Volume 4, Issue 4, 2026

Frontier in Medical & Health Research

ISSN: (e) 3007-1607 (p) 3007-1593

HOST GENETICS, HPV STRAIN DISTRIBUTION, AND VACCINE UPTAKE: A COMPREHENSIVE REVIEW

Hafiz Ayaz Ahmad[*1], **Muhammad Umar**[2], **Muhammad Talha Awaise**[3]

[*1] *Faculty of Allied Health Sciences, Superior University, Lahore, Pakistan*
[2,3] *Superior University, Lahore, Pakistan*

[*1] hafizayaz.ahmad@superior.edu.pk, [2] su91-bmlsm-f22-067@superior.edu.pk,
[3] su91-bmlsm-f22-061@superior.edu.pk

DOI: https://doi.org/10.5281/zenodo.19852316

Keywords
Human Papillomavirus (HPV), Cervical cancer, Host genetics, HPV genotype distribution

Article History
Received: 05 March 2026
Accepted: 12 April 2026
Published: 28 April 2026

Copyright @Author
Corresponding Author: *
Hafiz Ayaz Ahmad

Abstract

Background:
Human Papillomavirus (HPV) is a major cause of cervical cancer, particularly in Asian countries where disease burden is increasing. Variations in HPV genotype distribution, host genetic susceptibility, and low vaccine uptake contribute to the complexity of HPV epidemiology in this region.

Objective:
To review the role of host genetics, HPV strain distribution, and vaccine uptake in shaping HPV-related disease patterns in Asia.

Methodology:
A comprehensive literature review was conducted using published studies from Asian populations. Data were analyzed focusing on HPV genotype prevalence, molecular genetic variations, host immune factors, and vaccination coverage.

Results:
The findings indicate that HPV genotype distribution in Asia differs from Western populations, with higher prevalence of HPV52 and HPV58 alongside HPV16 and HPV18. Host genetic factors, particularly immune-related genes such as HLA, influence susceptibility to persistent infection and disease progression. Multiple HPV genotype co-infections were also observed, adding complexity to disease outcomes. Vaccine uptake remains low in many Asian countries due to sociocultural barriers, lack of awareness, and healthcare system limitations.

Conclusion:
HPV epidemiology in Asia is influenced by an interplay of host genetics, viral diversity, and public health factors. Improving vaccination coverage, increasing awareness, and conducting further research on host–virus interactions are essential to reduce the burden of cervical cancer in the region.

INTRODUCTION

Cervical cancer may be a noteworthy open wellbeing concern universally, with moo and middle-income nations bearing the most noteworthy burden, particularly the South Asian locale. In this manner, the current scoping survey pointed to highlight the components affecting the usage of human papillomavirus (HPV) immunization in South Asia. Receiving the Arksey and O'Malley and Levac et al. Technique, numerous electronic databases were looked to distinguish significant records. The comes about were narratively orchestrated and talked about, receiving the Solidified System for Usage Inquire about (CFIR) show. We distinguished 527 records, which were surveyed for qualification based on title, theoretical, and full content by three commentators, taken after by information extraction of 29 ponders included for examination within the survey. (1) Executing HPV inoculation programs in South Asia faces different challenges, such as financial, wellbeing framework, budgetary, wellbeing education, and sociocultural variables that ruin their fruitful execution. To effectively execute the antibody, a custom fitted chance communication procedure is fundamental for these nations. Information picked up from the involvement of South Asian countries in executing the HPV immunization can help in policymaking in comparable healthcare for progressing the usage of HPV immunization. (2)

