MINI-REVIEW

Human Papillomavirus Genotype Distribution among Thai Women with High-Grade Cervical Intraepithelial Lesions and Invasive Cervical Cancer: a Literature Review

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Abstract

Infection with high-risk human papillomavirus (HR-HPV) is an essential cause of cervical cancer. Because of substantial geographical variation in the HPV genotype distribution, data regarding HPV type-specific prevalence for a particular country are mandatory for providing baseline information to estimate effectiveness of currently implemented HPV-based cervical cancer prevention. Accordingly, this review was conducted to evaluate the HR-HPV genotype distribution among Thai women with precancerous cervical lesions i.e. cervical intraepithelial neoplasia grade 2-3 (CIN 2-3), adenocarcinoma in situ (AIS), and invasive cervical cancer by reviewing the available literature. The prevalence of HR-HPV infection among Thai women with CIN 2-3 ranged from 64.8% to 90.1% and the three most common genotypes were HPV 16 (38.5%), HPV 58 (20.0%), and HPV 18 (5.5%). There were high squamous cell carcinoma/CIN 2-3 prevalence ratios in women with CIN 2-3 infected with HPV 33 and HPV 58 (1.40 and 1.38, respectively), emphasizing the importance of these subtypes in the risk of progression to invasive cancer among Thai women. Data regarding the prevalence and genotype distribution of HR-HPV in Thai women with AIS remain unavailable. Interesting findings about the distribution of HPV genotype in cervical cancer among Thai women include: (1) a relatively high prevalence of HPV 52 and HPV 58 in invasive squamous cell carcinoma; (2) the prevalence of HPV 18-related adenocarcinoma is almost double thepreviously reported prevalence, and (3) 75% of neuroendocrine carcinomas are HPV18-positive when taking into account both single and multiple infections.

Keywords: Human papillomavirus - genotype distribution - cervical intraepithelial neoplasia

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Introduction

More than 90% of worldwide estimated human papillomavirus (HPV)-related cancer mortalities are secondary to invasive cervical cancer (Cutts et al., 2007). There are sufficient evidences to conclude that cervical cancer are virtually caused by complicated infection with high-risk (HR) or carcinogenic types of HPV. According to the recent classification proposed by the International Agency for Research on Cancer, twelve HR-HPV genotypes including type 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59 are classified as one of 114 agents that are carcinogenic to human, or the so-called "*group A*"(IARC, 2006).

As a substantial geographical variation in the HPV genotype distribution has been observed (Li et al., 2011), data regarding HPV type-specific prevalence in each country are therefore mandatory for providing baseline information to predict how the genotype-specific HPV vaccination and HPV-based screening will influence cervical cancer prevention. Accordingly, we evaluated the genotype distribution of HPV in high-grade intraepithelial lesions and invasive cervical cancer in Thai women by reviewing the available literature and compared with the data in the other regions.

Methodological Approach

Source of study identification

An electronic literature search was performed through PubMed, Scopus, Google Scholar, and Thai database of health science journals (thailand.digitaljournals.org). A systematic search strategy was developed based on a preliminary scope of studies involving HPV prevalence and genotype distribution among Thai women who had high-grade cervical intraepithelial lesions and invasive cervical cancer. High-grade cervical intraepithelial lesions were defined as cervical intraepithelial neoplasia grade 2-3 (CIN 2-3) and adenocarcinoma in situ (AIS).

Search terms were formulated based on an interpretation of the population/problem of interest, intervention and context (PICO) framework (Cooke et al., 2012). We

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also manually searched the reference lists of identified publications to ascertain additional relevant articles. The last update searching was performed in May, 2015.

Study selection and data extraction

We solely included studies that used PCR-based assays to identify HPV. Abstracted data included: (1) year of publication, (2) area of sample, (3) histology subtype, (4) type of specimens, (5) polymerase chain reaction (PCR) primer used, (6) overall prevalence and type-specific of HPV infection stratified by histological classification, (7) single or multiple infection, and (8) prevalence obtained from combined single and multiple infections. The authors may be contacted for more information if necessary.

