

HPV prevalence and type-distribution in cervical cancer and premalignant lesions of the cervix: A population-based study from Northern Ireland

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27 **ABSTRACT:**

Introduction: Assessment of Human papillomavirus (HPV) prevalence and genotype distribution is important for monitoring the impact of prophylactic HPV vaccination. This study aimed to demonstrate the HPV genotypes predominating in pre-malignant and cervical cancers in Northern Ireland (NI) before the vaccination campaign has effect.

32 Methods: Formalin fixed paraffin embedded tissue blocks from 2,303 women aged 16-93 years 33 throughout NI were collated between April 2011 and February 2013. HPV DNA was amplified by PCR 34 and HPV genotyping undertaken using the Roche[®] linear array detection kit.

35 Results: In total, 1,241 out of 1,830 eligible samples (68.0%) tested positive for HPV, with the 36 majority of these [1,181/1,830 (64.5%)] having high-risk (HR) HPV infection; 37.4% were positive for 37 HPV-16 (n=684) and 5.1% for HPV-18 (n=93). HPV type-specific prevalence was 48.1%, 65.9%, 81.3%, 38 92.2% and 64.3% among cervical intraepithelial neoplasias (CIN) grades I-III, squamous cell 39 carcinomas (SCC) and adenocarcinoma (AC) cases, respectively. Most SCC cases (81.3%) had only one 40 HPV genotype detected and almost a third (32.0%) of all cervical pathologies were HPV negative 41 including 51.9% of CIN I (n=283), 34.1% CIN II (n=145), 18.7% of CIN III (n=146), 7.8% of SCC (n=5) 42 and 35.7% of AC (n=5) cases.

43 **Conclusions:** This study provides important baseline data for monitoring the effect of HPV 44 vaccination in NI and for comparison with other UK regions. The coverage of other HR-HPV 45 genotypes apart from 16 and 18, including HPV-45, 31, 39 and 52, and the potential for cross 46 protection, should be considered when considering future polyvalent vaccines.

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Keywords: human papillomavirus, cervical cancer, cervical intraepithelial neoplasia, frequency,
population-based.

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53 **INTRODUCTION**

54 Annually 3,000 women are diagnosed with, and almost 1,000 die from cervical cancer in the United 55 Kingdom (UK), making it the 12th most common cancer diagnosis and 17th most common cancer 56 death [Cancer Research UK, 2014]. Two main subtypes exist, squamous cell carcinoma (SCC) and 57 adenocarcinoma (AC). Persistent infection with high-risk (HR) oncogenic human papillomavirus 58 (HPV) family *alpha-Papillomaviridae* is a necessary, but insufficient cause, for invasive cervical cancer 59 [IARC Working Group on the Evaluation of Carcinogenic Risks to Humans., 2012]; with HPV-16 and 60 HPV-18, the most common oncogenic types, contributing to around 70% of all cases worldwide 61 [WHO/ICO Information Centre on HPV and Cervical Cancer, 2010].

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63 HPV is highly sexually transmissible with 80% of women expected to have a HPV infection at some 64 point during their sexually active life [Alexander et al, 2012]. Many women are repeatedly infected, 65 with most infections occurring in those aged under 25 years [de Sanjosé et al, 2007; Smith et al, 66 2008; Anderson et al, 2013]. However, despite frequent exposure to HPV, development of cervical 67 cancer is uncommon with most HPV infections being transient and spontaneously regressing within 68 two years with no residual abnormality [Castellsagué, 2008]. In some cases HPV infection may 69 persist [Trottier et al, 2009], with some HPV genotypes more persistent than others [Louvanto et al, 70 2010]. Recent studies indicate a higher proportion of CIN II and CIN III lesions progressing to invasive 71 cancer in HPV-16 positive lesions, often within as little as 10-20 years [Jaisamrarn et al, 2013; Vink et 72 al, 2013; Wentzensen et al, 2013]. Many aspects of the natural history of HPV infection remain to be 73 fully elucidated, including the probable existence of latent infections and potential reactivation.

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Although HPV-16, 18, 31, 52 and 58 are cited among the top 10 most common HPV genotypes worldwide [Bruni *et al*, 2010], there is significant variation in the reported prevalence of HR-HPV genotypes between countries. We previously reported that the prevalence of any HPV infection in Northern Ireland (NI) women having a pap smear was 17.1%, ranging from 42.5% in those aged 20-

79 24 years to 4.2% in women aged 60-64 years; HPV prevalence was lower in women with normal 80 cytology at 13.2% increasing in those with cervical disease [Anderson *et al*, 2013]. However, this 81 study was underpowered to detect the prevalence of HPV genotypes in high-grade cervical 82 abnormalities (n=72).

