Research Article

Cancer Epidemiology, Biomarkers & Prevention

A Comparison of Human Papillomavirus Genotype-Specific DNA and E6/E7 mRNA Detection to Identify Anal Precancer among HIV-Infected Men Who Have Sex with Men

Philip E. Castle[1], Stephen Follansbee[2], Sylvia Borgonovo[2], Diane Tokugawa[4], Lauren M. Schwartz[6], Thomas S. Lorey[4], Brandon LaMere[5], Julia C. Gage[6], Barbara Fetterman[4], Teresa M. Darragh[3], Ana Cecilia Rodriguez[1,7], and Nicolas Wentzensen[6]

Abstract

Background: Human papillomavirus (HPV) RNA detection is reportedly more specific for the detection of anogenital precancer than HPV DNA but it is unknown whether this is due to detection of RNA or due to HPV genotype restriction.

Methods: A total of 363 human immunodeficiency virus (HIV)–positive men who have sex with men had two anal cytology samples taken and were evaluated using high-resolution anoscopy and biopsies of visible lesions. Anal specimens were tested for E6/E7 RNA for five carcinogenic HPV genotypes (HPV16, 18, 31, 33, and 45) and tested for the DNA of 13 carcinogenic HPV genotypes.

Results: DNA testing was more likely to be positive than RNA testing (53% vs. 48%; $P = 0.02$) for the same five HPV genotypes in aggregate. When restricted to five HPV genotypes targeted by the RNA test, the sensitivity to detect anal precancer was the same for DNA and RNA (81%), whereas RNA was more specific than DNA (65% vs. 58%; $P = 0.007$). In comparison, DNA detection of all 13 carcinogenic HPV genotypes was more sensitive (96% vs. 81%; $P = 0.001$) but much less specific (65% vs. 33%; $P < 0.001$) as compared with RNA detection of the five HPV genotypes.

Conclusion: After controlling for HPV genotypes, RNA was only slightly more specific than DNA detection for anal precancer.

Impact: DNA or RNA testing for a subset of the most carcinogenic HPV genotypes may be useful for distinguishing between those HPV-positive men at higher and lower risk of anal precancer and cancer. *Cancer Epidemiol Biomarkers Prev; 22(1); 42–49. ©2012 AACR.*

Introduction

Anal cancer is a relatively uncommon malignancy, with approximately 6,000 cases projected for 2012 (1). Men who have sex with men (MSM), especially human immunodeficiency virus (HIV)–infected MSM, are at an elevated risk of anal cancer (2–4). Human papillomavirus (HPV), the necessary cause of cervical cancer, is the primary cause of anal cancer. Although less well studied than the cervix, the natural history of HPV and anal cancer is believed to be analogous to that of HPV and cervical cancer. The key steps in HPV-induced carcinogenesis are HPV acquisition, HPV persistence (vs. clearance or HPV infection becoming undetectable), progression of persistent HPV infection to precancer, and development of invasive cancer from a precancer. MSM who participate in receptive anal intercourse expose susceptible squamous epithelium of the anal canal to HPV infection. HIV-infected MSM are at a higher risk of anal cancer than HIV-uninfected MSM presumably because of their impaired immune response reduces their ability to clear HPV infections. As a consequence, HIV-infected MSM have a very high prevalence of anal HPV, with a 73.5% prevalence for anal carcinogenic HPV (4), which is 2-fold greater prevalence for anal carcinogenic HPV in HIV-negative MSM (4) and cervical carcinogenic HPV in young (<20 years) women (5).

In anal and cervical cancer screening, most subjects who screen positive by HPV DNA testing or cytology do

Authors' Affiliations: [1]Albert Einstein College of Medicine, Bronx, New York; [2]Kaiser Permanente Medical Center; [3]University of California, San Francisco; [4]Kaiser Permanente TPMG Regional Laboratory, Berkeley; [5]Women's Health Research Institute, Division of Research, Kaiser Permanente, Oakland, California; [6]Division of Cancer Epidemiology and Genetics, National Cancer Institute, NIH, Rockville, Maryland; and [7]Proyecto Epidemiológico Guanacaste, Fundación Instituto Costarricense de Investigación y Enseñanza en Nutrición y Salud, San José, Costa Rica

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P.E. Castle is a Visiting Professor in Epidemiology and Population Health, Albert Einstein College of Medicine, Bronx, NY.

