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RESEARCH ARTICLE

Type-Specific Human Papillomavirus Distribution in Invasive Squamous Cervical Carcinomas in Tunisia and Vaccine Impact

Emna Ennaifer^{1,3*}, Faten Salhi^{1,3}, Thalja Laassili^{1,3}, Emna Fehri^{1,3}, Nissaf Ben Alaya², Ikram Guizani¹, Samir Boubaker³

Abstract

Background: High risk human papillomaviruses (HPVs) are the leading cause of cervical cancer (CC) and Pap smear screening has not been successful in preventing CC in Tunisia. HPV vaccination that targets HPV16 and 18 offers a new efficient prevention tool. Identification of HPV types in CC is thus essential to determine the impact of HPV vaccine implementation. The aim of this study is to provide specific data from Tunisia. **Materials and Methods:** A total of 89 histological confirmed paraffin embedded samples isolated from patients with CC diagnosed between 2001 and 2011 were collected from five medical centres from Northern and Southern Tunisia. HPV DNA was detected using a nested PCR (MY09/MY11-GP5+/GP6+) and genotyping was assessed using a reverse blot line hybridisation assay that enables the detection of 32 HPV types. **Results:** HPV DNA was detected in all samples. Twelve high risk types were detected; HPV16 and/or 18 were predominant, accounting together for 92.1% of all the CC cases (HPV16: 83.1%). Single infections accounted for 48.8% of the cases and were mostly linked to HPV 16 (32.6%) and less frequently to HPV 18 (2.4%). The other high risk HPV single infections were linked to HPV 35 (4.6%), 45 (4.6%), 58 (2.3%) and 59 (2.3%). Multiple infections with mixing of 2 to 4 genotypes predominately featured HPV16 and/or 18 with HPV 35 and 45 (96.6 %) and less frequently with HPV 59, 40, 66, 73 and 58. There was no statistically significant variation in the relative distribution of HPV types with age. **Conclusions:** These results strongly indicate that prophylactic HPV vaccines can have a major impact in preventing CC in Tunisia

Keywords: Cervical cancer - human papillomavirus - genotypes - vaccine - Tunisia

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Introduction

HPV infection is the most common sexually transmitted infection all over the world and persistent infection with high risk HPV (HR-HPV) is the cause of cervical cancer (CC) (Walboomers M et al., 1999; Coglian et al., 2005). The estimates CC burden in the world indicate an incidence of 529.000 cases/year and 275.000 deaths/year (Ferlay et al., 2010). Eighty percent of CC cases are killing women in under-resourced countries. Future projections have statute that the incidence will reach 1.000.000 cases/year in 2050 (Ferlay et al., 2010). Among Tunisian women, this cancer now ranks third after breast and colorectal cancer (Ben Abdallah et al., 2009). However, since preventable, it is considered as a public health priority. In Tunisia, Pap smear screening programs have not been successful in preventing CC so the introduction of prophylactic HPV vaccination needs to be considered. Prophylactic HPV vaccines are designed to prevent HPV 16 and 18 infections and are considered efficient in reducing the burden of

CC. Despite a constant rate distribution of HPV 16 and 18 in CC all over the world (Kulkarni et al., 2011; Shen et Liu., 2013; Abdul Raub et al., 2014), regional variations have been documented (Clifford et al., 2003; Clifford et al., 2006). Thus, identification of HPV genotypes in CC is of great importance to determine the effectiveness of prophylactic vaccines implementation. The aim of the present study is therefore to determine using standardized protocols, HPV genotypes distribution in Tunisian specimens of squamous cell carcinoma (SCC) the most represented histotype of CC.

Materials and Methods

Study population

The study was conducted at Pasteur Institute of Tunis (IPT), in the HPV unit Research of the "Laboratory of Molecular Epidemiology and Experimental Pathology applied to infectious diseases" with straight collaboration of the Department of Human and Experimental Pathology.

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Recruitment was performed in the period ranging from 2001 to 2011. 89 archival selected paraffin embedded samples of diagnosed SCC were collected. The aim of the selection process was to avoid Bouin fixation that is unfortunately widely used and that causes DNA alterations (Longy et al., 1997; Benerini Gatta et al 2012). Biopsies and surgical specimens were assembled from 4 medical centers across the country: 68 samples from 3 Northern centers (24 from IPT, 30 from La Marsa hospital and 14 from Nabeul hospital) and 21 samples from the hospital of Sfax located in the center of Tunisia. The diagnosis of primary SCC was confirmed by histopathology for all samples.

Preparation of the paraffin samples

To ensure that HPV typing is performed onto DNA extracted from cancer tissue, a 4 μ m thick section was stained with haematoxylin and eosin and evaluated by a pathologist of the Department of Human and Experimental Pathology (IPT). Four other sections of 10 μ m thick each were further obtained from each paraffin block and kept in Eppendorf tubes for DNA extraction. To reduce the risk of cross-contamination, the blades were changed for each specimen and the microtome extensively washed with ethanol solutions. For each sample, a deparaffinization process eliminates the surrounding paraffin edges of the tissue section using a sterile crowbar. Then 3 washing steps in 65° Xylène and 4 washing steps with decreasing concentrations of ethanol were achieved at room temperature. A final heating of the samples was performed at 45°C to exclude paraffin remnants.

