# **DISPERSAL AND GENETIC VARIABILITY OF** *Sonchus oleraceus* **L. IN RELATION TO ITS RESISTANCE TO ALS-INHIBITING HERBICIDES**

# **Robin. S. St John-Sweeting**

R.D.A., Grad.Dip.Ag., Master of Applied Science (Agriculture)

This thesis is submitted in fulfilment of the requirements

for the degree of

### **Doctor of Philosophy**

In the

Faculty of Sciences School of Agriculture, Food and Wine

**The University of Adelaide Waite Research Institute South Australia**

September, 2011

# **DISPERSAL AND GENETIC VARIABILITY OF**  *Sonchus oleraceus* **L. IN RELATION TO ITS RESISTANCE TO ALS-INHIBITING HERBICIDES**



*Sonchus oleraceus* **L. (common sowthistle) An annual weed with potential to distribute numerous wind borne seeds.**

> *" To win the secrets of a weed's plain heart." James Russell Lowell (Sonnet XXV).*

### **TABLE OF CONTENTS**



### **CHAPTER 1**

























# **Abstract**

The work described in this thesis investigates the existence and level of acetolactate synthase (ALS)-inhibiting herbicide resistance in *Sonchus oleraceus* in Australia. It further discusses the sensitivity of different *S. oleraceus* populations to different dose rate treatments of the ALS-inhibiting herbicide, chlorsulfuron. Thirdly the movement or not of the resistance gene between *S. oleraceus* plants. Gene movement is investigated in light of *S. oleraceus* being self pollinated and possessing a wind dispersed seed. Finally using molecular tools the genetic diversity and seed movement in *S. oleraceus* is investigated.

Although much is known about the evolution of plant based genetic resistance to herbicides there is less known as to the specific resistance gene movement in differing weed species.

The first approach undertaken in this study was to collect a broad spectrum of *S. oleraceus* seed from a number of Australian states and test the progeny from this seed for resistance to chlorsulfuron. Subsequent to this DNA extractions were made from *S. oleraceus* plant material for use in AFLP and sequencing techniques.

The results of this study indicate that ALS-inhibiting herbicide resistance to chlorsulfuron in *S. oleraceus* is now widespread in Australia. The movement of the resistance gene within populations is low (<4%), however, population dendrograms indicate seed has been dispersed across large distances in Australia facilitating the movement of the resistance gene. In addition sequence analysis indicates numerous independent mutation events. With the identification of previously unknown levels of resistance in Australia and gene movement knowledge, extension of improved management practises is possible.

# **Declaration**

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution to Robin St. John-Sweeting and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference is made in the text.

I give consent to this copy of my thesis when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

The author acknowledges that copyright of published works contained within this thesis (as listed below) resides with the copyright holder(s) of those works.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library catalogue, the Australasian Digital Theses Program (ADTP) and also through web search engines, unless permission has been granted by the University to restrict access for a period of time.

Robin St. John-Sweeting 22 September, 2011

# **Publications, Posters and Conference Proceedings**

### **Poster and one page paper at 15th Australian Weeds Conference, Adelaide.**

St. John-Sweeting, R.S., Preston, C., Baker, J., Walker, S. and Widderick, M. (2006) Herbicide resistant sowthistle (*Sonchus oleraceus* L.) in South Australia, northern New South Wales and Queensland. Proceedings of the 15<sup>th</sup> Australian Weed Conference, eds. C. Preston, J.H. Watts and N.D. Crossman, pp. 3-13. (Weed Society of South Australia, Adelaide).

#### **Poster judged in top 10 of 63 higher degree posters**

St. John-Sweeting, R.S., Preston, C., Baker, J., Walker, S. and Widderick, M. (2006) Gene movement in herbicide resistant sowthistle (*Sonchus oleraceus* L.). Proceedings of the 2007 Research Day, (University of Adelaide, Adelaide).

### **Presented 3 page paper at 16th Australian Weeds Conference, Cairns.**

St. John-Sweeting, R.S., Preston, C., Baker, J., Walker, S. and Widderick, M. (2008) Gene movement in herbicide resistant sowthistle (*Sonchus oleraceus* L.). Proceedings of the 16<sup>th</sup> Australian Weed Conference, eds. R.D. van Klinken, V.A. Osten, F.D. Panetta and J.C. Scanlan, pp. 113-115. (Weed Society of Queensland, Cairns).

#### **Poster**

St. John-Sweeting, R.S., Preston, C., Baker, J., Walker, S. and Widderick, M. (2008) Genetic Variability and Resistance of *Sonchus oleraceus* L.to Acetolactate Synthase– inhibiting herbicides. Proceedings of the 2008 Research Day, (University of Adelaide, Adelaide).

### **Presented 4 page paper at 17th Australasian Weeds Conference, Christchurch.**

St. John-Sweeting, R.S., Preston, C., Baker, J., Walker, S. and Widderick, M. (2010) Genetic diversity among ALS-inhibiting herbicide resistant and susceptible populations of Sonchus oleraceus L. (sowthistle) in Australia. Proceedings of the 17<sup>th</sup> Australasian Weed Conference, Christchurch New Zealand, eds. S. and R. Zydenbos, pp. 281-284. (New Zealand Plant Protection Society (Inc) ).