Where available, invasive cervical cancer (ICC) was independently classified into squamous cell carcinoma (SCCA), adenocarcinoma (ADCA), adenosquamous carcinoma (ASCA), and neuroendocrine carcinoma (NECA). If histology-specific HPV genotype distribution was not reported, they were classified as unspecified ICC.

Review Findings

Cervical intraepithelial neoplasia grade 2-3 (CIN 2-3)

In general, CIN 2-3 has been accepted as a threshold of initiating definite treatment of precancerous lesion of SCCA (Massad et al., 2013). Identifying HPV genotype distribution in CIN 2-3 lesions that potentially progress to SCCA is utmost important in gaining insight into the oncogenic potential of the different HPV genotypes, designing protocol for screening, and estimating the efficacy of type-specific HPV vaccine.

Table 1. Prevalence Ratio of Type-Specific HR-HPV between SCCA and CIN 2-3

	Clifford et al (2003)*			Aromseree et al (2014)‡		
HPV type	SCCA	CIN 2-3	SCCA/CIN 2-3	SCCA	CIN 2-3	SCCA/CIN 2-3
16	54.3	45	1.21	39.4	38.5	1.02
18	12.6	7.1	1.79	20	5.5	3.64
31	4.2	8.8	0.48	-	1.1	-
33	4.3	7.2	0.59	3.07	2.2	1.4
35	1	4.4	0.22	-	2.2	-
39	0.4	1.1	0.35	-	-	-
45	4.2	2.3	1.85	3.07	1.1	2.79
52	2.5	5.2	0.48	-	1.1	-
56	0.7	3	0.23	-	2.2	-
58	3	6.9	0.43	27.7	20	1.38
59	0.8	1.5	0.55	-	-	-
66	0.2	2.1	0.1	-	-	-
68	0.5	1	0.5	-	-	-

*HR-HPV, high-risk human papillomavirus; SCCA, squamous cell carcinoma; CIN, cervical intraepithelial neoplasia; *the meta-analysis study; ‡the study conducted in Thai women

Table 2. HR-HPV Positivity Rate and Genotype Distribution o in AIS

Authors	Year	Number of patients	Positive rate	Genotypes
Rabelo-Santos et al	2009	5	100%	HPV 16: 3 (60.0%) HPV 18: 2 (40.0%)
Quint et al	2010	33	100%	HPV 16: 16 (48.5%) HPV 18: 8 (24.2%) HPV 16+18: 1 (3.0%) HPV 16+other: 6 (18.2%) HPV 35: 1 (3.0%) HPV 45: 1 (3.0%)
Ault et al	2011	22*	95.50%	HPV 16: 7 (31.8%) HPV 18: 5 (22.7%) HPV 16+18: 1 (4.5%) HPV 16 + other: 4 (18.2) HPV 18+other: 1 (4.5%) HPV 16+18+other: 3 (13.6%)
Andersson et al	2013	22	95.50%	HPV 18/45: 13 (59.1%) HPV 16: 3 (13.6%) HPV 18/45+59: 2 (9.1%) HPV 16+18/45:1 (4.5%) HPV 16+18/45+33/53/58: 1 (4.5%) HPV 16+33/53/58: 1 (4.5%)

*HR-HPV, high-risk human papillomavirus; AIS, adenocarcinoma in situ; *One case was negative for 16/18/31/33/35/39/51/52/56/58/59, and had missing data about the positivity of type 45

Table 3. HPV in Invasive Cervical Cancer Worldwide, Overall and Stratified by Histological Subtype in the Meta-Analysis Conducted by Li et al. (2011)