Corresponding Author: Nicolas Wentzensen, Division of Cancer Epidemiology and Genetics, National Cancer Institute, 6120 Executive Blvd, Room 5024, Rockville, MD 20852. Phone: 3014353975; Fax: 3014020916; E-mail: wentzenn@mail.nih.gov

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not have concurrent precancer. The challenge is then differentiating the screen-positive subjects with benign, transient HPV infections (or cytologic abnormalities caused by those infections) from those that have a precancerous lesion. This is especially true in anal cancer screening of HIV-infected MSM with the very high background of anal HPV infection.

There are a number of new, promising HPV-related biomarkers that may better differentiate between high- and low-risk HPV infections, but more validation studies are needed. One of these promising biomarkers is the high-level expression of HPV E6 and/or E7 oncoprotein. In numerous studies of HPV-related anogenital disease (6–15), detection of HPV E6/E7 mRNA for HPV16, 18, 31, 33, and 45 together has been shown to be more specific albeit less sensitive for precancer than DNA detection of all carcinogenic-HPV genotypes.

We conducted a study of HIV-infected MSM in Northern California to evaluate some of these promising new biomarkers for anal cancer screening including E6/E7 mRNA detection of HPV16, 18, 31, 33, and 45. We previously confirmed that mRNA detection of the 5 HPV genotypes is more specific but less sensitive for anal precancer than DNA detection for 13 carcinogenic HPV genotypes. Here, we extended the analysis to differentiate the effects of mRNA detection versus type restriction on clinical specificity of E6/E7 mRNA detection.

Materials and Methods

Study population

We conducted a cross-sectional screening study at an anal cancer-screening clinic in San Francisco, California run by Kaiser Permanente Northern California (KPNC). We enrolled men who were identified as HIV-infected through the Kaiser HIV registry, who were 18 years or older, who were not diagnosed with anal cancer before enrollment, and who provided informed consent. In total, 363 HIV-positive men on antiretroviral therapy were enrolled between August 2009 and June 2010. The study was reviewed and approved by the Institutional Review Boards at KPNC and the U.S. National Cancer Institute (NCI). All participants were asked to complete a self-administered questionnaire to collect risk factor information. Additional information on HIV status and medication, sexually transmitted diseases, and histopathology results were abstracted from the KPNC clinical database. For 87 subjects of 271 without histologically confirmed high-grade anal intraepithelial neoplasia [anal intraepithelial neoplasia grade 2 (AIN2) or grade 3 (AIN3)] identified at the enrollment visit, follow-up information from additional clinic visits up to December 2011 was available and included in the analysis to partially reduce the misclassification of disease status at enrollment due to the imperfect sensitivity of high-resolution anoscopy (HRA; refs. 16, 17).

High-resolution anoscopy, cytology, and histology

During the clinical examination, 2 specimens were collected by inserting a wetted flocked nylon swab (18) into the anal canal up to the distal rectal vault and withdrawing with rotation and lateral pressure. Each specimen was placed into separate vials with PreservCyt medium (Hologic) for cytology and HPV DNA and biomarker testing. A third specimen was collected for routine *Chlamydia trachomatis* and *Neisseria gonorrhea* testing. After specimen collection, participants underwent a digital rectal examination followed by HRA. Suspicious-appearing lesions visualized during HRA were biopsied and sent for routine histopathologic review by KPNC pathologists. From the first specimen container, a liquid-based cytology slide was prepared for routine Pap staining and read independently by 2 pathologists, who showed moderate agreement (19). Cytology results were reported analogous to the 2001 Bethesda classification for cervical cytology (20): negative for squamous intraepithelial lesion (SIL) or malignancy ("negative"), atypical squamous cells of undetermined significance (ASC-US), low-grade SIL (LSIL), high-grade SIL (HSIL), and ASCs cannot rule out HSIL (ASC-H). The study pathologists made a further distinction of HSIL by categorizing them as either HSIL-AIN2 or HSIL-AIN3 based on severity.

Histology results were reported as negative, condyloma, and AIN grades 1 to 3.