## **Acknowledgements**

I am grateful for the financial support for this project supplied by the Cooperative Research Centre for Australian Weed Management and the University of Adelaide.

This support made it possible for me to travel widely to achieve my project aims, attend educational workshops and attend the 16<sup>th</sup> Australian Weeds Conference in Cairns, Australia to present a paper entitled "Gene movement in herbicide resistant sowthistle (*Sonchus oleraceus* L.)". Thanks to Dr. Richard Groves for his support and kind words of encouragement at the commencement of my PhD.

 I express my sincere thanks to my principal supervisor Associate Professor Dr. Christopher Preston of the University of Adelaide who provided me with invaluable guidance, encouragement, support and discussions throughout this study. His kind arrangements of visits to the Queensland Department of Primary Industry and a number of educational workshops significantly enhanced my work.

 My sincere appreciation to Dr Jeanine Baker of the Weeds and Pest Animal Section, Sustainable Resources Management Division, Department of Agriculture, Fisheries and Forestry, Canberra, Australia who guided me through my molecular biological and population genetics disciplines. Her patience and great support throughout all aspects of my study is gratefully acknowledged. I am indebted to her agreeing to continue to supervise my work after her new appointment in Canberra in the latter years of my study.

 My sincere appreciation goes to my co-supervisors based in Toowoomba with the Queensland Primary Industries, Dr. Steve Walker and Dr. Michael Widderick who facilitated my travels through the Queensland Darling Downs and northern New South Wales on seed collecting expeditions. I gratefully acknowledge their guidance in my research, their critical input into publications and thesis and their continuing interest throughout the course of my study. Thanks to Geoff Robinson for guidance and assistance in my first seed collecting expedition through the Darling Downs and northern New South Wales.

 Special thanks to the staff of Weed Science group, Dr. Peter Boutsalis, Dr. Angela Wakelin, Dr Fleur Dolman, Dr Jenna Malone, Sarah Morran and Patrick Krolikowski for their friendship comments and criticism during discussions for making the lab an interesting dynamic and pleasant place to work.

 Professor Stephen Powles, Director of the Western Australian Herbicide Resistance Institute, University of Western Australia for critical discussions and suggestions which enhanced my work.

 Dr. Anita Juen, of the Institute of Ecology Technikerstr. 13 6020 Innsbruck, Austria, for her critical discussion and molecular problem solving suggestions.

Angelica Jermakow CSIRO for Technical Assistance with AFLP analysis.

 Thanks to Dr. Julian Taylor for his assistance with computer operations, biometry and statistical analysis.

 My appreciation to Janine Guy and Zoe Goodhand for their enthusiastic and precise and valuable work with seed biological work, plant culture and assistance with gene band scoring.

 I am grateful to David Cooke of the South Australian Department of Water, Land, Biodiversity and Conservation for support and assistance with plant taxonomy and to Roseworthy Farm Manager, John Matheson for assistance with field records and field work at Roseworthy Agricultural College.

 I am extremely grateful to the staff of the Australian Genome Research Facility, Plant Genomics Centre, Urrbrae, particularly Dr. John Stephen and Nicole Burtt.

 Library research was possible with the co-operation of the staff of the Roseworthy, Woolhouse and Barr Smith libraries.

 I am grateful to the postdoctoral, my fellow postgraduate and honours students, Kieren Arthur, Stephen Coventry, Amanda Benger, Jason Emms, Kelly Bailey, Alice Yi Quing Lu, Anh Vu, Arezou Yazarlou, Ben Fleet, Cathryn Todd, Ellena King, Bonny Vogelzang, Mahammed Mohamed Aman and Deborah Blackman.

 Thanks to Kueh Kiong Hook and Yazid Bostamam and Asmah Salowi from Bornio, Malaysia for their friendship, interesting discussions and support.

 Thanks to my family and friends for their ongoing support and special thanks to my father and mother and my children Kellie, Caren and Andrew (deceased).

 Finally I am grateful to those who may have been inadvertently omitted who gave of their time and information.

# **Abbreviations**



# **List of Figures**



# **List of Tables**



# **List of Plates**



# **Glossary of Terms**



#### **1 GENERAL INTRODUCTION**

#### **1.1 BACKGROUND**

*Sonchus oleraceus* L. (common sowthistle) is a weed of major importance of cropping areas in the northern grain region of Australia (NGRA). The species is a weed prominent in fallows, using moisture and interfering with crop harvest. It is also a weed of lesser importance in cropping systems in the southern and western grain growing regions. Competitive crops will greatly reduce *S. oleraceus* weed biomass and potential weed seed production and, when effectively managed, this weed has minimal effect on the farming enterprise (Widderick 2002). However, in the last two decades, numerous populations of *S. oleraceus* in southern Queensland have evolved resistance to acetolactate synthase (ALS) inhibiting herbicides, such as chlorsulfuron and metsulfuron-methyl. There is a risk of more weeds evolving resistance to ALS-inhibiting herbicides in winter rotations where these herbicides are used intensively (Walker *et al.,* 2005b). The evolution of ALS-inhibiting herbicide resistance complicates management of this weed. Herbicide resistance threatens the efficiency and profitability of agricultural enterprises both nationally and worldwide. General principles and strategies have now been developed and applied to avoid the increasing development of herbicide resistance in weeds.

