DNA methylation is one of the main epigenetic mechanisms of turning genes “on” and “off”. In principle it is a process of addition of methyl groups to cytosines within DNA strand. It is generally accepted that the methylation of all adjacent cytosines in gene promoter abolishes gene transcription and accumulation of changes of methylation status at adjacent cytosines is considered a hallmark of neoplastic transformation, similar to accumulation of mutations in a cell.

In study leading to this proposal we have shown that the phenomenon of different methylation of adjacent cytosines, referred to as disordered methylation and so far attributed only to neoplastic cells, occurs also in healthy cells and tissues. Moreover, the patterns of discordant methylation in healthy cells are very stable, tissue-specific and undergo dysregulation in neoplastic cells. We also preliminarily showed that discordantly methylated cytosines may play a role in maintaining of a cell nucleus architecture and indirect regulation of gene expression.

Current models of epigenetic inheritance do not provide molecular mechanisms for transmission of phenomenon that we identified to daughter cells. Thus, the main aim of the research in this proposal is to elaborate the biology and physiological function of the discordant methylation patterns in healthy and neoplastic cells. We will also investigate potential use of the discordant methylation in early cancer diagnostics.