Summary

Genetic predisposition to cancer increases the probability of its occurrence during a person's life. It is conditioned by specific sequence changes in genes involved in processes related to cell cycle control and maintaining the integrity of the genome. One of the challenges of contemporary molecular studies is the effective detection of pathogenic sequence changes in the genetic material of a patient. Detection of mutations, especially in severe cancer syndromes, is crucial because identifying people from risk groups allows proper prophylactic care. In case a disease occurs, this gives a possibility to respond rapidly in its early stages, thus increasing the chance of remission. It also enables the exclusion of family members without inherited risk factor from the expensive diagnostic tests.

Cancer predisposition may be caused by both small sequence changes and large rearrangements of the genome. Detection of the genetic basis of a patient's condition currently requires a series of separate techniques. The development of molecular diagnostics is heading toward reducing time and costs necessary to perform the analyses, as well as increasing their productivity, sensitivity and throughput. New methods of mutation detection contribute to a better understanding of the genome structure or functioning, and help to improve medical care.

The doctoral dissertation, consisting of three original papers, describes the development and validation of new methods of detecting genetic predisposition to cancer based on selected diseases. It includes methodology for the detection of small mutations of the *STK11* gene in patients diagnosed with Peutz-Jeghers syndrome, comparative – high resolution melting analysis (C-HRM), which is a novel method for simultaneous detection of small mutations and large rearrangements, and description of the practical application of the C-HRM in detecting the most common changes in the *CHEK2* gene.

The developed methodologies improve genetic diagnostics of patients by reducing the cost of such analyses as well as by facilitating their implementation. Therefore, it is possible to cover a larger group of patients, and at the same time, increase the efficiency of identification of people at risk. High resolution melting (HRM) is one of the most cost-effective screening tools, and the development of the C-HRM, which enables the simultaneous detection of large rearrangements (CNVs) without changing the specificity of the method further increase its applicability.