HUMAN PAPILLOMAVIRUS TYPE DISTRIBUTION AND GENETIC VARIABILITY IN WOMEN WITH AND WITHOUT CERVICAL LESIONS FROM SOUTHERN BRAZIL

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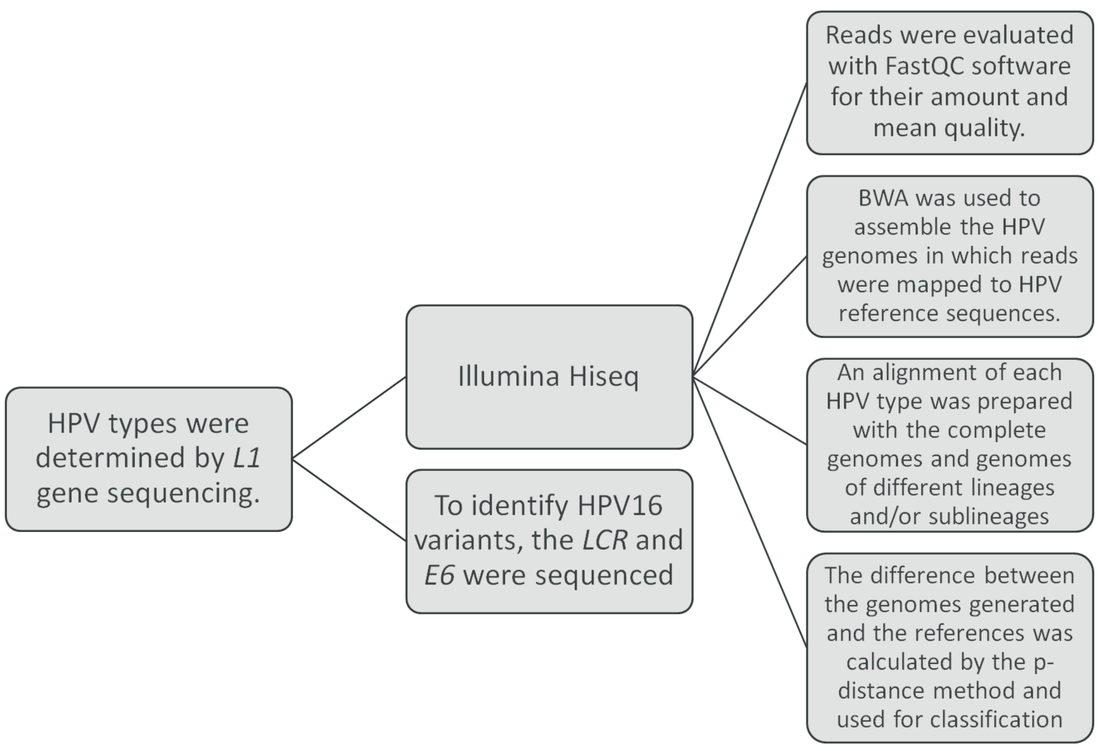
INTRODUCTION

Increasing evidence suggests that human papillomavirus (HPV) intratype variants (specific lineages and sublineages) are differentially associated with pathogenesis and progression from HPV infection to persistence and the development of cervical cancer.

OBJECTIVES

This study aimed to verify the prevalence of HPV infection, distribution of HPV types and intratype variants in Southern Brazil in women with and without cervical lesions.

METODOLOGY



RESULTS

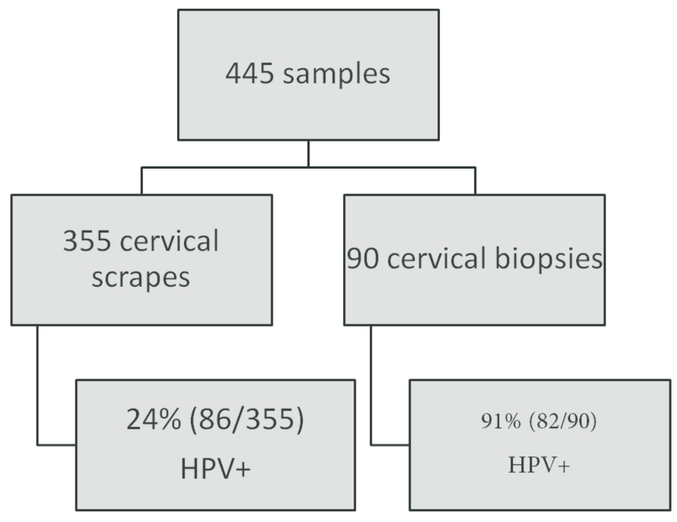


Table 1. HPV genotyping of cytology samples negative from HIV-1-positive and -negative women

