Analyses of human papillomavirus genotypes and viral loads in anogenital warts.

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2   **Analyses of human papillomavirus genotypes and viral loads in anogenital warts.**

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11

12   Running title: HPV genotypes and viral loads in anogenital warts

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1

1   **Abstract**

2   *Condylomata acuminata* (genital warts) are the most common sexually transmitted viral

3   diseases. These lesions are caused by infection with mucosal human papillomaviruses (HPVs).

4   However there is limited information on HPV strain distribution involved in the molecular

5   pathogenesis of these lesions. To address this, the strain prevalence and the frequency of

6   multiple HPV infections were determined in wart tissue obtained from 31 patients attending a

7   wart clinic. These lesions were bisected and subjected to parallel DNA and mRNA extractions.

8   HPV-type prevalence and incidence of multiple infections were determined by the Roche Linear

9   Array assay. qPCR compared HPV6, 11 16 and 18 viral loads and RT-qPCR measured HPV 6 and

10 11 E6 genomic expression levels. 71% of these samples were infected with multiple HPVs. Only

11 1 sample was negative for HPV6 or 11 DNA. 48% of samples were positive for a high risk

12 (oncogenic) HPV. The results show that multiple infections in tissue are frequent and the

13 subsequent analysis of HPV6 and 11 E6 DNA viral loads suggested that other HPVs could be

14 causing lesions. Further analysis of HPV6/11 E6 mRNA levels showed that there was no

15 discernable relationship between HPV6 E6 DNA viral load and relative HPV 6 or 11 E6 mRNA

16 levels thereby questioning the relevance of viral load to lesion causality.

17 **Keywords:** HPV. Genital warts. E6 DNA viral loads. E6 mRNA.

1 **Introduction**

2 Infection with Human papillomaviruses (HPVs) results in a major global disease burden. In

3 particular, HPVs infecting mucosal tissue cause very significant morbidity and mortality. Those

4 HPVs fall into 2 groups; the so-called 'low risk' strains that cause warts and the 'high risk'

5 (oncogenic) strains (particularly HPV 16 and 18) that are the cause of ano-genital and oro-

6 pharangeal cancers [Winder et al., 2009; zur Hausen, 2002].

7 In the uterine cervix, multiple HPV infections are frequent [Schmitt et al., 2010]. Studies using

8 highly sensitive PCR based methods for HPV strain detection in ano-genital lesions indicate that

9 multiple types (including both high and low risk strains) can also be detected in *Condylomata*. In

10 such circumstances it is difficult to assign causality to a specific HPV strain, although over 90%

11 of these lesions are positive for HPVs 6 and 11 DNA [Brown et al., 1999]; [Aubin et al., 2008];

12 [Chan et al., 2009] and there has been a significant decline in incident wart disease since the

13 introduction of a quadrivalent L1 VLP vaccine (Gardasil™) raised against HPVs 6 and 11 together

14 with the oncogenic HPVs 16 and 18 in 2007 ([Fairley et al., 2009]; [Munoz et al., 2010]).

15 Clarification of the clinical relevance of the multiple HPV strains found in a wart sample from an

16 individual patient is important for understanding which HPV strain is causal and these data will

17 be informative in any cases of vaccine failure.

18 In this study, the HPV strain prevalence, the frequency of more than 1 type in *condylomata* and

19 the relevance of viral DNA load to early gene expression have been determined in order to in

20 assign lesion causality to HPV 6 or 11.

3

1 **Materials and methods:**

2 **Clinical specimens and sample preparation.**

3 The study was approved by the local Research Ethics Committee and all patients provided

4 written informed consent for their tissues to be used for research. A total of 31

5 immunocompetent male and female patients attending the Department of GU/HIV Medicine,

6 St Mary's Hospital, London, UK, were recruited to the study. Genital wart samples were

7 obtained under local anaesthesia and the tissue bisected and snap frozen at the time of biopsy

8 for DNA and RNA extraction.