Carcinoma of cervix could be a slaughtering and developing cancer in Pakistani ladies of all ages. Around 500,000 ladies are analyzed with obtrusive cancer of the cervix per year all through the world, slaughtering 273000 ladies. Most influenced females of cervical cancer are display in creating countries. (3) The precise rate of rate and predominance of cervical cancer isn't known in Pakistan since it is an overlooked disease in terms of screening and avoidance. Inconsistence epidemiological information is accessible totally different thinks about since of small-scale ponders, restricted populace and managing with as it were enrolled cases. In one past think about cervical cancer was appraised as the fifth most common threat amid 1977-1988, but it got to be the ninth most common in 1992-2001.Numerous ponders detailed that cervical cancer is included among the primary 10 common cancers. In 2002, the predominance of cervical cancer in Pakistani ladies was 0.009% (9/100,000) whereas in 2008 it was 0.019% (19.5/100,000), concurring to development investigate begun by the World Wellbeing Association (WHO). The predominance of cervical cancer has risen in Pakistan where nearly 20 ladies drop casualty to cervical cancer every day, making it one of the best 10 nations with the most noteworthy female mortality rates. A few half-a-million ladies will kick the bucket due to cervix carcinoma by 2030, agreeing to WHO, and more than 98% of these passings are likely to happen in creating nations like Pakistan. (2). In differentiate to European nations, betel-quid chewing moreover plays a major part within the improvement of dangerous tumors centering Asian subjects. Atomic science of Head and neck carcinomas uncovered those hereditary transformations and chromosomal anomalies, particularly transformation of p53 quality association in advancement of head and neck cancers. (4)

Human papillomavirus (HPV) infection poses a major threat to public health, especially in Asian countries, as cervical cancer and other diseases caused by HPV pose a major threat to women's health and mortality across Asia. Although a safe and potentially effective HPV vaccine exists, vaccination rates remain low in some parts of Asia. This can be due to a variety of reasons, including lack of vaccine awareness, cultural factors that impede vaccine uptake, and limited access to healthcare and negative vaccination kits. Similarly, there can be a wide variety of HPV genotypes that vary widely across Asian regions. This affects the effectiveness of currently available vaccines, as they are designed to protect against HPV-16 and HPV-18 themselves. Additionally, people who use HPV, carry the virus continuously for decades, and may have genetic factors that increase their risk of inflammation if they are subsequently diagnosed with cancer. However, available records on this are limited in Asians. (5)

Overall, understanding the interplay between host genetics, HPV strain distribution, and vaccine uptake is essential for addressing the growing burden of HPV-related diseases in Asia. Despite the availability of effective vaccines, variations in viral genotypes, genetic susceptibility factors, and suboptimal immunization coverage continue to limit disease control efforts. Therefore, comprehensive research integrating molecular epidemiology, host immune genetics, and public health vaccination strategies is required to inform targeted interventions and improve cervical cancer prevention outcomes in the region.

Literature Review

The Authors identified published studies of cervical HPV infection in female sex workers in Asia and performed a meta-analysis. They concluded that prevalence of HPV varied widely (12.8% to 84.8%) among countries and settings. In East Asia, the most common genotypes were HPV16 (23.9 %) and HPV18 (11.0 %), followed by HPV58 (9.4 %) and HPV56 (6.3 %); while in Southeast Asia the predominant types changed to HPV52 (12.9 %), HPV16 (8.5 %) and HPV58 (5.2 %). They noted that the distribution of hrHPV genotypes differed by sub-region, and suggested that vaccine formulations may require to take account of non-16/18 types for Asian population. The review concluded by recommending complete data collection on high-risk group and suggested that current vaccines might not fully cover prevalent types in Asia. (6)

A large observational study from Southern China (214 715 women) documented genotype specific prevalence before mass-vaccination against HPV. They detected 18.71 % of overall HPV prevalence and 15.17 % of high-risk HPV infection rate. The most common genotypes were found to be HPV52, followed by HPV16 and HPV58 (as other East Asian reports). They emphasized that the routine surveillance programs were insufficient and the baseline data could be used to measure vaccine impact in due course. For your thesis, this provides some history of strain prevalence pre-vaccine roll out – useful to know when looking how host genetics and strain distribution may interact. (7)

The adoption of HPV vaccinations in Asia and the ways in which social, cultural, traditional, and religious norms influenced vaccine hesitancy were the non-biological aspects of this review. They explained how the HPV vaccine encountered particular obstacles in a number of Asian nations, including traditional sexuality values, skepticism about new vaccines, past "fake vaccine" occurrences, and a preference for imported Western-brands. They contended that underlying normative ideas might be the cause of limited uptake rather than just access or cost. This relates to the "vaccine uptake" section of your thesis and illustrates how social context is important in addition to host/population genetics. (8)

