PP48. Prognostic significance of the HPV status in early stage cervical carcinoma

K. Kubelka-Sabit, I. Prodanova, G. Yashar, G. Zografski, N. Basheska
Department of Histopathology and Clinical Cytology, Institute of Radiotherapy and Oncology, Clinical Center, Skopje, Macedonia
e-mail: *catkubelka@yahoo.co.uk*

Aims: In order to evaluate their prognostic significance, the parameters of the human papilloma virus (HPV) status were correlated to the lympho-nodal and tumor status, maximal diameter, minimal thickness of uninvolved stroma, histologic type, grade of differentiation, lympho-vascular space invasion, degree of lymphocytic inflammatory stromal reaction at the invasion front, age and the disease-free survival (DFS) of the patients with early stage invasive cervical carcinomas. Material and methods: 77 cases of cervical carcinomas, limited to the uterus, surgically treated and postoperatively irradiated, were selected for this retrospective study. HPV DNA status (presence and HPV type, type of hybridization signal and number of positive cells per sample) was evaluated using sensitive in situ hybridization detection kit with catalyzed signal amplification with biotinylated probes for types 6/11, 16/18 and 31/33 or 31/33/51. Results: The presence of HPV DNA was detected in 45 (58.4%) cases. Thirty-two (71.1%) showed positivity for HPV type 16/18, 8 (17.8%) for 31/33, whereas multiple infection was detected in (8.9%) 4 cases. Dot hybridization signal was found in 31 (68.9%), diffuse in 2 (4.4%) and mixed in 12 (26.7%) cases. More than five positive nuclei per sample were found in 37 (82.2%) of the cases. Only the presence of HPV was associated with absence of regional lymph node involvement, presence of moderate/abundant lymphocytic infiltration and longer 5 and 10-year DFS. Conclusions: According to our results, more extensive studies are needed to assess the real prognostic influence of the other parameters of HPV status in early stage cervical carcinomas.

PP49. Analysis of MTHFR C677T mutation in patients with pancreatic cancer

I. Nisevic[1], J. Dinic[1], S. Lukic[2], M. Ugljesic[2], A. Nikolic[1]
1. Institute of Molecular Genetics and Genetic Engineering, Belgrade, Serbia and Montenegro 2. Department of Gastroenterology, Clinical Center of Serbia, Belgrade, Serbia and Montenegro
e-mail: *qwert@eunet.yu*

Pancreatic cancer is one of the leading causes of cancer deaths in the world. Main risk factors for pancreatic cancer include cigarette smoking, age, diet, occupational exposure to certain carcinogenes, some medical conditions, chronic pancreatitis and inherited susceptibility. Several genes are suspected to modify the risk of pancreatic cancer, but although they have been extensively studied, their part in the etiology of this disease has not been revealed yet. 5,10-Methylenetetrahydrofolate reductase (MTHFR) plays an important role in DNA methylation, synthesis and repair, which makes MTHFR gene attractive as a candidate cancer-modifying gene in many malignant disorders, including panceratic cancer. This study has encompassed 41 patients with pancreatic cancer and 50 healthy saubjects with history of smoking. All subjects were tested for the presence of MTHFR C677T polymorphism by PCR-RFLP method. Mutation C677T was detected on 28 of 82 analyzed chromosomes in patients and on 33 of 100 analyzed chromosomes in controls. Allelic frequencies of this mutation did not significantly differ between the group of adenocarcinoma patients (34%) and control group (33%). The obtained results suggest that MTHFR C677T is not a risk factor for pancreatic cancer. However, these results can be considered only preliminary, due to the small number of analyzed patients and a possibility of combined effect with other genes.