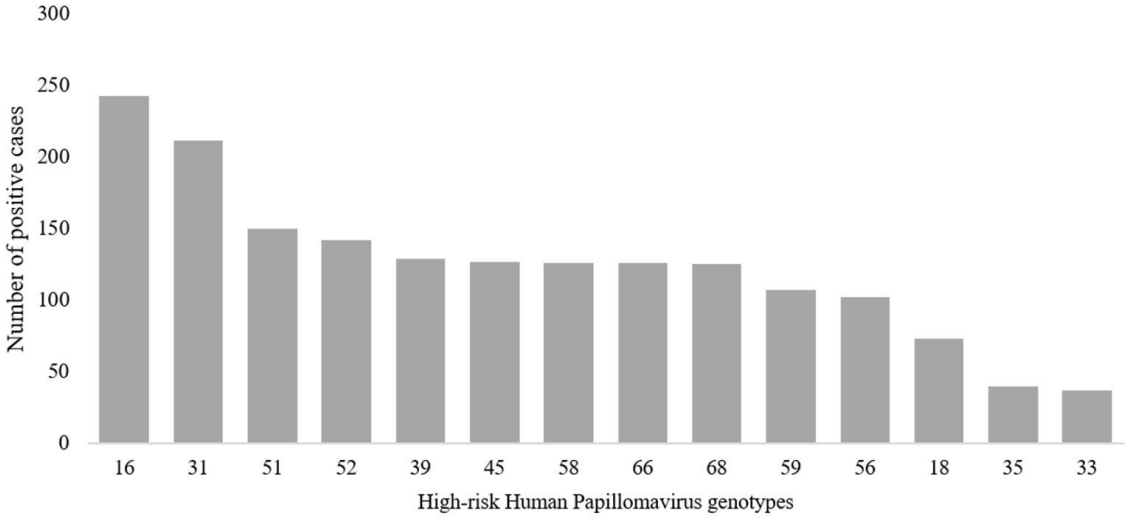


Figure 1 Distribution of high-risk genotypes of the Human Papillomavirus

Total prevalence of HPV-HR infection. Of the 6274 samples analyzed by real-time PCR at CIGMO INLASA, 1320 were positive for HPV-HR, with an overall prevalence of 21 % (95 % CI: 20.95-21.13). By department, the prevalence was 21.8 % (95 % CI: 21.73-21.95) in La Paz (*n*=4935*)* and 18.1 % (95 % CI: 17.88-18.26) in Pando (*n*=1339*).*

At the municipal level, it reached 24.1 % in Nuestra Señora de La Paz (95 % CI: 22.54-25.68), 18.1 % in El Alto (95 % CI: 16.41-19.81) and 18.4 % in Cobija (95 % CI: 16.11-20.67).

Specific distribution of genotypes. Of the 1320 positive samples, the most frequent genotype was HPV 16 with 243 cases (14.0 %), followed by HPV 31 with 212 cases (12.2 %) and HPV 51 with 150 cases (8.6 %) (Figure 1).

In La Paz, the predominant genotypes were HPV 16 (13.70 %), and HPV 31 (12.79 %). In the municipality of Nuestra Señora de La Paz HPV 16 (14.22 %), while in El Alto, HPV 31 (14.32 %) predominated.

In Pando, HPV 16 was also the most frequent (15.26 %), followed by HPV 68 (10.71 %), followed by HPV 31 (9.42 %) Figure 2.

Distribution by age groups. The 30-40-year-old group concentrated the highest proportion of samples analyzed (45.6 %), followed by the 41-50 group

(29.0 %). The 21-30 and 51-60 age groups accounted for 11.3 % (712 cases) and 11.7 % (735 cases), respectively. The age extremes were of lower participation: ≤ 20 years (34 cases; 0.5 %) and ≥ 61 years (114 cases; 1.8 %).