9 **DNA extraction and HPV detection.**

10 DNA was extracted with DNeasy™ blood and tissue kit (Qiagen, Crawley, UK), following the

11 manufacturer's instructions. HPV types in 62.5ng of sample DNA were identified using the

12 Roche Linear Array (Roche Diagnostics Ltd, Burgess Hill, UK)[Woo et al., 2007].

13 **Measurement of viral load**

14 For Taqman™ qPCR, primers and probes were synthesised by Sigma Genosys, Gillingham, UK.

15 The primers and probes for human GAPDH [Coleman et al., 2008], HPV6, 11 and 18 E6/7 DNA

16 and β-globin (A) [Tucker et al., 2001] and for HPV16 E6/7 DNA, and human β-Globin (B) [de

17 Boer et al., 2007] have been previously described (Supplementary table S I). Amplification was

18 performed in 20μL using 10ng sample DNA and Hotstart Taq (Qiagen, Crawley, UK) with cycling

19 conditions as follows: initial Taq activation and template denaturation at 95°C for 15 min,

20 followed by 45 cycles of 15s at 95°C and 60s at 60°C, with acquisition of fluorescent signal at 60

21 seconds. Amplification was performed on a Rotor-Gene 3000 (Corbett Life Science, Qiagen,

22 Crawley, UK) and data analysed using the Rotor-Gene software, v6.1. All optimisation

4

1   experiments were performed in triplicate at least 3 times. It was determined that HPV18 and

2   HPV16 could be multiplexed with the additional GAPDH internal control but all other HPV

3   amplification reactions were performed separately in parallel with control reactions. Standard

4   curves were constructed using purified placental human DNA (Sigma-Aldrich, Gillingham, UK)

5   and purified plasmids containing the HPV of interest. Serial dilutions of 1 in 5 were constructed

6   (containing 100ng to 6.4pg human DNA and 10^5 to 6.4 copies of HPV per reaction). The

7   specificity of primers was determined under identical conditions with genomic HPV DNA (HPVs

8   1a, 2a, 3, 5, 6, 7, 8, 10, 11, 14, 16, 17, 18, 20, 31, 49, 50 or 57) at a concentration of 10^6

9   copies/μL. No significant non-specific reactions were observed. Viral load was expressed as

10   number of virus particles/cell assuming 1ng DNA ~150 cells [Leyva and Kelley, 1974]. Viral loads

11   < 0.01 copies/cell were deemed as insignificant.

12   **mRNA extraction, purification and cDNA synthesis.**

13   The second half of the bisected tissue sample was shredded at the time of excision and stored

14   at -80°C in RNAlater™ (Qiagen, Crawley, UK). The tissue was later resuspended in 200μL Trizol™

15   (Invitrogen, Paisley, UK) in a lysing matrix D tube (MP Biomedicals, Solon OH, USA) and

16   pulverised using a Bulletblender™ machine (Next Advance, Averill Park, NY,USA). RNA was

17   precipitated with isopropranol and resuspended in 50μL H_2O. After DNAse I digestion, RNA was

18   recovered by column purification using PureLink™ RNA extraction kit (Invitrogen, Paisley, UK)

19   following manufacturer's instructions and a maximum of 5μg reverse transcribed using

20   Bioscript™ (Bioline, London, UK) after pre-incubation with random hexamer primers for 5min at

21   65°C. Reactions were performed as follows: 25°C for 10min, 42°C for 60min and 70°C for 15min.

22   No-RT controls were performed without the addition of enzyme. The resulting cDNAs were

1   diluted 1/10 with pure water before qRT-PCR analysis. RT-qPCR for HPV 6 and 11 E6/E7 was

2   performed as per qPCR with supplementary internal control primers (Supplementary table S II).

3   To enable multiplexing of mRNA internal controls, primer-pairs and probes were examined for

4   any potential primer-dimer pairs using

5   Autodimer™(http://www.cstl.nist.gov/div831/strbase/AutoDimerHomepage/AutoDimerProgra

6   mHomepage.htm). RT-qPCR was performed for all HPVs as a single-plex assay using primers and

7   probe as listed in Table I.

8   **Measurement of viral RNA load**

9   Values of HPV mRNA copy number were determined by standard curves of genomic HPVs (as

10   described for DNA viral load). Relative cellular mRNA was determined by normalising CT values

11   of TBP (TATA-Box binding protein), YWHAZ (tyrosine 3-mono-oxygenase/tryptophan 5-mono-

12   oxygenase activation protein, zeta polypeptide) and HMBS (hydroxymethylbilane synthase)

13   triplex RT-qPCR to calibrator sample (sample 9). Primers and probes sequences were first

14   reported for TBP, YHWAZ and HMBS by [Radonic et al., 2005], [Ohl et al., 2006] and [Qian et al.,

15   2002] respectively.

16   **Data analysis and statistics**

17   The results from the Linear Array assay were compared to those obtained by qPCR. Unweighted

18   Kappa statistics were calculated by online software

19   (http://www.graphpad.com/quickcalcs/kappa1.cfm). Kappa values determined were ranked as

20   moderate, substantial or near perfect as described by Viera et al. [Viera and Garrett, 2005].

21

6

1 **Results**

2 DNA from all 31 genital wart samples was positive for β-globin and HPV using the Linear Array

3 assay. All the warts harboured at least one low-risk HPV (Table I), and, as expected, HPV 6 and

4 11 dominated and were present in 97%, with HPV 6 in 28 (90%) and HPV 11 in 10 lesions (32%).

5 In 9 lesions (29%), only HPV 6 was found. The frequency distribution of HPV strains in this

6 cohort of tissue is featured in figure 1.

7

8 22 of the warts (71%) were multiply infected (Table II). In 7 (22%), more than one low-risk HPV

9 was detected and in 15 (48%) a mixture of low- and high-risk types were found. 11 (35%) of the

10 samples contained HPV16 or 18 or both. Only one sample (sample 25) was not infected by HPV

11 6 or 11, but was infected by other low risk types 40, 84 and CP6108 in addition to the oncogenic

12 strains 16, 18, 33 and possibly 52. Other low and high risk strains detected are shown in Table II.

13

14 Viral load was assayed using 10ng of sample DNA as standardization experiments had shown

15 that the Taqman™ qPCR was unbalanced with 100ng or more DNA. A threshold level for copy

16 numbers of specific HPV E6/E7 DNA was assumed to be 10 copies/cell indicating the HPV in

17 question to have been replicated and so likely to be involved in the pathogenesis of the clinical

18 lesion [Doorbar, 2006]. In addition, the sample DNA was obtained from tissue containing both

19 epithelium and stroma, so the concentration of HPV in infected keratinocytes is likely to be

20 higher than the values obtained for the full biopsy.

21

1 Of the 28 warts positive for HPV 6 in Linear Array, 18 had a copy number of HPV 6 above

2 threshold value. 5 warts, in which there was co-detection of HPV 11, had a copy number of HPV

3 11 exceeding 10 copies/cell (Table II). 8/31 samples (26%) did not have viral loads above

4 threshold value of either HPV 6 or 11. In 3 of these, however, HPV 16 was detected at a level

5 above 10 copies/cell and was also positive in the Linear Array assay. In 4 of these 8 samples,

6 other low risk HPV strains, which were not tested by qPCR, had been detected in the Linear

7 Array assay and so potentially could have been causal in these lesions.

8

9 HPV 6 or 11 E6/E7 transcripts were detected and quantified in 23 samples. No tissue was

10 available for RNA extraction in 3 cases. In all samples where HPV mRNA was quantified at a

11 measurable level, the same HPV type had been found by the Linear Array assay. Only sample 8

12 had very low HPV6/11 DNA and mRNA levels, suggesting that one or more of the other low risk

13 HPVs present (55, 62, or 84) could have been causal in these lesions.

14

15 These data show that relatively small DNA viral loads are capable of producing high mRNA

16 levels as, for example, sample 1 had only 2 copies of HPV 6 per cell, but generated a relative

17 amount of 1163 copies of HPV 6 mRNA per reaction. The converse is also true, as the sample

18 with the largest HPV 6 DNA viral load (namely sample 15 with 870 copies/cell), did not yield the

19 largest E6/7 mRNA load. Five multiply infected samples (namely 1, 4, 8, 17 and 22) had low HPV

20 6 DNA viral loads (<10 copies/cell) suggesting that another HPV was responsible for the lesion.