HPV testing

The test manufacturers conducted HPV DNA (Roche Molecular Systems) and RNA (NorChip AS) testing on the second PreservCyt specimen according to their instructions, blinded to all study data.

Specimens were tested for the DNA of 37 HPV genotypes (6, 11, 16, 18, 26, 31, 33, 35, 39, 40, 42, 45, 51–56, 58, 59, 61, 62, 64, 66–73, 81–84, 82v, and 89) using HPV (LA-HPV) assay (Roche; refs. 21, 22). HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, and 68 were classified as carcinogenic HPV genotypes (23).

Specimens were tested for the E6 and E7 mRNA of 5 HPV genotypes (HPV16, 18, 31, 33, and 45) by real-time multiplex nucleic acid sequence–based amplification using the PreTect HPV-Proofer assay (NorChip) as previously described (7–11). DNA/RNA was first isolated from 5 mL PreservCyt specimens by using the NucliSENS easyMAG system (bioMerieux). To avoid false-negatives due to degradation of mRNA, primers and probes against human U1A mRNA are included in the PreTect HPV-Proofer Kit as a performance and integrity control.

Statistical analysis

We calculated the basic agreement statistics (percentage agreement, percentage-positive agreement, and κ value) for comparing paired DNA and RNA test results. We tested for differences in percentage of test positives and the number of HPV genotypes detected for paired tests using an exact version of a symmetry χ^2 test. A nonparametric test (24) was used to assess the trends in

Table 1. Agreement for DNA and E6/E7 mRNA detection of 5 HPV genotypes (HPV16, 18, 31, 33, and 45) individually and in aggregate ("any") in anal cytologic specimens

		DNA+	RNA+	DNA+ RNA+	DNA+ RNA−	DNA− RNA+	DNA− RNA−	% Agreement	% Positive agreement	κ	*P*
HPV16	*n*	92	88	79	13	9	233	93.4%	78.2%	0.83	0.5
	Row%	28%	26%	24%	4%	3%	70%				
HPV18	*n*	35	31	27	8	4	295	96.4%	69.2%	0.80	0.4
	Row%	10%	9%	8%	2%	1%	88%				
HPV31	*n*	50	48	37	13	11	273	92.8%	60.7%	0.71	0.8
	Row%	15%	14%	11%	4%	3%	82%				
HPV33	*n*	38	36	31	7	5	291	96.4%	72.1%	0.82	0.8
	Row%	11%	11%	9%	2%	1%	87%				
HPV45	*n*	40	39	30	10	9	285	94.3%	61.2%	0.73	1
	Row%	12%	12%	9%	3%	3%	85%				
Any	*n*	178	161	146	32	15	141	85.9%	75.6%	0.72	0.02
	Row%	53%	48%	44%	10%	4%	42%				

percentage of test positives with increasing severity of the cytologic interpretation and older age, categorized into groups based on approximate quartiles in age (<46, 46–51, 52–59, and 60 years and older). Standard clinical performance characteristics [sensitivity, specificity, negative (NPV) and positive (PPV) predictive value, negative (LR−) and positive (LR+) likelihood ratio, and OR with 95% confidence interval (95% CI)] were calculated for the 2 tests for identifying subjects with anal precancer.

Results

We restricted our analysis to the 334 of 363 (92.0%) participants who had complete HPV DNA and E6/E7 mRNA results; 20 were missing DNA results, 8 were missing RNA results, and 1 was missing both DNA and RNA. The median and mean age and the range of ages were 52, 53, and 32 to 79 years, respectively. The description of the population can be found in the Supplementary Table. Approximately 80% of the participants completed the short questionnaire. The population was predominantly White and well educated. Most MSM (74%) had 10 or more anal intercourse partners in their lifetime. Approximately 80% of the subjects had CD4 counts of 350 or greater per microliter and more than 80% had HIV viral loads of less than 75 viral copies/mL of blood.

