Abstract

Endometrial cancer is a heterogeneous group of tumours of the endometrium, which are characterized by different pathogenesis, course of disease and response to treatment. Traditional classification is based on clinical or histopathological features. Observations of the last decade have shown that endometrial cancer is a biologically, clinically, morphologically and genetically diverse group of tumours. Traditional classifications rarely reflect this diversity and, although they carry prognostic information, they fail to predict treatment response. The main objective of hereby thesis was to find molecular markers of diagnostic, prognostic and predictive importance in endometrial cancer using molecular techniques. The project was based on a comprehensive analysis of markers which could: better differentiate endometrial cancer, correlate with clinical and pathological characteristics, correlate with patients’ survival, and allow for treatment optimization. Detailed aims of the research included: determination of the copy number variation of 10 genes (TOP2A, ERBB1, ERBB2, ERBB3, ERBB4, MYC, CCND1, PI3K, RAD21, ESR1) by quantitative PCR (qPCR); determination of the expression level of genes MGB1, RAD21, RUNX1, CD133, SNAIL, SLUG by qPCR preceded by reverse transcription (RT-qPCR); determination of the expression level of 14 proteins (ESR1, PGR, ERBB1, ERBB2, ERBB3, ERBB4, PIK3CA, phosphorylated AKT1, MYC, TOP2A, CDKN2A, TP53, RAD21, RUNX1) by immunohistochemical staining (IHC). In total, 30 markers have been tested for the potential use in endometrial cancer. All the results were analyzed statistically, including clinicopathological data and survival of patients. The results are contained in the following publications: