Summary

Cytokinins (CKs) are important group of plant hormones involved in a wide range of physiological and developmental processes. Endogenous levels of CKs as well as proportions of individual CK forms and derivatives are not constant and differ among plant species. The amounts of biological active CK forms (free bases and ribosides) are regulated through tangled machinery of metabolic conversions including biosynthesis, conjugation and degradation pathways. The main object of this thesis was to characterize the metabolic pathways involved in the regulation of bioactive CK levels in plants especially *via* CK biosynthesis with aspect to the environmental stimuli and *via N*-glucosylation pathway.

It was shown, that light signal is an important input for modulating some CK-related genes and CK levels in Arabidopsis plants. The complex diurnal expression profiles of CK-biosynthetic genes (*AtIPT1* – *AtIPT9*) in Arabidopsis plants indicated a strong dependence of *AtIPT1* and *AtIPT5* on light/dark phase in leaf rossetes. In contrast, no diurnal oscillation of *AtIPT* transcript levels was recorded in roots. Although the content of endogenous CKs was not constant in plants and varied during a day, no statistically significant correlation between light/dark cycle and oscillation in CK levels was revealed in shoots as well as in roots. Using Arabidopsis photoreceptor mutants with disrupted perception of red (*phyAphyB*) and blue (*cry1cry2*) light, it was demonstrated that blue light affects transcript abundance of *AtIPT1* and *AtIPT5* in higher extent than red light. Subsequently, characterization of two tomato biosynthetic genes, *SlIPT3* and *SlIPT4* in response to salt stress showed a strong repression in tomato roots, and different transcripts abundance in young and old leaves after salt stress treatment. Tight connection of *SlIPT3* and *SlIPT4* with regulation of CK feedback mechanism was demonstrated after *trans*-zeatin application. Moreover, *SlIPT3* overexpression in tomato resulted in an altered phenotype, high accumulation of CK-*N*-glucosides (especially N^6-(Δ^2-isopentenyl)adenine 7-glucoside), modifications of CK biosynthesis-, signaling- and degradation-gene expression and enhanced tolerance to salinity. Based on these results the hypothetical scheme of *SlIPT3* and *SlIPT4* action during early salt stress has been proposed. It was also shown that CK-*N*7- and *N*9-glucosides display some biological activity *per se* in bioassays suggesting that *N*-glucosylation pathway is not necessarily the final step in bioactive CK inactivation. From evolutionary point of view it is demonstrated that other mechanisms controlling bioactive CK levels and differing from higher plants might exist in cyanobacteria and algae to substitute a substantially suppressed or even missing CK-*N*-glucosyltransferase and CKX catalysing CK metabolic pathways. It is therefore evident that the current knowledge concerning regulation of bioactive CK levels in plants *via N*-glucosylation needs to be reconsidered and expanded.