The aim of the present study was therefore to provide an estimate of the background prevalence of HPV infection and age-specific HPV type distribution, and to highlight the HPV genotypes most frequently present in cervical cancer tissue and precursor lesions, before the HPV vaccination programme alters the distribution of HPV infection in NI. Of note, unpublished data from the present study has been recently incorporated into a pooled analysis of the HPV type-specific prevalence in invasive cervical cancers in the UK [Mesher et al, 2014] where the overall prevalence of any HR-HPV was found to be 95.8%; data that will be valuable in future HPV vaccine monitoring and effectiveness studies. More detailed data on the prevalence of all detected HPV genotypes stratified by five year age-bands, inclusive of CIN I-III and cervical pathologies are reported herein.

105 **METHODS**

106 Sample selection

Prospectively derived formalin fixed paraffin embedded (FFPE) cervical tissue blocks (processed at all four pathology laboratories in NI) pertaining to routine diagnostic samples collected between April 2011 and February 2013 from all women attending for cervical screening across NI (populationbased cohort), and which were determined to have cervical abnormalities, were eligible for inclusion. No age or histological restrictions were applied to the cohort during specimen collection.

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113 Through data supplied by the Public Health Agency Northern Ireland, we estimate that only a small 114 proportion of samples may have been derived from previously HPV vaccinated women (5.9%), thus 115 the majority of samples included in this study are from HPV unvaccinated women. Following routine 116 examination of the biopsy in each reporting laboratory, consultant pathologists selected the most 117 appropriate FFPE block containing the highest grade of disease reported. The selected cervical 118 tissue blocks were sent to the Department of Cellular & Molecular Pathology, Northern Health & 119 Social Care Trust for HPV determination. For the purposes of the present study, analysis was 120 restricted to samples identified as cervical intraepithelial neoplasia (CIN) grades I, II and III, SCC and 121 AC. On reception of the FFPE tissue blocks, pathology records were accessed and clinical pathological 122 information including patient age, sample type and histology, were extracted. A unique study 123 number was then assigned to each case and the link to the original case broken, ensuring 124 confidentiality and complete anonymisation of the results. Ethical approval for the study was 125 granted from the Office of Research Ethics Committees NI (ORECNI ref: 08/NIIR02/104).

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127 Specimen processing

FFPE tissue blocks underwent tissue microtomy and were processed under molecular pathology
conditions, to reduce the risk of cross contamination. Tissue lysis was performed using the QIAGEN
ATL (EDTA and 10% sodium dodecyl sulphate) buffer (P/N 19076, Qiagen, Crawly, West Sussex, UK),

131 in the presence of 20µl of proteinase K (P/N 19131, Qiagen, Crawley, West Sussex, UK). The tissue 132 was incubated at 56°C \pm 2°C for 24 hours with occasional vortex mixing during this incubation 133 period. During post enzymatic incubation, the lysate was added to processing tubes and was 134 subjected to automated DNA extraction on the Roche COBAS® 480 X module as per manufactures 135 protocols. Extracted DNA was eluted into buffer EB and stored at -20°C until amplification. Detection 136 of HPV genotypes were undertaken using a modified Roche Linear Array HPV genotyping test (LA 137 HPV GT P/N:04391853 190) and the Linear Array detection kit (LA DK P/N: 03378179 190, Roche 138 Molecular Systems, Inc. Branchburg, NJ, USA). The modification from manufactures protocol 139 consisted of the addition of a compound into the HPV MasterMix, to allow for compatibility with the 140 DNA extracted from the COBAS® 480 X module. Extracted DNA was quantified via NanoDrop 141 spectrophotometry with all samples standardised to a concentration of 24ng/ul; the optimum level 142 determined in-house to allow for successful HPV detection in the background of human DNA and 143 reduce the number of test failures due to an "overloaded" PCR reaction. Of note, the Roche linear 144 array uses multiple type (mixed) probes to detect DNA from HPV-52 which limits the assay's ability 145 to discriminate HPV-52 status in the presence of HPV 33, 35 and/or 58 infections. The HPV-52 146 genotype was thus derived as positive if co-infection of HPV 33, 35 and 58 was not present in the 147 sample. Cervical SCC samples that tested HPV negative were revisited, DNA isolated and retested to 148 ensure the result. Samples were considered HPV negative only when a linear array negative result 149 was obtained and confirmed by repeat testing.

150

151 Specimen Reporting

The term HR-HPV is used to describe a number of HPV genotypes that have been shown to be associated with an increased risk of cervical cancer and include: HPV-16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59 (carcinogenic), 68 (probably carcinogenic) and 66 (possibly carcinogenic) based on the World Health Organization (WHO) HPV categorizations [Cogliano *et al*, 2005]. The term 'low-risk

HPV' covers all other HPV genotypes detected by the Roche HPV linear array genotyping test. AllHPV types identified by the Roche linear array are shown in Table 3.