21 However, analysis of relative mRNA levels revealed measurable HPV 6 E6 transcription in 4

8

1   samples (1, 4, 17 and 22) thus HPV 6 could still be causing these lesions. As HPV 6 E6 mRNA was

2   not measurable in sample 8, other low risk HPVs present (55, 62 or 84) may have been causal.

3

4   3 samples (3, 22 and 25) had copies of HPV 16 DNA viral loads above 10 copies/cell, raising the

5   possibility that these lesions could be caused by HPV 16. For sample 3, HPV 11 and 16 were

6   detected by the Linear Array assay, subsequent qPCR and RT-qPCR revealed HPV 11 E6 DNA and

7   E6 mRNA levels to be negligible whilst HPV 16 DNA was present at 177 copies/cell. These data

8   suggest HPV 16 is causing the lesion, although in the absence of HPV 16 mRNA measurement it

9   can only be speculated. In sample 22 (positive for HPV 6 and 16 DNA) HPV 6 mRNA was

10   abundant even though the HPV 6 DNA load was <10 copies/cell.

11

12   Sample 25, however was negative for HPV 6 and 11 on the Linear Array assay, but positive for

13   HPV 40, 84, CP, 16, 18, 33 and 52. The absence of measurement of the low risk HPVs 40, 84 and

14   CP6108 mRNAs meant that their contribution to the pathogenesis of this lesion could not be

15   discounted and it would be incautious to conclude that HPV 16 caused this lesion.

16

17   Inter-assay concordance values were derived using Cohen's κ algorithm (Table III) [Viera and

18   Garrett, 2005]. For all comparisons agreement was considered better than 'moderate' (κ>0.41),

19   except between Linear Array results and relative mRNA levels for HPV 6 which was determined

20   to be 'fair'. These data suggest that the presence of HPV 6 L1 DNA as determined by the Linear

21   Array assay does not predict E6 genomic expression as measured by the RT-qPCR.

9

1 **Discussion**

2 This detailed DNA and RNA analysis of HPVs in genital warts attempted to identify not just the

3 HPV strains present in or on the lesion, but also to gather evidence of the HPV strains that could

4 be causing the lesions and producing infective virions. To our knowledge, there are no previous

5 published data for this type of analysis in *condylomata acuminata*. Most studies of HPV types in

6 genital warts have used surface swabs and PCR amplification with sequencing or hybridization

7 methods to identify multiple infections [Chan et al., 2009; Greer et al., 1995; Giuliano et al.,

8 2008; Sanclemente et al., 2007]. These sensitive methods can also detect HPV DNAs in the

9 anogenital region in asymptomatic individuals [Nielson et al., 2009]. The potential risk from

10 analysis of surface samples is that the HPVs detected may reflect carriage but not necessarily

11 permissive viral growth. The analysis of lesion tissue should minimize false positive results due

12 to other non-lesion associated HPVs within this body area.

13

14 It was no surprise to find HPV 6 was the most frequently detected in these lesions with HPV 11

15 as the second most prevalent type. This is in accordance with previous data for other studies

16 using the Linear Array assay in genital wart swabs [Aubin et al., 2008; Chan et al., 2009] and

17 tissue [Potocnik et al., 2007]. The finding of high risk HPVs in 35% of samples in this

18 immunocompetent group is in keeping with other reports of high risk types detected in 14-44%

19 of non-immunosuppressed individuals [Brown et al., 1999; Potocnik et al., 2007] but below that

20 found in patient groups with a higher HIV positive prevalence where high risk HPVs may be

21 present in 47-100% of genital warts [Brown et al., 1999; Müller et al., 2010; Schlecht et al.,

22 2010].

10

1

2   This data from immunocompetent patients show that 71% excised wart samples contained dual

3   or multiple HPV types, agreeing with previous estimates [Brown et al., 1999; Aubin et al., 2008,

4   Chan et al., 2009]. The Linear Array assay has the advantage of simultaneously detecting the

5   presence of 37 genital HPV types [Woo et al., 2007] and is considered the most sensitive test of

6   its kind [van Ham et al., 2005; van Hamont et al., 2006]. The advantage of qPCR is the ability to

7   estimate viral load, allowing comparison of specific HPV subtypes in multiply infected samples.

