Manipulation of isoprenoid metabolism in potato tubers: implications for nutritional quality and the potato tuber life-cycle

Laurence Ducreux[1], Wayne Morris[1], Paul Fraser[2], Christophe Lacomme[3], Steve Millam[3,4] and Mark Taylor[1]

1.Quality, Health and Nutrition and 3. Gene Expression, Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA, UK.

2. School of Biological Sciences, Royal Holloway, University of London, Egham, Surrey TW20 OEX, UK.

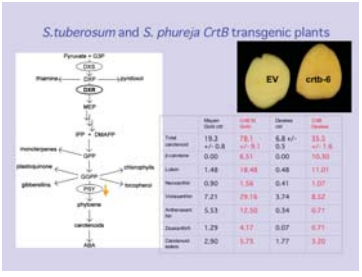
4. Current address: Daniel Rutherford Building, Institute of Molecular Plant Sciences, Kings Buildings, University of Edinburgh, Edinburgh, EH9 3JR.

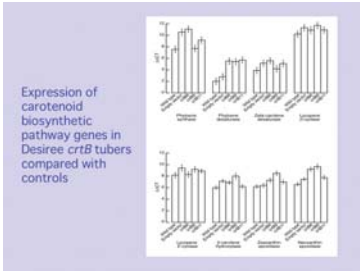
Introduction

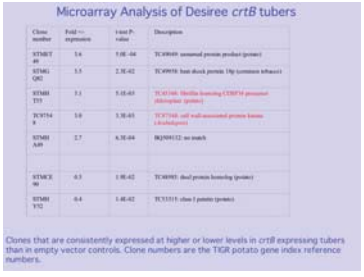
Using a metabolic engineering approach, we have attempted to perturb aspects of isoprenoid metabolism in potato tubers. Our aims are to determine the extent to which it is possible to enhance the accumulation of nutritionally important isoprenoids such as carotenoids, and to learn more about the integrated regulation of isoprenoid metabolism.

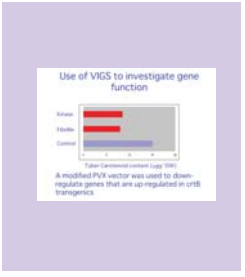
Development of a provitamin A containing potato

In one example we have produced transgenic potato plants expressing an *Erwinia uredovora crtB* gene encoding phytoene synthase, specifically in the tuber of *Solanum tuberosum* L. cultivar Desiree, which normally produces tubers of low carotenoid content and also in *Solanum phureja* L. DB337, which produces yellow-fleshed tubers of higher carotenoid content. Expression of the *crtB* gene resulted in significant increases in the contents of carotenoids with a particularly large increase in lutein and an accumulation of the provitamin A β-carotene, a carotenoid that is not normally detectable in potato tubers.



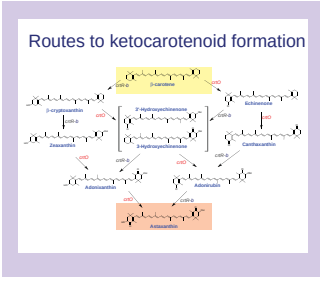


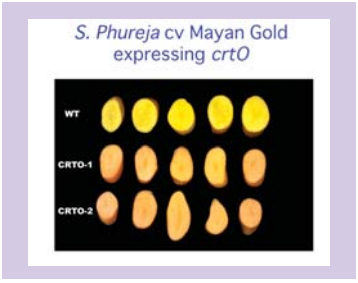


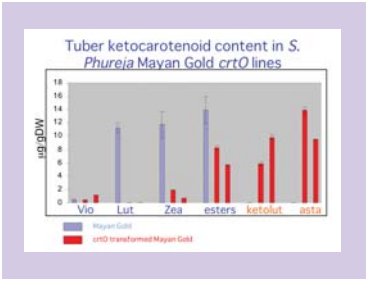


Ketocarotenoid accumulation in transgenic tubers

Increasingly, the health benefits associated with ketocarotenoid consumption are becoming apparent. Over-expression of an algal *crtO* gene encoding β-carotene-oxygenase results in the accumulation of astaxanthin and ketolutein in the tuber.

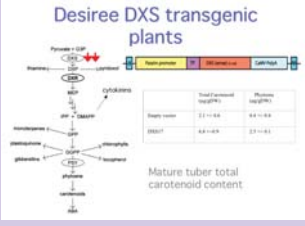


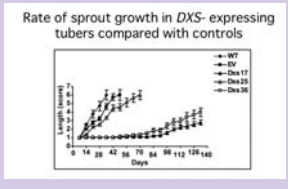


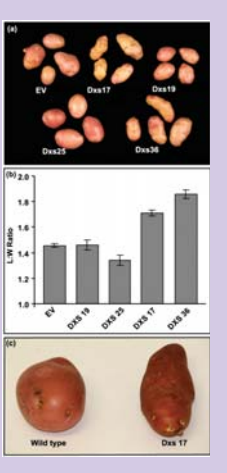


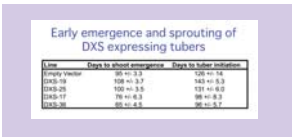
DXS over-expression effects tuber shape and severely reduces tuber dormancy

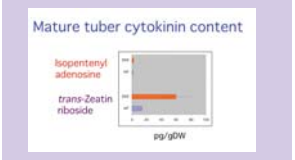
Perturbation of plastidic isoprenoids also has a drastic effect on the tuber life-cycle. Expression of a bacterial 1-deoxy-D-xylulose 5-phosphate synthase gene in the tuber plastid leads to modest changes in carotenoid levels, but a distinct tuber phenotype characterised by elongated tubers with greatly reduced bud dormancy – this phenotype reveals different phases in dormancy release and sprouting. Associated with DXS expression was a 4-fold increase in tuber cytokinin content.











Acknowledgements

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