159 Statistical analysis

The overall prevalence, genotype and age-specific HPV prevalence among pre-malignant lesions (CIN I-III) and cervical cancers (SSC and AC) were estimated for all samples. The frequency of those testing positive for HPV-16 and HPV-18 with or without other HR-HPV genotypes was investigated. Women within the study were stratified into five year age bands, this was further classified into three age groups for the following reasons; under 25 years (outside the age range for the current NI Cervical Screening Programme, but current at the time of our previous prevalence study in the screened population); 25 to 34 years (reported to have a higher transient HPV infection risk with no significant underlying disease [Khan et al, 2005]), over 35 years (this group of HR-HPV positive is said to have a higher chance of significant pathological outcome [Khan et al, 2005]). STATA IC/11.2 (StataCorp, College Station, TX, USA) was used for all analyses.

182 **RESULTS**

In total, 2,303 samples were received between April 2011 and February 2013. Figure 1 is a flow diagram providing justification for the selection of study samples. Exclusions included 58 samples that were not tested due to overrepresentation in the low-grade dyskaryosis groups, a further 200 were excluded at the post-analytical phase of the study due to insufficient tissue remaining for molecular analysis. 218 samples were also excluded as they were not SCC, AC or CIN I-III pathologies. A total of 1,827 eligible samples were included for analysis, the majority of which were acquired through large loop excisions of the transformation zone (64.8%) or punch biopsies (34.2%).

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191 Prevalence of HPV infection:

In total, 1,243/1,827 samples (68.0%) tested positive for HPV, with the majority 1,183/1,827 (64.8%) having HR-HPV infection. A total of 584/1,827 (32.0%) of samples were HPV negative, 37.4% were positive for HPV-16 (n=684) and 5.1% for HPV-18 DNA (n=93). Figure 2 outlines the overall HPV genotype profile among the cohort and HPV multiplicity. The five most common HPV genotypes detected across all cervical pathologies examined were HPV-16 (n=684), HPV-31 (n=150), HPV-52 (n=125), HPV-18 (n=93) and HPV-33 (n=91) (Figure 2).

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HPV type-specific prevalence:

200 The majority of samples were from CIN III cases (42.6%). HPV DNA was detected in 262/545 (48.1%) 201 of CINI samples, 280/425 (65.9%) of CIN II lesions, 633/779 (81.3%) of CIN III specimens, 59/64 202 (92.2%) of SCCs and 9/14 (64.3%) of AC samples. Table 1 details the number of HPV genotypes 203 detected by pathological subtype. Half of all samples (49.7%) had only one HPV genotype detected 204 (n=908). Multiple HPV genotypes (>1) were more common in CIN I-III lesions than other cervical 205 pathologies. Among SCC specimens, 7.8% had no HPV DNA detected and most (81.3%) had only 1 206 HPV genotype persisting, Table 1. HPV-16 and/or HPV-18 DNA was present in the majority of SCC 207 (82.8%) and AC (64.3%) cases and over half (56.2%) of CIN III samples, Table 2. Other HR HPV

208 genotypes were more prevalent in CIN I-III pathologies, and present in less than 10% of SCCs and AC 209 cases. LR-HPV genotypes were most common in lower grade cervical lesions and absent in cervical 210 cancer specimens, Table 2. Almost a third (32.0%) of all pathologies were HPV negative. The 211 distribution of HPV genotypes detected within each cervical pathology is detailed in Table 3. The 212 current HPV vaccination genotypes (HR-HPV 16 and or HR-HPV 18) were found in at least 82.8% of 213 women with SCC of the cervix. For cervical SCC, HPV-16 (n=51/64), HPV-18 (n=3/64), HPV-45 214 (n=3/64) and HPV-52 (n=5/64) made up 96% of the HPV positive samples. HPV-16 was the most 215 common HPV detected across all cervical pathologies, except for AC where HPV-18 predominated 216 with HPV-16, HPV-51 and HPV-54 making up the remaining HPV genotypes present, Table 3.

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218 Age-specific prevalence for HPV infection:

The pathological distribution of samples by five-year age group is shown in Table 4. The mean age of women included in the study was 32 years (range 16-93 years, standard deviation (SD) 9.4 years) and significantly differed between histopathological groups (P <0.001). In total, 375 samples were from women aged 24 years and under, 887 from women aged 25 to 34 years and 565 samples from those aged 35 years and over. CIN I was more common in younger women and CIN II and CIN III most common in those aged 25-29 years. SCC was most common in women aged 35-39 years, Table 4.