The Weed Science Society of America, after considering the influence of weed resistance in Australia, emphasised that it is imperative that research continues into weed resistance and management (Hall *et al.,* 2000). Corbett and Tardif (2006); Tranel and Wright (2002) highlight that ALS-inhibiting herbicides have been used worldwide due to their high activity, selectivity and wide spectrum. Due to the intensive and persistent use of these herbicides over 100 weed species have been reported to have evolved resistance to ALS-inhibitors (Heap 2010). Little is known about the spread of ALS resistance by wind dispersed seed and an understanding of the evolution and dispersal of this resistance is likely to be helpful not only in managing *S. oleraceus*, but also managing resistance to other herbicides in self pollinated wind dispersed weeds.

#### **1.2 BIOLOGY AND ECOLOGY**

*S. oleraceus* is an erect annual winter herb that reproduces only by seed (Hutchinson *et al*. 1984). It is common in disturbed habitats and waste places and usually grows to a height of 400 to 700mm, but has been known to reach a height of 1500mm. Its tap root is unbranched and stems are hollow with alternate pinnately-lobed leaves with small auricles. The inflorescence is irregularly cymose-umbellate carrying a number of capitulum, each containing approximately 150 bisexual yellow florets (Hutchinson *et al*., 1984). The flower buds increase in size until maturity at which time the bud opens exposing the yellow composite florets. Each floret has one ovule with the stigma and style extending upward through a tube containing grains of pollen, at which time self pollination occurs (Lewin 1975). The flower opens only one morning then closes and stays closed for approximately one week while the seed achenes mature. After maturation, the seed head opens in the afternoon and the seed with pappus attached is dispersed by the wind. However, Widderick pers. comm. (2008) reports seed dispersal in the morning in Queensland when the temperatures are high enough. The seed has little to no innate dormancy and has an intermittent and prolonged emergence period (Widderick 2002).

#### **1.3 AIMS AND SCOPE OF THIS THESIS**

#### **1.3.1 INTRODUCTION**

This study will focus on genetic diversity, gene flow and spatial distribution of ALS-inhibiting herbicide resistance in *S. oleraceus*. With the aid of molecular genetic tools, this project will assess the type and level of genetic variation within and between *S. oleraceus* populations with an emphasis on herbicide resistant populations.

Agricultural production is reduced by competition with weeds. Agriculturalists have used numerous weed management control methods to reduce the competitive effect of weeds, such as herbicides (Gressel and Segal 1982; Hashem and Bowran 2001). The use of herbicides has resulted in large increases in agricultural production (Mathews 1994). These increases are threatened with the evolution of plant based genetic resistance to these herbicides. Interest in assessing this evolution in weeds has focused on genetic mutations, gene flow and the selection of resistance genes in plant populations (Messeguer *et al*., 2001; Knispel *et al.,* 2008). Gene flow can have an important role in disseminating resistance and can affect the level of resistance and the consequent impact on crop production (Ashigh *et al*., 2008). The first recorded biotype of *S. oleraceus* resistant to ALS inhibiting herbicides in Australia was found at Goondiwindi, Queensland in 1991 (Boutsalis and Powles 1995a). This poses the question of where else resistance occurs in Australia. In addition, it is unknown how or whether resistance is moving over the landscape. Also it is not known how much genetic variation is present in Australian populations of *S. oleraceus.* The project aims to assess the pattern of ALS-resistance gene movement and genetic diversity of *S. oleraceus,* with particular emphasis on plants with resistance to herbicides. Literature relating to the biology and ecology of *Sonchus oleraceus*, herbicide resistance, population genetics and the evolution of herbicide resistance and molecular genetics will be thoroughly reviewed in Chapter 2. The general methods, including seed collection are covered in Chapter 3.

#### **1.3.2 HERBICIDE RESISTANCE IN AUSTRALIAN** *S. oleraceus*

Chapter 4 aims to assess the distribution of resistance alleles from *S. oleraceus* local populations in Queensland, New South Wales, South Australia, Western Australia, Victoria and Tasmania. Seed collections from 1991 and 1998 to 2001 were used along with new seed collections from 2005 to 2008. DNA was extracted and preliminary investigations conducted prior to selection of the most suitable methodology. Seed was propagated and treated with the Group B sulfonylurea herbicide chlorsulfuron to determine whether resistance existed. A dose response experiment with chlorsulfuron was conducted to determine the sensitivity of a number of different *S. oleraceus* populations to different dose rate treatments.

#### **1.3.3 POLLEN MOVEMENT IN** *S. oleraceus*

Chapter 5 investigates whether gene flow can occur by pollen movement between plants in *S. oleraceus.* Individual resistant and susceptible plants were propagated and pollen movement experiments conducted. Plants were placed outside and allowed to flower and set seed naturally. The seed from the susceptible plants was collected and tested for herbicide resistance to assess whether resistance genes had moved to the susceptible plants in pollen.

