**Identification of genomic rearrangements in white blood cells of colorectal cancer patients**

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Colorectal cancer is at the forefront of incidence and mortality associated with cancer globally as well as in Czech Republic. Currently, treatment is based on a combination of surgery followed by oncological treatment in the case of advanced or metastatic colorectal cancers. Appropriate prognostic and predictive markers are required to select the optimal treatment schedule. However, their use may be complicated by evolutionary changes in tumor tissue during treatment, which will affect the effectiveness of the therapy. Tracking these changes using a classic biopsy is often not possible, and therefore, efforts are increasingly being made to use the so-called "fluid" biopsy of free nucleic acids and circulating tumor cells. In this project, however, we focused on the analysis of genomic aberrations in white blood cells in patients with colorectal carcinoma.

In the study, we analyzed a total of 52 white blood cells from 21 patients with colorectal carcinoma. These white blood cells were collected by the micromanipulator from preparations of the peripheral blood nuclear cell suspensions that were used to detect circulating tumor cells. For individual white blood cells, their DNA was amplified using the SigmaAldrich WGA4 kit, the New England Biolabs NEBNext Ultra library was prepared and sequenced on the HiSeq instrument. By analyzing copy number variations in combination with the C5.0 algorithm, we were able to identify a region whose aberrations in white blood cells appear to be associated with duration of tumor-free survival.

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