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The number of HPV genotypes decreased with increasing age, with just over half (51.0%) of all HPV infections found in tissue from women aged between 25-29 years, Table 1. Most tissue samples had a single HPV genotype and this was more common in those aged over 60 years. Five or more HPV genotypes were detected in some women but this was largely limited to those aged under the age of 40 years, Table 1. 41.7% of women with cervical pathology had HPV-16 or HPV-18 detected, and the highest proportion HPV 16/18 positive were over the age of 65 years, Table 2. Other HR-HPV genotypes were more common in younger women, particularly those aged 35-39 years. LR-HPV

- 233 genotypes were most common in those aged 55-59 years, with women over the age of 60 years
- having no LR-HPV genotypes detected, Table 2.

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259 **DISCUSSION**:

260 This is the largest population-based study investigating the HPV genotype distribution in women 261 with CIN I-III and cervical SCC and AC in NI. The overall prevalence of any HPV in SCC samples was 262 92.2% and was 68.0% across all cervical samples investigated. HR-HPV was detected in 64.8% of all 263 samples with HPV-16 being the most common HPV genotype identified, which is consistent with that 264 described elsewhere in CIN cases across Europe in countries such as Spain, France and Germany 265 [García-Espinosa et al, 2012; Monsonego et al, 2012; de Jonge et al, 2013; Leinonen et al, 2013; 266 Rössler et al, 2013] and in invasive disease internationally [Bosch et al, 2008; de Sanjose et al, 2010; 267 Li et al, 2011]. As previously reported the prevalence of HPV increased through CIN I-III lesions in NI 268 [Anderson et al, 2013] from 48.1% in CIN I to 81.3% in CIN III cases. Most HPV positive samples had 269 HR-HPV genotypes with HPV-16 and/or HPV-18 present in 20.6%, 35.3% and 56.2% of CIN I-III cases 270 respectively.

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272 In an examination of FFPE tissue from more than 6,000 women from 17 European countries using 273 the SPF10-LiPA25 assay, including data from neighbouring Scotland, Ireland and Wales, Tjalma et al 274 found HPV-16 was the most frequent HPV type detected in both CIN and invasive cervical cancer 275 [Tjalma et al, 2013]. HPV-16 and/ or HPV-18 prevalence (among HPV positive cases) was reported as 276 45.8% in CIN II and 67.3% in CIN III cases [Tjalma et al, 2013], slightly higher than the current study. 277 The authors reported HPV-31, 33, 35, 51, 52, 58 and 68 as the most frequently detected genotypes 278 in women with high-grade CIN lesions. Apart from HPV-16, we similarly found that HPV-18, 31, 33, 279 45, 51 and 52 were the most common genotypes identified in high grade lesions. Building on 280 previous meta-analyses of type-specific HPV prevalence worldwide by specific grades of cervical 281 disease [Clifford et al, 2003, 2005; Smith et al, 2007; Li et al, 2011] Guan et al in a further meta-282 analysis of 423 studies (144 of which were from Europe) using PCR assays based on various primers 283 among cell or biopsy/tissue cervical diagnoses also showed an increasing HPV prevalence with 284 increasing severity of cervical disease, with HPV-16 the most frequently detected HR-HPV type in all 285 grades [Guan et al, 2012]. The prevalence (including HPV negative cases in the denominator) of HPV-286 16 was 27.6%, 39.8% and 58.2% and HPV-18 prevalence 9.0%, 10.0% and 7.4% in CIN I to CIN III 287 cases respectively [Guan et al, 2012], again higher than the estimates reported in the present study, 288 variation which may have arisen from methodological differences in HPV detection techniques. The 289 majority of SCCs (92.2%) in the present study were HPV positive, this is in accordance with the 290 proportions of invasive cervical cancers (the majority of which were SCCs) testing HPV positive in 291 other countries of the UK [Mesher et al, 2014], Sweden, Spain Italy and eastern Europe [Du et al, 292 2011; Alemany et al, 2012; Giorgi Rossi et al, 2012; Guan et al, 2012; Piana et al, 2013; Pista et al, 293 2013; Škamperle et al, 2013; Tjalma et al, 2013; Kjær et al, 2014; Simanaviciene et al, 2014].