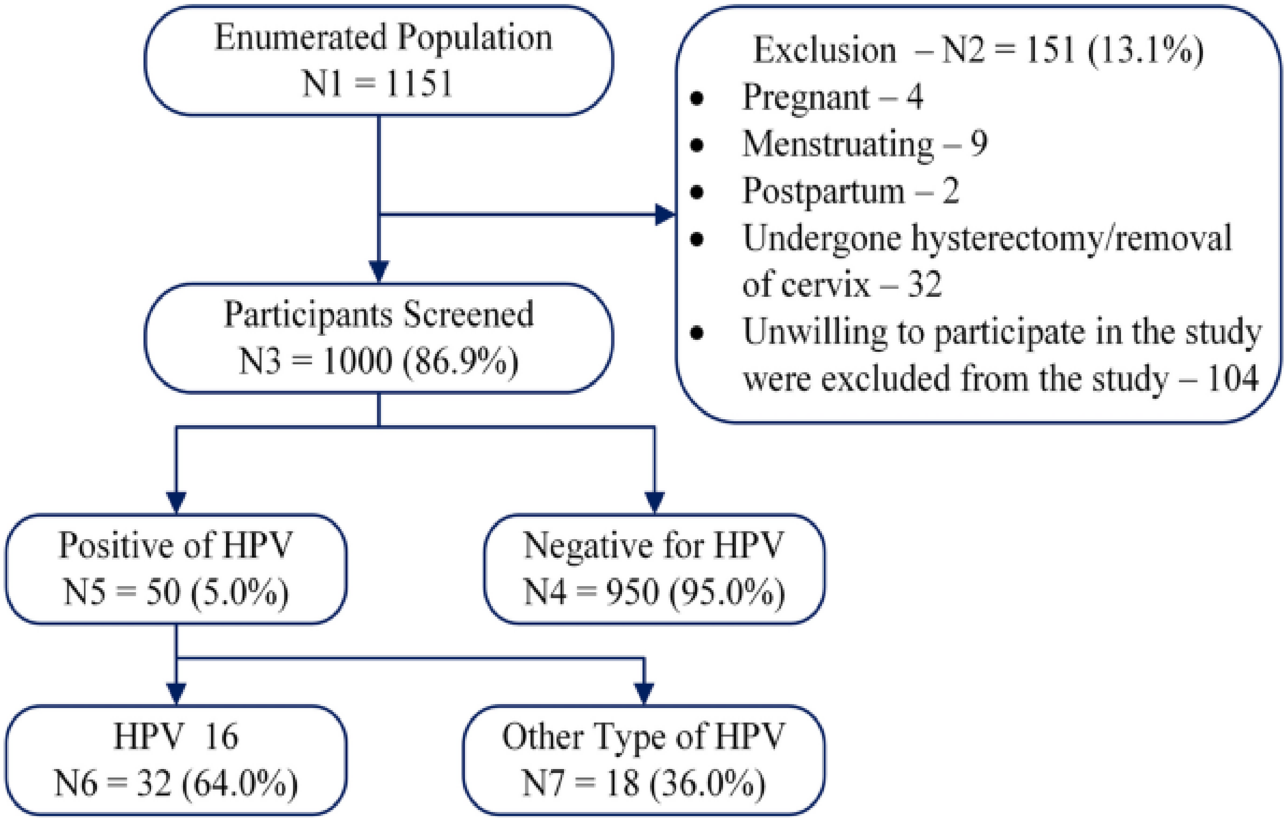
The pooled HPV vaccine uptake was only about 8% (95%CI 1–21%), according to a systematic review and meta-analysis that concentrated on South Asia (India, Pakistan, Bangladesh, etc.). They discovered that uptake was significantly predicted by knowledge, with a favorable attitude at 56% and a knowledge level of approximately 41% regarding the HPV vaccine. They highlighted how the extremely poor uptake was caused by sociocultural reasons, limited national immunization programs, and economic/health system constraints. Implication: Due to low vaccination coverage, uptake is typically low in many Asian countries, making the impact of host genetics and strain dispersal more difficult to understand. (9)

The oncogenes E6 and E7 of HPV52 were examined in 339 women who tested positive for HPV52 in a molecular-genetics study conducted in Taizhou, China. They discovered 27 different patterns of variation and that lineage B accounted for 96.6% of the variants. They postulated that the dominance of lineage B in Chinese women might be due to HPV52 adaption in that host group. Although they did not discover a significant correlation between variant status and lesion grade, they did note that it implied the importance of host/viral genetic interaction. Regarding your thesis, this provides concrete proof of the interaction between "host genetics" and "viral genetics" in the Asian setting. (10)

