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Original Research Article

Molecular Genotyping of Human Papilloma Virus (HPV) in Women with Normal Endo-Cervical Cytology in Senegal

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Abstract

Background: Cervical cancer (CC) is a major public health problem worldwide. In Senegal, it is the first female cancer before breast cancer. Human papillomavirus (HPV) has been described as responsible for CC and is the most common sexually transmitted infection in the world. Low risk HPV (HPV-LR) including HPV 6 and HPV 11 are responsible for most of mild infections while among high-risk HPV (HPV-HR) including genotypes 16, 18, 45, 31, 33, 52, 58, 35 in order of frequency are involved in almost 90% of cervical cancer. Objective: The general objective is to do molecular genotyping of HPVs and to assess the prevalence of HPV types among Senegalese women. *Materials and methods:* The study was done on a population of 198 sexually active women with normal cytology. DNA extraction is carried out using endocervical samples stored in Abbott Cervi-Collect Specimen Collection Kit tubes with the Zymo Research DNA Viral KITTM, USA www.Zymoresearch.com. Molecular identification of the HPV genotypes (19 HPV-HR and 9 HPV-LR) was carried out by multiplex PCR with the Anyplex[™]II HPV28 Detection kit from Seegene on a CFX96[™] Bio-Rad machine. Data analysis was performed by R Studio software (3.6.0), Pearson chi-square comparisons or Fisher's exact test. Odds Ratios were calculated to estimate the association between individual characteristics and HPV infection if P<5%. Results: 64.65% (128/198) Women were infected with HPV. HPV-HR and HPV-LR had respective prevalences of 57.07% (113/198) and 34.34% (68/128). 37.37% of the women presented a co-infection, that is to say hosting at least two genotypes. The most common genotypes were HPV56 (27.78%), HPV68 (12.12%), HPV52 (8.59%), HPV31 (8.08%), HPV58 and HPV82 (7.07% each) in HPV-HR and among HPV-LR HPV 42 (14.14%), HPV54 (8.08%), HPV43 and HPV44 (5.05%, each). HPV16 and HPV18 had a prevalence of 7.07% and 5.05% respectively and HPV-6 and HPV-11 also had a prevalence of 4.54% and 0.51% respectively. Our results showed that there was an association between HPV infection, age, marital status and contraception. Conclusion: Our results show high prevalence of HPV HPV-HR and HPV-LR in our population of women with normal cytology. The number of co-infected women who harbored at least two genotypes was high. The non-vaccine genotypes are mainly identified (HPV56, HPV42, HPV68, HPV52, HPV31, HPV54 et HPV82). The HPV16 and HPV18 genotypes were present at a moderate level. The woman's marital status, the woman's age and contraception were associated with HPV infection. These results contribute to a better understanding of the molecular epidemiology of HPV in Senegal. **Keywords**: HPV, Prevalence, AnyplexTM II HPV 28 Detection, Genotyping, Senegal.

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INTRODUCTION

The main cause of cervical cancer is the persistence of human papilloma virus (HPV) infection. This persistence of HPV can lead to cellular abnormalities, which in the natural development of the disease can lead to cervical cancer [1]. Nowadays more than 189 genotypes of HPV have been identified among them 120 types are susceptible to infect humans and of which the 40 genotypes are responsible for genital infections [2]. The latter are classified according to their

epidemiological association with cervical cancer. A distinction is made between low-risk HPV (HPV-LR) such as HPV types 6 and 11 can cause benign or low-grade changes in cervical cells, and are responsible for around 90% of genital warts [3] and high-risk HPV (HPV-HR), which can cause anal and genital cancers [4]. These HPV-HR are found in almost 100% of cervical cancers and in a variable proportion of other genital or oropharyngeal cancers. HPV-HR types 16 and 18 are found worldwide in around 70% of cancers linked to

HPV [5]. Genotypes 16,18, 45, 31, 33, 52, 58, 35, in order of frequency, are involved in almost 90% of cervical cancers [6].

HPV infection is among the most common human viral infections around the world; about 80% of sexually active people will be infected at some point in their lives. Human-to-human transmission occurs mainly through direct contact; however, their transmission is not exclusively sexual [7].

About 10.4% of women with normal cytological results in the cervix are infected with HPV. The least developed regions were particularly the most affected in particular in Africa (22.1%), in Central America and Mexico (20.4% each) compared to North America (11.3%) to Europe (8.1%) and Asia (8.0%) [8]. The hypothesis of the link between genital HPV infections and cervical cancer was suggested in the early 1976s and later confirmed by fundamental and epidemiological studies [9].