HPV type	Histological types		
	Overall	SCCA	ADCA
Single	79.00%	79.40%	73.40%
Multiple	11.20%	11.60%	9.30%
HPV 16	56.50%	59.30%	36.30%
HPV 18	16.00%	13.20%	36.80%
HPV 31	3.80%	4.00%	2.30%
HPV 33	4.60%	4.90%	2.20%
HPV 45	4.50%	4.40%	5.20%
HPV 52	3.40%	3.60%	1.20%
HPV 58	4.70%	5.10%	1.50%

*HPV, human papillomavirus; SCCS, squamous cell carcinoma; ADCA, adenocarcinoma

In a meta-analysis of 4338 cases with CIN 2-3, the five most common HPV genotypes in either single or multiple infections were HPV 16 (45.0%), HPV 31 (8.8%), HPV 33 (7.2%), HPV 18 (7.1%), and HPV 58 (6.9%) (Clifford et al., 2003). In population-based study conducted in Norway to determine HPV genotype distribution in CIN 2-3 cases, multiple HPV infections were more common than infection with a single HPV type. In this study, the common HPV genotype, as single and/or in concurrence with other types included HPV 16 (51.2%), HPV 31 (16.3%), HPV 33 (15.2%), HPV 52 (11.2%), HPV 18 (10.9%), and HPV 51 (9.3%) (Sjoeborg et al., 2010). In addition, HPV 16 and HPV 33 were associated with higher prevalence of CIN 3 suggesting a high oncogenic potential by nature of these two HPV genotypes for women in this region.

Table 4. Detailed HR-HPV Genotype Distribution among Invasive Cervical Cancer in Thailand

Data	Siriaunkgul et al	Siriaunkgul et al	Chinchai et al	Siriaunkgul et al	Natphopsuk et al
Years	2008	2011	2012	2013	2013
Areas	North	North	Central	North, South, Central	Northeast
Pathology	SCCA	NECA	Unspecified	ADCA	SCCA
Population	Hospital	Hospital	Hospital	Hospital	Hospital
HPV DNA source	Biopsy/ resection	Biopsy/ resection	Biopsy/ resection	Biopsy/ resection	Cells
PCR primers	GP5+/6+	GP5+/6+	SPF10	GP5+/6+	GP5+/6+
No.(patients)	99	111	155	150	198
HR-HPV positivity	96 (96.9)	93 (83.8)	147 (96.1)	145 (96.7)	152 (76.8)
Multiple infection	21 (21.2)	14 (12.6)	18 (11.6)	11 (7.3)	11 (5.5)
Single type					
16	56 (58.3)	15 (16.1)	69 (46.9)	40 (30.3)	86 (56.6)
18	6 (6.3)	57 (61.3)	27 (18.4)	86 (65.2)	20 (13.2)
31	1 (1.0)	0 (0)	0 (0)	1 (0.8)	0 (0)
33	4 (4.2)	1 (1.1)	5 (3.4)	0 (0)	6 (3.9)
45	2 (2.1)	0 (0)	5 (3.4)	4 (3.0)	3 (1.9)
52	1 (1.0)	0 (0)	9 (6.1)	0 (0)	2 (1.3)
58	3 (3.1)	3 (3.2)	6 (4.1)	0 (0)	22 (14.5)
Other	2 (2.1)	0 (0)	8 (5.4)	1 (0.8)	2 (1.3)
Multiple type					
16,18	0 (0)	11 (11.8)	0 (0)	2 (1.4)	1 (0.7)
16,52	7 (7.3)	0 (0)	4 (2.7)	0 (0)	1 (0.7)
16,33	3 (3.1)	0 (0)	0 (0)	0 (0)	0 (0)
16,58	4 (4.2)	0 (0)	2 (1.4)	0 (0)	4 (2.6)
16,31	2 (2.1)	0 (0)	0 (0)	1 (0.8)	0 (0)
16,35	2 (2.1)	1 (1.1)	0 (0)	0 (0)	0 (0)
16,18,52	2 (2.1)	1 (1.1)	0 (0)	1 (0.8)	0 (0)
16,33,35	1 (1.0)	0 (0)	0 (0)	0 (0)	0 (0)
18,52	0 (0)	1 (1.1)	1 (0.7)	1 (0.8)	0 (0)
33,58	0 (0)	0 (0)	0 (0)	0 (0)	2 (1.3)
Other	0 (0)	0 (0)	11 (7.5)	6 (4.1)	3 (1.9)