DNA extraction, HPV DNA detection and typing

DNA extraction was performed using the QIA amp DNA Mini Kit (Qiagen) according to the manufacturer's instructions. DNA quantification was assessed by spectrophotometry (A260/A280). HPV detection was performed with a nested PCR using MY09/MY11 and GP5+/GP6+ biotinylated primers as described by Carvalho Nde O et al (Carvalho Nde et al., 2010). The first PCR was performed in a final reaction volume of 50 μ L, containing 10 to 25 ng of DNA, 10 μ L of buffer [100 mM Tris-HCl, 500 mM KCl], 50 μ M of MgCl₂, 2.5 μ M of dNTPs, 10 μ M of each primer and 2.5 U of Taq DNA polymerase. The second PCR was performed in a final volume of 50 μ L, containing 1 μ L of the first reaction, 10 μ L of buffer [100 mM Tris-HCl, 500 mM KCl], 50 μ M of MgCl₂, 2.5 μ M of dNTPs, 10 μ M of each primer and 2.5 U of Taq DNA polymerase.

Genotyping was performed by a Reverse Line Blot hybridization assay using the different biotinylated probes in a Miniblotter system (World Health organization, 2009; Eklund et al, 2010). The oligonucleotides were covalently joined to a Biotin C membrane and activated with EDAC reagent (Sigma). The PCR products were denatured at 96°C, cooled on ice, and applied to each capillary of the Miniblotter. Hybridization was completed after 1 hour and the signal (peroxidase conjugate streptavidin Roche) was detected using a chemiluminescent autoradiography. This hybridization assay was performed for HLADQ and 32 HPV genotypes: HPV 6, 11, 16, 18, 26, 31, 33, 34, 35,

39, 40, 42, 44, 45, 51, 52, 53, 54; 55, 56, 57, 58, 59a, 59b, 66, 68, 69, 70, 73, 82, 83, 84.

Statistical analysis

All statistical analyses were performed using SPSS 13.0. Descriptive analysis was performed and the proportion of different genotypes was calculated. Comparison of mean age according to HPV genotypes was achieved using T-test. Chi-square test was used to compare the distribution of different genotypes by age groups.

Results

HPV detection

The study was conducted among 89 women aged from 33 to 88 years (mean 56.47 $\pm$ 12.86 years). HPV DNA was detected in all samples using nested PCR. Thus, among all subjects of this study, the prevalence of HPV infection in SCC was 100 %. Sixteen HPV genotypes were detected including 12 high risk types. The most prevalent genotypes were HPV16 and HPV 18 detected in respectively 83.1% and 42.7% of samples. When both single and mixed infections were considered, HPV16 and/or HPV18 were detected in 92.1% of the SCC. Single infections accounted for 48.8% of the specimens and were mostly linked to HPV 16 (32.6% of single infections) and less frequently to HPV 18 (2.4%). The others HR-HPV single infections

Table 1. Proportional Distribution of HR-HPV Types that were Detected in this Series of Invasive Cervical Carcinoma

HR-HPV type	Total	%	Single infections		Mixed infections	
			number	%	number	%
16	66	86.6	26	34.2	40	52.6
18	35	46	6	7.89	29	38.1
35	20	26.3	21	2.63	18	23.6
45	17	22.3	0	1.3	16	21
59	14	18.42	0	0	14	18.4
66	8	10.52	0	0	8	10.52
73	6	8.45	0	0	6	8.45
58	7	9.2	0	0	7	9.2
53	5	6.5	0	0	5	6.5
68	4	5.2	0	0	4	5.2
33	1	1	0	0	1	1
31	1	1	0	0	1	1

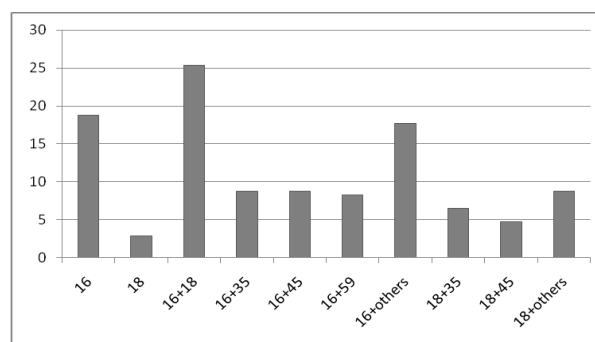


Figure 1. Proportional Distribution of Single and Mixed Infections with HPV16 and HPV 18 in this Series of Squamous Invasive Cervical Carcinoma

were linked to HPV 35 (4.6%), 45 (4.6%), 58 (2.3%) and 59 (2.3%). Multiple infections were mixing 2 to 4 HPV types and were predominately mixing HPV16 and/or 18 with HPV 35 and 45 (96.6 %), and less frequently HPV16 and/or 18 with HPV 59, 40, 66, 73 and 58 (Figure 1). Four low risk HPV types (HPV44, 40, 6 and 11) were detected in 22.4 % of SCC and were always mixed with HPV 16 and/or HPV18 and/or HPV35. The distribution of HR-HPV types is reported in table 1.