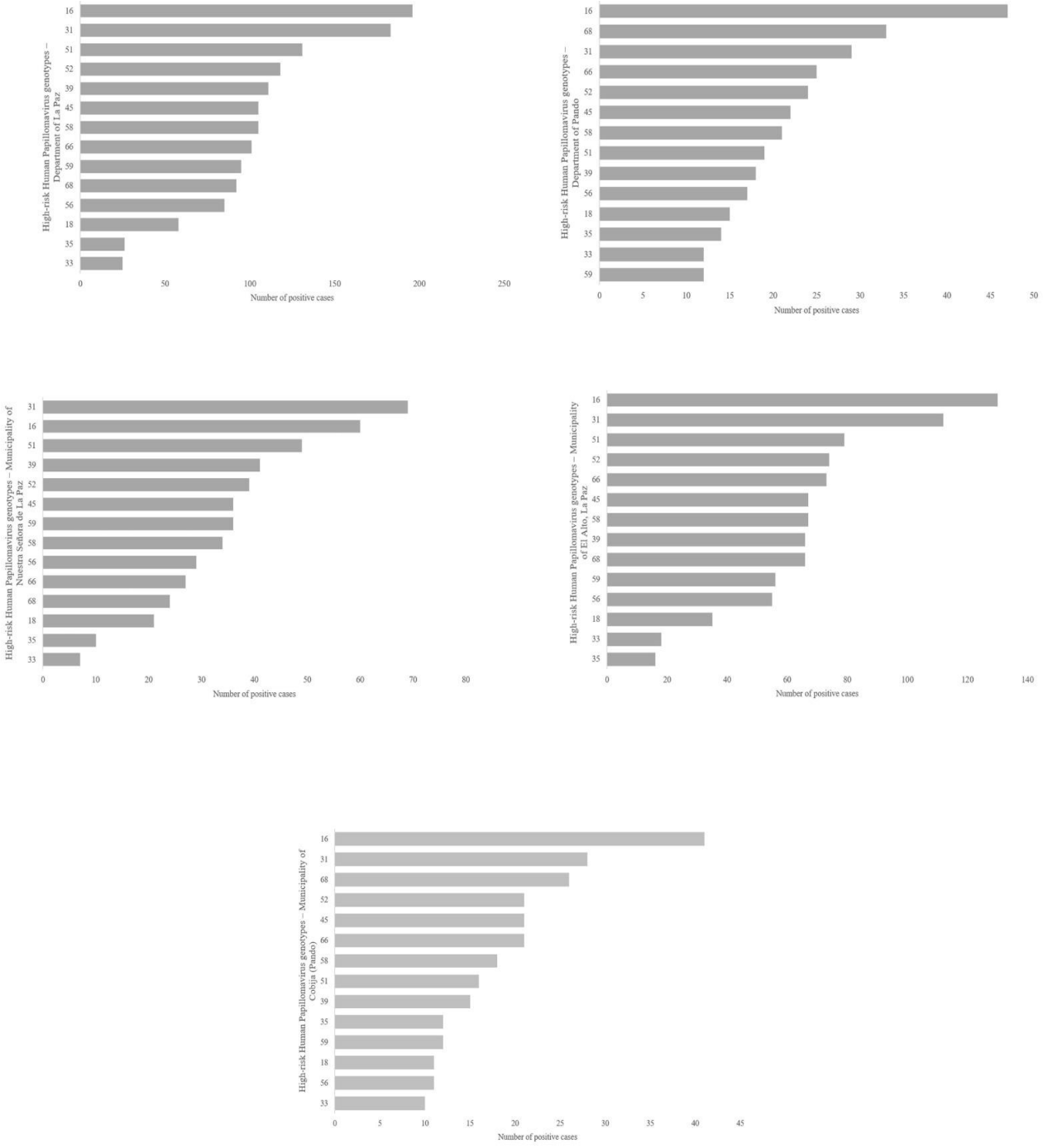


Figure 2 Distribution of high-risk genotypes of Human Papillomavirus by department and municipalities of capital cities

Of a total of 6274 samples, 79.0 % (4954) were negative and 21.0 % (1320) positive. The 31-40-year-old group had the highest proportion of positive results (615 cases; 46.6 %). A statistically significant association was evidenced between age group and test result ($p < 0.001$), as well as a significant linear trend ($p < 0.001$), indicating variations in positivity as age increases Figure 3.

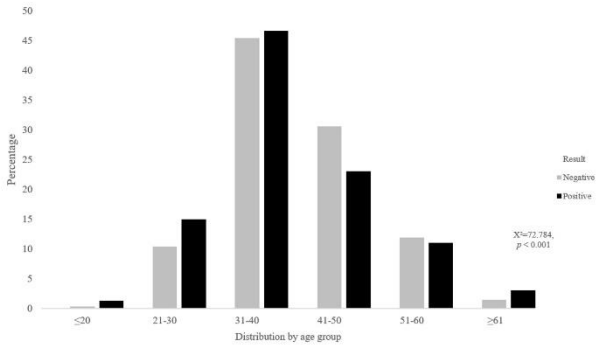


Figure 3 Distribution of positive and negative results by age group

Distribution of genotypes by age. In ≤ 20 years, HPV 31 (6 cases) and HPV 16 (4 cases) were the most frequent. In 21-30 years, HPV 16 (49 cases) predominated, followed by HPV 31 (37 cases) and HPV 52 (35 cases). In 21-30 years, HPV 16 (49 cases) predominated, followed by HPV 31 (37 cases) and HPV 52 (35 cases). In 31-40 years, HPV 16 (116 cases) and HPV 31 (95 cases) were the most common, along with HPV 51 (66 cases). In 41-50 years, HPV 16 (51 cases) and HPV 31 (49 cases) led, followed by HPV 45 (39 cases). In 51-60 years, the most frequent genotypes were HPV 51 (23 cases), HPV 66 (22 cases) and HPV 52 (19 cases).

