

## ABSTRACT

Cervical cancer (CC) is one of the most prevalent malignancies in females worldwide, in which one of its major causative agents is human papillomavirus type 16 (HPV16). The current HPV screening measures are responsible for reducing CC incidence; however, some limitations still persist which brings about the necessity to investigate novel biomarkers. The HPV16 genome contains several genes with one of them being E4 which plays a role in viral release and transmission during productive infection. This study investigated the potential of E4 as a novel biomarker by quantifying the E4 mRNA expression through two-step qRT-PCR in different stages of cervical precancerous lesions. Notably, the LSIL samples expressed E4 in all of the samples, showing a significant increase of expression compared to NILM. The samples diagnosed with NILM and HSIL had lower E4 expression levels, with some of them presenting E4-negative results. This signified that there was a reduction in E4 expression at high-grade lesions while it peaked at low-grade lesions, indicating productive infection; hence, this suggested the utilization of E4 as a novel potential early biomarker for screening of cervical carcinogenesis.

**Keywords:** *HPV16, E4, cervical precancerous lesion, viral carcinogenesis, biomarker, qRT-PCR*