In Table 1, we present the agreement between HPV DNA and E6/E7 mRNA detection of HPV16, 18, 31, 33, and 45 individually and collectively. An HPV DNA assay including the 5 genotypes would have a positivity of 53% in this population (corresponding to the referral rate), whereas the HPV mRNA assay for the 5 genotypes had an overall positivity of 48%. For the 5 individual HPV genotypes, the overall agreement ranged from 92.8% (HPV31) to 96.4% (HPV18 and HPV33), the positive agreement ranged from 60.7% (HPV31) to 78.2% (HPV16), and the κ values from 0.71 (HPV31) to 0.83 (HPV16). There were no statistically significant differences in the percentage positive between measures for each genotype although the percentage positive by DNA was consistently slightly higher than by RNA. For any of 5 HPV genotypes detected (regardless of whether agreement for the specific HPV genotypes was present), there was 85.9% total agreement, 75.6% positive agreement, and κ value of 0.72 (95% CI, 0.61–0.84) for the 2 measures. DNA testing for the 5 HPV genotypes in aggregate was more likely to be positive than RNA testing (53% vs. 48%, respectively; $P = 0.02$). Considering agreement for all 5 HPV genotypes individually (including agreement when multiple HPV genotypes are detected; $n = 1{,}670$; 334 subjects and 5 possible infections per subject), there was 94.7% total agreement, 69.6% positive agreement, and κ value of 0.79 (95% CI, 0.75–0.83) for the 2 measures. There were no significant differences in the individual detection for all 5 HPV genotypes ($P = 0.2$).

Shown in Fig. 1 is the prevalence (percentage positive) by age group for DNA and RNA detection for the

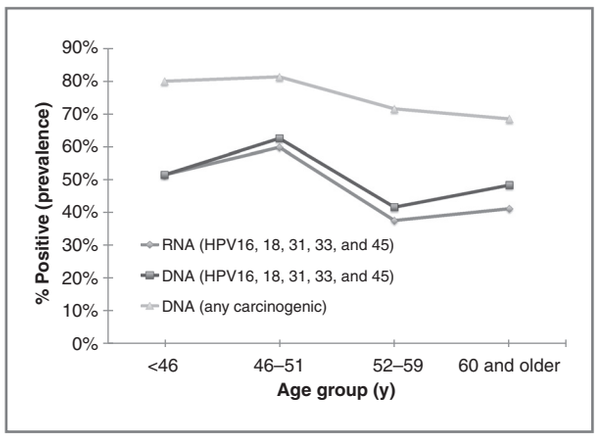

Figure 1. The age-group–specific prevalence (percentage positive) of HPV16, 18, 31, 33, and 45 in aggregate by DNA and E6/E7 mRNA detection and of all 13 carcinogenic HPV genotypes by DNA detection.

Table 2. Number of HPV16, 18, 31, 33, and 45 infections detected by HPV DNA and E6/E7 mRNA

			No. of HPV16, 18, 31, 33, 45 genoytpes (RNA)					
			0	1	2	3	4	Total
No. of HPV16, 18, 31, 33, 45 genoytpes (DNA)	0	*n*	141	12	2	1	0	156
		Cell%	42%	4%	1%	0%	0%	47%
	1	*n*	29	82	8	1	1	121
		Cell%	9%	25%	2%	0%	0%	36%
	2	*n*	2	6	28	4	0	40
		Cell%	1%	2%	8%	1%	0%	12%
	3	*n*	1	1	2	11	1	16
		Cell%	0%	0%	1%	3%	0%	5%
	4	*n*	0	0	0	0	1	1
		Cell%	0%	0%	0%	0%	0%	0%
	Total	*n*	173	101	40	17	3	334
		Cell%	52%	30%	12%	5%	1%	

5 HPV genotypes and DNA detection for all carcinogenic HPV. The age-group–specific prevalence as measured by RNA was similar to that of DNA but slightly, nonsignificantly lower in all age groups. The DNA prevalence for all carcinogenic HPV was approximately 20% to 30% greater than for the 5 HPV genotypes for all age groups. The trend of decreasing test positivity with older age groups was significant for RNA detection of 5 HPV genotypes ($P_{trend} = 0.04$) but was not for DNA detection of 5 HPV genotypes ($P_{trend} = 0.2$) and of 13 HPV genotypes ($P_{trend} = 0.06$).

The distribution for the number of HPV16, 18, 31, 33, and 45 genotypes detected by DNA and RNA testing is shown in Table 2. There was no significant difference ($P = 0.1$) in the number of HPV genotypes detected between tests. The main discrepancy between the 2 tests was that DNA was more likely to be positive for a single HPV genotype and RNA negative for any of the 5 targeted HPV genotypes than the converse (29 vs. 12, respectively).

