

CONCLUSION

The prevalence of HPV infection among 214 women who attended the gynecological clinic at Maharaj Nakorn Chiang Mai Hospital, Faculty of Medicine, Chiang Mai University was determined by using the PCR technique amplifying the L1 nucleotide sequence. Fifty-one out of 214 (23.83%) samples were positive for HPV DNA. Among those positive samples, 16 (15.38%) were from the preinvasive and 35 (72.92%) invasive stages. The HPV positive samples were studied further for genotype distribution by using the RFLP technique. HPV 16 was found most frequently in 21 of 51 (41.18%) samples followed by HPV-18 (13.73%), -35 (13.73%), -52 (9.8%), -6 (7.84%), -11 (1.96%) and -51 (1.96%). HPV-16 was also found most frequently among preinvasive and invasive cervical samples, 5 out of 16 (31.25%) and 16 out of 35 (45.17%), respectively. HPV-16 and -18 containing samples were analyzed further for E6/E7 gene expression by using RT-PCR with fluorescent-labeled primer. At least two subsets of HPV16 E6/E7 transcripts, E6*I and E6*II were observed in 18 of 21 samples. In HPV18, only E6*I was detected in 4 of 7 samples. The relative proportion of E6*I and E6*II was analyzed. No significant relationship between the patterns or relative proportion of the transcripts and the tumor histology was observed.