#### **1.3.4 GENETIC DIVERSITY & GENE MOVEMENT IN** *S. oleraceus*

Chapters 6 and 7 investigate the genetic diversity of *S. oleraceus* with particular emphasis on plants with resistance to herbicides. Genomic DNA was extracted from collection samples and analysed using fluorescent amplified fragment length polymorphisms. Amplified bands or peaks were scored as present or absent and genetic relationships tested. Evidence of widespread seed movement or multiple *de novo* mutations events can be drawn from the finding of the same genotype at multiple locations.

The findings of the research will be brought together and are discussed in Chapter 8 which will also include implications of the research and future research priorities in this study area.

#### **2 LITERATURE REVIEW**

#### **2.1 INTRODUCTION**

This literature review briefly covers the biology of members of the family Asteraceae and reviews relevant literature relating to *Sonchus oleraceus* L. (common sowthistle). It introduces the Australian agricultural environment as a habitat of *S. oleraceus*. Relevant aspects of weed science are covered; with an emphasis on the evolution of resistance to herbicides inhibiting acetolactate synthase (ALS) also called acetohydroxyacid synthase (AHAS). Within this group of herbicides the chemical family of sulfonylureas are a focus. The evolutionary development, genetics and molecular genetics of *S. oleraceus* are covered.

*S. oleraceus* is a weed of bare ground (Walker pers. comm. 2005). Martin *et al*., (1988) observed *S. oleraceus* as a weed of fallows rather than competing with crops. *S. oleraceus* is reported as a host to a number of pests and diseases of crops. Included among these pests and diseases are aphids, some species of which are vectors of the disease Lettuce Necrotic Yellow Virus (O'Loughlin and Chambers 1969), fungal pathogens, other insects and nematodes. Therefore, the weed's main impacts are as a user of resources in fallow, as a host for pests and diseases, a contaminant at harvest and as direct competition for resources in crops.

The introduction of chemicals for the control of weeds in the 1900s have included sodium chlorate (1910), 2,4-D (1942), diuron, amitrole, simazine, paraquat and numerous others in the 1950s (Anonymous 2004). Others chemicals including bromoxynil, chlorthal-dimethyl and oryzalin were developed in the 1960s and glyphosate and oxyfluorfen to name a few in the 1970s. The first sulfonylurea herbicide chlorsulfuron (Glean®) was released in 1979. Chlorsulfuron was followed by sulfometuron-methyl (Oust®) in 1980, Metsulfuron-methyl (Ally<sup>®</sup>) in 1985 and triasulfuron (Logran<sup>®</sup>) in 1985 (Anonymous 2004). Others sulfonylurea herbicidess have been released in the late 1980s and 1990s and are all ALS-inhibitors. Since the 1950s crop production has become increasingly dependant on the use of herbicides to control weeds with this benefit has been diminished as weeds have evolved resistance to the herbicides.

Throughout the world weed species are accumulating resistance mechanisms, evolving multiple resistances across many herbicides posing a great challenge to herbicide sustainability in world agriculture (Powles and Yu 2010). Herbicide resistance has evolved as a result of selection for individuals within weed populations that survive herbicide treatment (Tranel and Wright 2002; Holt *et al*., 1993; Tucker and Powles 1988). The first weed biotype resistant to ALS-inhibiting herbicides (*Lactuca serriola* L.) was identified in 1987 (Mallory-Smith *et al.*, 1990a). Although usually present at very low frequency, weed populations often contain individuals that are naturally resistant to ALS-inhibiting herbicides and which increase in numbers over generations as a constant selection pressure is applied (Preston and Powles 2002). It is also possible that a novel mutation could be introduced from outside the population, if none were present within a population. For *S. oleraceus*, like other selfpollinated weeds, resistant alleles are dispersed through seeds. This dispersal can be by wind, water, animal or mechanical means and once dispersed, establishment and reproduction can occur as the seed establishes new populations of resistant plants. The level of success of these dispersed populations rests with the fitness of the immigrant individuals compared to existing individuals. The emergence of herbicide resistance will depend on the fitness of individuals to survive the application of herbicides.

Factors that influence herbicide resistance evolution include the herbicide use pattern, the number of plants treated, the mode of inheritance of the gene endowing resistance and the initial frequency of the herbicide-resistant individuals (Powles *et al*., 1997). Resistant populations have been found in numerous geographic locations at various distances apart. Whether these populations originated from a single mutation conferring resistance of multiple mutation events can only be determined by further analysis of their genetic relationship (Ashigh and Tardif 2007).

The first recorded biotype of *S. oleraceus* resistant to ALS-inhibiting herbicides in Australia was found at Goondiwindi, Queensland in 1991 (Boutsalis and Powles 1995a). Adkins *et al*., (1997) reported *S. oleraceus* as one of 15 weed species resistant to the recommended rate of chlorsulfuron (15g a.i.  $ha^{-1}$ ) in a survey of weed resistance in the north-east grain region of Australia.