*HR-HPV, high-risk human papillomavirus; SCCS, squamous cell carcinoma; NECA, neuroendocrine carcinoma, ADCA, adenocarcinoma; PCR, polymerase chain reaction; Data are present as number (percentage)

Table 5. Distribution of HPV Genotype Present as Combined Single and Multiple Infections among Thai Women with Cervical Squamous Cell Carcinoma

Data	Siriaunkgul et al	Natphopsuk et al	Aromseree et al
Years	2008	2013	2014
Population	Hospital	Hospital	Hospital
HPV DNA source	Biopsy/ resection	Cells	Biopsy/ resection
PCR primers	GP5+/6+	GP5+/6+	GP5+/6+
HR-HPV type			
16	80.20%	62.50%	39.40%
18	8.30%	15.10%	20.00%
31	3.10%	0.70%	0%
33	8.30%	5.30%	3.10%
45	2.10%	1.90%	3.10%
52	10.40%	1.90%	0%
58	7.30%	19.70%	27.70%
Other	2.10%	1.90%	0%

*HR-HPV, high-risk human papillomavirus; PCR, polymerase chain reaction

Table 6. Distribution of HPV Genotype Present as Combined Single and Multiple Infections among Thai Women Invasive Cervical Cancer (Other than Squamous Cell Carcinoma)

Data	Siriaunkgul et al 2011	Chinchai et al 2012	Siriaunkgul et al 2013
Pathology	NECA	Unspecified	ADCA
Population	Hospital	Hospital	Hospital
HPV DNA source	Biopsy/ resection	Biopsy/ resection	Biopsy/ resection
PCR primers	GP5+/6+	SPF10	GP5+/6+
HR-HPV type			
16	30.10%	51.00%	30.30%
18	75.30%	20.00%	65.50%
31	0%	0%	2.10%
33	1.10%	4.50%	1.40%
45	0%	3.90%	3.40%
52	2.10%	10.30%	2.10%
58	3.20%	5.80%	0.70%
Other	0%	9.20%	4.80%

HR-HPV, high-risk human papillomavirus; NECA, neuroendocrine carcinoma, ADCA, adenocarcinoma

The prevalence of HR-HPV infection among Thai women with CIN 2-3 ranged from 64.8% to 90.1% (Suthipintawong et al., 2011; Aromseree et al., 2014). The three most common HR-HPV genotypes noted among Thai women with CIN 2-3 were HPV 16 (38.5%), HPV 58 (20.0%), and HPV 18 (5.5%)(Aromseree et al., 2014). The prevalence of HPV 58 infection among Thai women with CIN 2-3 is notably high when compared to the findings in a previous meta-analysis (20.0% versus 6.9%, respectively) (Clifford et al., 2003; Aromseree et al., 2014)

Table 1 shows the prevalence ratio of type-specific HPV between SCCA and CIN 2-3 which has been proposed as an indicator of potential likelihood of progression to invasive stage (Clifford et al., 2003). In a meta-analysis conducted by Clifford et al. (2003), HPV 45, HPV 18, and HPV 16 showed SCCA/CIN 2-3 ratios of 1.85, 1.79, and 1.21, respectively, highlighting that these HPV genotype may be more likely to progress from CIN 2-3 to SCCA than other high-risk genotypes which had SCCA/CIN 2-3 prevalence ratios between 0.10 and 0.59 (Clifford et al., 2003).