Overall, HPV 16 was the most prevalent genotype in all age groups, especially in the youngest, reaching proportions close to 50-60 % in some subgroups. Other genotypes such as HPV 18/31/58 were less frequent, with variations according to age (Figure 4).

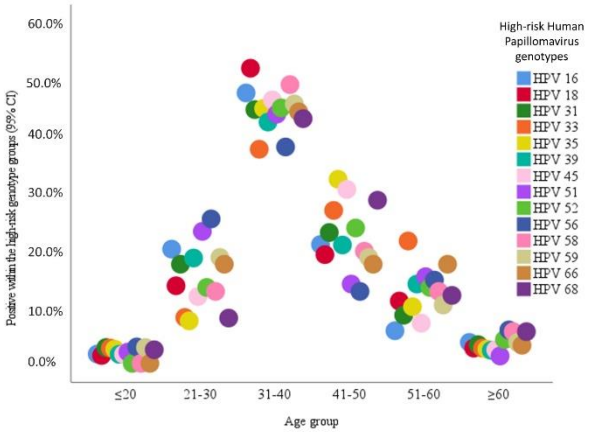


Figure 4 Distribution of high-risk genotypes of the Human Papillomavirus by age group

Association between genotypes and age groups. A statistically significant association was observed between the presence of HPV 16 ($p = 0.014$), HPV 51 ($p = 0.002$), HPV 56 ($p = 0.002$) and HPV 68 ($p = 0.046$) with the different age groups, suggesting an association between these infections and the age of the individuals. In contrast, no significant association was identified for HPV 18 ($p = 0.954$), HPV 31 ($p = 0.191$), HPV 33 ($p = 0.257$), HPV 35 ($p = 0.589$), HPV 39 ($p = 0.641$), HPV 45 ($p = 0.232$), HPV 52 ($p = 0.551$), HPV 58 ($p = 0.271$), HPV 59 ($p = 0.499$) or HPV 66 ($p = 0.089$).

Infection trends by genotype according to age. Infection frequencies varied between genotypes and age groups: i) HPV 16; higher prevalence in young people (23.5 % in ≤ 20 years and 24.7 % in 21-30 years), decreasing in older adults (9.6 % in 51-60 years). (ii) HPV 18; low frequency (5.5 %) and stable in all groups. (iii) HPV 31; 16.1% positivity, with a higher proportion in ≤ 20 years (35.3 %) and progressive decrease with age (12.3 % in 51-60 years). (iv) HPV 33/35; low frequency (< 3 %), with peaks in ≤ 20 years and in 51-60 years. (v) HPV 39/45; around 10

% positivity, with moderate variations according to age. (vi) HPV 51; 11.4 % positivity, more frequent in ≤ 20 years (17.6 %) and 51-60 years (15.8 %). vii) HPV 52/56/58/68: they were more frequent in extreme age groups (≤ 20 years and ≥ 61 years), reaching up to 17.5 % in some cases.

For HPV 59/66; low prevalence (< 10 %), with no significant variations between groups. *Monoinfection and multiinfection*. Of the total number of positive cases, 15.8 % (*n*=989*)* corresponded to monoinfections and 5.3 % *(n*=331*)* to multiple infections. Monoinfections; the most frequent genotype was HPV 16 (160 cases; 16.2 %), followed by HPV 31 (133 cases; 13.5 %). Multiinfections; most corresponded to co-infections with two genotypes (76.7 %; *n*=254*)*, followed by three *(*20.2 %; *n*=67*)*, four *(*2.7 %; *n*=9*)*, and five genotypes (0.3 %; *n*=1*)*. The genotypes with the highest infection rate were HPV 16 (11.1 %), HPV 51 (10.7 %), and HPV 31 (10.5 %). The most frequent combinations were HPV 16/31 (10 cases), HPV 16/51 (9 cases) and HPV 66/58 (8 cases).

Discussion

The global burden of HPV infection has evolved significantly in recent decades. In 2012, the global prevalence in women without cervical anomalies was estimated at 16 % in Latin America[17], currently the high risk continues to be incidence and mortality in women, particularly in South America[18].