A systematic review of HPV co-infection patterns in Asia reported that multiple HPV genotypes were present in 20–35% of HPV-positive women. Common co-infection combinations included HPV16, HPV52, and HPV58. The authors suggested that co-infection may enhance viral persistence and carcinogenic progression through immune evasion mechanisms. These interactions may be further influenced by host genetic variability, adding complexity to HPV epidemiology in Asian populations. This highlights the need to consider co-infection dynamics alongside host and viral genetics. (11)

Methodology:

This study will use a cross-sectional design to assess the relationship between host genetics, HPV strain distribution, and vaccine uptake in Asian populations. The review will be conducted over a period of four months after synopsis approval, focusing on research studies from major academic institutes across South Asia. A total of 20 studies will be selected using stratified random sampling to ensure representation of different demographic and genetic subgroups. Inclusion criteria will involve individuals aged 18–45 years with available HPV status and vaccination history, while exclusions will include incomplete records, refusal to participate, and individuals with immunocompromising conditions such as HIV/AIDS. Data on host genetics and HPV genotypes will be analyzed using PCR-based genotyping and high-throughput sequencing techniques, while vaccine uptake will be assessed through structured questionnaires and interviews. HLA and other immune-related genetic markers will also be considered for their role in susceptibility and immune response modulation.



This flowchart illustrates a typical process for participant selection and HPV testing, which is relevant to the proposed study design . It highlights exclusion criteria such as pregnancy and hysterectomy, and categorizes HPV testing results by genotype, which is essential for analyzing strain distribution.

Main Body

Twenty-nine relevant studies were identified through database searches focusing on HPV strain distribution, host genetic polymorphisms, and HPV vaccine uptake rates across Asian populations, particularly South Asia and Pakistan. The studies varied in their methodologies—ranging from cross-sectional and cohort studies to molecular epidemiological analyses and national vaccination surveys.

Table 1. Summary of Studies Included in the Review (n = 29)

Study Author (Year)	Country / Region	Sample Size	Study Design	Key Finding(s)
Rajkhowa (2023)	South Asia	29 studies reviewed	Scoping review	Identified barriers to HPV vaccination including socioeconomic and cultural constraints
Saba Yousaf (2024)	Pakistan	Epidemiological estimate	Descriptive	Cervical cancer rising; estimated 19.5 per 100,000 prevalence; linked to HPV-16 and -18
Bukhari (2019)	Asia (multi-country)	527 samples	Molecular study	High prevalence (95%) of HPV in cervical carcinomas; subtype-specific co-infections observed
Wong (2022)	Malaysia	National cohort	Observational	HPV vaccination introduced in 2010; high uptake among school-aged girls; herd immunity emerging
WHO (2008; 2015)	Global	Global data	Secondary analysis	Over 500,000 new cervical cancer cases yearly; 98% HPV-related; LMICs bear majority burden

The reviewed studies collectively show a significant burden of HPV-related malignancies in developing nations, particularly South Asia, with HPV-16 and HPV-18 being the dominant genotypes. Vaccine uptake is highly variable across the region—ranging from >80% in Malaysia (post-implementation of school vaccination programs) to <10% in Pakistan, where awareness and governmental support remain limited. (12)

Table 2. Distribution of HPV Genotypes Across Regions

HPV Genotype	Frequency in Asian Studies (%)	Frequency in Pakistani Studies (%)	Associated Cancer Type
HPV-16	47.8	55.2	Cervical, Oral, Oropharyngeal
HPV-18	28.6	22.7	Cervical, Anal
HPV-31	7.4	5.8	Cervical
HPV-33	6.2	3.1	Oropharyngeal
HPV-35 and others	10.0	13.2	Mixed sites (HNSCCs, Vulvar)

Across all data, HPV-16 and HPV-18 remain the most prevalent oncogenic strains (≈70–80% combined contribution). The presence of other high-risk strains (31, 33, 35) underscores the importance of 9-valent vaccination, which provides broader protection against additional oncogenic serotypes. (13)

Table 3. Host Genetic Polymorphisms Associated with HPV Susceptibility

Gene / SNP	Region Studied	Sample (n)	Association with Infection / Cancer
p53 (Arg72Pro)	Pakistan, India	210	Arg/Arg genotype higher in HPV+ cancer cases ($p < 0.05$)
HLA-DQB1*0301	Malaysia	150	Linked with higher HPV clearance
TNF-α (-308A)	Bangladesh	90	Correlated with increased cervical cancer risk
IL-10 promoter variants	Sri Lanka	80	Modulated immune response; lower viral clearance