8   The inter-assay agreement levels between the Linear Array assay and qPCR was good and

9   validated the use of either assay for screening.

10

11 The identification of HPV strains other than 6 or 11 causing genital warts will be important for

12 future vaccination strategies, although the reduction of anogenital warts since the introduction

13 of the quadrivalent vaccine, Gardasil™ [Fairley et al., 2009; Munoz et al., 2010], supports

14 confirmation presented here of the role of HPV 6 or 11 in causing lesions, even in multiply

15 infected samples or when their DNA loads are low. One concern is that if lesions caused by HPV

16 6 and 11 are eradicated, other HPVs may become more prevalent and therefore more

17 important for identification, and subsequent confirmation of which HPV is causal. Confirmation

18 and quantitation of other HPV mRNAs would be desirable, but as yet there is no equivalent of

19 the Linear Array assay for HPV mRNA analysis and this study was limited to the primer and

20 probe sets in the laboratory. The PreTect™ HPV Proofer and Aptima™ systems are designed for

21 the detection of high-risk HPV mRNA only [Halfon et al., 2010; Molden et al., 2007; Keegan et

22 al., 2009] and so would be unsuitable for *Condylomata*.

11

1

2   The choice of E6/E7 transcript in this study was based on their known roles in the viral

3   infectious cycle [Doorbar, 2006]. Studies investigating the DNA and mRNA loads of oncogenic

4   HPVs in cervical intraepithelial neoplasia (CIN) have concluded that E6 RNA load is a better

5   predictor of lesion severity [de Boer et al., 2007; Cattani et al., 2009; Ho et al., 2010] and

6   progression levels [de Boer et al., 2007], and although malignant progression was not likely in

7   these lesions, E6 RNA abundance probably reflects viral contribution to lesion pathogenesis. As

8   demonstrated in this report, DNA loads of low-risk subtypes, HPV 6 and 11, do not correlate

9   with their respective mRNA E6 transcript levels and is similar to that observed in HPV 16-

10 associated CIN [de Boer et al., 2007; Cattani et al., 2009]. Therefore, viral genome copy number

11 does not directly reflect viral activity.

12

13 HPV16 is not thought to produce *Condyloma*-like lesions [zur Hausen, 2002] although one

14 reported case [Chrisofos et al., 2004] based on DNA analysis alone, suggests that it may. The

15 DNA analysis shows 3 samples in which HPV 16 DNA was detected by the Linear Array assay and

16 also at a significant level by qPCR, suggesting that this oncogenic type is amplified within these

17 lesions, but this can only be confirmed by quantitation of the mRNA which was not performed

18 in this study.

19

20 These data provide evidence for multiple subtype infection as a common event in the natural

21 history of *Condylomata acuminata,* but with significant replicative activity of usually HPV 6 or

22 11. DNA viral loads alone are insufficient to truly determine which HPV is causal, and mRNA

12

1   analysis is required to discount the contribution of HPV 6 and/or 11 when DNA loads are low. In

2   order to confirm these findings, a prospective study including larger numbers of patients, rather

3   than an unselected collection of warts should be performed. It is likely that analysis of HPV

4   mRNA would provide data informative for HPV vaccines and will be especially useful in the

5   event of vaccine failure.

