

Control Of The Potato Tuber Life-cycle

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Introduction

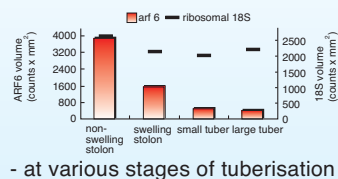
The manipulation of the potato tuber life cycle, in order to improve the timing of tuberisation, tuber-size distribution and dormancy characteristics is a major economic target. An understanding of the processes that lead to stop-start cycles in the growth of the potato tuber apical meristem is important to achieve this aim. ESTs representing genes that are up-regulated in the tuber apical bud

on dormancy release have been isolated. Our study focuses on the characterisation of two transcription factors: one encodes an auxin response factor whereas the other contains sequence encoding a recently defined TCP domain, a motif found in proteins regulating growth and development.

Results

We have used suppression subtractive hybridisation to produce a library of genes up-regulated in the tuber apical bud on dormancy release. The sequences of cDNAs representing 385 different genes were determined.

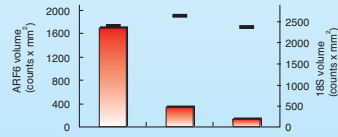
Semi-quantitative *ARF6* RT-PCR analyses.



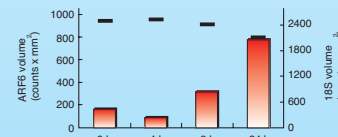
- at various stages of tuberisation



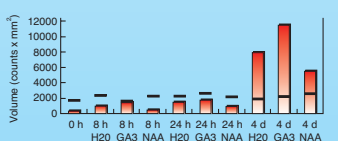
- in dormant and sprouting buds,



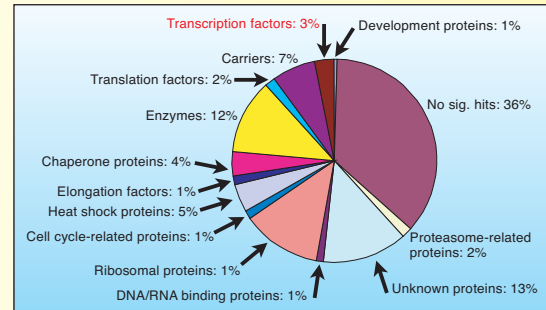
- in stem axillary buds (sprout system)



- on axillary meristem activation



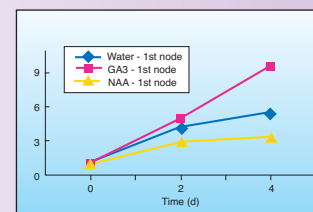
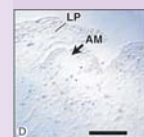
- in stem axillary buds treated or not with 10 M GA₃ or 10 M NAA during a 4 day time course



Auxin Response Factor6 (*ARF6*)

Bar graph and solid lines represent phosphoimager quantification of *ARF6*-specific/18S ribosomal RNA-specific RT-PCR products respectively

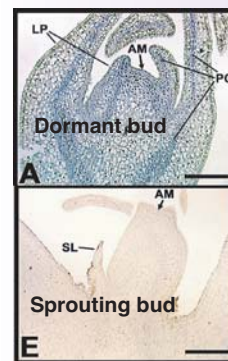
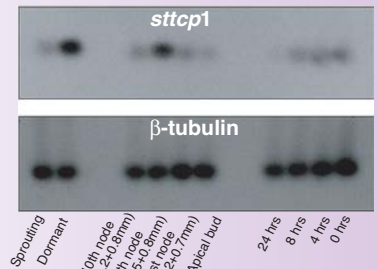
in situ hybridisations in tuber apical buds and adjacent tissues on dormancy release



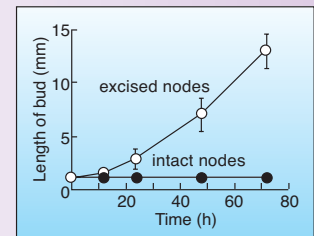
Rate of axillary bud outgrowth from the 1st node in etiolated potato sprouts

TCP domain transcription factor (*sttcp1*)

RT-PCR analysis of *sttcp1* RNA extracted from: sprouting buds, dormant buds, buds from the 10th, 5th, 1st nodes and apex of etiolated potato sprouts, and from the bud from the 5th node 24, 8, 4 and 0 hours after excision



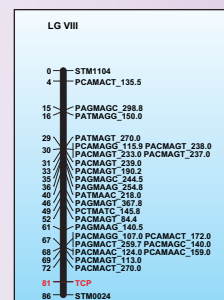
in situ hybridisations in tuber apical buds and adjacent tissues on dormancy release



Rate of axillary bud outgrowth from the 5th node in etiolated potato sprouts. Bud growth in excised nodal sections is compared with the rate of growth in the 5th node from intact plants



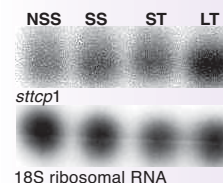
sprout system



sttcp1 maps on potato chromosome VIII

Conclusions

ARF6 and *sttcp1* transcript levels appeared to correlate with the rate of meristem growth during the potato tuber-life cycle. Whereas *ARF6* transcript level increases on meristem activation, *sttcp1* transcript level decreases. The data presented here clearly demonstrate that *ARF6* expression level is a marker for meristem activation status in potato. It will be interesting to see if similar results are found on bud activation in other species.



RT-PCR analysis of *sttcp1* RNA extracted from the different stages of tuberisation: non-swelling stolon, swelling stolon, small tuber and large tuber

Acknowledgements

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