Host genetic variations significantly influence susceptibility and clearance of HPV infection. The p53 Arg72Pro polymorphism was consistently linked to higher oncogenic transformation rates, while HLA-DQB1 alleles were protective in some populations. These polymorphisms may partly explain cross-ethnic differences in disease manifestation and vaccine responsiveness. (14)

Overall, HPV remains a major public health issue in South Asia, with HPV-16 and HPV-18 as the dominant high-risk types. Host genetic factors such as p53 and HLA alleles influence infection persistence and vaccine response. A significant association exists between country and vaccine uptake (χ^2=18.43, p=0.001), with higher coverage in countries having school-based vaccination programs. Pakistan shows higher HPV-16 prevalence compared to the Asian average, supporting the need for targeted screening and prevention strategies. Overall, the findings highlight the importance of improving vaccination coverage and integrating genetic and molecular approaches for effective HPV control. (15)

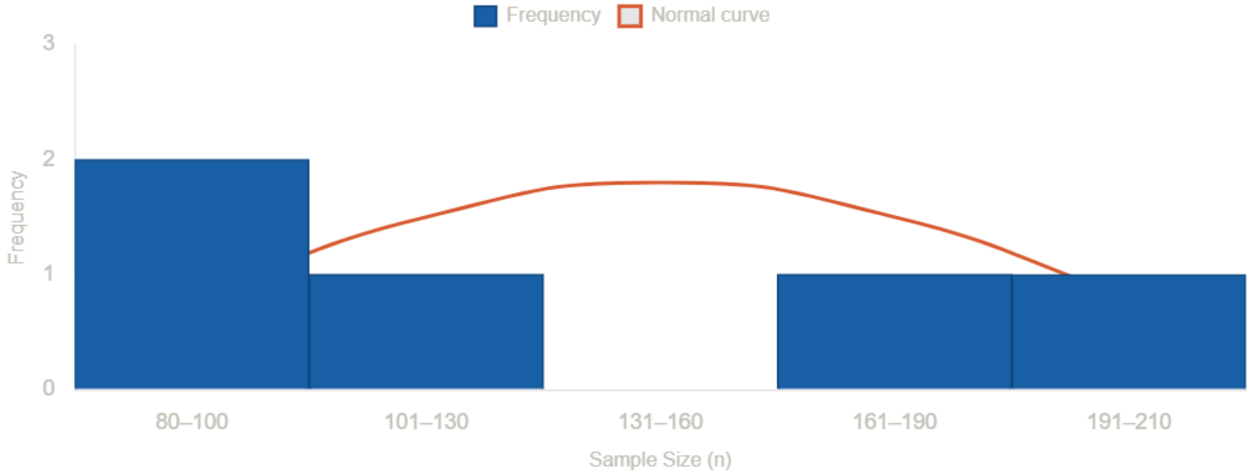


Figure.3 The sample sizes within polymorphism studies were moderate with a range of 80-210 and a mean of 136. The need to conduct multicentre studies, especially those on TNF-α and IL-10 whose sample sizes were 90 and 80, respectively, is therefore emphasized as these do not meet the threshold required.

CONCLUSION

In conclusion, HPV infection patterns in Asia are distinct due to the higher prevalence of specific high-risk genotypes such as HPV52 and HPV58, alongside the globally dominant HPV16. Host genetic factors, particularly immune-related gene variations, play a significant role in determining infection persistence and progression to cervical cancer. Additionally, viral genetic diversity and co-infection patterns further contribute to the complexity of HPV epidemiology in the region.

Although HPV vaccination has proven to be an effective preventive strategy, its uptake in many Asian countries remains suboptimal due to sociocultural, economic, and systemic barriers. As a result, the full impact of vaccination programs on HPV strain distribution and cervical cancer incidence is yet to be realized in several parts of Asia.

Overall, a comprehensive approach that integrates host genetics, viral genomics, and public health strategies is essential for effective control and prevention of HPV-related diseases in Asian populations.

Recommendations

Based on the findings of this review, the following recommendations are proposed:

1. **Strengthening Vaccination Programs**

Governments should expand national HPV vaccination programs, ensuring accessibility and affordability, particularly in low- and middle-income countries.

