Prevalent HPV genotypes among Hispanic women along the Texas-Mexico border

Christina Gutierrez[1], Jane Montealegre[2], Michael Scheurer[2], Laura Dillon[3], Karen Adler-Storthz[3], Thelma Carrillo[1], Leonid Fradkin[4], Michele Follen[4], Zuber D. Mulla[1]

[1]Department of Obstetrics & Gynecology, PLFSOM, Texas Tech University Health Sciences Center, El Paso, Texas 79905; [2]Baylor College of Medicine, Houston, Texas 77030; [3]University of Texas Health Science Center at Houston- School of Dentistry, Houston, Texas 77054, [4]Brookdale University Hospital and Medical Center, Brooklyn, New York, 11212

Introduction

There are 13 oncogenic (high-risk) types of human papillomavirus (HPV) that are causally associated with cervical cancer, specifically types 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68. HPV 16 and 18 are causally related to 70% of cervical cancers and 50% of precancerous lesions worldwide and are the primary targets for the two commercially-available HPV vaccines. However, there is evidence that HPV 16 and 18 are detected in a significantly lower proportion of high-grade cervical lesions among Hispanic women when compared to non-Hispanic white women. The purpose of this study was to identify prevalent high-risk (HR) HPV genotypes among Hispanic women living along the Texas-Mexico border.

Methodology

Parent Study

Patients in this analysis represent a subset of patients participating in a clinical trial to evaluate molecular imaging for the identification of cervical neoplasia (the Multispectral Digital Colposcopy trial). Trial participants are consenting patients presenting at an academic colposcopy clinic in El Paso, Texas with an abnormal Papanicolau test result. Other eligibility criteria include: ≥ 18 years of age, understand English or Spanish, not pregnant at time of enrollment, no history of hysterectomy. As part of the parent trial, a subset of participants were administered a demographics and health history survey and asked to provide a cervical swab for HPV genotyping.

HPV Genotyping

Swabs were sent to the University of Texas School of Dentistry for genotyping using the Roche Linear Array.

Instruments

An interviewer administered questionnaire was used to ascertain demographic characteristics and behavioral risk factors. A medical record review form was used to collect pathology results. Histologic diagnosis were based on biopsies evaluated by a certified pathologist and represent the histology of the most severe biopsy.

Statistical Analysis

Descriptive statistics of the demographic survey and HPV genotyping results were used to determine prevalent HPV genotypes. *p*-value was generated with either χ^2 or Fisher's exact test using software, "OpenEpi: Open Source Epidemiologic Statistics for Public Health."

Results

To date, we have performed HPV genotyping for 81 participants. Of these, 76 (94%) were of Hispanic origin. Among Hispanic women, the median age was 34 years and 45% were born in Mexico. There were significant demographic differences between U.S. and Mexican-born women. U.S.-born women were significantly more likely to be 35 years of age and younger, single, and to have more than a high school education. U.S.-born women were also significantly more likely to have received at least one dose of the HPV vaccine.

Overall, eighty seven percent of Hispanic women (n=66) were infected with HPV. 55% of HPV-infected women expressed a single strain, whereas 46% expressed multiple strains. U.S-born women were significantly more likely to be infected with multiple strains (56% versus 31%). Overall, 63% (n = 35) of infected women were infected with HR-HPV. There were no significant differences between U.S.- and Mexican-born women in regard to HR-HPV infection.

Among U.S-born women, prevalent HR-HPV types were HPV52 (14%), HPV31 (11%), and HPV16 (present in 10% of HR-HPV positive samples.

Among Mexican-born women, prevalent HR-HPV types were HPV16 (21%), HPV 31 (13%), and HPV66 (11%).

Among all Hispanic women with CIN2 and CIN3 (n=9), the most common HR-HPV types were HPV 16 and 31 (both present in 3 of 9 samples).

Table 1. Demographic data of Hispanic TTUHSC enrolled patients based on the 76 patients that submitted samples for HPV genotyping.

