

Evaluation of CDH1 Promoter Methylation and HPV Infection Status in the Development of Parotid Pleomorphic Adenoma

F. Ozen¹, Z. Yegin^{2*}, G. O. Acar³, C. Avsar⁴ and T. Zenginkinet⁵

¹*Department of Medical Genetics, Goztepe Research and Training Hospital, Istanbul Medeniyet University, Istanbul, Turkey*

^{2*}*Medical Laboratory Techniques Program, Vocational School of Health Services, Sinop University, Sinop, Turkey
E-mail: zyegin@sinop.edu.tr*

³*Department of Otorhinolaryngology, Göztepe Training and Research Hospital, Istanbul Medeniyet University, Istanbul, Turkey*

⁴*Department of Biology, Faculty of Science and Arts, Sinop University, Sinop, Turkey*

⁵*Department of Pathology, Goztepe Research and Training Hospital, Istanbul Medeniyet University, Istanbul, Turkey*

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ABSTRACT Both benign and malignant salivary gland tumors are clinically heterogeneous and they display different histology. Researchers aimed to elucidate the potential roles of both CDH1 methylation and high-risk oncogenic human papilloma virus (HPV) types HPV16 and HPV18 in parotid pleomorphic adenoma. Genomic DNA samples extracted from formalin-fixed paraffin-embedded (FFPE) samples of parotid pleomorphic adenoma and control tissues were subjected to methylation specific PCR (MSP) for hypermethylation analyses. HPV infection presence was evaluated using both GP5+/GP6+ consensus primers and type-specific primers for HPV16 and HPV18. Both CDH1 promoter hypermethylation and HPV16 infection partially seemed to be responsible in the occurrence of the tumors. According to the best of the researchers' knowledge, this is the first study investigating the possible roles of both CDH1 methylation and HPV involvement in parotid pleomorphic adenoma. Multicentered studies with larger sample cohorts could be highly beneficial to strengthen this study's results and thus draw a more precise conclusion