The direct economic and environmental impact to Australian ecosystems caused by *S. oleraceus* in the late 1990s was described as being relatively low (Widderick 2002). However, this is likely to increase with selection for an increased frequency of resistant plant biotypes in populations. Recent surveys conducted in 2001 of cotton growers in southern Queensland and northern NSW found *S. oleraceus* to be a common problem weed (Walker *et al.,* 2005a; Alemseged *et al*., 2001).

Gilbey (1974) outlined the relationship between the density of the broad leafed weed *Emex australis* and found that 10 plants per  $m^2$  reduced wheat yields by 10% and 120 plants per  $m^2$ reduced yields by 50%. Since *S. oleraceus* is also a broad leaf weed and is likely to have similar competitive effects to *E. australis,* it could be assumed that without appropriate management strategies to control populations of *S. oleraceus*, their increased presence will reduce crop yields. Strategies to prevent, or minimise, the risk of resistance are now in place (Walker *et al.,* 2005b): However, farmers and land managers must be convinced to adopt such strategies based on a sound understanding of the weeds ecology.

This project will investigate gene flow among *S. oleraceus* populations and the implications that movement of herbicide resistance between *S. oleraceus* populations will have on resistance management. It will investigate the genetic diversity and the dispersal and spread of *S. oleraceus* on a landscape scale and suggest development of resistance management programs based on the results.

#### **2.1.1** *Sonchus oleraceus* **IN THE AGRICULTURAL ENVIRONMENT**

The Australian agricultural environment is mainly situated in the rain-fed areas within 600 km of the coast as most of the centre of Australia is arid or semi arid. The grain growing regions are divided into the western, southern and northern grain regions of Australia (Figure 2.1).

The climate in much of the southern and western grain regions is similar to that of countries around the Mediterranean basin, parts of Chile and Argentina in South America, South Africa, parts of south western Asia and the western United States of America. Winters are mild and humid and summers are hot and dry. The southern grain region of Australia (SGRA) and western grain region of Australia (WGRA) have a temperate climate, while the northern grain region of Australia (NGRA) ranges from temperate to sub tropical in New South Wales through to sub tropical in southern Queensland. *S. oleraceus* has been recorded in all of these regions. Widderick (2002) found that *S. oleraceus* is a common weed throughout the NGRA and it infests all important crops and fallows using moisture and interfering with harvest**.** Although geographically widespread, *S. oleraceus* is not very competitive and growing a competitive crop greatly reduces the weed's biomass and potential seed production (Widderick 2002). Common sowthistle is currently the most prevalent weed of cropping in southern Queensland where it has increased in importance in the last few decades as farming systems have moved towards reduced or zero tillage (Widderick pers. comm. 2009).



**Figure 2.1** Location of the western, southern and northern grain regions of Australia. (WGRA = western grain region of Australia, SGRA = southern grain region of Australia and NGRA = northern grain region of Australia). Note: Locations are generalised areas.

The surface (0-1 cm) seed bank is depleted by germination following rain and via other means, such as predation or decay. In contrast, up to 12% of seeds buried below a depth of 2 cm persisted for at least 30 months (Widderick 2002).

#### **2.2 TAXONOMY, BIOLOGY AND ECOLOGY**

#### **2.2.1 THE FAMILY ASTERACEAE**

The Asteraceae is the largest angiosperm family with 1100 genera worldwide and 200 genera native to Australia (Black 1986). Judd *et al*., (1999) lists the characteristics that plants in the family Asteraceae share: an inflorescence with a capitulum flower head, anthers with stamens fused together at their edges forming a tube, ovary with basal arrangement of the ovules, one ovary per ovule, an achene fruit with a tuft of hair (pappus).

#### **2.2.2 THE GENUS** *Sonchus*

#### **2.2.2.1** *Sonchus* **in the world**

There ar e 55 species of *Sonchus* worldwide ( Boulos 1972) . B oulos ( 1972) had linked the genus *Sonchus* with the g enus *Embergeria.* This c aused s ome c ontroversy, but now i t i s generally regarded separately as *Sonchus.* 

#### **2.2.2.2** *Sonchus* **in Australia**

There are 2 native and 4 naturalised species of *Sonchus* (with 2 *asper* subspecies) in Australia

(Table 2.1). This study will focus on *S. oleraceus*, a member of the family Asteraceae.

**Table 2.1.** *Sonchus* species in Australia (Boulos 1972).

 NOTE: This table is included on page 10 of the print copy of the thesis held in the University of Adelaide Library.

#### **2.2.2.3 Geographic distribution of** *S.oleraceus*

#### *Origin and world distribution of S.oleraceus*

The already wide geographical distribution of *S. oleraceus* globally makes determining the geographic origin difficult (Mitich 1998). Guertin and Halvorsen (2003) report that *S. oleraceus* is a native to Africa (Mediterranean region), temperate Asia, tropical Asia, and Europe. Lewin (1948) described *S. oleraceus* as a weed that had followed the spread of civilization to the temperate and sub-tropical zones of both hemispheres and high altitudes in the tropics to their present distribution worldwide (Figure 2.2).