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295 There were only 14 cases of AC included in the current investigation, and therefore our study is likely 296 underpowered to investigate HPV prevalence in this subgroup. Of note however, HPV-18 was the 297 most common HPV type in AC cases with a prevalence of 42.9% in the current study, akin to a recent 298 Scottish estimate of 44.0% (among HPV positive cases) [Powell et al, 2013] which examined HPV 299 DNA in FFPE tissue detected using the SPF10-DEIA/LiPA25-PCR assay. The prevalence of HPV-16 300 and/or HPV-18 was 64.3%, lower than reported in an English multi-site investigation of HPV DNA in 301 cervical cytology and cervical cancer biopsies using the Roche Linear array typing system (81.9%, 302 among HPV positive cases) [Howell-Jones et al, 2010] and among AC cases from other European 303 studies (94.6%) [Tjalma et al, 2013]; perhaps due to a lower HPV-18 rate.

304

The number of HPV genotypes detected in the current study varied across pathological grade, with the lowest percentage of single genotypes (31.0%) in CIN I lesions and the highest proportion (81.3%) in cervical SCCs, indicative that a single HPV genotype remains persistent in patients that progress. Although HPV persistence has been shown to vary by geographical region, HPV-16, 18, 31, 33, 45, 52 and 58 are the most persistent HPV genotypes reported among women with invasive cervical cancer [Bernard *et al*, 2013; Rositch *et al*, 2013]. The most frequent single genotypes in the

311 current investigation in SCCs were HPV 16, 18, 45, 31, 39 and HPV 52. Notably, this profile includes 312 several HPV genotypes which are not currently incorporated in the present HPV vaccine programme. 313 These should be considered in the next generation of anti-HPV vaccines. In line with the UK HPV 314 vaccination programme, in September 2012 NI began using the quadrivalent vaccine Gardasil® 315 (Gardasil, Sanofi Pasteur MSD), with a relatively high uptake of 86.8% for all three doses in girls aged 316 12-13 years [HSC Public Health Agency Northern Ireland, 2014]. Markov modelling has shown that 317 the UK HPV vaccination programme would require 80% uptake to have a reduction of 66% in the 318 prevalence of high-grade precancerous lesions and a 76% reduction in cervical cancer deaths [Kohli 319 et al, 2007]. Therefore the HPV genotypes covered by the current HPV vaccination programme will 320 lower the prevalence of HPV 16/18, as has already been evidenced in Scotland [Kavanagh et al, 321 2014], and should prevent the majority of cervical cancers in NI. The formerly used bivalent vaccine 322 (Cervarix®) offers some cross-protection for HPV genotypes of the A7 species including HR HPV-31, 323 33 and 45 [Paavonen et al, 2009; Malagón et al, 2012; De Vincenzo et al, 2013; Verdenius et al, 324 2013]. The potential effects of vaccine cross protection against other oncogenic non-target 325 genotypes should also be considered when conducting future cost-benefit analyses.

326

The principal strength of this study is its size and population-based design. The study was able to report the identification of high and low-risk HPV genotypes as well as the prevalence of multiple HPV infections. When comparing the HPV prevalence between countries it is important to consider that variations in HPV positivity may be explained by differences in the quality and type of samples analyzed (biopsies, surgical specimens or fresh tissue), as well as the methods of HPV detection and assessment.

333

While it is frequently reported that 99.7% of cervical SCCs are HPV positive [Walboomers *et al*, 1999], women have been shown to have cervical disease without testing HPV positive using current methods. In a pooled analysis of 3 large Italian case series using three different PCR methods, 24

337 (4.2%) of 574 invasive cervical cancers were found to be 'true' HPV negative cases [Giorgi Rossi et al, 338 2012]. Similarly, Tjalma et al in large-scale data from 17 European countries found that 8.2% of 339 invasive cervical cancers were HPV negative [Tjalma et al, 2013]. HPV-negative carcinoma, if it exists 340 at all, is likely to be rare. In the present study 10/78 invasive cervical cancers (12.8%) tested HPV 341 negative. Although other aetiologic factors, such as mutations within the p53 gene, may explain 342 some HPV negative cases [Fogel et al, 1995] the potential for false negative results arising from 343 differences in analytic sensitivity for different HPV types particularly in the presence of multiple 344 infections, low titer or copy number of HPV DNA and inadequacy of the specimen should be 345 carefully considered. For instance, HPV genotyping analysis in the present study was undertaken 346 using the Roche linear array detection kit. Importantly, this assay uses PGMY L1 consensus primers 347 to amplify a 450-bp fragment. As it is well known that formaldehyde fixation provides low yields of 348 extractable DNA due to protein cross-linking and strand cleavage, such a large amplicon size 349 provides the potential for false negative results on FFPE tissue. Whilst the detection of HPV in fresh 350 frozen tissue appears superior [Odida et al, 2010], this would have been difficult to acquire and 351 process in a large population-based study such as this.