We then compared the DNA and RNA test results for the pool of 5 HPV genotypes to cytology and histology results as shown in Table 3. For both DNA and RNA, the percentage positive increased with increasing severity of cytology or histology. The percentage positive for DNA and RNA for cytologic categories as read by the 2 pathologists was as follows: (i) 35% to 37% and 27% to 30%, respectively, for negative cytology; (ii) 50% to 57% and 46% to 53%, respectively, for ASC-US or LSIL; and (iii) 82% to 84% and 76% to 81%, respectively, for high-grade cytology (ASC-H or HSIL cytology). The trend of increasing test positivity with increasing severity of the cytologic interpretation was significant for all 4 combinations of test and cytology results ($P_{trend} < 0.001$). The percentage positive also increased with greater certainty of the presence of anal precancer. The percentage DNA or RNA positive for AIN2 ($n = 40$) and AIN3 ($n = 22$) was approximately 85% and was 100% for AIN2/3 with both cytologic interpretations read as high-grade ($n = 25$). HPV DNA testing was more likely to be positive than RNA for the same 5 HPV genotypes among subjects whose cytology was read as negative by pathologist 1 (37% vs. 30%; $P = 0.1$) or negative by pathologist 2 (35% vs. 27%; $P = 0.03$), or who had histologic diagnosis of less severe than AIN2 or did not have a diagnosis (46% vs. 40%; $P = 0.01$).

Using a *post hoc* definition of anal precancer as anyone with histology of AIN2/3 and/or with high-grade cytology as read by both pathologists ($n = 96$), we calculated the clinical performance statistics for HPV DNA and RNA (Table 4). Comparing RNA and DNA detection for the common 5 HPV genotypes, we observed identical sensitivity (81%) for both, whereas RNA detection was slightly more specific than DNA detection (65% vs. 58%, respectively; $P = 0.007$) for high-grade anal disease. Thus, RNA detection had a slightly better overall performance than DNA for detection of the same 5 HPV genotypes. PPV and NPV were very similar for both assays. Including the DNA detection of other carcinogenic HPV genotypes into the definition of the test resulted in an incremental improvement in sensitivity (from 81% to 96%) but reduced the specificity by almost half (from 58% to 33%) compared with the DNA detection of only the 5 HPV genotypes. Consequently, the DNA test for all 13 carcinogenic HPV genotypes was more sensitive ($P = 0.001$) but much less specific ($P < 0.001$) for high-grade anal disease than the RNA test for HPV16, 18, 31, 33, and 45. Conversely, restricting the tests to HPV16 and HPV18, the 2 most carcinogenic HPV genotypes, resulted in a less sensitive but more specific test, and the DNA test for HPV16 and HPV18 was significantly less sensitive but more specific test than the RNA test for 5 HPV genotypes ($P < 0.001$ for both). Similar results were observed using different definitions of cases (data not shown).

Table 3. Percentage positive for DNA and E6/E7 mRNA detection of 5 HPV genotypes (HPV16, 18, 31, 33, and 45) stratified by cytology and histology results

		HPV16/18/31/33/45		
	N	%DNA+	%RNA+	*P*
Cytology				
Pathologist 1				
Missing/unsatisfactory	19	37%	37%	1
Negative	103	37%	30%	0.1
ASC-US/LSIL	127	50%	46%	0.2
High-grade cytology (ASC-H or HSIL)	85	82%	76%	0.1
Pathologist 2				
Missing/unsatisfactory	9	44%	44%	1
Negative	143	35%	27%	0.03
ASC-US/LSIL	107	57%	53%	0.3
High-grade cytology (ASC-H or HSIL)	75	84%	81%	0.4
Both pathologists				
No high-grade cytology[a]	233	41%	36%	0.1
One high-grade cytology	42	79%	62%	0.02
Both high-grade cytology	59	85%	85%	1
Histology				
<AIN2	272	46%	40%	0.01
AIN2	40	88%	85%	1
AIN3	22	82%	86%	1
Histology and cytology				
No high-grade cytology[a] or histology	206	36%	31%	0.1
Any high-grade cytology or histology	128	81%	76%	0.1
AIN2/3 and any high-grade cytology	35	91%	91%	1
AIN3 and any high-grade cytology	14	93%	93%	1
AIN2/3 and both high-grade cytology	25	100%	100%	1
AIN3 and both high-grade cytology	11	100%	100%	1

[a]Includes HPV results for those with missing/unsatisfactory cytology results.

