Abstract

Blood cancers are caused by the accumulation of mutations in haematopoietic stem cells. This creates a malignant clone that has a selection advantage due to improved survival and unrestricted proliferation, a process of leukaemia development called leukemogenesis. Leukemogenesis is a complex process and it is difficult to identify a single mutation that is responsible for the transformation of haematopoietic cells. In addition to transcriptional deregulation caused by oncogenic fusion proteins, mutations in specific genes that regulate critical signaling pathways play a critical role in leukemogenesis. Examples of such genes include mutations in the isocitrate dehydrogenase 1 and 2 genes (*mutIDH1/2*). These genes are thought to play an important role in the development of leukaemia, as indicated by their increasing frequency in the progression of myelodysplastic syndrome to acute myeloid leukaemia. The functions of *mutIDH1/*2 include epigenetic regulation, changes in metabolism and redox homeostasis. It has been shown that regulation of reactive oxygen species (ROS) production and elimination, so-called redox homeostasis, is important for the proper function of haematopoietic stem cells and its disruption is a frequent phenomenon accompanying malignant transformation of these cells. Some mutations, including mutIDH1/2, affect the production and elimination of ROS and thus disrupt redox homeostasis. As a result, redox cascades are affected through protein modifications that contribute to leukemogenesis. The consequences of these changes include unrestricted proliferation and impaired differentiation of haematopoietic stem cells. The aim of this study is to describe the redox metabolism aspect of mutIDH1/2 in leukemogenesis.