352

In conclusion, HPV-16 was identified as the main HPV genotype associated with cervical disease in NI, contributing to around 83.0% of the cervical SCCs investigated. Provided there is sustained high HPV vaccine coverage in NI, the current HPV vaccination programme should prevent the majority of cervical cancers but coverage of other HR-HPV genotypes with high prevalence and oncogenic potential including HPV-31, 39, 45 and 52 and the potential influence of cross protection, should be considered in any future polyvalent vaccines.

359

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- 367 HSC Trust).
- 368 **FIGURE LEGENDS**:
- 369 Figure 1: Flowchart of sample selection and eligibility
- 370 **Figure 2:** Overall HPV genotype profile denoting the prevalence of single and multiple HPV infections
- 371

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Number of HPV Genotypes detected (% of each pathology)									
Pathology	HPV negative	1	2	2 3 4		5 or more	Total n (%)		
CIN I	283 (51.9)	169 (31.0)	63 (11.6)	19 (3.5)	9 (1.7)	2 (0.4)	545 (100.0)		
CIN II	145 (34.1)	217 (51.1)	46 (10.8)	15 (3.5)	1 (0.2)	1 (0.2)	425 (100.0)		
CIN III	146 (18.7)	462 (59.3)	129 (16.6)	32 (4.1)	4 (0.5)	6 (0.8)	779 (100.0)		
SCC	5 (7.8)	52 (81.3)	6 (9.4)	1 (1.6)	0 (0.0)	0 (0.0)	64 (100.0)		
AC	5 (35.7)	8 (57.1)	0 (0.0)	1 (7.1)	0 (0.0)	0 (0.0)	14 (100.0)		
Age group (yrs)	HPV negative	1	2	3	4	5 or more	Total n (%)		
Under 25	115 (30.7)	172 (45.9)	64 (17.1)	18 (4.8)	3 (0.8)	3 (0.8)	375 (100.0)		
25-29	152 (28.7)	270 (51.0)	79 (14.9)	21 (4.0)	6 (1.1)	1 (0.2)	529 (100.0)		
30-34	110 (30.7)	186 (52.0)	44 (12.3)	14 (3.9)	1 (0.3)	3 (0.8)	358 (100.0)		
35-39	74 (33.3)	119 (53.6)	23 (10.4)	4 (1.8)	1 (0.5)	1 (0.5)	222 (100.0)		
40-44	51 (33.8)	77 (51.0)	16 (10.6)	6 (4.0)	1 (0.7)	0 (0.0)	151 (100.0)		
45-49	41 (44.6)	39 (42.4)	9 (9.8)	2 (2.2)	1 (1.1)	0 (0.0)	92 (100.0)		
50-54	24 (49.0)	17 (34.7)	6 (12.2)	1 (2.0)	1 (2.0)	0 (0.0)	49 (100.0)		
55-59	10 (35.7)	13 (46.4)	3 (10.7)	1 (3.6)	0 (0.0)	1 (3.6)	28 (100.0)		
60-64	3 (33.3)	6 (66.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	9 (100.0)		
65+	4 (28.6)	9 (64.3)	0 (0.0)	1 (7.1)	0 (0.0)	0 (0.0)	14 (100.0)		
TOTAL	584 (32.0)	908 (49.7)	244 (13.4)	68 (3.7)	14 (0.8)	9 (0.5)	1,827 (100.0)		

Table 1: Percentage distribution of the number of HPV genotypes detected bypathological subtype and 5-year age group.

CIN = Cervical Intraepithelial Neoplasia (grades I-III), SCC = Squamous cell carcinoma, AC = Adenocarcinoma

Pathology	HPV-16 and or HPV-18	Other High-risk HPV genotypes*	Low risk HPV genotypes Only	HPV negative	Total	
i athology	n (%)	n (%)	n (%)	n (%)	n (%)	
CIN I	112 (20.6)	121 (22.2)	29 (5.3)	283 (51.9)	545 (100.0)	
CIN II	150 (35.3)	110 (25.9)	20 (4.7)	145 (34.1)	425 (100.0)	
CIN III	438 (56.2)	184 (23.6)	11 (1.4)	146 (18.7)	779 (100.0)	
SCC	53 (82.8)	6 (9.4)	0 (0.0)	5 (7.8)	64 (100.0)	
AC	9 (64.3)	1 (7.1)	0 (0.0)	5 (35.7) 14 (100.0)		
Age group (yrs)						
Under 25	154 (41.1)	93 (24.8)	13 (3.5)	115 (30.7)	375 (100.0)	
25-29	237 (44.8)	127 (24.0)	13 (2.5)	152 (28.7)	529 (100.0)	
30-34	151 (42.2)	82 (22.9)	15 (4.2)	110 (30.7)	358 (100.0)	
35-39	84 (37.8)	59 (26.6)	5 (2.3)	74 (33.3)	222 (100.0)	
40-44	59 (39.1)	36 (23.8)	5 (3.3)	51 (33.8)	151 (100.0)	
45-49	34 (37.0)	12 (13.0)	5 (5.4)	41 (44.6)	92 (100.0)	
50-54	18 (36.7)	5 (10.2)	2 (4.1)	24 (49.0)	49 (100.0)	
55-59	12 (42.9)	4 (14.3)	2 (7.1)	10 (35.7)	28 (100.0)	
60-64	4 (44.4)	2 (22.2)	0 (0.0)	3 (33.3)	9 (100.0)	
65+	9 (64.3)	1 (7.1)	0 (0.0)	4 (28.6)	14 (100.0)	
TOTAL n (%)	762 (41.7)	421 (23.0)	60 (3.3)	584 (32.0)	1,827 (100.0)	

