



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

Cassandra Collins

Candidate for the degree of
Doctor of Philosophy

University of Adelaide,
Department of Horticulture, Viticulture and
Oenology, Waite Campus

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TABLE OF CONTENTS

SUMMARY.....	6
DECLARATION AND AUTHORITY OF ACCESS TO COPYING.....	9
ACKNOWLEDGMENTS.....	10
LIST OF TABLES.....	11
LIST OF FIGURES.....	12
CHAPTER 1 GENERAL INTRODUCTION.....	16
1.1 AUSTRALIAN BUSHFOOD AND ITS COMMERCIAL POTENTIAL.....	17
1.2 THE FAMILY SOLANACEAE.....	20
1.3 THE GENUS <i>SOLANUM</i>	21
1.4 <i>SOLANUM CENTRALE</i>	22
1.5 PROJECT AIMS.....	25
CHAPTER 2 LITERATURE REVIEW.....	26
2.1 BUSH TOMATO PRODUCTION.....	26
2.1.1 <i>History and culinary uses of bush tomatoes</i>	26
2.1.2 <i>Cultivation, propagation and market considerations</i>	27
2.1.3 <i>Nutritional value</i>	28
2.2 DOMESTICATION.....	30
2.2.1 <i>Propagation</i>	31
2.3 ALKALOIDS AND STEROIDAL ALKALOIDS.....	31
2.3.1 <i>Alkaloids</i>	31
2.3.2 <i>Steroid alkaloids in Solanum</i>	32
2.3.3 <i>Common steroidal alkaloids</i>	34
2.3.4 <i>Toxicity of steroidal alkaloids</i>	35
2.3.4.1 <i>Factors affecting steroidal alkaloid toxicity</i>	35
2.3.4.2 <i>Symptoms of steroidal alkaloid poisoning</i>	36
2.3.5 <i>History of steroidal alkaloid extraction</i>	36
2.3.6 <i>Analysis of steroidal alkaloids</i>	37
2.4 FLORAL BIOLOGY.....	38
2.4.1 <i>Self-incompatibility</i>	39
2.4.2 <i>Pollination in Solanaceae and Solanum</i>	39
2.5 GENETIC MARKERS IN PLANTS.....	40
2.6 GENETIC DIVERSITY.....	41
2.6.1 <i>Molecular identification</i>	41
2.6.1.1 <i>Isozymes</i>	41
2.6.1.2 <i>DNA fingerprinting</i>	43
2.6.1.2 <i>RFLPs</i>	43
2.6.1.3 <i>PCR</i>	44
2.6.1.4 <i>AFLP</i>	45
2.6.1.5 <i>Microsatellites</i>	46
2.6.1.6 <i>RAPDs</i>	47

2.6.1.8	Marker Analysis	50
2.7	CONCLUSION	51
CHAPTER 3	PLANT MATERIAL	52
3.1	SOURCES OF PLANT MATERIAL.....	52
3.1.1	<i>Northern Territory</i>	52
3.1.1.1	Utopia Station.....	52
3.1.1.2	Alice Springs	56
3.1.1.2.1	Fresh material	56
3.1.1.2.2	Herbarium seed store material.....	56
3.1.2	<i>Western Australia</i>	60
3.2	WAITE CAMPUS PLANTATION	62
3.3	POTTED PLANTS	66
3.4	PESTS AND DISEASES OF <i>SOLANUM CENTRALE</i>	69
CHAPTER 4	PROPAGATION.....	73
4.1	INTRODUCTION	73
4.2	SEED GERMINATION.....	73
4.2.1	<i>Materials and methods</i>	74
4.2.2	<i>Results</i>	75
4.3	VEGETATIVE PROPAGATION	78
4.3.1	<i>Materials and methods</i>	78
4.3.2	<i>Results</i>	79
4.4	DISCUSSION.....	82
CHAPTER 5	INVESTIGATIONS INTO THE EXTRACTION AND MEASUREMENT OF STEROIDAL ALKALOIDS	83
5.1	INTRODUCTION	83
5.2	MATERIALS AND METHODS.....	83
5.2.1	<i>Extraction and clean up methods</i>	83
5.2.2	<i>Steroidalkaloid standards</i>	85
5.2.3	<i>Extraction analysis</i>	85
5.2.3.1	High performance liquid chromatography.....	85
5.2.3.2	Thin layer chromatography.....	86
5.3	RESULTS.....	86
5.3.1	<i>Extraction and clean-up methods</i>	86
5.3.2	<i>Steroidalkaloid standards</i>	86
5.3.3	<i>Extraction analysis</i>	86
5.3.3.1	High performance liquid chromatography.....	86
5.3.3.2	Thin layer chromatography.....	87
5.4	DISCUSSION.....	93
CHAPTER 6	INVESTIGATIONS OF BREEDING SYSTEM AND DEVELOPMENT OF HYBRIDISATION TECHNIQUES FOR <i>SOLANUM CENTRALE</i>.....	95
6.1	INTRODUCTION	95
6.2	REPRODUCTIVE BIOLOGY OF <i>SOLANUM CENTRALE</i>	95
6.3	MATERIALS AND METHODS.....	97
6.3.1	<i>Plant material</i>	97
6.3.2	<i>Sequence of floral development</i>	97
6.3.3	<i>Pollen viability</i>	97