In our study, relevant differences were observed between departments of La Paz 21.84 % (95 % CI: 21.73-21.95 %) higher than that of Pando 18.07 % (95% CI: 17.88-18.26 %) These variations could be related to population factors, urbanization and access to health services.

The most frequent genotype was HPV 16 (13.97 %), followed by HPV 31 (12.19 %) and HPV 51 (8.63 %). These findings coincide with international studies, such as the one conducted in Italy that reported a high frequency of these genotypes[12]. However, previous research in rural communities of La Paz identified a higher prevalence of HPV 56/39/31, followed by (HPV 16/18)[19]. In addition, other studies have reported similar frequencies of genotypes, such as HPV 52 (17.6 %), HPV 31 (15.7 %), and HPV 16 (12.9 %)[20]. Worldwide, HPV 16/18 is the main culprit of cervical cancer, corroborated in multiple studies[17,21-23], along with other common genotypes such as (HPV 52/31/58) [21-23].

The highest prevalence of infection was observed in women aged 31-40 years (46.6 % among all positive cases), consistent with previous reports[24-26].

The analysis by age indicated that HPV 16 predominated in young groups ≤ 20 and 21-30 years, decreasing at older ages, suggesting greater persistence in young women, in accordance with previous studies[25,27]. Other genotypes such as HPV 18/31/68 presented specific patterns, although without significant associations in all age groups, reflecting population variability.

Regarding the form of infection, 15.8 % corresponded to monoinfections, with HPV 16 being the most frequent with a prevalence of 16.18 %, while 5.3 % were multiinfections. This finding is clinically relevant, since co-infections can increase the risk of progression to malignant lesions[28,29]. The discrepancy with studies that report higher rates of monoinfection[30,31] could be due to methodological or population differences.

The most common associations in our study were HPV 16/31, HPV 16/51 and HPV 66/58, while worldwide the most frequent are usually (HPV 16/18)[30,32-35].

Finally, significant associations were identified between age and certain genotypes (HPV 16/51/56/68), suggesting a greater propensity of these types to infect certain age groups. In contrast, genotypes such as HPV 18/33 did not indicate a relationship with age, which indicates that their distribution could depend on other epidemiological or biological factors.

Funding Source

This study was funded by the National Program to Fight Cancer (PNLCC). The National Institute of Health Laboratories (INLASA), the host institution, provided complementary support through the provision of its own institutional resources, infrastructure and operational support.

Conflicts of interest

All authors declare no conflicts of interest in relation to this study

Acknowledgements

We thank the technical and administrative staff of CIGMO-INLASA for their operational and logistical support, as well as the support of the Coordination of the Diagnostic Division and the National Program to Fight Cancer. Finally, Dr. Luisa Valentina Hurtado López and Dr. Milton Pedro Soria Humerez for being pioneers in the implementation of real-time PCR for human papillomavirus at INLASA.

Ethical considerations

The study was carried out respecting the bioethical principles of confidentiality, anonymity and protection of personal data, in accordance with current national and international regulations. The integrity and rights of the participants were guaranteed throughout the research process.

Limitations in research

The authors note that there were no limitations to the research.

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Contribution of the authors in the article

Simón Quispe-Quispe, design, data collection, data analysis, interpretation and writing of the article, results and discussion. *María Esther Chuquimia-Choque*, material and methods, literature review for material, discussion, analytical and post-analytic phase. *María Isabel Pocoma-Rodríguez*, pre-analytical, analytic phase. *María Elena Flores-Rojas*, pre-analytical, *Giovanni Rodrigo García-Rada*, supervision of all phases of the research, revision and correction of the manuscript.

Informed consent

Participation in the study was voluntary and conditional on the signing of the informed consent form, included in the epidemiological file. Only those par-

ticipants who expressed their acceptance by signing the document were included, authorizing the use of their samples for research and publication purposes, with the guarantee of keeping their identity in strict confidentiality.

Use of artificial intelligence

In the present study, no AI-based tools were used for data collection, processing, or analysis, or for the generation of graphs, figures, or any other type of visual representation. Similarly, the writing and preparation of this manuscript were carried out exclusively by the authors, without the intervention of artificial intelligence technologies or other automated systems.

Imaging Disclosure

All the figures and diagrams were made by the authors, no artificial intelligence tool was used in their realization.

Data Access

Autorizamos el acceso, uso y tratamiento de los datos únicamente para las multas especificadas, garantizando la confidencialidad y cumpliendo con la normativa vigente sobre protección de datos.

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