

## **Abstract**

Members of the AHL (AT-hook motif nuclear-localized) gene family have been found in all sequenced plant land species, hence a link between divergence of AHL genes and colonization of terrestrial environments by plants is assumed. One of the adaptations of plants to the terrestrial environment was the development of a root system. Currently there is only a few information about the possible function of AHL genes in root system establishment and development. A typical characteristic of AHL genes is the presence of an AT-hook motif and a highly conserved PPC domain. Many studies have confirmed the involvement of AHL genes in a wide range of plant processes. They are potentially strong regulators of transcription at different levels. They function as transcription factors, interact with other transcription factors through the PPC domain, and are capable of chromatin remodeling through histone modifications.

We selected candidate genes based on publicly available transcriptomic data: AHL18, AHL19, AHL20, AHL21, AHL22, AHL23, AHL27, and AHL28 with predicted function in root formation and development. The first aim of this thesis was to investigate possible involvement of AHL genes in lateral root development. For AHL19, AHL20, AHL21, AHL23, AHL27, and AHL28, we examined transcription rates at the root tip and at different stages of the developing primordia. Based on the results obtained, we choose the gene with the highest transcription intensity in the primordia for further experiments. In the second part, we focused on the effect of modulation of AHL20 gene expression on lateral root development.