At present, more than 20% of total cultivated lands and 33% of irrigated agricultural land is estimated to be affected by salinity, worldwide. This problem is increasing with the rapid climate changes and the excess use of irrigation water. Salinity is one of the most destructive abiotic stresses which severely affects the agricultural productivity. It is estimated that by the 2050, more than 50% of the arable land will be contaminated by the excess of salt. Dependent on the rate of salt accumulation in the soil, either the salt stress or the salt shock may occur. The former results from the gradual increase in salt levels. The latter is caused by instant exposure to a high level of salinity. Salt shock rarely occurs in either agricultural practice or in natural ecosystems because salt concentration in soils usually increases gradually. Plant's response to adverse conditions requires profound reprogramming of the metabolic pathways. These changes are controlled by a complex network of signaling pathways incorporating transcellular membrane sensors, Ca^{2+} channels and Ca^{2+}-binding proteins, histidine kinases, G-protein-coupled receptors and other signaling molecules. Resulting alterations involve the onset of processes triggering the acclimation to environmental challenge. Concurrently, numerous processes, which are not mandatory for survival, are silenced, to save energy resources for coping with stress. Because these changes are largely due to the transcriptional up- or down-regulation of specific groups of genes, it is of utmost importance to identify the chief regulators which orchestrate the change in gene expression under stress. This role is played by transcription factors (TFs) since most of them are encoded by early stress-responsive genes and control the expression of a set of downstream target genes. Identifying the stress-dependent TFs in crops, opens the way for their application for stress tolerance improvement in plants. In the course of the recent studies on the salt-induced gene expression patterns in beet leaves, we found that the gene encoding the transcription factor bHLH137 as strongly up-regulated by salt treatments in leaves of sugar beet and its wild ancestor, the see beet (*Beta maritima*). The TF was transcriptionally up-regulated by salt, irrespective of the mode of salt treatment (salt stress *vs* salt shock) and on dose-dependent manner. Furthermore, the bHLH137 was the sole salt upregulated TF, identified in our study. These findings rise the idea that the bHLH137 plays a prominent role in the regulation of transcriptomic response to salt in beets. Consequently, the purpose of the present study is to assess the role of bHLH137 in the control of gene expression during response to salinity in beets and its involvement in salt tolerance in sugar beet and its wild ancestor, the sea beet. The purpose of the study is to assess the role of bHLH137 in salt tolerance. In order to meet this goal, the stable transformants, either constitutively overexpressing bHLH137 or the ones with silenced expression of this transcription factor will be generated. We hypothesize, that if the TF is important for salt tolerance trait in beets, the silencing of the bHLH137 expression would reduce plant performance under salt treatment. In parallel, it will be tested whether the bHLH137-overexpressing plants display increased salt tolerance. Assessment of acclimatization to stress will be accompanied by transcriptomic and epigenetic analyzes. The results of the study will clarify the role of bHLH137 in salt tolerance in beets. If it turns out, that the salt tolerance in beets may be manipulated by altering the expression of bHLH137, an efficient way of breeding sugar beet varieties with higher salinity tolerance would become available.