The current world distribution of *S. oleraceus* is very broad and covers areas of northern Europe and Canada through the tropics to South America and South Africa (Holm *et al*., 1977), United States of America (Peschken 1982), Canada (Hutchinson *et al*., 1984) and England (Mitich 1998).



**Figure 2.2** Global distribution of Sonchus oleraceus L (Holm *et al*. 1977) (Australian Virtual Herbarium 2009).

#### *Australian distribution of S. oleraceus*

*S. oleraceus* is widespread throughout Australia (Auld and Medd 1987; Australian Virtual Herbarium 2009). In Queensland, *S. oleraceus* is found in the regions of Moreton, eastern Darling Downs, western Darling Downs, Maranoa and central Queensland. In New South Wales, it is found in the Central-West Slopes and Plains, North-West Plains and North-West Slopes. It is a lso w idespread t hroughout S outh A ustralia, V ictoria, W estern A ustralia,

Tasmania and the Northern Territory (Figure 2.3).

 NOTE: This figure is included on page 12 of the print copy of the thesis held in the University of Adelaide Library.

**Figure 2.3** Australian distribution of *Sonchus oleraceus* L. derived from existing physical herbarium records (Australian Virtual Herbarium 2009).

#### **2.2.2.4 Morphology and variation**

*S. oleraceus* stems are commonly 20 t o 150 c m in height, hollow, septate at the nodes and more or less pentagonal in section by reason of the decurrent midribs in the leaves (Alex *et al.,* 1980). The leaves are not spinous or glossy and can vary in shape, even within the same plant. T he pl ant i s g labrous e xcept f or a c aducous tomentum around the young leaf and flower buds (Hutchinson *et al*., 1984). Clapham *et al*., (1987) point out a large amount of leaf shape variation in the species. *S. oleraceus* plants from the northern grain region of Australia are m orphologically di verse va rying i n l eaf c olour, l eaf s erration, rosette form, height, fecundity and time of flowering (Widderick 2002). Andersson (1991) reported that selfpollinating weed species, such as *S. oleraceus*, are more likely to form distinct biotypes compared with species with a tendency to out-cross. A survey conducted in the northern grain region of Australia highlighted that: *S. oleraceus* is widespread and prevalent; that it is probable that biotypes of *S. oleraceus* exist; and that the weed's ability to adapt may partly be responsible for its prevalence (Widderick 2002). A high degree of morphological variation (Widderick 2002) may indicate a high level of cross pollination and genetic variation; however, this is perplexing as the plant is regarded as a self pollinator (Barber 1941). Whatever the reason for these morphological differences the fact is that self pollination will perpetuate them.

#### **2.2.2.5 Habitat and ecology**

In general, climate is the main limiting factor to the potential distribution of a plant species. The climatic limitations of *S. oleraceus* are not fully understood; however, the distribution of *S. oleraceus* would indicate a broad tolerance of climatic variation (Hutchinson *et al*. 1984). In Australia, *S. oleraceus* is found in areas with climate ranging from arid to tropical, including both dry and wet summer areas (Widderick 2002). In Canada, the distribution of annual *Sonchus* spp. is within a range of precipitation from 300 to 3000mm (Guertin and Halvorson 2003). *S. oleraceus* prefers well drained, slightly acid to alkaline soils and is tolerant of saline soils (Lewin 1948). Hutchinson *et al.,* (1984) reports *S. oleraceus* likes nutrient-rich, not too dry, nitrogen containing soils with textures that are loamy sands or stony.

#### **2.2.2.6 Plant development**

There is no vegetative reproduction in *Sonchus* and unfavourable periods of growth are mitigated by a large seed bank that can persist for up to 30 months (Lewin 1948, Widderick 2002). In the northern hemisphere specimens that have survived the winter commence flowering about the middle of March to the end of April. Achenes are produced abundantly between May and November and in suitable conditions will germinate (Lewin 1948). Mature achenes are produced about a week after flowering. Capitular bracts open when the achenes are mature and then the pappus-borne achenes are dispersed by the wind (Hutchinson *et al*., 1984). In the southern hemisphere, specimens flower from October through the summer and into autumn depending on the time of germination, which can be variable (Widderick 2002).

#### **2.2.2.7 Karyology**

The chromosome number of *S. oleraceus* is 2n=32. Cooper and Mahony (1935) described it as a tetraploid and that there is some evidence of secondary association of bivalents on the metaphase plate in the first division of the pollen mother cells. Stebbins *et al*., (1953) described *S. oleraceus* as an allotetraploid or amphidiploid with a chromosome number of 32 with 18 chromosomes coming from *S. asper* and 14 chromosomes from *S. tenerrimus* L. It is interesting to note the findings of Stebbins *et al.,* (1953) indicate that the two different species of *Sonchus* can cross, producing fertile progeny when *S. oleraceus* is the female. However, data compiled by Hsieh *et al*., (1972) indicated that *S. oleraceus* is an autotetraploid. As a point of interest, Marchal (1920) reported a diploid (2n=16) variant.