Discussion

We found that the patterns of HPV detection by DNA and RNA were much alike. While we observed that there was a consistent pattern of lower positivity of RNA than DNA detection, the differences in detection for individual HPV genotypes were minor so that only pooling of the 5 targeted HPV genotypes showed a statistically significant difference in relative specificity of approximately 10% for identifying HIV-positive MSM with anal precancer. Inclusion of all the carcinogenic HPV genotypes into the definition of a positive DNA test incrementally increased sensitivity while drastically reducing the

Table 4. Clinical performance of DNA and E6/E7 mRNA detection of different combinations of carcinogenic HPV genotypes for identification of anal precancer

	Se	Sp	LR+	LR−	PPV	NPV	OR (95% CI)
HPV16/18 RNA	62%	81%	3.3	0.48	57%	84%	6.8 (4.1–12)
HPV16/18 DNA	62%	77%	2.8	0.50	53%	83%	5.6 (3.3–9.3)
HPV16/18/31/33/45 RNA	81%	65%	2.3	0.29	48%	90%	8.1 (4.5–14)
HPV16/18/31/33/45 DNA	81%	58%	1.9	0.32	44%	89%	6.0 (3.4–11)
Carcinogenic[a] HPV DNA	96%	33%	1.4	0.13	37%	95%	11 (4.0–32)

Abbreviations: Se, sensitivity; Sp, specificity.
[a]HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, and 68.

specificity compared with a HPV E6/E7 mRNA test targeting 5 HPV genotypes, as previously observed.

We previously showed that mRNA detection of the 5 HPV genotypes is more specific but less sensitive for anal precancer than DNA detection for 13 carcinogenic HPV genotypes (25). On the basis of our data, we suggest that the improved specificity of RNA testing compared with DNA testing observed in the previous studies of anogenital disease (6–15) can be explained in a large part to restricting detection to 5 highly carcinogenic types. However, the RNA test showed a small significant increase in specificity compared with the type-restricted DNA test, suggesting that there is a small independent effect of RNA testing leading to improved specificity. The PreTect HPV-Proofer assay targets the most carcinogenic HPV genotypes, HPV16, 18, 31, 33, and 45, which together are responsible for causing 80% to 85% of all cervical cancer and a similar percentage of cervical intraepithelial neoplasia grade 3 (CIN3). HPV16, 18, 31, 33, and 45 cause similar or more anal cancer (26, 27) and AIN2/3 (27–29), although the exact percentage of AIN2/3 caused by these types in HIV-infected MSM populations is difficult to estimate precisely because of the frequent presence of multiple HPV infections (26, 28) and the challenges associated with attribution in the context of multiple infections (30). Adding weaker carcinogenic HPV genotypes (e.g., HPV59 and HPV68), which rarely cause cervical cancer (23, 31, 32) and may never cause anal cancer (27), into the test provides better sensitivity and improved NPV for CIN3 and AIN3, desirable for a screening test to rule out who is at risk, but reduces the diagnostic accuracy because of poorer specificity and PPV. In contrast, restricting DNA and RNA detection to HPV16 and HPV18, the 2 most carcinogenic HPV genotypes, further improved specificity and PPV compared with detection of the 5 HPV genotypes targeted by PreTect HPV-Proofer but reduced sensitivity.

On the basis of the effects observed for 5 carcinogenic types, we would predict that if the PreTect HPV-Proofer targeted all 13 carcinogenic HPV genotypes, we would observe significantly lower specificity versus RNA detection of the 5 HPV genotypes and a 10% relative improvement in the specificity versus the DNA detection of the 13 carcinogenic HPV genotypes. This would be consistent with previous reports comparing carcinogenic DNA detection and Aptima (33, 34), a recently U.S. Food and Drug Administration (FDA)–approved E6/E7 mRNA test for 14 carcinogenic HPV genotypes[1], for the detection of cervical precancer.