In Thailand, data regarding type-specific HR-HPV prevalence ratio of cervical cancer and CIN 2-3 was available in only one study conducted in Northeast Thailand. HPV 18 and HPV 45 infections among Thai women showed high SCCA/CIN 2-3 prevalence ratios (3.64 and 2.79, respectively) which are consistent with trends reported in a previous meta-analysis. The interesting findings among Thai women was a considerably high SCCA/CIN 2-3 prevalence ratios observed in HPV 33 and HPV 58 infection (1.40 and 1.38, respectively), emphasizing a regional variation of HPV genotypes distribution in CIN 2-3 and the importance of HPV 33 and HPV 58 infection in the risk of progression from CIN 2-3 to invasive cancer among Thai women (Aromseree et al., 2014). Further large scale studies are warranted to confirm these compelling results.

Adenocarcinoma in situ (AIS)

AIS has been acknowledged as pre-invasive lesion of adenocarcinoma (Zaino, 2002). However, incidence of AIS is relatively low (Kietpeerakool et al., 2006; Srisomboon et al., 2007). Similar to the pre-invasive lesion of cervical squamous cell carcinoma, almost all AIS lesions have evidences of HR-HPV infection. Table 2 displays the incidence and genotype distribution of HR-HPV among women with AIS. The most common HPV genotypes found in AIS lesion are HPV 16 and 18, which account for more than 90% of cases (Rabelo-Santos et al., 2009; Quint et al., 2010; Ault et al., 2011; Andersson et al., 2013). AIS lesions infected with multiple HPV genotypes are commonly observed among young women (Andersson et al., 2013). In the HPV vaccine trial, almost all AIS lesions (96%) were noted to be positive for HR-HPV testing but only 9.1% had glandular abnormality on concomitant cervical cytology (Ault et al., 2011). This observation indicates the potential benefit of incorporating HR-HPV testing into cervical cytology screening to better identifying AIS. However, data regarding the prevalence and genotype distribution of HR-HPV infection in AIS specific for Thai women remain unavailable.

Invasive cervical cancer (ICC)

In the recent meta-analysis conducted by Li et al (2011)

which aimed to determine the HPV genotype distribution among 30,848 ICC worldwide, the overall prevalence of HPV in the studies published during 1990-1999 and 2006-2012 were approximately 86% and 93%, respectively. Prevalence of multiple HPV infection was noted in 11.2% of ICC specimens. Table 3 displays the distribution of HPV reported from this meta-analysis (Li et al., 2011).

The high prevalence of HR-HPV infection among Thai women with ICC also has been consistently reported across the regions ranging from 77% to 97% (Tungsinmunkong et al., 2006; Siriaunkgul et al., 2008; Siriaunkgul et al., 2011; Chinchai et al., 2012; Natphopsuk et al., 2013; Siriaunkgul et al., 2013; Aromseree et al., 2014). In addition, more than 60% of ICC was HPV 16 and/or 18-related supporting that the majority of ICC in all regions is associated with HPV16 and/or 18. Multiple HPV infection in Thai women varied widely from approximately 6% to 20% depending on histologic subtypes of ICC (Table 4) (Siriaunkgul et al., 2008; Siriaunkgul et al., 2011; Chinchai et al., 2012; Natphopsuk et al., 2013; Siriaunkgul et al., 2013).

For SCCA, five most prevalent HPV types as single and multiple infection among Thai women, in order of decreasing prevalence, were HPV 16, HPV 18, HPV 58, HPV 52, and HPV 33 (Table 5) (Siriaunkgul et al., 2008; Natphopsuk et al., 2013; Aromseree et al., 2014). More than 75% of SCCA were HPV 16 and/or 18-related which was comparable to the reported result of 72.5% from the meta-analysis (Li et al., 2011). However, HPVgenotypes following HPV 16/18 observed in this meta-analysis, in descending order, were HPV 58, HPV 33, and HPV 45. Interestingly, this meta-analysis reported that the relatively high prevalence of HPV 52 and HPV 58 infection in ICC is unique for Eastern Asia. The third and fourth most common HPV infections after HPV 16 and HPV 18 in ICC specimens obtained from Eastern Asia were HPV 58 and HPV 52, respectively which was similar to the findings in Thai women (Li et al., 2011).

