

Summary

In plants, members of gene families differ in function and mode of regulation. Fine-tuning of the expression of individual genes helps plants to cope with a variable environment. Genes encoding proline dehydrogenase (*PDH*), the key enzyme in proline degradation, and the proline biosynthetic enzyme, Δ^1 -pyrroline-5-carboxylate synthetase (*P5CS*), play an important role in responses to osmotic and drought stresses. We have compared the expression patterns of three *PDH* and two putative *P5CS* genes during drought stress progression and subsequent recovery. Whereas the *NtPDH1* gene was little affected by dehydration or rehydration, the *NtPDH2* gene responded rapidly to both conditions, being down-regulated under drought. The *CIG1* gene, encoding cytokinin-inducible PDH, exhibited an intermediate transcription pattern. The *P5CS A* gene was highly up-regulated during drought stress. *CIG1* and *NtPDH1* transcription was not activated and *P5CS A* was only partially reduced in leaves within 24-h after rehydration, a re-watering period sufficient for large physiological changes to occur. The lack of activation of tobacco *PDH* genes and incomplete reduction of the *P5CS A* gene in leaves within 24-h of rehydration may reflect the need for the protection of chloroplasts against reactive oxygen species (ROS). The data indicate that recovery is a specific physiological process following different scenario in leaves and roots.