

Possible role of negative human papillomavirus E6/E7 mRNA as a predictor of regression of cervical intraepithelial neoplasia 2 lesions in hr-HPV positive women.

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ABSTRACT

BACKGROUND: The aim of this study was to evaluate the regression rate of CIN2 p16 positive lesions in women over 25 years of age and identify possible predictors of regression.

METHODS: A total of 128 CIN2 p16 positive patients over 25 years old were considered. The women met the following inclusion criteria: HPV genotype 16, 18, 31, 33, 45 positive, HPV E6 / E7 mRNA test positive, without immune system pathologies, not pregnant and had completed at least two years of follow-up. At each follow-up examination patients were examined by colposcopy, HPV test, E6/E7mRNA, targeted biopsy and p16 protein detection. The final state after the two years of follow-up was classified as progression if the histology showed a CIN3, persistence if the lesion was a CIN2, regression if negative or LSIL. The predicted regression factors evaluated were: HPV E6/E7mRNA, protein p16.

RESULTS: Overall, we had 35.1% (45 cases) of progression to CIN3, 41.4% (53 cases) of persistence and 23.4% (30 cases) of regression. The regression rate was higher in women with negative mRNA 92.8% (26/28), OR 312 (34.12-1798.76) $p = 0.0001$, while women with p16 negative had a regression of 22.6% (7/31), OR 0.94 (95% CI 0.36-2.46), p was not significant. We found no significant difference in regression between p16 positive (23.7%) and p16 negative (22.6%) CIN2 p16 lesions. p16 had a VPN of 22.6 (CI 95% 0.159-0.310), indicating that a p16 negative lesion does not exclude a CIN2 + .

CONCLUSIONS: We had a regression rate of 23.4%, which was low if we consider that in the literature the regression rates vary from 55 to 63%. The discrepancy in the results may indeed be explained by the fact that all lesions in our study were hr-HPV positive and belonged to "older women" reflecting a more "high-risk" population. As regression factors we studied p16 and HPV E6/E7 mRNA. The results of our study show that HPV mRNA, if negative, appears to be able to identify CIN2 lesions with a higher probability of regression and underlines how a p16 negative is not an indicator of regression.