Singly or in combination, five most common HPV types among Thai women with ADCA included HPV 18 (65.5%), HPV 16 (30.3%), HPV 45 (3.4%), HPV 52 (2.1%), and HPV31 (2.1%)(Table 6). Interestingly, the prevalence of HPV 18-related ADCA among Thai women was notably high as compared to the findings from the meta-analysis (65.5% versus 36.8%) (Li et al., 2011; Siriaunkgul et al., 2013). Further studies are warranted to confirm this different finding.

NECA is an uncommon histological subtype of ICC accounting for approximately 1% of the cases (Siriaunkgul et al., 2011). Data regarding prevalence and genotype distribution among women with NECA, an aggressive cell type, are limited due to its rarity. Available evidences based on only a constrained number of NECA cases demonstrate that almost all of NECA cases are associated with HPV 16 and/or HPV 18. However, in contrast to that noted in SCCA, the most prevalent HPV type among NECA cases is HPV 18, followed by HPV 16 (Masumoto et al., 2003; Ishida et al., 2004; Wang et al., 2006). In a study from Northern Thailand which is the largest study conducted to determine HPV genotype distribution in NECA, almost 90% of cases of NECA are HPV 16 and/or HPV 18-related. Interestingly, approximately 75% of NECA were HPV18-positive when combined single and multiple infections. The next most prevalent HPV types in NECA were HPV 16 (30.1%), HPV 58 (3.2%), HPV 52 (2.1%), and HPV 33 (1.1%) (Table 6) (Siriaunkgul et al., 2011).

Conclusion

Limited data are available for describing HPV genotype distribution in cervical cancer precursor lesions. In women with ICC, more than 60% is HPV 16 and/or 18-related supporting that a majority of ICC in all world regions are associated with HPV16 and/or 18. Three interesting findings about the distribution of HPV genotype in ICC among Thai women have been observed including (1) a relatively high prevalence of HPV 52 and HPV 58 in SCCA; (2) the reported prevalence of HPV 18-related ADCA is almost double of incidence reported in the meta-analysis of cervical cancer worldwide, and (3) 75% of NECA are HPV18-positive when combined single and multiple infections. This review provides not only important baseline data for estimating the effectiveness of currently implemented HPV-based cervical cancer prevention but also for guiding the clinical application of newly HPV-based interventions to strengthen the public health benefits.

References

Andersson S, Mints M, Wilander E (2013). Results of cytology and high-risk human papillomavirus testing in females with cervical adenocarcinoma. *Oncol Lett*, **6**, 215-9.

Aromseree S, Chaiwongkot A, Ekalaksananan T, et al (2014). The three most common human papillomavirus oncogenic types and their integration state in Thai women with cervical precancerous lesions and carcinomas. *J Med Virol*, **86**, 1911-9.

Ault K A, Joura EA, Kjaer SK, et al (2011). Adenocarcinoma in situ and associated human papillomavirus type distribution observed in two clinical trials of a quadrivalent human papillomavirus vaccine. *Int J Cancer*, **128**, 1344-53.

Chinchai T, Chansaenroj J, Swangvaree S, et al (2012). Prevalence of human papillomavirus genotypes in cervical cancer. *Int J Gynecol Cancer*, **22**, 1063-8.

Clifford GM, Smith JS, Aguado T, et al (2003). Comparison of HPV type distribution in high-grade cervical lesions and cervical cancer: a meta-analysis. *Br J Cancer*, **89**, 101-5.

Cooke A, Smith D, Booth A (2012). Beyond PICO: the SPIDER tool for qualitative evidence synthesis. *Qual Health Res*, **22**, 1435-43.

Cutts FT, Franceschi S, Goldie S, et al (2007). Human papillomavirus and HPV vaccines: a review. *Bull World Health Organ*, **85**, 719-26.

IARC monographs on the evaluation of carcinogenic risks to humans, volume 90, human papillomaviruses. Lyon: International Agency for Research on Cancer; 2006.

