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Gene expression profiling reveals novel candidate genetic biomarkers of ovarian carcinoma prognosis and metastasisRadka Vaclavikova^{1,5}, Katerina Elsnerova^{1,5}, Marie Ehrlichova^{1,5}, Lukas Rob², Martin Hruda², Petr Skapa³, Alena Bartakova⁴, Jiri Bouda⁴ and Pavel Soucek^{1,5}¹National Institute of Public Health, Czech Republic²Vinohrady University Hospital, Czech Republic³Motol University Hospital, Czech Republic⁴University Hospital in Pilsen- Charles University, Czech Republic⁵Charles University, Czech Republic

Epithelial ovarian cancer (EOC) has the highest mortality among gynecological carcinomas. Given the diversity in responses to the therapy, there is a need for identification of reliable biomarkers of prognosis, progression and prediction of EOC therapy outcome. The aim of our study was (i) to explore differences in expression of 94-gene panel connected to drug transport (ABC, SLC transporters), metabolism and cell cycle regulation in a set of primary EOC tissues (n=60), intraperitoneal metastases (n=29) and control ovarian tissues (n=14) as well as in a validation set of EOCs (n=57) using quantitative real-time PCR; (ii) to investigate associations of gene expression level with prognosis, development of metastasis and progression-free survival of EOC patients. Different gene expression profiles were found in ovarian carcinomas when compared with controls. Expression of ABCA7 significantly increased and that of ESR2 decreased in the order control ovarian tissues - primary EOCs - EOC metastases. The most important associations between gene expression and clinicopathological data were found for membrane transporters (*ABCA2/9/10*, *ABCG2*, *SLC16A14*) and cell cycle regulators (*PLK1*, *CIT*, *PRC1*). Transporters from the ABCA family, ABCG2 and ESR2 are involved mainly in lipid metabolism, membrane transport and cell proliferation. These processes are thus probably important for EOC progression. In conclusion, we have proposed novel genetic biomarkers of ovarian carcinoma prognosis and progression potentially useful as therapeutic targets.

Biography

Radka Vaclavikova has completed her PhD from Charles University in Prague, CZ and conducted her Post-doctoral studies in cooperation with Faculty of Medicine, University of Oslo, Norway. She is a Principal Investigator in Toxicogenomics Unit, National Institute of Public Health in Prague, CZ and in Laboratory of Pharmacogenomics, Biomedical Center in Pilsen, CZ. She has published 34 papers in impacted journals (450 citations, H Index 12) and serves as a Mentor of doctoral studies under Faculty of Medicine, Charles University in Prague.

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