
P-37; GENETIC VARIABILITY IN E6 AND E7 PROTEINS OF HPV-81 CIRCULATING IN ITALY

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Background and Aims: HPV types known to infect the genital tract are classified as “Low Risk” (LR) and High Risk” (HR) on the basis of their oncogenic potential, related to E6 and E7 proteins, inactivating p53 and pRB, respectively. Little is known concerning the molecular variants of LR-types with limited diffusion, as most data concern E6 and E7 variants in HPV-16 and -18 and HPV-6 and -11. In the present study we analysed the E6 and E7 genetic variability of HPV-81.

Materials and Methods: The E6 and E7 genes were amplified from 6 HPV-81 positive cervical cytobrush by specific primers. PCR products were cloned and sequence analysis was performed.

Results: Neither frame shifts, nor insertion were observed in all analysed sequences. For E6, maximal divergence from the prototype ranged from 0.6% to 2.5%. Several amino-acids (R56, R78, L111, W133), significant in modulating maintenance of viral episomes in both HR and LR, were conserved in all HPV-81 analysed clones. In E7, maximal intervariant diversity ranged from 1% to 5.1%. Altogether 9 mutations resulting in amino-acid changes were identified of which R65K and T89A were the most prevalent (86% and 23%, respectively). Comparison the pRB binding domain of the HPV-16 and -18 and HPV-6 and -11 with those of HPV-81 clones revealed the presence of D21 in all HPV-81 clones versus G22 present in HPV-6 and -11. The G in HPV-6 and -11 confer less affinity to bind pRB, and maybe the D residues in HPV-81 could increase its oncogenic activity.

Conclusions: Our data indicate that genetic variability in E6 was less than in E7. In particular, regarding the R65K and T89A changes observed in E7 region, further studies should be planned to determine their importance for biological properties of the protein and their involvement for host immune recognition.