TITLE: The role of PRDM-family transcription factors in the development and progression of different types of acute leukaemia	
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Summary: Leukaemia is a type of blood disorder, which on cellular level it is represented by abnormal, underdeveloped blood cells (blasts). It originates in the bone marrow where a combination of genetic and environmental factors impairs the hematopoietic stem cells differentiation, leading to their transformation into leukaemia cells. Acute leukaemia (AL) is the rapid increase of these abnormal cells that leads to their quick accumulation and the need for timely and intensive treatment. A lot of efforts have been applied to reveal the genetic basis for this disorder and some progress has been made. The most common reasons for leukaemia development are chromosomal errors and gene mutations. Altered DNA sequence or signal transducers, chromatin modifiers (CM), transcription factors, splicing factors, and cohesion complexes are directly or indirectly involved in the disease pathogenesis. Among them, the class of CMs are of particular interest since by altering the chromatin state, they change the expression of other factors in leukaemia, they are frequently mutated in cancers and could be attractive drug targets. Underexplored concerning leukaemia are the CMs belonging to the family of PRDM transcription factors, which comprises about 20 members. Their function is context-dependent, and the same member may have an antagonistic action based on its type of protein interactions. Though there are studies about the role of the PRDM factors in tumorigenesis, less is known about their impact on AL. We propose to make a complete screening of samples from AL patients and healthy donors of the PRDM mRNA, check the expression levels and sequence them. The factors that are up- or downregulated will be analysed at the protein level using immunofluorescence microscopy to determine their cellular localisation, expression, and protein interactions. Finding the potential role of PRDMs in AL would contribute to a profound understanding of the disease, which is required to improve the prognosis of AL.

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