

Human papillomavirus (HPV) is responsible for one of the most frequent sexually transmitted infections. The first phylogenetic analysis of LCR region was performed by Ho et al. Currently, 4 variants have been described: African (Af-1; Af-2), Asian-American (AA) and European (E). Smith proposed sub-lineages of the E variant and other investigators claim that specific mutations in the E6 and LCR sequences could be related to persistent viral infections. The aim of this study was the phylogenetic study of HPV16 sequences of cervical samples in order to detect the circulating lineages and analyze the presence of mutations related to malignancies. Fifteen samples of HPV16 were studied, they were analyzed by PCR for L1, E6 and LCR regions and sequenced. Phylogenetic trees were constructed by Maximum Likelihood with parameters suggested by JModelTest 3.7, with bootstrap and 1000 pseudoreplica. The phylogenetic analysis determined that 86% of the samples belonged to the variant E, to AF-1 7% and to AF-2 another 7%. The most frequent mutation detected in LCR sequences was G7521A, in 80% of the analyzed samples; it affects the binding site of a transcription factor (YY1) that could contribute to carcinogenesis. Other nucleotide changes were detected in LCR which could affect the regulation positive or negative of HPV transcription. In the E6 sequences, the most common mutation was T350G (L83V) in 67% of the samples, associated with increased risk of persistent infection. These results are the first contribution on molecular epidemiology of HPV16 in Cordoba. The high detection rate of the E variant is consistent with the patterns of human migration. The importance of the study of circulating variants and the analysis of the presence of changes in the nucleotide structure is significant, in two areas: in molecular epidemiology and also in the impact of these variations on Public Health Affairs when they are correlated to the evolution towards malign processes.