6.3.4	<i>Timing of stigma receptivity</i>	97
6.3.5	<i>Techniques used for emasculation and pollen transfer</i>	98
6.3.6	<i>Compatibility</i>	102
6.4	RESULTS.....	102
6.4.1	<i>Sequence of floral development</i>	102
6.4.2	<i>Pollen Viability</i>	106
6.4.3	<i>Timing of stigma receptivity</i>	106
6.4.4	<i>Compatibility</i>	106
6.5	DISCUSSION.....	108
CHAPTER 7 MORPHOLOGICAL DIVERSITY		111
7.1	INTRODUCTION	111
7.2	MATERIALS AND METHODS.....	111
7.2.1	<i>Plant material</i>	111
7.2.2	<i>Morphological characters and measurements</i>	112
7.2.3	<i>Data analysis</i>	119
7.3	RESULTS.....	119
7.3.1	<i>Morphological variability within Utopia population</i>	119
7.3.2	<i>Morphological variability between ten Australian populations..</i>	125
7.4	DISCUSSION.....	131
7.4.1	<i>Morphological variability within Utopia population</i>	131
7.4.2	<i>Morphological variability between ten Australian populations..</i>	131
CHAPTER 8 GENETIC DIVERSITY OF POPULATIONS OF <i>S. CENTRALE</i>		134
8.1	INTRODUCTION	134
8.2	MATERIALS AND METHODS.....	135
8.2.1	<i>Plant material</i>	135
8.2.2	<i>DNA isolation</i>	135
8.2.3	<i>Polymerase chain reaction (PCR) technique</i>	136
8.2.4	<i>Agarose gel electrophoresis</i>	137
8.2.5	<i>Primer screening</i>	137
8.2.6	<i>Data analysis</i>	138
8.3	RESULTS.....	138
8.3.1	<i>Primer screening</i>	138
8.3.2	<i>Genetic variability within Utopia population</i>	141
8.3.3	<i>Genetic variability between ten Australian populations</i>	145
8.4	DISCUSSION.....	153
8.4.1	<i>Genetic variability within Utopia population</i>	153
8.4.2	<i>Genetic variability between ten Australian populations</i>	154
CHAPTER 9 GENETIC MARKER FOR NON-PRICKLINESS IN <i>S. CENTRALE</i>		156
9.1	INTRODUCTION	156
9.2	MATERIALS AND METHODS	159
9.2.1	<i>Plant material</i>	159
9.2.2	<i>DNA extraction</i>	159
9.2.3	<i>Preparation of bulked DNA samples</i>	159
9.2.4	<i>Screening primers</i>	159
9.2.5	<i>Confirmation of marker in progeny</i>	159
9.3	RESULTS.....	160
9.4	DISCUSSION.....	162

CHAPTER 10 SEQUENCE TAGGED SITE FOR THE RAPD MARKER LINKED TO NON-PRICKLINESS IN *S. CENTRALE*.....163

10.1 INTRODUCTION 163

10.2 MATERIALS AND METHODS 163

 10.2.1 *Isolation and purification of RAPD fragment* 163

 10.2.2 *Cloning and transformation of DNA* 164

 10.2.3 *Mini plasmid preparation*..... 165

 10.2.3 *Preparation of plasmid DNA for sequencing* 166

 10.2.4 *Design and analysis of sequence specific primers* 166

 10.2.5 *Test of sequence homology*..... 167

10.3 RESULTS 167

 10.3.1 *Isolation and purification of RAPD fragment* 167

 10.3.2 *RAPD fragment cloning and sequencing* 167

 10.3.3 *Sequence specific primers analysis* 167

 10.3.4 *Comparison of RAPD and STS sequences* 168

10.4 DISCUSSION 172

CHAPTER 11 GENERAL DISCUSSION174

REFERENCES179

APPENDIX.....205

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.