The chromosome number is important in understanding the genetic nature of the plant and the position of resistant alleles on the chromosome as they are mapped. There are also implications for genetic diversity and mutation. Chromosomal variation is widespread in plants and animals. It often contributes to the genetic barriers preventing gene flow between species and hence its role in species diversification has been heavily debated (White, 1978; King, 1993; Rieseberg, 2001). Our understanding of these phenomena has progressed considerably recently as a result of theoretical research on hybridization and genome duplication and technical advances in Polymerase Chain Reaction (PCR).

14

#### **2.2.2.8 Reproduction**

#### *Floral biology and flowering*

Unlike the glabrous stems and leaves, the flower buds have caducous tomentum and glandular hairs sometimes present on the branches and involucres of the inflorescence, which is irregularly cymose-umbellate (Lewin 1948). The involucres are about 1.5cm long and the span of the capitulum when open is 2 to 2.5cm. The florets are ligulate and yellow. The pappus is white and silky (Lewin 1948). Percival (1955) observed the duration of pollen presentation to be between 7 am and 12 noon, with a peak period of 8 to 9 am. On 84% of the days, pollen was present during this peak period. In addition, from observations of 86 plant species, it was noted that *S. oleraceus* produced the least amount of pollen, but that nectar was available and that pollen collection did not occur by bees. Percival (1955) also states that anthesis in *S. oleraceus* occurs at the highest relative humidity level of 95%, with free anthesis at 15 to  $22.8^{\circ}$ C and that rain limited flower opening. The capitulum contains some 200 florets each of which consist of an ovary, pappus and anther-collar tube through which the stigma and style emerge.

#### *Pollination*

Pollination is an important factor in the flow of genes from one plant to another. Barber (1941) states that *S. oleraceus* is self fertile and attempts to cross artificially were unsuccessful, although Stebbins *et al*., (1953) indicated crossing was possible when *S. oleraceus* was the maternal donor. Lewin (1975) reported that true hybrids involving *S. oleraceus* were rare and that it was unlikely that many of the reported "hybrids" between *S. oleraceus* and *S. asper* were of mixed descent. Barber (1941) describes an undoubted hybrid, which arose spontaneously in cultivation in which the chromosome number was 25 (*S. oleraceus,* 2n=32: *S. asper,* 2n=18), but the plant was sterile both in pollen and in the ovules.

There are some contradictory findings on the success of outcrossing, although the reasons for these differences are not clearly understood. Fitzpatrick *et al*., (2003) found that the level of gene flow in the cross pollinated plant, *Medicago sativa* (lucerne/alfalfa) to be 1.39% at 500 ft separation, 0.28% at 900 feet, 0.08% at 1500 feet and 0.0% at 2000 feet. Their work further indicated that with separation distances of greater than 900 feet that this isolation standard is sufficient to produce seed with 99.7% varietal purity. So, it is clear that distance between donor and source can affect the level of gene flow. However, for the purpose of this study, and consistent with the findings of Pupilli *et al*., (2004) and Lu *et al*., (2008), it will be assumed that *S. oleraceus* is self pollinated and produces seed that is genetically identical to the mother plant.

#### *Seed production, dispersal and viability*

The tall stems of sowthistles aid the seed dispersal process by elevation above the crop canopy (Sheldon and Burrows 1973). *S. oleraceus* achenes are distributed by wind, with the pappus enhancing dispersal, but have also been reported to have been dispersed by water and birds (Andersson 1991; Holm *et al.,* 1977; Hutchinson *et al.,* 1984). Methods of reducing the spread of wind dispersed seeds may be impractical on a large scale. However, Davies and Sheley (2007) suggest a conceptual framework for preventing spatial dispersal of invasive plants by identifying vectors of dispersion and management strategies. This recognises that preventing invasive plants from infesting new areas is more cost-effective and efficient than trying to restore the system after it is infested.

Salisbury (1964) reports that seed may germinate after ingestion and excretion by birds and mammals. For example 27% of the achenes of *S. asper* fed to a cow germinated in the manure (Dorph-Peterson 1924). This demonstrates the hardy seeds, particularly since the cow is a ruminant. Zollinger and Parker (1999) report *Sonchus* achenes found tangled in the wool or hair of animals. Guertin and Halvorson (2003) report from Holm *et al*., (1977) that *Sonchus* seeds have been collected by aircraft on a screen at 600m. This shows the potential for achenes to blow widely over the landscape and hitchhike on animals.

Shields *et al*., (2006), using remote controlled model aircraft, collected *Conyza candensis* (horseweed) seeds, a member of the Asteraceae also with wind-borne seed, up to 140m above the ground and suggested that seeds can easily be dispersed more than 500km in a single dispersal event. Lebeda *et al.,* (2004) found that of populations of *Lactuca* spp. collected in Europe, 59% originated in Europe, 37% in Asia and 2% from Africa and 2% from America. This highlights the mobility of wind dispersed seed or human mediated movement.