Demographics	Total Hispanics (n=76), %	Nativity: Hispanic U.S-Born (n=41), %	Nativity: Hispanic Mexico-Born (n=34), %	U.S-born versus Mexico-born *p* value*
Age				
21-35	65.8	85.4	41.2	<0.0001
≥ 36	34.2	14.6	58.8	
Marital Status				
Married	19.7	9.8	32.4	
Divorced, Widowed, Separated	36.8	31.7	44.1	0.001
Never Married	35.5	53.7	11.8	
Member unmarried couple	7.9	4.9	11.8	
Education Level				
≤ High School	51.3	26.8	79.4	<0.0001
≥ college	48.7	73.1	20.6	
Annual Income **				
< $20,000	48.7	43.9	52.9	0.35
≥ $20,000	25.0	29.3	20.6	
HPV Vaccination (at least one) **				
Yes	21.1	34.1	5.9	0.002
No	73.7	61.0	91.2	

*p-value generated with either χ^2 or Fisher's exact test as appropriate
**Some subjects refused/did not know the annual household income or if they received an HPV vaccination

Table 2. HPV and cervical dysplasia characteristics of TTUHSC enrolled patients.

	Total Hispanics	Hispanic U.S-Born	Hispanic Mexico-Born	U.S-born versus Mexico-born *p* value, χ^2
Cervical Dysplasia	(n=75), %	(n=41), %	(n=34), %	
Low-grade dysplasia/Negative for Dysplasia , ≤ CIN1	85.3	87.8	79.4	0.47
High-grade dysplasia, ≥ CIN2				
CIN2/CIN3	12.0	12.2	11.8	
Carcinoma *In-situ*	16.0	-	5.9	
HPV Infection	(n=66), %	(n=36), %	(n=29), %	
Multiple Strain	45.5	55.6	27.6	0.02
Single Strain	54.5	44.4	72.4	
HPV Infection	(n=66), %	(n=36), %	(n=29) %	
High Risk	77.3	80.6	72.4	0.49
Low Risk	22.7	19.4	27.6	
HPV Genotypes*	(n=112), %	(n=71),%	(n=38), %	
High Risk Genotypes	63.4	64.8	60.1	
HPV16	13.4	9.9	21.0	
HPV18	-	-	-	
HPV31	11.6	11.3	13.2	
HPV33	0.9	1.4	-	
HPV35	4.5	5.6	-	
HPV45	2.7	1.4	5.3	
HPV51	3.6	4.2	2.6	-
HPV52**	10.7	14.1	2.6	
HPV56	4.7	4.2	5.3	
HPV58	2.7	4.2	-	
HPV59	0.9	1.4	-	
HPV66	7.1	5.6	10.5	
HPV68	0.9	1.4	-	
Low Risk Genotypes	36.7	35.2	39.4	

*Statistical analysis not performed due to the inclusion of multiple records for certain patients; to clarify, some subjects were infected with multiple genotypes.
**Linear Array assay does not have separate detection for HPV52. If signal band for HPV 33, 35, 52, and 58, and three separate bands for HPV 33, HPV 35, and HPV 58 are present, the patient is said to have a co-infection of the separate band and HPV 52. Patient is HPV 52 positive if the HPV 33/35/52/58 signal is present and the HPV 33, HPV35, and HPV 58 signals are absent.

Conclusion

In our sample of Hispanic women living along the Texas-Mexico border, HPV16 and 31 were the most prevalent HR-HPV types among both U.S.- and Mexican-born women. HPV 16 and 31 were also the most prevalent genotypes among women with CIN2/3. HPV18 was not present in any samples. Although limited by our small sample size, these preliminary data suggest that the distribution of HPV genotypes among Hispanic women along the Texas-Mexico border may be different from that of other populations and includes genotypes that are not targeted by the two commercially-available HPV vaccines.

Acknowledgements

TTUHSC IRB: Development and Application of a Multispectral Digital Colposcope and Probe Algorithm for Detection of Cervical Intraepithelial Neoplasia, E121147.
This work was supported by the Optical Technologies and Molecular Imaging for Cervical Neoplasia grant 3 P01 CA082710-14.