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Distribution of Human Papillomavirus Genotypes in Condylomata Acuminata: An Austrian Cohort Study

Elisabeth Juelg[a] Michaela Busch[a] Andrea Lueger[a] Emmanuella Guenova[b]
Martina Schuetz-Bergmayr[a] Wolfram Hoetzenecker[a]

[a]Department of Dermatology, Kepler University Hospital, Linz, Austria; [b]Department of Dermatology, University Hospital Zurich, Zurich, Switzerland

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HPV types · Sexually transmitted infections · Frequency · Human papillomavirus · Genotypes

Abstract
Introduction: Condylomata acuminata are caused by various genotypes of human papilloma viruses (HPV). ***Methods:*** We assessed the frequency of 33 different HPV DNA types in 49 patients with condylomata acuminata by the polymerase chain reaction technique. ***Results:*** Forty-two percent of the patients were infected with low-risk genotypes, and 21% of the patients tested positive for high-risk genotypes. Multiple infections with low- and high-risk genotypes were detectable in 36% of the patients. ***Conclusion:*** As our results are in line with previous large-scale reports, our data might serve as a basis for monitoring the efficacy of HPV vaccination in Austria.

Introduction

The number of daily acquired sexually transmitted infections (STI) worldwide topped the million mark, with the most common sexually transmitted pathogen being human papilloma virus (HPV) [1]. Many HPV infections appear to be transient and may not result in clinically significant outcomes [2–4]. However, persistent infections play an important role in the development of condylomata acuminata (genital warts) and are the main risk factor for cervical cancer [5–10]. HPV types 6 and 11 are associated with approximately 90% of all genital warts, whereas approximately 70% of the cervical and other genital cancers are caused by HPV types 16 and 18 [5–10]. Furthermore, extragenital HPV is common in patients with genital warts [10]. Up to now, over 170 types of HPV have been identified, which are classified into low- and high-risk genotypes [11]. Today, HPV vaccination is available in most Western countries; e.g., the 9-valent HPV vaccine was introduced to the public Austrian vaccination plan recently. Follow-up data indicate that HPV incidence and morbidity is declining following the implementation of vaccination [12–16].

There is a lack of data on the frequency and distribution of HPV genotype infections in condylomata acuminata in Austria, especially besides the main genotypes 6 and 11. Thus, we assessed the frequency of 33 different HPV genotypes in patients with condylomata acuminata at the Department of Dermatology, Kepler University Hospital Linz, over a period of 6 months.

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E-Mail karger@karger.com
www.karger.com/drm

Wolfram Hoetzenecker, MD, PhD
Department of Dermatology, Kepler University Hospital
Krankenhausstrasse 9
AT–4020 Linz (Austria)
E-Mail wolfram.hoetzenecker@kepleruniklinikum.at

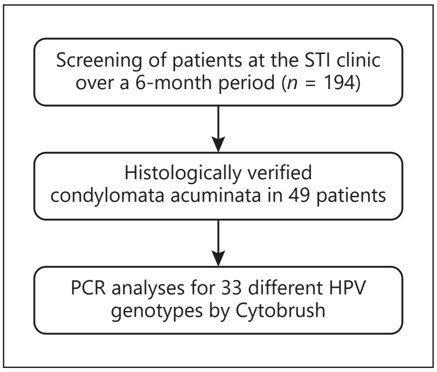

Fig. 1. Flowchart of Methods.

Table 1. Patients and diagnostic characteristics

	Total	*Condylomata*
Patients	194	49
Sex		
Female	76 (40)	15 (29)
Male	118 (60)	34 (71)
Age, years		
Median	37.5	34
Minimum	6	20
Maximum	90	68
Age groups		
0–30 years	63 (33)	21 (42)
31–50 years	80 (41)	25 (50)
>50 years	51 (26)	3 (8)
HPV-PCR		
Negative	–	2
Positive	–	47

Values in parentheses are percentages. Tabular overview of the sex and age-specific characteristics of the total patient collective and patients with condylomata acuminata.

Methods

For further details, see the supplementary materials (see www.karger.com/doi/10.1159/000500908 for all suppl. material) (Fig. 1), (Table 1).