Table 2: Type of HPV genotypes detected by cervical pathology and 5-year age group.

* Including high-risk HPV genotypes other than HPV 16/18 i.e.: HPV-31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 and 68. CIN = Cervical Intraepithelial Neoplasia (grades I-III), SCC = Squamous cell carcinoma, AC = Adenocarcinoma

HPV genotype	AC	CIN I	CIN II	CIN III	SCC	Total	
HPV 16	3 (21.4)	87 (16.0)	136 (32.0)	407 (52.3)	51 (79.7)	684 (37.4)	
HPV 31	0 (0.0)	35 (6.4)	29 (6.8)	84 (10.8)	2 (3.1)	150 (8.2)	
HPV 52	0 (0.0)	22 (4.0)	33 (7.8)	65 (8.3)	5 (7.8)	125 (6.8)	
HPV 18	6 (42.9)	29 (5.1)	17 (4.0)	39 (5.0)	3 (4.7)	93 (5.1)	
HPV 33	0 (0.0)	18 (3.3)	15 (3.5)	58 (7.5)	0 (0.0)	91 (5.0)	
HPV 51	1 (7.1)	17 (3.1)	25 (5.9)	28 (3.6)	0 (0.0)	71 (3.9)	
HPV 45	0 (0.0)	14 (2.6)	10 (2.4)	31 (4.0)	3 (4.7)	58 (3.2)	
HPV 39	0 (0.0)	20 (3.7)	12 (2.8)	14 (1.8)	1 (1.6)	47 (2.6)	
HPV 58	0 (0.0)	11 (2.0)	13 (3.1)	17 (2.2)	0 (0.0)	41 (2.2)	
HPV 66	0 (0.0)	22 (4.0)	6 (1.4)	10 (1.3)	0 (0.0)	38 (2.1)	
HPV 35	0 (0.0)	9 (1.7)	12 (2.8)	16 (2.1)	0 (0.0)	37 (2.0)	
HPV 59	0 (0.0)	14 (2.6)	8 (1.9)	8 (1.0)	0 (0.0)	30 (1.6)	
HPV 56	0 (0.0)	18 (3.3)	3 (0.7)	5 (0.6)	0 (0.0)	26 (1.4)	
HPV 6	0 (0.0)	7 (1.3)	9 (2.1)	9 (1.2)	0 (0.0)	25 (1.4)	
HPV 73	0 (0.0)	9 (1.7)	6 (1.4)	8 (1.0)	0 (0.0)	23 (1.3)	
HPV 53	0 (0.0)	9 (1.7)	5 (1.2)	5 (0.6)	0 (0.0)	19 (1.0)	
HPV 70	0 (0.0)	4 (0.7)	4 (0.9)	9 (1.2)	0 (0.0)	17 (0.9)	
HPV 42	0 (0.0)	9 (1.7)	2 (0.5)	3 (0.4)	0 (0.0)	14 (0.8)	
HPV 61	0 (0.0)	6 (1.1)	1 (0.2)	7 (0.9)	0 (0.0)	14 (0.8)	
HPV 54	1 (7.1)	2 (0.4)	3 (0.7)	5 (0.8)	0 (0.0)	12 (0.7)	
HPV 11	0 (0.0)	5 (0.9)	2 (0.5)	4 (0.5)	0 (0.0)	11 (0.6)	
HPV 68	0 (0.0)	4 (0.7)	5 (1.2)	2 (0.3)	0 (0.0)	11 (0.6)	
HPV CP6108	0 (0.0)	4 (0.7)	0 (0.0)	6 (0.8)	0 (0.0)	10 (0.6)	
HPV 82	0 (0.0)	1 (0.2)	0 (0.0)	8 (1.0)	0 (0.0)	9 (0.5)	
HPV 62	0 (0.0)	2 (0.4)	1 (0.2)	4 (0.5)	0 (0.0)	7 (0.4)	
HPV 84	0 (0.0)	3 (0.6)	2 (0.5)	2 (0.3)	0 (0.0)	7 (0.4)	
HPV 81	0 (0.0)	6 (1.1)	0 (0.0)	1 (0.1)	0 (0.0)	7 (0.4)	
HPV 69	0 (0.0)	2 (0.4)	1 (0.2)	2 (0.3)	0 (0.0)	5 (0.3)	
HPV 55	0 (0.0)	3 (0.6)	1 (0.2)	0 (0.0)	0 (0.0)	4 (0.2)	
HPV 83	0 (0.0)	2 (0.4)	1 (0.2)	1 (0.1)	0 (0.0)	4 (0.2)	
HPV is39	0 (0.0)	0 (0.0)	2 (0.5)	1 (0.1)	0 (0.0)	3 (0.2)	
HPV 67	0 (0.0)	3 (0.6)	0 (0.0)	0 (0.0)	0 (0.0)	3 (0.2)	
HPV 40	0 (0.0)	1 (0.2)	0 (0.0)	1 (0.1)	0 (0.0)	2 (0.11)	
HPV 26	0 (0.0)	1 (0.2)	0 (0.0)	1 (0.1)	0 (0.0)	2 (0.1)	
HPV 64	0 (0.0)	1 (0.2)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.1)	
HPV 72	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	
HPV 71	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	
TOTAL	11 (78.5)	400 (73.6)	364 (85.6)	861 (110.8)	65 (101.6)	1701 (93.3)*	
AC = adenocarcinoma, CIN = Cervical Intraepithelial Neoplasia (grades I-III), SCC = Squamous Cell Carcinoma * This figure does not add up to 1,243 (i.e.: the number HPV positive) as several patients may have had multiple HPV genotypes on testing							