Ishida GM, Kato N, Hayasaka T, et al (2004). Small cell neuroendocrine carcinomas of the uterine cervix: a histological, immunohistochemical, and molecular genetic study. *Int J Gynecol Pathol*, **23**, 366-72.

Kietpeerakool C, Srisomboon J, Prompittayarat W, et al (2006). Can adenocarcinoma in situ of the uterine cervix be predicted before cervical conization? *Asian Pac J Cancer Prev*, **7**, 522-4.

Li N, Franceschi S, Howell-Jones R, et al (2011). Human papillomavirus type distribution in 30,848 invasive cervical

cancers worldwide: Variation by geographical region, histological type and year of publication. *Int J Cancer*, **128**, 927-35.

Massad LS, Einstein MH, Huh WK, et al (2013). 2012 updated consensus guidelines for the management of abnormal cervical cancer screening tests and cancer precursors. *Obstet Gynecol*, **121**, 829-46.

Masumoto N, Fujii T, Ishikawa M, et al (2003). P16 overexpression and human papillomavirus infection in small cell carcinoma of the uterine cervix. *Hum Pathol*, **34**, 778-83.

Natphopsuk S, Settheetham-Ishida W, Pientong C, et al (2013). Human papillomavirus genotypes and cervical cancer in northeast Thailand. *Asian Pac J Cancer Prev*, **14**, 6961-4.

Quint KD, de Koning MN, van Doorn LJ, et al (2010). HPV genotyping and HPV16 variant analysis in glandular and squamous neoplastic lesions of the uterine cervix. *Gynecol Oncol*, **117**, 297-301.

Rabelo-Santos SH, Derchain SF, Villa LL, et al (2009). Human papillomavirus-specific genotypes in cervical lesions of women referred for smears with atypical glandular cells or adenocarcinoma in situ. *Int J Gynecol Pathol*, **28**, 272-8.

Siriaunkgul S, Suwiwat S, Settakorn J, et al (2008). HPV genotyping in cervical cancer in Northern Thailand: adapting the linear array HPV assay for use on paraffin-embedded tissue. *Gynecol Oncol*, **108**, 555-60.

Siriaunkgul S, Utaipat U, Settakorn J, et al (2011). HPV genotyping in neuroendocrine carcinoma of the uterine cervix in northern Thailand. *Int J Gynaecol Obstet*, **115**, 175-9.

Siriaunkgul S, Utaipat U, Suthipintawong C, et al (2013). HPV genotyping in adenocarcinoma of the uterine cervix in Thailand. *Int J Gynaecol Obstet*, **123**, 226-30.

Sjoeborg KD, Trope A, Lie AK, et al (2010). HPV genotype distribution according to severity of cervical neoplasia. *Gynecol Oncol*, **118**, 29-34.

Srisomboon J, Kietpeerakool C, Suprasert P, et al (2007). Factors affecting residual lesion in women with cervical adenocarcinoma in situ after cone excisional biopsy. *Asian Pac J Cancer Prev*, **8**, 225-8.

Suthipintawong C, Siriaunkgul S, Tungsinmunkong K, et al (2011). Human papilloma virus prevalence, genotype distribution, and pattern of infection in Thai women. *Asian Pac J Cancer Prev*, **12**, 853-6.

Tungsinmunkong K, Suwiwat S, Sriplung H (2006). Detection of human papillomavirus in intraepithelial lesions and carcinoma of the cervix uteri in southern Thai women. *Asian Pac J Cancer Prev*, **7**, 427-30.

Wang KL, Yang YC, Wang TY, et al (2006). Neuroendocrine carcinoma of the uterine cervix: A clinicopathologic retrospective study of 31 cases with prognostic implications. *J Chemother*, **18**, 209-16.

Zaino RJ (2002). Symposium part I: adenocarcinoma in situ, glandular dysplasia, and early invasive adenocarcinoma of the uterine cervix. *Int J Gynecol Pathol*, **21**, 314-26.