Somatic embryogenesis in potato

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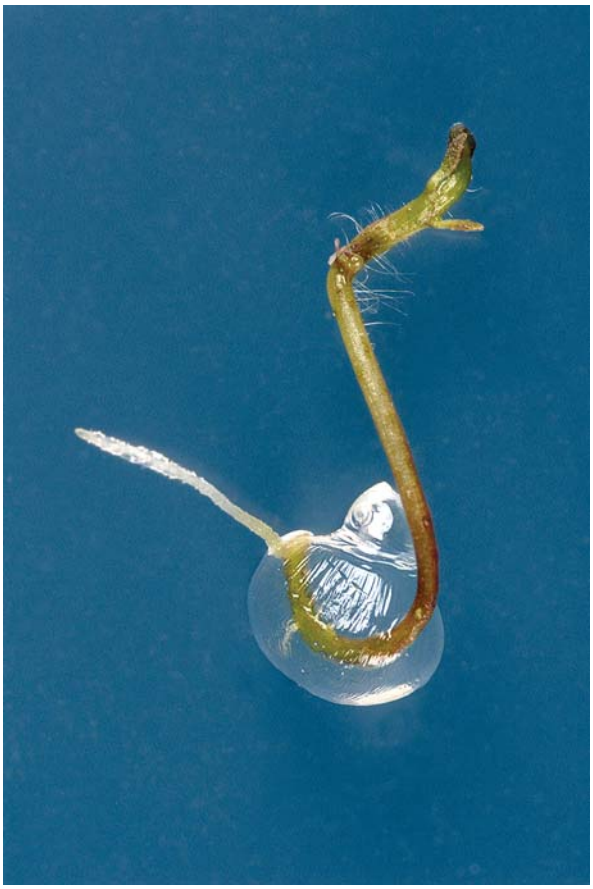
Potato, the world fourth most important food crop, is largely propagated via tubers from the previous crop. Tissue culture techniques, mainly micropropagation, have substantially augmented the supply of potato planting material, the demand for which is rapidly rising, driven by increasing markets in China and India and the development of specialist cultivars for the home market. Micropropagation can reduce the time required for the release of new cultivars from more than a decade to as little as three years and has a vital role in any plant breeding programme in the rapid bulking of advanced breeding material. Clonal *in vitro* propagation methods not only maintain crop uniformity, but also preserve health status as the planting material has reduced exposure to soil-borne and other diseases, principally viruses. We have recently developed an efficient somatic embryogenesis (SE) system for potato (Sharma & Millam 2004), which has considerable promise for rapid propagation of potato material. In this process tissue culture material is used to induce the formation of embryonic structures from callus tissue, by a series of manipulations of the growth conditions.

Despite the advantage of rapid propagation (up to 40 times faster in the early stages than micropropagation) one concern about SE, and indeed all clonal propagation methods, relates to the level of genetic stability of the material generated. It is of fundamental importance that micropropagated plants, irrespective of their development through either organogenesis or embryogenesis, remain 'true-to-parental' type. Potato is known to be subject to low levels of somaclonal variation, which can be due to both genetic and epigenetic causes. In our studies, Desiree plants obtained through different propagation routes (SE, axillary bud proliferation, microtubers) were evaluated for somaclonal variation using phenotypic, cytological and molecular (amplified fragment length polymorphism, AFLP) approaches. In our study, no phenotypic or cytological differences were observed. However, low levels of AFLP variation were seen for SE (0.66% bands polymorphic) and microtuber grown plants (0.44%), and intriguingly, this variation was only observed when AFLPs were performed using methylation sensitive restriction enzymes. This suggests a possible role for methylation in the generation of somaclonal variation,



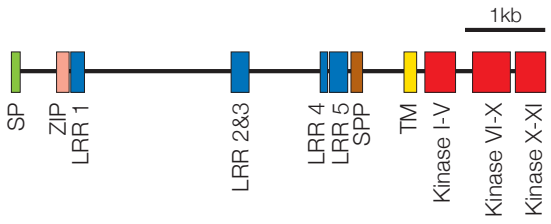


Figure 1 a. Photograph of germinating potato somatic embryo contained in sodium alginate bead.
b. Generalized structure of StSERK1, 'SP' denotes signal peptide, 'ZIP' Zip domain, 'LRR' Leucine Rich Repeats, 'SPP' Proline rich domain containing SPP (Ser-Pro-Pro) motif, 'TM' alanine-rich hydrophobic trans-membrane domain, 'Kinase' serine-threonine kinase domains.

although further detailed studies are required to investigate this phenomenon.

Another goal of our research has been to gain a better understanding of the molecular events taking place during SE. A primary objective has been the isolation of a potato orthologue of a class of gene known to play an important role in SE in other plants, such as Arabidopsis. We have cloned and characterised a *SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE* (*SERK*) gene from potato, using a range of molecular approaches. *SERK* genes have been shown to mark and enhance embryogenic competence in somatic cells of model plant species. Sequence analysis of *StSERK1* reveals very high levels of similarity to other plant *SERK*s, as well as a conserved intron/exon structure which is unique to members of this family. Monitoring of *StSERK1* expression during the progression of potato SE revealed increased expression during the 'induction' phase of SE, and we also observed up-regulation of *StSERK1* expression in somatic embryos. We believe that the *SERK* gene family may serve as a marker of tissue pluripotency, rather than embryogenesis in the strict sense (for further details see Sharma et al., 2008). A second elucidatory approach has been to monitor global gene expression changes during SE using a 10K spotted potato microarray developed at The Institute for Genomic Research (TIGR). Analysis of these data, still in progress, has identified a number of genes implicated in the molecular changes occurring during the establishment of SE, as well as several parallels with other plant SE systems. This integrated study is the first of its kind in potato embryogenesis and offers information for potential uptake in a wide range of crop improvement and basic research programmes.

References

Sharma, S.K., & Millam, S. 2004. Somatic embryogenesis in *Solanum tuberosum* L.: a histological examination of key developmental stages. *Plant Cell Reports* **23,** 115-119.

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