Results

Over a 6-month period, we screened 194 patients who attended the STI clinic at the University Hospital Linz, Austria, for the presence of condylomata acuminata (Table 1). Condylomata acuminata were verified by histology in 49 patients, and subsequent polymerase chain reaction (PCR) analyses for 33 different HPV genotypes were performed. Twenty (42.6%) patients were infected with low-risk genotypes, and 10 (21.3%) patients tested positive for high-risk genotypes (Fig. 2a). Combinations of infections with low- and high-risk genotypes were detectable in 17 (36.2%) patients. In 2 patients, PCR revealed negative results. As shown in Figure 2b, a total of 86 HPV infections with 20 different genotypes were detected in those 47 patient cases. The most common HPV genotype was genotype 6, which was confirmed in 29 samples (61.7% of all cases). In 9 (17.6%) HPV-positive patients, concomitant sexually transmitted diseases or other disease affecting the genital area were detectable.

Discussion

The main aim of the present study was to assess the prevalence rates of 33 different HPV genotypes in anogenital condylomata acuminata. We found that (i) approximately 42% of the condylomata acuminata cases were positive for low-risk HPV genotypes; (ii) 21% were infected with high-risk genotypes; and (iii) multiple infections with both low- and high-risk genotypes were detectable in 36%. Besides the main HPV types 6 and 11 that are associated with approximately 90% of all genital warts, not much is known about the prevalence of other genotypes in genital warts. In a comprehensive study, Sturegård et at. [8] analyzed 621 patients with condylomata for HPV infections. The authors identified 35 different genital HPV types, with HPV6 (62%), HPV16 (13%), and HPV11 (10%) being the most common [8]. In another study including 256 females and 260 males, the most prevalent genotypes were 6 (69%), 11 (16%), and 16 (9%) [9]. In our study, the low-risk HPV genotype 6 was found in 61.7% of the cases, HPV16 in 19.5%, and HPV11 in 12.7%, respectively. HPV66/68 was detected in 15% of our patient cohort.

Importantly, we detected multiple HPV infections in around 36% of our patients. This is in line with data from Sturegård et al. [8] with 32% of subjects positive for more than one HPV genotype.

The genotypes HPV6/11 were present in 74% of our patients. This proportion is similar to the rates reported in other large-scale studies [8, 9, 17] but lower than the estimates in most of the smaller studies [6, 18–22]. Whereas Sturegård et al. [8] explain that the consecutive enrollment of patients in their study was a reason for a lower HPV6/11 ratio, our patients were preselected due to re-

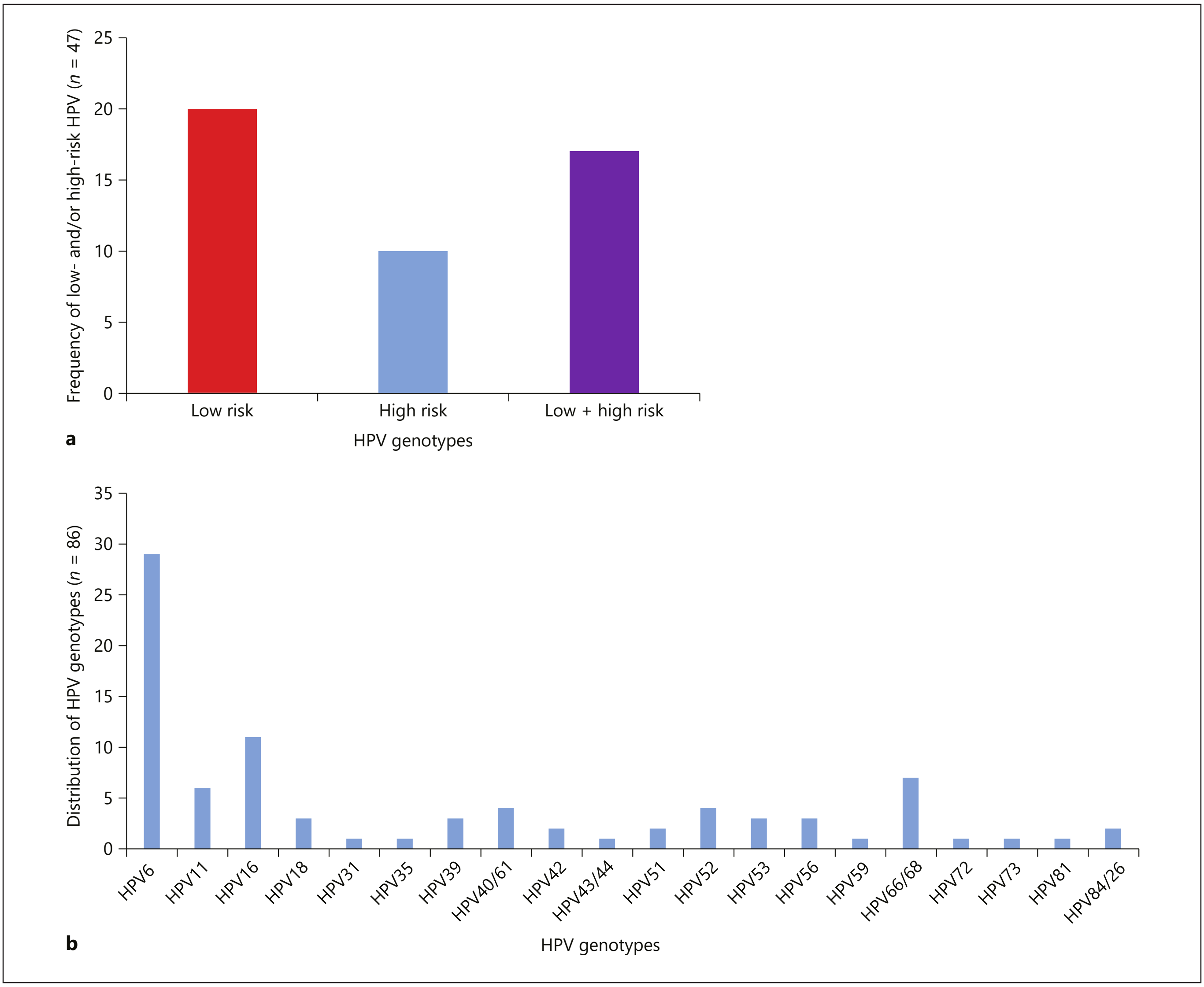

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Fig. 2. a Frequency of low-risk and high-risk HPV genotypes. Distribution of low-, high-, and low-/high-risk HPV genotypes in condylomata acuminata (*n* = 47). Genotypes were detected by the PCR technique from Cytobrush samples. **b** Distribution of HPV genotypes. Screening revealed 24 different genotypes in 47 cases. Genotypes were detected by the PCR technique from Cytobrush samples of condylomata acuminata.

ferral to our STI clinic. This might have resulted in a higher prevalence as the "typical" STI patient often represents with concomitant anogenital warts.

In our cohort, 21.3% of the patients tested positive for high-risk genotypes only, and 36.2% of the patients were infected with both low-risk and high-risk HPV DNA types. This proportion is in line with other studies, which report 33–48% high-risk infections [9, 17–19].

It is of great interest that 17.6% of the HPV-positive patients had additional sexually transmitted diseases (*Neisseria gonorrhoeae*, *Chlamydia trachomatis*, or *Treponema pallidum*) or other disease affecting the genitals (data not shown). These observations expand data as the previous large-scale studies only focused on HPV prevalence in anogenital warts [8, 9] and suggest that physicians should look out for other STI in HPV patients and vice versa.

There are several limitations to our study. First, the number of study patients is rather small. This might result in incorrect data of the distribution of HPV genotypes in condylomata acuminata. However, our findings are essentially in line with large-scale studies that report similar results (e.g., low- vs. high-risk HPV genotypes, prevalence of HPV6/11) [8, 9]. Second, our study population might have been preselected, as only patients who have been referred to the STI clinic were included. However, our data are similar to observations of Sturgegård et al. [8] who used a consecutive enrollment of patients with condylomata diagnosed at primary centers in their study design. Third, there might be differences in the sampling methodology as some studies used biopsy material to detect HPV infections, whereas we utilized Cytobrush techniques.

The key observation of our study is the fact that 1 out of 5 patients with condylomata acuminata was infected with high-risk HPV DNA types. This is of clinical importance, as these genotypes are a main risk factor for cancer. Based on our data, we suggest performing HPV typing of condylomata acuminata on a routine basis to identify patients with high-risk genotype infections. Furthermore, regular HPV typing might serve as a basis for monitoring the efficacy of HPV vaccination, which has been proven to be an effective tool to decrease the incidence of condylomata and HPV morbidity [12–16].

Key Message

In this study, we assessed the frequency of different HPV DNA types in patients with condylomata acuminata. Because a significant number of patients were infected with high-risk genotypes, we recommend performing HPV typing on a routine basis in patients with condylomata acuminata.

Acknowledgments

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Statement of Ethics

All procedures were in accordance with the ethical standards of the responsible committees on human experimentation (institutional and national) and with the Helsinki Declaration of 1983.

Disclosure Statement

The authors have no conflicts of interest to disclose.

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