Introduction

Classical Hodgkin lymphoma (cHL) is a cancer of the lymphatic tissue which is one of the most common lymphomas of the Western world. It affects B-lymphocytes (white blood cells) that in consequence completely change their appearance and functionality. The tumor cells of cHL called Reed–Sternberg cells are giant cells with multiple nuclei. The cHL shows high prevalence in adolescents and young adults. Main symptoms of this neoplasm are mainly fevers, drenching sweats, unexplained weight loss. The genetic causes are not fully known, however it's believed that infections of viruses such as HIV and EBV, organ transplantation and positive history of autoimmune conditions may be responsible for increased incidence of cHL. Despite the availability of efficient therapy of cHL the molecular background of this neoplasm, especially epigenetics, still remains enigmatical.

Aim of the project

The aim of our project is to expand the knowledge on genetic and epigenetic background of cHL. We focus on non-coding regions of the genome. These regions usually contain promoters and transcription factor binding sites which are crucial for proper gene expression. Any genetic variants present in such regions may lead to changed expression of the genes involved in pathogenesis of cHL. Our goal is to identify such variants and describe a novel mechanism of genes deregulation important in cHL development.

The description of the research

We have previously performed several high-throughput experiments which allow us to detect regulatory region harbouring variants potentially important in cHL. Furthermore we plan to confirm our preliminary results with use of commonly known experimental methods such as Sanger sequencing. Next, we intend to establish the alternative mechanism of altered gene expression as hipermethylation of abovementioned regions using pyrosequencing. Finally we would like to validate the potential influence of the identified variants by using functional analysis (reporter assays).

The reason of undertaken research

The epigenetic background of cHL is not fully understood yet. The potential influence of alterations in regulatory regions in the context of cHL still remain elusive. We intend to fill the existing gap of knowledge.

Expected impact and effects of the research

Our research will allow better understanding of the epigenetic background of cHL by indication of alterations in regulatory regions of this neoplasm. As a consequence, our research may facilitate the discovery of diagnostic biomarkers and targets for novel therapy of this lymphoma.