HPV Types	HIV-1-negative N = 55	HIV-1-positive N = 23	Total N = 78
HPV6	7 (13%)	2 (9%)	9 (14%)
HPV16	12 (21%)	7 (31%)	19 (24%)
HPV18	3 (5%)	-	3 (4%)
HPV31	2 (4%)	2 (9%)	4 (5%)
HPV33	3 (5%)	2 (9%)	5 (7%)
HPV35	1 (2%)	-	1 (1%)
HPV44	2 (4%)	1 (4%)	3 (4%)
HPV45	7 (13%)	-	7 (9%)
HPV53	2 (4%)	-	2 (2%)
HPV58	8 (14%)	3 (14%)	11 (14%)
HPV61	1 (2%)	1 (4%)	2 (2%)
HPV67	1 (2%)	1 (4%)	2 (2%)
HPV68	-	1 (4%)	1 (1%)
HPV70	1 (2%)	1 (4%)	2 (2%)
HPV82	4 (7%)	1 (4%)	5 (7%)
HPV83	-	1 (4%)	1 (1%)
HPV85	1 (2%)	-	1 (1%)

- In the HIV-1- samples with LSIL (n = 6), the genotypes detected were HPV6, HPV31, HPV33 and HPV82; in the sample with HSIL (n = 1), HPV16 was identified.
- From the HIV-1+ women, HPV16 was detected in the sample with HSIL.

Table 2. Human papillomavirus (HPV) genotyping of biopsy samples (n = 77) *

Genotype	No lesions (N = 17)	LSIL (N = 30)	HSIL (N = 30)	Total (N = 77)
HPV11	1 (6%)	-	-	1 (1%)
HPV16	10 (58%)	14 (47%)	20 (66%)	44 (57%)
HPV18	1 (6%)	6 (20%)	2 (7%)	9 (12%)
HPV31	-	2 (7%)	2 (7%)	4 (5%)
HPV33	1 (6%)	-	-	1 (1%)
HPV53	1 (6%)	1 (3%)	-	2 (3%)
HPV58	2 (12%)	4 (13%)	4 (13%)	10 (13%)
HPV70	1 (6%)	-	-	1 (1%)
Multiple infections	-	3 (10%)	2 (7%)	5 (7%)

HSIL: high-grade squamous intraepithelial lesions; LSIL: low-grade squamous intraepithelial lesions.

* Seventy-seven (94%) of the 82 HPV-positive biopsy samples were genotyped.

- 75% of the HPV16-positive samples were classified into lineages

Table 3. HPV16 lineage distribution in cervical samples according to histopathology.

HPV16 lineage	Normal histology (N = 21)	LSIL (N = 12)	HSIL (N = 16)	Total (N = 49)
A	19 (90%)	10 (84%)	14 (88%)	43 (88%)
B	-	1 (8%)	-	1 (2%)
D	2 (10%)	1 (8%)	2 (12%)	5 (10%)

HSIL: high-grade squamous intraepithelial lesions; LSIL: low-grade squamous intraepithelial lesions.

- Double or multiple infections were detected by NGS in 53% (8/15) of the previously typed samples, and 14 infections of different HPV types were found in some samples that had not been previously detected by Sanger sequencing.

Table 4. Distribution of HPV types, multiple infections, percent nucleotide distance of each HPV complete genome and identified lineages and sublineages by next-generation sequencing infecting women followed-up at University Hospital of the Federal University of Rio Grande

Sample	HPV type by Sanger sequencing*	HPV type(s) by NGS	Complete genomes assembled	Distance (%)	Lineage(s)/ sublineage(s) assigned
01	6	6	6	0.1	B3
02	6	6	6	0.1	B1
03	6	6	6	0.2	A
04	16	16, 31	---	---	---
05	18	18	18	0.1	A3
06	31	31, 68	31	0.3	C2
			68	0.3	C1
07	33	68	68	0.2	C1
08	35	35, 39	35	0.3	A1
			39	0.1	A1
09	58	51, 58	51	0.2	A1
10	58	58	58	0.1	A2
11	67	31, 67, 85	67	0.1	A2
			85	0.1	A
			31	0.3	B2
12	82	56, 61, 82	56	0.2	A2
			61	0.1	A1
			82	0.1	A2
13	82	82	82	0.1	A2
14	83	31, 82, 83,	---	---	---
15	83	6, 74, 82, 83	---	---	---

CONCLUSIONS

This study identified highly diverse HPV oncogenic types (HPV 16, 18, 31, 33, 45, and 82) and identified a high frequency of European and North American HPV16 lineages, consistent with the genetic background of the human population in Southern Brazil. This is also the first report describing the distribution of HPV intratype lineages of high and low oncogenic risk in asymptomatic women from Southern Brazil.

CNPq Conselho Nacional de Desenvolvimento Científico e Tecnológico
FAPERGS Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul

Projeto Gráfico: Setor de Edição e Informação Técnico-Científica / INCA

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