Statistical results

There was not any significant change in the relative distribution of the detected HPV types according to age using Chi-square test.

Discussion

The Tunisian CC incidence is similar to that seen in developed countries despite much lower screening (Cancer incidence in Five Continents, vol IX, 2007). According to the 2008 North cancer Tunisian registry of cancer, CC has moved from second to third women cancer after breast and colorectal cancer (Ben Abdallah et al., 2009). However, there is no statistics indicating a real decrease of its incidence and CC remains a national health problem and a national priority as it is a preventable cancer. Pap smear screening programs have not been efficient in preventing the disease (Njah et al, 1994; Hsairi et al., 2013; Lazzar et al., 2014) and vaccine implementation, considered as a valuable tool for CC control (Human Papillomavirus vaccines. WHO, 2009) is under investigation in Tunisia. Thus, collecting epidemiological data and information about HPV genotype distribution in CC is the keys to study the effectiveness of prophylactic strategies such HPV vaccination. HPV16 and 18 are the target of the two affordable HPV prophylactic vaccines and they have been established as the most common HPV types found in CC worldwide despite consistent regional variations (Munoz et al., 2004; De Sanjose et al., 2010; Sjoeborg., 2010). Efficacy of these vaccines in reducing CIN2/ CIN3 lesions associated with HPV 16 and 18 types has been estimated to 93%-100% (Harper et al., 2006; Villa et al., 2006).

The first North African report describing HPV genotypes in CC was from Morocco (Chaouki et al., 1998). The study published in 1998, shows that HPV 16 and 18 are predominant (53.3% and 7.9 %). The second (Hammouda et al., 2005) reports a majority (95 %) of HPV 16 and 18 isolates from Algerian patients with CC. In our Tunisian series, we show that HPV 16 and/or 18 are present in 92.13 % of tested SCC. Two previous Tunisian studies showed similar findings. Missaoui et al report (Missaoui et al., 2010) shows using PCR technique and consensus GP5/GP6 primers, that HPV 16 is the most frequent detected genotype (47.6%) in the samples isolated from their patients. HPV 16 and 18 were also the most reported genotypes in a series of 146 cases collected in the Tunisian cancer Institute (KrennHrubic et al., 2011). Our results also show that multiple infections were seen in 51.7 % of cases and were mainly mixing HPV 16, 18, 35 and 45 and less frequently HPV 59, 40, 66, 73 and 58. Multiple infections have to be taken in consideration

since the emergence of HPV genotype other than HPV16 and HPV18 after vaccination could alter the effectiveness of vaccination. However, we could also consider that the immune response to HPV vaccine type can lead to a cross-protection against the closely related species. Indeed, HPV 16 belongs to the A9 species which also includes types 31, 33, 52, 58, and 35. HPV 18 belongs to the A7 species which also includes types 45, 59 and 39 and it has recently shown a cross protection for HPV35 and 45 (Paavonen et al., 2009).

At a technical level, while the usual HPV detection rate among formalin fixed and paraffin embedded samples is under 99 %, all the samples tested in our study were positive for HPV DNA. DNA fragmentation in formalin fixed paraffin embedded tissues are significantly more frequent compared to fresh tissues so DNA integrity usually decreases overtime in those samples and the probability to get false negatives increases (Mc Sherry et al., 2007; Fattorini et al., 2009; Webersinke et al., 2013). This can be overcome in part by the use of the general primers GP5 and GP6 elongated at their 3' ends with adjacent highly conserved sequence (De Roda et al., 1995; Lee, 2012) or the use of a nested PCR performed with MY09/MY11 and GP5+/GP6+ biotinylated primers as we did in our study (Carvalho et al., 2010). High levels of DNA concentration combined with these PCR conditions allow a detection of HPV DNA in 100 % of the samples. That was close to the findings of the Moroccan study that has been using a similar PCR protocol (Chaouki et al., 1998).

Our study shows that the prevalence of HPV 16 and/or 18 is highly predominant in our Tunisian SCC series suggesting that the current prophylactic vaccines might be potentially effective in preventing the disease. If current screening policies need to be revised in Tunisia, these results indicate that HPV vaccination can have a major impact on CC preventive guidelines. Mixed infections are crucial when considering second generation vaccines with broader coverage of HPV types and the potential benefits of cross-protection with current vaccines. The prevalence of HPV 35 and 45 in our study is interesting to notice when considering the cross protection that has been described with HPV 35 and 45 (Paavonen et al., 2009).

Cost-effectiveness analyses has been done in various parts in the world and has been conducted based on available data of HPV prevalence. The most important surveys have been assembled in a global meta-analysis. Besides differences in the PCR technologies used (Clifford et al., 2006), this analysis has provided relevant information for designing HPV vaccines and determining their impact in all world regions. Further documentation about HPV prevalence at a national level and its distribution according to age is needed to study the cost-effectiveness of vaccine implementation in preadolescent girls and for the initial catch-up efforts in elder women (C Kitchener et al., 2014).

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