Each year, there are approximately 569 847 new cases with an estimated 311 400 deaths. Which makes cervical cancer (CC) a major public health problem worldwide [10]. It is the second most frequently diagnosed cancer and the third leading cause of death from cancer in women in developing countries [11]. In Senegal it is the first female cancer in 2018 with around 1876 new CCs diagnosed each year [12]. Although HPV infection is common, studies suggest that around 90% of infections disappear over the years [13]. Three types of prophylactic vaccines are available and have been developed based on epidemiological data from Western countries. They therefore targeted HPV types 6,11,16,18 and several other subtypes [14]. However, in our African countries other non-vaccine genotypes are revealed but which seems to pose a problem as shown by various studies carried out in an African environment [15]. Since HPV-HR infection is a cause of cervical cancer, HPV-HR detection tests based on the detection of viral DNA by molecular techniques have been proposed as a complementary tool to cervical cytology [16]. Large-scale use in specialized laboratories allows early management of HPV infections and effective prevention of cervical cancer.

The objective of our study was to do a molecular genotyping of HPVs and to assess their prevalence in a population of Senegalese women with normal endo-cervical cytology.

MATERIALS AND METHODS

Study Type and Population

This descriptive and analytical cross-sectional study was carried out in the molecular biology laboratory of the Armed Forces AIDS Control Program at the Ouakam Military Hospital Dakar, Senegal, from February 2016 to May 2019. The target population was 198 women who came to undergo cervical cancer screening or prescription screening from various health facilities with free and informed consent. Each woman responded to a survey sheet collecting information on identity, socio-demographic parameters such as age, marital status abortion age of first sexual intercourse, the number of sexual partners, contraception has been filled. To be eligible women had to be sexually active and able to undergo a vaginal speculum examination.

Samples

198 endo-cervical samples were taken using a cytobrush by swabbing the endocervix. The cytobrush is then introduced into a transport tube of the Abbott multi-sample collection kit (Abbott GmbH Co. KG Max Plank, Germany) and the sample is stored at -80°C before the test.

DNA extraction and nanodrop DNA assay

The extraction of viral DNA was done using the Zymo DNA kitTM Research, USA, www.zymoresearch.com according to the manufacturer's protocol of 200μ l of endocervical sample. Viral DNA extract was analyzed using NanoDropTM Lite [17] to assess its quality and quantity and then stored at -20°C before PCR.

Molecular Genotyping

The molecular analysis was carried out by multiplex PCR with the Seegene Anyplex II HPV28 Detection kit on the CFX96 real-time Biorad machine according to the manufacturer's protocol. The Anyplex II HPV28 Detection method makes it possible to detect 28 HPV genotypes in vitro in cytological fluids or cervical samples. This technique makes it possible to detect genotyping and quantify individually 19 HPV-HR (16, 18, 26, 31, 33, 35, 39, 45, 51, 52,53, 56, 58, 59, 66, 68, 69, 73, 82) and 9 HPV-LR (6, 11, 40, 42, 43,44, 54, 61, 70) by using DPO (double priming oligonucleotide) and TOCETM (Tagging Oligonucleotide Cleavage and Extension) technology [18], a fragment of the β -globin gene was co-amplified as an internal control.

Data entry and Analysis

All information collected from the questionnaires was recorded in an Excel database. Data analysis was performed by R Studio software (3.6.0). Proportional comparisons were made using the Pearson chi-square test or the Fisher exact test.

The significance rate is P <5%. Odds Ratios were calculated to estimate the association between individual characteristics and HPV infection and P<5%.

RESULTS

Prevalence of HPV in the general population

64.65% (128/198) patients had an HPV infection (Table-1). The respective prevalence of HPV-HR and HPV-LR were 57.07% and 34.34%.

Multi-infection was present in 37.37% of women, that means hosting at least two HPV genotypes (Table-2).

Identification of HPV genotypes in the study population

Our study method makes it possible to detect 28 genotypes. We have described the most representative types of HPV in our study population. The genotypes HPV56, HPV42, HPV68 were the main viruses identified with a prevalence of 27.78%, 14.14% and 12.12%. Secondly follow the genotypes HPV52 (8.59%) HPV31 and HPV54 (8.08%) and HPV58 and HPV82 (7.07%). Due to their highly oncogenic nature, we are interested in the HPV16 and HPV18 genotypes and their prevalence was 7.07% and 5.05% respectively. Due to their strong presence in genital warts, types HPV6 and HPV11 were also found with a prevalence of 4.54% and 0.51% (Table-2).

Prevalence of HPV by age

The median age of the patients was 43 years with extremes of 20 and 73 years. To study the age-HPV infection relationship, our cohort was classified into three groups. The prevalence of HPV was 67.9%, 51.8% and 79.7% respectively in age groups <35 years, [35-50] and \geq 50 ans. Women aged <35 years and \geq 50 years were more infected than those aged between 35-50 years (p=0.002) (Table-1).

