Title of the project: The clinicopathological and molecular factors detected in liver metastases predicting treatment response in colon cancer patients.

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Starting date: 01.05.2019    Duration (years): 4

Total funds allocated for project - Kč (thousands): 9941

Summary of 2019 results

Title of the presentation: Liver metastases in colon cancer patients – do we have new predicting clinicopathological and molecular biomarkers?


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Abstract.
The aim of this project is to identify molecular and immunological patterns associated with adverse outcomes (i.e. early relapse following resection and chemoresistance) in patients with colorectal cancer (CRC), who underwent curative therapy for the primary tumor and subsequently developed liver metastases. Furthermore, we seek to identify molecular and immunological factors associated with response to induction (neoadjuvant) bio-/chemotherapy preceding liver resection.

We plan to enroll 54 patients (retrospective analysis) and 14 patients (prospective analysis) during the first year. Mutational analysis using next-generation sequencing will be performed in paired samples – from the primary tumor and correspondent liver metastases. Considering that clonal evolution takes part in disease progression and metastasizing, this will allow us to identify shifts in molecular patterns associated with liver metastases. Furthermore, this analysis will help us identify factors associated with resistance to adjuvant chemotherapy for the primary tumor. Some of the patients will be candidates for induction (neoadjuvant) chemotherapy. In this case, the depth of response will be assessed and potential molecular markers associated with response to bio-/chemotherapy will be analyzed.

The tasks during the first year include: Recruitment of patients and sampling of biological material, collection of clinical data and storage of processed/unprocessed biological samples, DNA and RNA isolation from tumor samples, adjacent non-malignant mucosa, metastasis and peripheral blood lymphocytes (PBLs), and library preparation for RNA sequencing (discovery set). A database including both clinical data and laboratory results will be created to allow complex statistical analysis.

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