



ELSEVIER

Contents lists available at ScienceDirect

Virology

journal homepage: www.elsevier.com/locate/yviro

Analysis of human papillomavirus 16 variants and risk for cervical cancer in Chinese population

Dong Hang^{a,1}, Yin Yin^{a,1}, Jing Han^a, Jie Jiang^a, Hongxia Ma^a, Shuanghua Xie^b, Xiaoshuang Feng^b, Kai Zhang^c, Zhibin Hu^{a,d}, Hongbing Shen^{a,d}, Gary M. Clifford^e, Min Dai^b, Ni Li^{b,*}

^a Department of Epidemiology and Biostatistics, School of Public Health, Nanjing Medical University, Nanjing 211166, China

^b National Office for Cancer Prevention and Control, Cancer Institute and Hospital, Chinese Academy of Medical Sciences, Beijing 100021, China

^c Department of Cancer Prevention, Cancer Institute and Hospital, Chinese Academy of Medical Sciences, Beijing 100021, China

^d State Key Laboratory of Reproductive Medicine, Nanjing Medical University, Nanjing 211166, China

^e Infections and Cancer Epidemiology, International Agency for Research on Cancer, Lyon 69372, France

ARTICLE INFO

Article history:

Received 6 September 2015

Returned to author for revisions

13 November 2015

Accepted 16 November 2015

Keywords:

Human papillomavirus 16

Variant

Cervical cancer

Case-control study

Meta-analysis

ABSTRACT

HPV16 is the most carcinogenic HPV type, but only a minority of HPV16 infections progress to cancer. Intratype genetic variants of HPV16 have been suggested to confer differential carcinogenicity. To investigate risk implications of HPV16 variants among Chinese women, a case-control study was conducted with 298 cervical cancer patients and 85 controls (all HPV16-positive). HPV16 isolates were predominantly of the A variant lineage, and variants of A4 (previously named “Asian”) sublineage were common. A4/Asian variants were significantly associated with increased risk of cervical cancer compared to A1–3 (OR=1.72, 95% CI=1.04–2.85). Furthermore, a meta-analysis including 703 cases and 323 controls from East Asia confirmed the association (OR=2.82, 95% CI=1.44–5.52). In conclusion, A4 variants appear to predict higher risk of cervical cancer among HPV16-positive women, which may provide clues to the genetic basis of differences in the carcinogenicity of HPV16 variants.

© 2015 Published by Elsevier Inc.

Introduction

Cervical cancer ranks as the fourth most common malignancy in females worldwide, with a relatively high burden in developing countries, including in China (Ferlay et al., 2015). Infection with a subset of human papillomavirus (HPV), termed high-risk types, is a necessary pre-requisite for this disease (zur Hausen, 2002). Notably, although approximate 80% of women will have acquired cervical HPV infection by age 50, less than 1% of persistent infections will ultimately lead to invasive cancer (Myers et al., 2000; Schiffman et al., 2011). Factors that influence the outcome of HPV infection are not fully understood, but HPV intratype variants have been suggested to play a critical role in cervical carcinogenesis, and are recognized as an important marker for research on viral transmission, persistence, and carcinogenicity (Wang and Hildesheim, 2003; Xi et al., 2014).

* Correspondence to: National Office for Cancer Prevention and Control, Cancer Institute and Hospital, Chinese Academy of Medical Sciences, No. 17 Panjiayuananli, Chaoyang District, Beijing 100021, China. Tel.: +86 10 8778 7394; fax: +86 10 8778 7054.

E-mail address: lini1240@hotmail.com (N. Li).

¹ These authors contributed equally to this paper.

Of the 13 key genital high-risk human papillomavirus types (HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, and 68), HPV16 is the most prevalent type, and causes more than half of cervical cancer cases worldwide (Guan et al., 2012). Based on whole HPV genome sequencing, HPV16 variants have been classified into four major lineages: (1) A, that includes A1–3 (previously named European), and A4 (Asian) sublineages; (2) B (African 1); (3) C (African 2); and (4) D (including Asian–American [AA] and North-American [NA]) (Burk et al., 2013).

Epidemiological studies have suggested that certain HPV16 variants, particular D lineages, might promote viral persistent infection and cervical cancer development (Berumen et al., 2001; Schiffman et al., 2010; Xi et al., 2007). However, D lineages are rare in East Asia, where A lineages predominate (Cornet et al., 2013; Yamada et al., 1997). In particular, the prevalence in cervical cancer of A4/Asian variants (most commonly classified by the polymorphism T178G in E6) is much higher in Asia (65.5% in China, 85.2% in Korea, and 44% in Japan) than in Europe (2%) and North America (3%) (Kang et al., 2005; Matsumoto et al., 2000; Wu et al., 2006; Yamada et al., 1997). However, in comparison to a number of relevant studies in European and American populations, little is known about the oncogenic potential of HPV16 variants in Asian women. A4/Asian variants were associated with a higher risk of

Table 1
Nucleotide polymorphisms identified at HPV16 E6 gene.

Variant ^a HPV16 reference	94	109	111	131	132	136	145	154	168	173	176	178	184	188	193	219	241	267	276	286	295	310	315	335	350	442	516	Predicted amino acid change	Case (N=298)	Control (N=85)	Total
	G	T	A	A	G	G	G	A	C	C	G	T	A	G	T	G	T	G	A	T	T	T	C	C	T	A	C				
A1-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	98	35	133
a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	6	18	
a	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25N	1	2	3	
a	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	D25N/L83V	1	0	1	
a	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E	10	1	11	
a	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	T	-	-	D25E/H78Y	1	0	1	
a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	S71C	1	0	1	
a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	H78Y	1	2	3	
a	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	L83V	0	1	1	
c	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	L83V	0	1	1	
-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K11N	1	0	1	
-	-	-	-	-	-	-	-	G	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	T22S/L83V	1	0	1	
-	-	-	-	-	-	-	-	-	-	T	C	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	H24Y/D25H/E29Q	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25N	9	0	9	
-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25H	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25Y	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	g	-	-	-	-	-	-	-	-	-	-	D25N	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I27M	0	1	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	E29Q	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	R39Q	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	g	-	-	-	-	-	-	-	-	-	-	-	7	4	11	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	N58S	1	2	2	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	D64E	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	G	-	-	D64E/L83V	2	1	3	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F69L	1	0	1		
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	G	-	H78Y/L83V	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	C	H78Y/E113D	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	L83V	3	1	4	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	C	-	L83V/E113D	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	G	-	L83V/S138C	0	1	1	
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	E113D	1	0	1	
A4/Asian	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E	117	24	141	
c	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E	0	1	1	
C	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q3P/D25E	1	0	1	
c	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E	11	2	13	
c	-	-	-	-	-	-	-	-	-	-	G	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E/E29Q	1	0	1	
-	-	-	-	-	-	-	-	G	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	T22S/D25E/L83V	2	0	2	
-	-	-	-	-	-	-	-	-	-	-	G	-	-	c	-	-	-	-	-	-	-	-	-	-	-	-	D25E	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	g	-	-	-	-	-	-	-	-	-	-	D25E	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E/R55L	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D25E/H78Y	1	0	1	
-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	D25E/S138C	0	1	1	
D	-	-	-	-	C	-	T	-	-	-	-	-	-	-	-	-	-	-	-	a	-	-	-	-	-	-	R10T/Q14H/H78Y	1	0	1	

^a Variant classification based on the E6 sequences.

Download English Version:

<https://daneshyari.com/en/article/6138882>

Download Persian Version:

<https://daneshyari.com/article/6138882>

[Daneshyari.com](https://daneshyari.com)