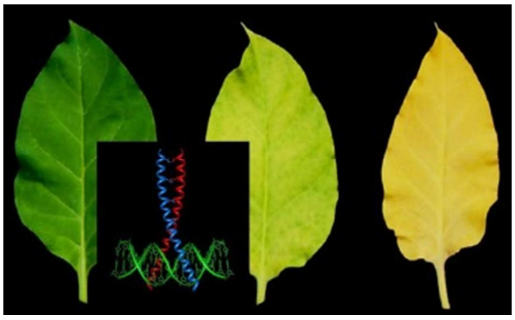
Plant basic region/leucine zipper (bZIP) transcription factors, stress and sugar



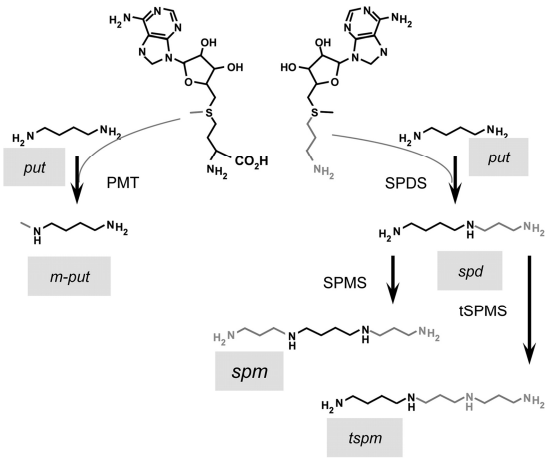
Transcription factors play crucial roles in all biological processes which are based on differential gene expression. Structurally, transcription factors are usually classified by their DNA-binding domains: basic region/leucine zipper (bZIP) transcription factors have a basic region which binds to DNA and a leucine zipper motif for dimerization. Proteins of the bZIP-type are present in all eukaryotic organisms analysed to date. In *A. thaliana*, there are 75 members of the bZIP protein family. These are divided into ten subgroups on the basis of the length of the peptides, common motifs, and the position of the bZIP domain, among other criteria (Jakoby et al. 2002).

Within the bZIP gene family of transcription factors in plants, we characterised a subfamily which codes for the shortest bZIP proteins of 140-150 amino acids in length. This subfamily, which can be categorised into the group S of *A. thaliana* bZIP-proteins, was named lip19-subfamily because the first member has initially been described as cDNA clone number 19 coding for a low-temperature induced protein from rice. We found that the expression of members of the lip19-subfamily from rice, maize, *Arabidopsis* and tobacco is induced during the process of leaf senescence and by abiotic stress conditions. Interestingly the transcripts of these small bZIPs contain long untranslated regions at their 5´-ends (5´-UTRs). These are involved in the expression regulation of the mRNAs through the sugar sucrose. The process is called Sucrose Induced Repression of Translation (SIRT).

Currently the regulation of expression of the lip19-subfamily of bZIPs on posttranscriptional level and the target genes of these transcription factors are investigated by transgenic techniques. We could show that the transgenic expression of the bZIP cDNA with deleted uORF escapes the control of SIRT and eventually leads to enhanced sugar levels in tobacco leaves and tomato fruits.

Cooperation with Prof. T. Kusano at Tohoku-University, Sendai, Japan.

Polyamines in plant adaptation to environmental stress

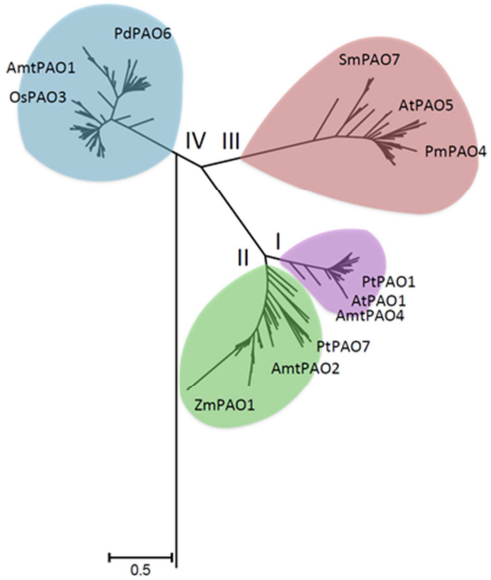


Polyamines (PAs) are low molecular weight, aliphatic polycations found in the cells of all living organisms. Due to their positive charges, polyamines bind to macromolecules such as DNA, RNA, and proteins. They are involved in diverse processes, including regulation of gene expression, translation, cell proliferation, modulation of cell signalling, and membrane stabilization. They also modulate the activities of certain sets of ion channels. Because of these multifaceted functions, the homeostasis of polyamines is crucial and is ensured through regulation of biosynthesis, catabolism, and transport.

Obviously polyamines are essential for growth and survival. In plants, diamine putrescine, triamine spermidine and tetraamines spermine and thermospermine are the most abundant polyamines. Spermine is not essential for normal growth and development as displayed by normal growth of an Arabidopsis mutant plant that does not produce spermine. However, this mutant was hypersensitive to high salinity and drought stresses suggesting a role of spermine in these stress responses. Indeed exogenously applied spermine could rescue the mutant plant from the stresses by means of inducibility of certain stress-responsive genes.

Besides the function of spermine in abiotic stress responses, we proposed that a spermine-mediated signal transduction pathway is involved in the hypersensitive response (HR) induced by tobacco mosaic virus (TMV) in tobacco plants. Regulatory components of this pathway, such as a Cys2/His2 type zinc-finger protein have been identified. Our research focuses on the detailed analysis of the signaling pathways in which PAs are involved and how the pathways contribute to abiotic and biotic stress responses.

Evolution of the polyamine synthesis and catabolic pathways in plants



The biosynthesis pathway of polyamines in plants is well understood and the genes involved are identified. Recently this has also been uncovered for the catabolic pathway. We showed that the catabolic enzymes polyamine oxidases (PAO) differ in their cellular localization, their pH optima and in their substrate specificity. Especially the class of enzymes represented by Arabidopsis PAO5 (AtPAO5) was shown to be specific to thermospermine (T-Spm) rather than spermine. Furthermore, a balanced level of T-Spm was shown to be necessary for proper development of the vascular system in plants. Phylogenetic analysis revealed that PAOs from vascular plants are classified into four clades (I-IV) and that the class of AtPAO5-related proteins form a distinct clade (III) which lacks in non-vascular plants. The clade III members, which function as T-Spm oxidase in Arabidopsis and rice, are most closely related to animal PAOs. Furthermore, PAO genes in clades I, II and IV usually contain 7 to 9 introns, whereas the clade III genes are intron-less or contain a single intron, suggesting the occurrence of a horizontal gene transfer of ancestral clade III polyamine oxidase gene(s) from primitive animals. Currently we try to confirm this hypothesis and further investigate the phylogenetic origin of enzymes involved in PA metabolism.

Cooperation with Prof. T. Kusano at Tohoku-University, Sendai, Japan.