D14 Transgenic 14-3-3 isoforms in plants
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The 14-3-3s constitute a family of highly homologous proteins, first discovered in brain tissue and now thought to be present in all eukaryotic cells. They are modulators of enzyme activities. They mediate in the formation of protein complexes involved in signal transduction and the subcellular location of proteins. Six 14-3-3 full-size DNAs from potato plant have been cloned and sequenced, and their high sequence homology established. All the isoforms are present in each analysed tissue. However, the level of a given isoform strongly varied dependent on plant age and the tissue investigated. The antisense plants shows a decrease in tuber number and an increase in tuber size and lose chlorophyll faster during their growth than the control plants. The plants were analysed for enzyme activities and metabolite levels. Sucrose phosphate synthase and nitratereductase were the most highly affected of the enzymes measured in transgenic tubers and leaves, respectively.

In in vitro experiments these enzymes were also significantly affected by 14-3-3 proteins. Thus the results obtained are consistent with those from transgenic plants analysis and the in vitro data can be directly transferred to in vivo situation.

Of many measured in transgenic tuber metabolites the significant increase in sucrose, starch, aspartic and glutamic acids, glutamine, malic and citric acids was detected which suggest the potential role of 14-3-3 in TCA cycle regulation.

D15 Phosphorylation-independent interaction between 14-3-3 protein and the plant plasma membrane H⁺-ATPase
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A large number of proteins interact with and seems to be regulated by 14-3-3 proteins. Among primary transport systems, IgF₁-ATP synthase and plant P-type H⁺-ATPase are inhibited and activated, respectively. The mechanism by which 14-3-3 proteins bind to their targets has been extensively studied. In most cases, 14-3-3 protein targets contain a common interacting epitope involving a phosphothreonine motif: R-S-x-pS-x-P. However, epitopes distant from the phosphosine motif have been examined. One such example is the plant plasma membrane H⁺-ATPase AHA2. Here 14-3-3 interacts with a phosphothreonine motif H-Y-pT-V in the extreme C-terminal end of the H⁺-ATPase molecule. Phosphorylation-independent binding of 14-3-3 protein to the H⁺-Y-T-V motif can be induced by the fungal phytotoxin fusicoccin. The molecular basis for the phosphorylation-independent interaction between 14-3-3 and H⁺-ATPase in the presence of fusicoccin has been investigated. Fusicoccin binds to a heterodimeric receptor that involves 14-3-3 protein and H⁺-ATPase. Binding of fusicoccin is independent on the phosphorylation status of the H⁺-ATPase and requires residues further upstream of the H⁺-Y-T-V motif.

Apparently, 14-3-3 protein interacts with the unusual epitope in H⁺-ATPase via its conserved amphipatic groove. This implies that diverse epitopes bind to a common structure in the 14-3-3 protein.

D16 Plants call 14-3-3 for transport assistance
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Turgor pressure is a cellular parameter, important for a range of physiological processes in plants, like cell elongation, gas exchange and gravitropic/phototropic bending. Regulation of turgor pressure involves ion and water transport at the expense of metabolic energy (ATP). The primary pump in the plasma membrane (the H⁺-ATPase) is a key player in turgor regulation since it provides the driving force for ion uptake (followed water influx through osmosis). Using the phytotoxin fusicoccin (a well known activator of the ATPase) as a tool, 14-3-3 proteins were identified as regulators of the H⁺-ATPase. Since fusicoccin has a dramatic effect on K⁺ accumulation and cellular respiration as well, we studied whether 14-3-3 proteins play a role in the regulation of the mitochondrial FoF₁-ATP synthase and ion channels in the vacuolar and plasma membrane. Besides the plasma membrane H⁺-ATPase, we have identified thus far at least four other transport proteins that are regulated by 14-3-3 proteins. The mechanism of regulation will be described and the possibility that 14-3-3 proteins act as coordinators of ion transporters with varied but interdependent functions will be discussed.

E1 X-ray crystallographic studies of IgG-FcγR interactions
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Human Fc receptors (FcγRs) for the Fc portion of immunoglobulin G are major mediators of the adaptive immune response. Crystal structures of their extracellular domains were recently solved and showed that they obey a common fold resulting in a heart shaped structure. Together with the multifunctional Fc fragment whose structure was already deciphered in the 1970s, the complex of a FcγR with Fc could recently be crystallised. Its crystal structure indicates that despite the dimeric character of the Fc fragment, only one FcγR can bind to Fc due to an introduced asymmetry within the homodimeric Fc, as well as by binding to symmetrically related residues of both Fc chains. Homology modelling suggested that the other FcγRs bind the Fc in a similar manner. The resolved complex structure can be regarded as a paradigm for immunoglobulin binding to Fc receptors and serves as a solid base for the design of compounds interfering with complex formation. Such molecules would be of invaluable benefit for the therapy of immunological disorders.