Table 3: HPV genotype distribution by cervical pathologyCervical histology

Table 4: Pathological distribution of cohort (numbers of cases) by five-year age group

	Mean ageAGE (years)years (± SD; range)AGE (years)							n (%)				
PATHOLOGY n (%)		<25	25-29	30-34	35-39	40-44	45-49	50-54	55-59	60-64	65+	TOTAL
CIN I	32 (10; 16-69)	144 (26.4)	136 (25.0)	82 (15.1)	55 (10.1)	51 (9.4)	42 (7.7)	19 (3.5)	11 (2.0)	3 (0.6)	2 (0.4)	545 (100.0)
CIN II	32 (9; 18-80)	83 (19.5)	120 (28.2)	92 (21.7)	51 (12.0)	40 (9.4)	17 (4.0)	11 (2.6)	6 (1.4)	1 (0.2)	4 (0.9)	425 (100.0)
CIN III	31 (8; 18-64)	146 (18.7)	268 (34.4)	169 (21.7)	94 (12.1)	53 (6.8)	27 (3.5)	12 (1.5)	7 (0.9)	3 (0.4)	0 (0.0)	779 (100.0)
SSC	43 (14; 23-93)	1 (1.6)	3 (4.7)	12 (18.8)	19 (29.7)	7 (10.9)	5 (7.8)	7 (10.9)	3 (4.7)	1 (1.6)	6 (9.4)	64 (100.0)
AC	42 (16; 23-73)	1 (7.1)	2 (14.3)	3 (21.4)	3 (21.4)	0 (0.0)	1 (7.1)	0 (0.0)	1 (7.1)	1 (7.1)	2 (14.3)	14 (100.0)
TOTAL n (%)		375 (20.5)	529 (28.9)	358 (19.6)	222 (12.2)	151 (8.3)	92 (5.0)	49 (2.7)	28 (1.5)	9 (0.5)	14 (0.8)	1,827 (100.0)

CIN = Cervical Intraepithelial Neoplasia (grades I-III), SCC = Squamous Cell Carcinoma, AC= Adenocarcinoma

±SD = Standard deviation

N.B.: Please note that certain pathological groups were overrepresented in this study, so the proportions above may not be a true reflection of the distribution of cervical pathologies within each age category in Northern Ireland.





HPV genotypes omitted above (no. of single/multiple infections): HPV 16 (480/204), HPV CP6108 (1/9), HPV 82 (0,9), HPV 62 (0/7), HPV 84 (1/6), HPV 81 (3/4), HPV 69 (1/4), HPV 55 (0/4), HPV 83 (2/2), HPV IS39 (1/2), HPV 67 (2/1), HPV 40 (0/2), HPV 26 (1/1), HPV 64 (0/1), HPV 72 (0/0), HPV 71 (0/0).