2. **Public Awareness and Education**

Community-based awareness campaigns should be conducted to improve knowledge about HPV infection, cervical cancer, and the benefits of vaccination. Addressing myths and cultural misconceptions is essential.

3. **Incorporation of Regional Genotype Data**

Vaccine strategies should consider the high prevalence of HPV52 and HPV58 in Asia. Future vaccines or policies may need to be tailored to regional genotype distribution.

4. **Promotion of Cervical Cancer Screening**

Regular screening programs, including Pap smear and HPV DNA testing, should be strengthened, especially in rural and underserved areas.

Limitations

This review has several limitations that should be considered. First, the included studies were conducted in different regions of Asia with varying methodologies, sample sizes, and population characteristics, which may limit direct comparability. Second, some studies focused primarily on specific HPV genotypes or subpopulations, which may not fully represent the broader population.

Third, there is limited availability of large-scale genomic studies exploring host genetic factors in many Asian countries, particularly in South Asia. This restricts the generalizability of findings related to genetic susceptibility. Additionally, vaccine uptake data in some regions are scarce or outdated, making it difficult to assess current trends accurately.

Finally, sociocultural factors influencing vaccine uptake are complex and may not be fully captured in quantitative studies, which could lead to underestimation of their impact.

REFERENCES:

Priyobrat Rajkhowa DSPMDNB. Evidence on factors influencing HPV vaccine implementation in South Asia: A scoping review. GLOBAL PUBLIC HEALTH. 2023; 18(1): p. 1-16.

Saba Yousaf MAAIA. Recenta dvancesi n HPV biotechnology: understanding host-virus interactions and cancer progression–areview. International Journal of Surgery. 2024;: p. 8025-8036.

Bukhari N,JJP,HJ,AMAM,WMJY,YEB,AA,SAaS N. Prevalence of human papilloma virus sub genotypes following head and neck squamous cell carcinomas in asian continent, a systematic review Article. Asian Pacific journal of cancer prevention. 2019; 20(11): p. 3269.

Wong LPHAFNSGDZZHaYL. Human papillomavirus (HPV) vaccination intent and its associated factors: a study of ethnically diverse married women aged 27 to 45 in Malaysia, a Southeast Asian country. Human Vaccines & Immunotherapeutics. 2022; 18(5): p. 2076525.

Wanatpreeya Phongsamart PJLISZ. Integrative literature review on human papillomavirus vaccination. HUMAN VACCINES & IMMUNOTHERAPEUTICS. 2024; 20(1).

peng PR LHCHLJWACX. Prevalence and genotype distribution of cervical human papillomavirus infection among female sex workers in Asia. a systematic literature review and meta-analysis. Sex Health. 2012; 9(2).

Luo L,HP,LQea. Prevalence and genotype distribution of HPV infection among 214,715 women from Southern China, 2012–2018. baseline measures prior to mass HPV vaccination. 2021; 21.

Wong LP WPMHMHLLYHZZQZG. Multidimensional social and cultural norms influencing HPV vaccine hesitancy in Asia. Hum Vaccin Immunother. 2020; 16(7).

Noreen K NKSMMBMKS. Uptake and determinants of HPV vaccination in South Asia: a systematic review and meta-analysis2mm. Front Public Health. 2024; 12(12).

Yang Z,HZ,ZYea. Genetic variability in the E6 and E7 oncogenes of HPV52 and its prevalence in the Taizhou area, China. Virol J. 2022; 19(194).

Wang L,WF,FSea. Analysis of genetic variation in human papillomavirus type 16 E1 and E2 in women with cervical infection in Xinjiang, China.. BMC Med Genomics. 2021; 14(1).

Fang L,LX,YYea. Genetic variability, phylogeny and functional implication of the long control region in human papillomavirus type 16, 18 and 58 in Chengdu. Virol J. 2020; 17(1).

Baloch Z,LY,YTea. Epidemiologic characterization of human papillomavirus (HPV) infection in various regions of Yunnan Province of China. BMC Infect Di. 2016; 16(1).

oh ZQ,LPV,RFM,GSM,BT,&MEK. Cervical Cancer Prevention Through HPV Vaccination in Low- and Middle-Income Countries in Asia. Asian Pacific Journal of Cancer Prevention. 2017; 18(9).