Abstract

Chronic lymphocytic leukemia (CLL) represents the most prevalent leukemia in Europe and USA. CLL affects predominatly elderly people (median age, 70y). This lymphoproliferative disorder is characterised by an accumulation of mature B-cells in the peripheral blood, bone marrow and lymph nodes. The lifespan of CLL cells is longer than normal healthy B-cells due to impaired cell cycle and apoptosis. CLL cells dysplay several chromosomal aberations and genetic abnormalities. The next generation sequencing revealed many somatic mutations in CLL cells. Analysis of these somatic mutations in CLL facilitates detail understanding at the disease molecular basis and opens new possibilities to the personalised therapy.

The main aim of this thesis is brief description of CLL as disease and to summarise the recent knowledge in the field of next generation sequencing with attention to CLL.