6

7   Disclosure of Conflicts of Interest

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1 **Figures**

2

3 **Supplementary table S I**

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Target	Accession Number	Forward Primer	Reverse Primer	Probe	Optimised primer concentration (nM)
HPV6	AF092932	GTTCATAAAGCTAAATTGTACGTGGAA	TGTGAATCTTGTCCGTCCACTT	[6FAM]-ACAATATCCTTTAGGGTAACATGTCTTCCATGCATG - [TAMRA]	75
HPV11	M14119	GCTTCATAAAACTAAATAACCAGTGGAA	TGCGTCTTGTTTGTCCACCTT	[6FAM]-CTATATCCTTTAGGGTAACAAGTCTTCCATGCATGTTG- [TAMRA]	75
HPV16	K02718	CCGGACAGAGCCCATTACAAT	ACGTGTGCTTTGTACGCAC	[6FAM]-TGTTGCAAGTGTGACTCTACGCTTCGGT-[BHQ1]	100
HPV18	NC_001357	CAACCGAGCACGACAGGAA	CTCGTCGGGCTGGTAAATGTT	[6FAM]-AATATTAAGTATGCATGGACCTAAGGCAACATTGCAA-[BHQ1]	100
β-globin (A)	NG_000007	CAGGTACGGCTGTCATCACTTAGA	CATGGTGTCTGTTTGAGGTTGCTA	[TET]-GCCCTGACTTTTATGCCCAGCCCTG-[BHQ1]	500
β-globin (B)	NG_000007	GACAGGTACGGCTGTCATCA	TAGATGGCTCTGCCCTGACT	[TET]-CTAGGGTTGGCCAATCTACTCCCAG-[BHQ1]	100
GAPDH	NM_002046	CGGCTACTAGCGGTTTTACG	AAGAAGATGCGGCTGACTGT	[Cy5]-CACGTAGCTCAGGCCTCAAGACCT-[BHQ3]	300

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6

7 Supplementary table I.

8 **Primers and probe sets used in qPCR assay of viral load.**

9 Primer/probe sets used for the detection of HPV and Human DNA in DNA samples

10 generated from wart tissue. Sequences are represented 5'-3' and the 5' fluorescent labels

11 indicated (6FAM - 6-carboxyfluorescin, TET - tetrachloro-6-carboxyfluorescein or Cy5 -

12 cyanine). Tetramethylrhodamine (TAMRA), Black Hole Quencher 1 (BHQ1) or Black Hole

13 Quencher 3 (BHQ3) was incorporated at the 3' end of each probe.

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1   **Supplementary table S II**

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Target	Accession Number	Forward Primer	Reverse Primer	Probe	[Primer] (nM)
TBP (233)	NM_003194	TTCGGAGAGTTC TGGGATTGTA	TGGACTGTTCTTC ACTCTTGGC	[6FAM]-CCGTGGTTCGTGGCTCTCTT ATCCTCAT- [BHQ1]	60
YWHAZ (196)	NM_145690	AAGTTCTTGATCC CCAATGCTT	GTCTGATAGGAT GTGTTGGTTGC	[TET]-TATGCTTGTTGTGACTGATC GACAATCCCT-[BHQ2]	80
HMBS (82)	NM_000190	ACTTTCCAAGCG GAGCCAT	CGAATCACTCTC ATCTTTGG	[Cy5]-CGGCTGCAACGGCGGAAG AAAAC-[BHQ3]	100

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5   Supplementary table S II.

6   **mRNA housekeeping/internal control primer sequences and probe sets.**

7   Primer/probe sets used for the detection of internal control housekeeping transcripts in cDNA

8   samples. Sequences are represented 5'-3' and the 5' fluorescent labels indicated (6FAM - 6-

9   carboxyfluorescin, TET – tetrachloro-6-carboxyfluorescein or Cy5 - cyanine). Tetramethylrhodamine

10   (TAMRA), Black Hole Quencher 1 (BHQ1) or Black Hole Quencher 2 (BHQ2) was incorporated at the

11   3' end of each probe. Amplicon size is in brackets (number of base pairs).

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1   **Table I**

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	Number of samples (%)
HPV positive	31 (100)
HPV6+	28 (90)
HPV6 plus other	21 (68)
HPV11 +	10 (32)
High Risk HPV+	15 (48)
Single Infections	9 (29)
Dual infections	11 (35)
Triple Infections	3 (10)
More than 3 HPVs present	8 (26)

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6   Table I.

