

## RESEARCH ARTICLE

# Human Papillomavirus Genotypes Profile in Cervical Cancer Patients at Dr. Hasan Sadikin General Hospital, Bandung, Indonesia

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### Abstract

**Background:** As in other developing countries, cervical cancer is the most frequent gynecologic malignancy in Indonesia. Persistent high risk genotypes of human papillomavirus (HPV) that infect the cervical tissue have been established as the etiology of cervical cancer. This study aimed to explore the profile of cervical cancer patients and the infected HPV genotypes at Dr. Hasan Sadikin General Hospital-Bandung. **Materials and Methods:** During the year 2010, 554 cervical cancer patients were registered. In a subset of the patients during July – November 2010, 40 randomized fresh biopsies were tested for HPV genotype after obtained informed consent. The distribution of HPV genotypes and the association to risk factors were analysed. **Results:** The result showed that 62.5% of the tested biopsies were infected by multiple HPV infections, with HPV-16 found in most of the cervical cancer patients (90%). Marriage at age younger than 16 years old was statistically significant in relation to multiple HPV infection ( $p=0.003$ ), but not parity more than three times ( $p=0.59$ ). **Conclusions:** Although high parity in our study was not associated with multiple HPV infection, good family planning programs and reproductive health education need to be emphasized in Indonesia as high parity and marriage at young age might increase the chance of cervical cancer development.

**Keywords:** Bandung - cervical cancer - HPV - multiple HPV infections - high parity - young marriage

*Asian Pac J Cancer Prev*, 15 (14), 5781-5785

### Introduction

Persistent human papillomavirus (HPV) infection has been established as a key determinant of cervical carcinogenesis (Castellsague, 2008). The new cases of cervical cancer remain high despite the HPV vaccine availability, and the cases are increasing being the second highest incidence rate in the world among women after breast cancer (Ferlay et al., 2012). Studies conducted in several countries have shown that highrisk (hr) HPV genotypes infect the cervical cancer tissue (de Sanjose et al., 2010), with genotype HPV-16 is the most commonly hrHPV genotype found in squamous cell carcinoma and HPV-18 in adenocarcinoma (Altekruse et al., 2003). The distribution in HPV genotype that infect the women differs in various regions, and the hrHPV infections can infect the cervical cancer tissue either in a single or multiple HPV infections (Vaccarella et al., 2010; Resende et al., 2014). Implication of knowing the status of hrHPV infection whether it is single or multiple HPV infection may give a clear prediction for successful therapy. Therefore, individual screening is needed, since multiple HPV

infection is known to be associated with poor response of radiotherapy and bad prognosis in locally invasive cervical cancer (Munagala et al., 2009). Data on HPV distribution is necessary and should be available in every area for a better treatment and prevention of cervical cancer.

Next to persistent HPV infections, there are well known risk factors for having cervical cancer, known as reproductive risk factors such as early sexual intercourse, multiple partners, the number of parity, the number of abortions, the use of oral contraceptive (Kumar and Bhasker, 2013). Other riskfactors that may attribute to cancer developing are smoking behavior (Vaccarella et al., 2008), several host genetics determinants (Nunobiki et al., 2011; Mei et al., 2012) and other factors that may associate with socio-cultural factors of the population (Nessa et al., 2013).

Based on the histopathological data in Indonesia, cervical cancer is the most common gynecologic cancer occurring among women (Azis et al., 2009). Meta analysis in HPV prevalence across Asia region showed that only one study reported from Indonesia (Bruni et al., 2010). Therefore, we aimed to further explore the profile of

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