Predictive and prognostic factors in gastric cancer

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Introduction: Gastric cancer is one of malignant diseases which have the worst prognosis. Unfortunately, there are most patients with advanced-stage disease who have to be treated in a palliative way. Patients suffered from the same type of tumor, being at the same stage of disease and treated with the same chemotherapy have various rates of survival, which can be caused by diverse expression of selected genes impacting on the mechanism of cytostatic effects. The determination of these genes or microRNAs which regulate these genes could be used as a predictive factor for prediction of effects of administered chemotherapy. The determination of some microRNAs, or in the combination with suitable plasmatic factors, could be used as a prognostic factor for patients with gastric cancer. It is also possible to use this combination for early diagnosis of cancerogenesis

Object: The aim is to verify the possibility to use expression of selected genes and some microRNAs in tumor tissue as a prognostic factor or a predictor for therapeutic effects of chemotherapy in patients with gastric cancer.

Methodology: We retrospectively evaluated the group of 1258 patients with gastric cancer who had been treated in our department in the course of fourteen years. We selected 54 patients who had not undergone resection surgery and had been administered chemotherapy (conditions for predixtion). These patients were determined expression of 33 various microRNAs and 4 genes in paraffin-embedded tissue samples in. Afterwards, these obtained data were in conntection with the type of chemotherapy, the length of survival and time to progression.

Results: We succeeded in proving predictive significance of miR181b, miR150, miR192 and miR 342 for 5-fluorouracil and capecitabine as well as predictive signficance of miR221, miR224, miR520 and miR375 for platin derivates. We proved predictive significance of the thymidylate synthase gene in tumor tissue for therapeutic effects of platin derivates. On the basis of results obtained by us, we can state that the determination of expression of miR150, miR342, miR224 and the determination of gene expression of ERCC1 RT2 can be used as a prognostic factor in patients with gastric cancer.

Discussion: It is necessary to verify the possibility to use predictive significance of miRNAs in patients after resection, too because in these patients, this administered chemotherapy is targeted at residual cells in their bodies. Results of published study works show that some phenotypic features of cells which left a primary tumor differ from features of cells of the original tumor. Nowadays, it is also possible to determine miRNAs in the peripheral blood, which can significantly make the determination much easier. However, there is a need to compare miRNA levels in tumor tissue with peripheral blood level. Besides, miRNAs can be determined with the combination with other serum factors to detect early cancerogenesis. Here are numerous questions which have to be replied before determining right conclusions.

Conclusion: The determination of microRNAs is certainly very auspicious and means a great chance for the future. Use of expression of selected microRNAs directly in tumor tissue can serve as a predictive and prognostic factor in patients with gastric cancer. It is possible to use the determination of expression of some genes in the same way, too. Thanks to prediction of effects of given chemotherapy, we can differ the patients who will profit from chemotherapy administered to them. The other patients will avoid useless administration of chemothepy for whom it is not effective and which could make quality of their lives worse and increase total treatment costs.