7   **Summary of Linear Array results.**

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1　**Table II**

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Sample Number	Linear Array Result (HPV type present)		Taqman™ qPCR results. (copies/cell)				Relative HPV RNA load (copies/reaction)	
	Low risk	High risk	HPV6	HPV11	HPV16	HPV18	HPV6	HPV11
1	6, 40	18	2	-	-	-	1163	-
2	6		13	-	-	-	354	-
3	11	16	-	-	177	-	-	-
4	6, 42		3	-	-	-	53	-
5	6		27	-	-	-	NA	NA
6	6, 11		-	51	-	-	-	71
7	6, 42, 54, CP	31, 39	198	-	-	-	18	-
8	6, 55, 62, 84	45	-	-	-	-	-	-
9	6, 11		46	-	-	-	4764	-
10	6, 11		-	123	-	-	-	6905
11	6	18	14	-	-	-	5630	-
12	6		351	-	-	-	20	-
13	6, 11, CP	16	-	190	-	-	-	21604
14	6		35	-	-	-	NA	NA
15	6	18, 45, 51, 59	870	-	-	-	4036	-
16	6		59	-	-	-	21735	-
17	6, 67	52? 58	8	-	-	-	243	-
18	6	18	12	-	-	-	2712	-
19	6, 11		456	-	-	-	51	-
20	6, 11, 69, 84	16	-	251	-	-	6	67
21	6		26	-	-	-	493	-
22	6	16	3	-	16	-	141	-
23	6		147	-	-	-	616	-
24	6		12	-	-	-	959	-
25	40, 84, CP	16, 18, 33, 52?	-	-	11	-	-	-
26	6, 11		85	-	-	-	3715	13
27	6	45	203	-	-	-	-	-
28	6	18, 59	61	-	-	-	3289	-
29	6, 11, 84		19	558	-	-	676	7662
30	11, 42, 64	18	-	284	-	-	NA	NA
31	6		-	-	-	-	-	-

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4　Table II.

5　**Linear Array Results vs qPCR Viral Load and Relative RNA load.**

6　Samples were assayed for the appearance and DNA and RNA viral load of HPV as described in the methods

7　section. (-) denotes not significantly positive during assay (less than 1 copy/cell or 5 copies/reaction total RNA).

8　CP represents CP6108. 52? denotes positivity at the 52/33/35/58 band on the Linear Array, but also for

9　individual 33 and 58 markers, but where the presence of 52 cannot be discounted as described in the

10　manufacturer's instructions. NA denotes no tissue available for RNA analysis.

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1　**Table III.**

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Comparison between positive results	HPV6	HPV11
Linear Array vs qPCR DNA	0.415	0.67
Linear Array vs RT-qPCR RNA	0.323	0.731
qPCR DNA vs RT-qPCR RNA	0.825	0.887

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6　Table III.

7　**Interassay concordance data.**

8　Cohen's κ coefficients were derived as described in the methods section.

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1   **Figure 1**

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6   Fig. 1.
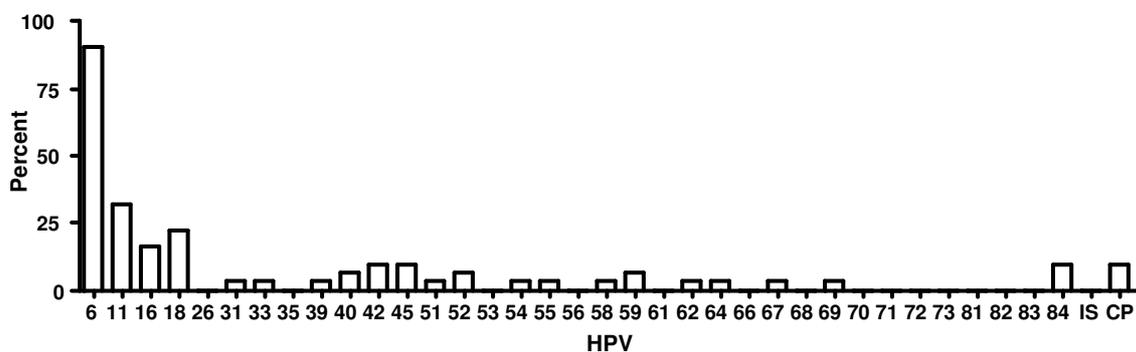
7   **Distribution of HPV types in wart tissue as determined by Linear Array.**

8   All occurrences of HPV were scored, regardless of being single or multiple infections.