Prevalence of HPV by marital status

We evaluated the carrying of the HPV according to the marital status of the patient. The

prevalence of HPV was 80% and 60.1% respectively for unmarried and married women. Prevalence of HPV was significantly higher in unmarried women, (p=0.01); OR=2.6 (Table-1).

Prevalence of HPV according to contraception

The evaluation of the carrying of HPV according to contraception showed a prevalence of HPV of 73.8% and 47.06% respectively in women without contraception and in those using contraception. Women who did not use contraception were more susceptible to HPV than those who did use contraception (p=0.0002; OR=3.2) (Table-1).

Prevalence of HPV by number of abortions

An HPV carrying rate of 65.7% and 63.2% was detected in women without abortion and in women with a history of abortion. Abortion is not considered here to be associated with HPV infection rates in women (p=0.75) (Table-1).

Prevalence of HPV by ethnicity

The relationship between the ethnic group and the carrying of the HPV-HR has been studied. Ethnic associations are grouped into three groups: Pulaars; Wolofs and others (Sérère, Jola, Soninké, Bambara etc.). The prevalence of HPV was 70.69%, 57.33% and 67.69% respectively among women of the Pulaars, wolofs and other ethnic groups. Ethnicity is not considered to be associated with HPV infection in women (p > 0.23) (Table-1).

| | Parameters (N) | HPV n (%) [IC 95%] | <i>P</i> -value | OR [IC 95%] |
|---|------------------------|--------------------------|-----------------|--------------------|
| | Prevalence HPV | 128 (64.65) | - | - |
| | (198) | [57.8–70.9] | | |
| Age | [20-35] (56) | 38 (67.9) | 0.002 | 0.51 |
| _ | | [54.8–78.6] | | [0.25-1.03] |
| | [35-50] (83) | 43 (51.8) | | 1 |
| | | [41.2-62.2] | | |
| | > 50 (59) | 47 (79.7) | | 0.27 |
| | | [67.7–87.9] | | [0.13-0.59] |
| Marital status | Non married (45) | 36 (80) | 0.01 | 2.6 |
| | | [66.2-89.1] | | [1.19-5.89] |
| | Married (153) | 92 (60.1) | | |
| | | [52.2-67.5] | | |
| Contraception | No (130) | 96 (73.8) | 0.0002 | 3.17 |
| | | [65.7-80.6] | | [1.71-5.88] |
| | Yes (68) | 32(47.06) | | |
| | | [35.6–58.8] | | |
| Abortion | No (102) | 67 (65.7) | 0.7 | - |
| | | [56.05-74.18] | | |
| | Yes (96) | 61 (63.5) | | |
| | | [53.57–72.48] | | |
| Ethnics | Others (65) | 44 (67.69) | 0.23 | - |
| | | [55.6–77.8] | | |
| | Wolofs (75) | 43 (57.33) | | |
| | | [46.05–67.9] | | |
| | Pulaars (58) | 41 (70.69) | | |
| | | [57.99-80.82] | | |
| N= | = sample size (num | ber), $n = HPV positive$ | e number | |
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Table-1: Prevalences of HPV as a function of socio-demographic parameters

| Table-2: Prevalence of individualized HPV genotypes in the general population | | | | | | |
|---|--------------|-----------|-------|-----------------|--|--|
| | Genotypes | Positives | (%) | IC à 95 % | | |
| HPV high risks (HPV-HR) | HPV-HR | 113 | 57.07 | [50.11 - 63.76] | | |
| | HPV 16 | 14 | 7.07 | [4.26 - 11.52] | | |
| | HPV 18 | 10 | 5.05 | [2.75 - 9.05] | | |
| | HPV 26 | 0 | 0 | [0.00 - 1.90] | | |
| | HPV 31 | 16 | 8.08 | [5.04 - 12.72] | | |
| | HPV 33 | 10 | 5.05 | [2.77 - 9.05] | | |
| | HPV 35 | 3 | 1.52 | [0.52 - 4.36] | | |
| | HPV 39 | 2 | 1.01 | [0.28 - 3.61] | | |
| | HPV 45 | 4 | 2.02 | [0.79 - 5.08] | | |
| | HPV 51 | 4 | 2.02 | [0.79 - 5.08] | | |
| | HPV 52 | 17 | 8.59 | [5.43 - 13.32] | | |
| | HPV 53 | 8 | 4.04 | [2.06 - 7.77] | | |
| | HPV 56 | 55 | 27.78 | [22.01 - 34.39] | | |
| | HPV 58 | 14 | 7.07 | [4.26 - 11.52] | | |
| | HPV 59 | 4 | 2.02 | [0.79 - 5.08] | | |
| | HPV 66 | 24 | 12.12 | [8.28 - 17.4] | | |
| | HPV 68 | 24 | 12.12 | [8.28 - 17.4] | | |
| | HPV 69 | 7 | 3.54 | [1.72 - 7.12] | | |
| | HPV 73 | 9 | 4.55 | [2.41 - 8.41] | | |
| | HPV 82 | 14 | 7.07 | [4.26 - 11.52] | | |
| HPV low risks (HPV-LR) | HPV-LR | 68 | 34.34 | [28.08 - 41.20] | | |
| | HPV 6 | 9 | 4.54 | [2.41 - 8.41] | | |
| | HPV 11 | 1 | 0.5 | [0.09 - 2.81] | | |
| | HPV 40 | 2 | 1.01 | [0.28 - 3.61] | | |
| | HPV 42 | 28 | 14.14 | [9.97 - 19.68] | | |
| | HPV 43 | 10 | 5.05 | [2.77 - 9.05] | | |
| | HPV 44 | 10 | 5.05 | [2.77 - 9.05] | | |
| | HPV 54 | 16 | 8.08 | [5.03 - 12.72] | | |
| | HPV 61 | 5 | 2.53 | [1.08 - 5.77] | | |
| | HPV 70 | 7 | 3.54 | [1.72 - 7.12] | | |
| | co-infection | 74 | 37.37 | [30.93 - 44.29] | | |

DISCUSSION

The prevalence of HPV in our general population is 64.65%. This rate is very high compared to the average in West Africa which was 27.8%% [19], however it is roughly equal to that described in Gabon (60%) [20]. It is much higher than those described in Senegal (12.7%) [21] and in Guinea (50.8%) [22], however a higher rate (76%) has been described in Morocco [23]. The variation in prevalence between countries may be linked to the difference in sexual practices and education. The difference in molecular techniques used in studies of HPV (panel of genotypes detected) may explain the variation in prevalence. HPV-HR genotypes were detected in 57.07% in our series. This rate is higher than the 13.6% reported in the Fiji Islands [24] but it is lower than the 72.6% described in Burkina Faso [25]. 37.37% of women had multiple infections. This multi-infection rate is above the 30% described in Senegal [26] but a higher rate of 77.42% has been described in Colombia [27]. These different rates may indicate that multiple infections are a common phenomenon since the modes of HPV transmission are identical. The most common genotypes in the population

were HPV56 (27.78%) HPV68 (12.12%), HPV52 (8.59%), HPV31 (8.08%), HPV82 (7.07%) among HPV-HR and HPV42 (14.14%) followed by HPV54 (8.08%) for HPV-LR. These results differ from those found in Senegal within the framework of a study carried out in five regions which had found a predominance of HPV 52 and 58 [28], and those found in Ethiopia where they had HPV16 followed by HPV35, HPV56, HPV58, HPV18, HPV31, HPV39, HPV45, HPV59 and HPV68 [29]. In our series, non-vaccine genotypes were predominant as in most Sub-Saharan countries Ouedraogo *et al.*, [24] and provide the risk of carcinoma of the cervix 2.94 times higher, [30]. HPV16 and HPV18 deserve special attention because they are involved in 70% of cervical cancers [31] in the whole world. Genotypes HPV16 and HPV18 had a prevalence of 7.07% and 5.05% respectively. These rates are lower than those found in Asia [32]. The socio-demographic factors of the patients and their relationship with the carriage of HPV in women were evaluated. Our results showed that there was an association between HPV infection and age (p = 0.002).

Women aged \geq 50 years and those aged <35 were the most infected and this U-shaped distribution was found in French Guiana [33] and in other countries by cross-sectional and cohort studies, with a first peak in women under 30 and a second peak in women 55 to 64 [34-36].

An association between HPV infection and marital status has also been shown (p=0.01). Single women were more infected with HPV. These results are in agreement with numerous studies notably those found in Senegal [21], Ouagadougou [25] and in Poland [37]. A strong association between HPV infection and contraception has also been shown (p=0.0002). Women who did not use any contraceptive method were more sensitive to HPV than others; these results corroborate those found in Burkina Faso [38]. However, our results differ from those found by numerous studies, which showed through numerous epidemiological studies that contraception was a risk factor for users [39, 40].

Our results showed that there was no association between HPV infection and the number of abortions by ethnicity.

CONCLUSION

Our results show high prevalence of HPV, HPV-HR and HPV-LR, in our population of women with normal endo-cervical cytology. The number of co-infected women who harbored at least two genotypes was high. The non-vaccine genotypes are mainly identified (HPV56, HPV42, HPV68, HPV52, HPV31, HPV54 and HPV82). The HPV16 and HPV18 genotypes responsible for 70% of cervical cancers were present at a moderate level. There was association between HPV infection and, age, marital status and contraception of women.

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