A study into the domestication of *Solanum centrale*, Australian bush tomato

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Summary

Solanum centrale L. the Australian bush tomato is a perennial, undershrub that is geographically restricted and a rare species. Mainly used as flavouring in value added products, this species is showing promise in both domestic and overseas markets. The supply of wild bush tomatoes is variable and hence unreliable. This has prompted the establishment of a number of commercial plantations in Australia to meet market demands.

The steps towards domestication covered by this study included improving methods of propagation, investigating the breeding system of the species and developing hybridisation techniques, investigating potential steroidal alkaloids in fruit, studying morphological and genetic diversity of *S. centrale* populations and identifying molecular markers for desirable traits. No serious domestication of *S. centrale* had taken place previously.

Vegetative methods of propagation were explored. Rooted cuttings with at least 90% survival rate were achieved with IBA at 3 000 and 8 000 ppm. A preliminary investigation of the reproductive biology of *S. centrale* with a view to artificial hybridisation was carried out. High levels of variability in the fertility of the plant were identified. This study indicated self-incompatibility and that this species can outcross under natural and artificial conditions. A controlled pollination method was developed.

The presence of steroidal alkaloids in the leaves and fruit was investigated. A number of methods of extraction and analysis were tested, confirming the presence of alkaloids in the immature fruit and leaves, but not in the mature fruit.

The pattern of morphological and genetic variability was investigated using plants grown from seeds collected from various wild populations found in natural habitats in Australia. Eight vegetative and floral characters were used with morphological data analysed using the hierarchical clustering method, unweighted pair group

arithmetic averaging (UPGMA) and the non-hierarchical ordination methods multidimensional scaling (MDS) and principal component analysis (PCA). The results for the population study of 100 individuals showed a high degree of morphological variation. For the study involving 10 isolated populations 10 clusters were produced each corresponding closely with the 10 different populations.

Diversity within the species was further investigated using RAPD-PCR, and analysed using hierarchical and non-hierarchical distance methods. Samples of DNA from individual plants were amplified with six different 10-mer primers to produce RAPD fragments. One hundred individual plants were selected and their DNA fingerprints compared. These were used to generate an UPGMA dendrogram based on similarity, an ordination derived by MDS and a minimum spanning tree (MST) to show the relative dissimilarities between the individuals tested.

The data subjected to MDS showed the presence of ten molecular clusters matching a dendrogram constructed using the simple matching coefficient with UPGMA clustering. The ten molecular clusters were significantly different. Each cluster consisted of the ten individuals from each of the populations investigated suggesting that there was a significant genetic differentiation between populations. The distribution of the clusters suggests that the gene flow and therefore pollination was localised within the populations.

For any crop species, the gains that can be made from selection depend to a large extent on the genetic variability of the population. The genetic similarities found between the 100 individuals from one population varied from 72% to 95%, confirming the existence of high genetic diversity in the gene pool. Two molecular clusters were identified, neither of which was significantly different indicating that random gene flow was a feature of this population.

A RAPD marker linked to non-prickliness was identified by bulked segregant analysis (BSA). To increase the utility of the RAPD marker for non-prickliness, it was converted to a sequence tagged site by developing primers specific for the sequence of the RAPD band. These primers were used to screen *S. centrale*

individuals for non-prickliness. This marker may facilitate the management of *S. centrale* breeding and selection for the bushfood industry, by providing an initial screening for non-prickliness.

This study contributed to the knowledge essential for further improvement of *Solanum centrale* as a commercial crop.