The additional approximately 10% in relative DNA positivity to RNA positivity for the 5 HPV genotypes did not seem to be associated with any disease. These DNA-positive, RNA-negative HPV infections seemed to be of low viral load: single infections that were DNA-positive but RNA-negative were more likely to have concurrent negative cytology and had a lower signal strength on a real-time PCR test for HPV (cobas4800, Roche) than those that were DNA- and RNA-positive (data not shown). It is probable that these are DNA detectable-only HPV infections, which are transient and have low risk for incident anal precancer and cancer.

We acknowledge several limitations of this study. First, there was limited number of histologic diagnoses of AIN3, which by analogy to CIN3 in cervix, is the most rigorous definition of precancer, and therefore the best surrogate for anal cancer risk (35). In addition, there were a number of men ($n = 34$) without AIN2 or worse histology and yet had high-grade cytology as read by both pathologists, suggesting that HRA had missed some anal precancer. We therefore included in our case definition of anal precancer those men with histologic AIN2 and/or confirmed high-grade cytology. It was reassuring that the patterns of HPV detection in these different groups included in our case definition were very similar to one another.

Second, our participants were from a single clinic site and their HIV infection in general was well managed, as indicated by the high percentage of MSM that had CD4 counts 350 per microliter or higher and HIV viral loads of less than 75 copies/mL. While our results may not be generalizable to a general population, there are no efforts to implement anal cancer screening in the general population, because the prevalence is so low. Thus, our participants are representative for the growing population of HIV-infected MSM, in which anal cancer is an increasing problem and in which screening and early detection options need to be evaluated. Furthermore, our results may apply to other populations with high HPV prevalence, in which distinguishing between benign HPV infections and those infections that have caused precancer is important.

In conclusion, once we accounted for the differences in the targeted HPV genotypes between RNA and DNA tests, we found only minor differences between detection of these 2 biomarkers of HPV infection in anal specimens from HIV-infected MSM to identify those anal precancer. E6/E7 expression is not exclusive to transforming infections, as E6/E7 must be expressed for genome maintenance in productive HPV infections (36). The E6/E7 mRNA test, which amplifies its target, may not effectively differentiate between E6/E7 expression detected in productive viral infections versus its overexpression detected in precancer. The clinical relevance of the incremental improvement in specificity of RNA over DNA detection will depend on the population in which the test is applied. In the high-risk population analyzed in this study, the improved specificity of RNA testing resulted only in a marginal increase of PPV. An algorithm similar as that used for cervical cancer screening (37), which may use HPV16/18 DNA detection, could serve as a model for anal cancer screening: rule out disease with

[1]http://www.fda.gov/MedicalDevices/ProductsandMedicalProcedures/DeviceApprovalsandClearances/Recently-ApprovedDevices/ucm278520.htm

carcinogenic HPV DNA detection and use DNA or RNA detection for a subset of highly carcinogenic HPV genotypes, perhaps in combination with cytology to determine which carcinogenic HPV-positive people need immediate HRA and directed biopsies. The choice between DNA and RNA detection may depend on laboratory ease of use and costs given the similarities in clinical performance characteristics.

Disclosure of Potential Conflicts of Interest

P.E. Castle is a consultant/advisory board member of Merck, BD, and Roche. T.M. Darragh is a consultant/advisory board member of Onco-Health and Arbor Vita. No potential conflicts of interest were disclosed by the other authors.

Authors' Contributions

Conception and design: P.E. Castle, S. Follansbee, J.C. Gage, N. Wentzensen
Development of methodology: P.E. Castle, S. Follansbee, N. Wentzensen
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): P.E. Castle, S. Follansbee, S. Borgonovo, D. Tokugawa, T.S. Lorey, B. Fetterman, T.M. Darragh
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): P.E. Castle, J.C. Gage, N. Wentzensen
Writing, review, and/or revision of the manuscript: P.E. Castle, S. Follansbee, L.M. Schwartz, T.S. Lorey, J.C. Gage, B. Fetterman, T.M. Darragh, A.C. Rodriguez, N. Wentzensen
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): L.M. Schwartz, B. LaMere, B. Fetterman
Study supervision: P.E. Castle, S. Follansbee, S. Borgonovo

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