Harper (1977) reported that in most plant species the population of dormant seed in the ground is often much greater than the above ground growing population. *S. oleraceus* seeds lack innate dormancy and readily germinate over a wide range of temperatures (Widderick 2002). Weeds that emerge with a crop can do far more competitive damage than weeds that emerge later in the crops' development (Sanyal *et al*., 2008). Although *S. oleraceus* is not very competitive, with an increased frequency of herbicide resistant plants would be expected to increase the potential for adverse competition.
## **2.2.2.9 Parasites and predators**

*S. oleraceus* is host to a number of insects including aphids, flies, leaf miners and seed borers (Hutchinson *et al.,* 1984). Berube (1978) reported two flies (*Tephritis dilacerate* and *T. formosa*) that occasionally lay eggs into the flower buds of *S. oleraceus* forming galls*. S. oleraceus* is host to a number of nematodes that reduce the vigour of the plant (Hutchinson *et al.,* 1984). An eriophyid mite which causes leaf edge curl and swelling has been found in Western Australia (McCarren pers. comm. 2007). This knowledge is of value in beginning the process of the selection of any biological control agent for the control of *S. oleraceus* in Australia. However, there is little evidence currently that specific predators are important in controlling populations of *S. oleraceus*.

## **2.2.2.10 Control measures**

# *Response to herbicides and other chemicals*

*S. oleraceus* is susceptible to a wide range of pre-emergence and foliar herbicides from a number of herbicide groups (Table 2.2). This suggests that developing a strategy to prevent the evolution of herbicide resistance to specific modes of action is achievable.

<b>Chemical Name</b>	Mode of Action
Chlorsulfuron and Metsulfuron-methyl	Acetolactate synthase (ALS)-inhibitors
Bromoxynil and Metribuzin	Inhibitors of photosynthesis at photosystem II
Pendimethalin & Chlorthal-dimethyl	Inhibitors of tubulin formation
Diflufenican	Inhibitors of carotenoid biosynthesis
Oxyfluorfen	Inhibitors of protoporphyrinogen oxidase
2,4-D & MCPA	Disrupters of plant cell growth
Propachlor	Herbicides with multiple sites of action
Glyphosate	Inhibitors of EPSP synthase

**Table 2.2** Selected herbicides for the control of *S. oleraceus.* (Source: Pest Genie and APVMA Pubcris 2010).

# *Biological control measures*

Classical biological control refers to weed management by natural enemies, such as insects or micro-organisms (Lovett and Knights 1996). Where a weed is a problem in its native environment the chances of finding a biological agent for a novel environment is reduced, although there is the possibility that an effective control agent may be present (Hutchinson *et al*., 1984). Groves (1991) cites from Julien (1982) that, at present, biological control programs have a success rate of between 25% and 40% and that the level of success is rarely predictable. Indeed, as with other single methods of control, the result may be that one weed replaces another. Peschken (1982) outlines the host specificity and biology of *Cystiphora sonchi* a candidate for the biological control of *Sonchus* species. Other than this, very few investigations into biological control of *Sonchus* species were found in the literature. This lack of information on possible biocontrol agents heightens concerns about options for controlling the weed should herbicide resistance become widespread. McCarren pers. comm. (2007) whilst searching for eriophyid mite that is common on *Sonchus* species collected seed from a number of *S. oleraceus* plants in Western Australia for use in this project.

#### **2.3 HERBICIDE RESISTANCE**

### **2.3.1 THE HISTORY OF HERBICIDE RESISTANCE**

The potential for weeds to evolve resistance to herbicides was predicted in the 1950s (Harper 1956). Numerous weed species have now evolved resistance to herbicides (Heap and Knight 1982; Holt and LeBaron 1990; LeBaron 1991; Holt 1992; Holt *et al*., 1993; Heap 2009). Resistance has evolved in numerous weed species worldwide with 348 herbicide resistant weed biotypes of which over 100 were reported to be resistant to ALS inhibitor herbicides (Heap, 2010).

### **2.3.2 BIOLOGY AND ECOLOGY OF HERBICIDE RESISTANCE**

#### **2.3.2.1 Basic understanding**

The evolution of herbicide resistance in weeds is influenced by the inheritance of the resistance allele, gene flow, selection pressure, plant fitness and seed bank characteristics (Tranel and Wright 2002; Gressel and Segel 1982; Powles 1993). Gressel and Segel (1982) outlined the rationale that resistance must initially be preceded by the presence of one or more alleles responsible for expressing resistant phenotypes in the population. The resistance trait can be dominant or recessive, but in most cases, a single dominant to semi-dominant gene is involved (Darmency 1994). The mechanism of herbicide resistance can be due to reduced herbicide uptake and translocation, enhanced herbicide metabolism or a modified site of action (Maneechote 1995). These are often the same mechanisms that provide selectivity to herbicides in beneficial plants (such as wheat).

#### **2.3.2.2 Gene flow**

Gene flow relates to the movement of genes among a population and this flow is capable of causing evolutionary change through the emigration (loss of genes) or immigration (gain of genes) within the population (Radosevich *et al.,* 1991). McDonald and Linde (2002) reported that organisms that have a high degree of gene flow often have greater genetic diversity than organisms with low levels. Gene flow increases the effective population size by increasing the size of the genetic pool. This will influence the maintenance of particular genotypes in a population. Gene flow processes can also directly alter the frequencies of resistant and susceptible alleles in a population (Maxwell *et al*., 1990).

Fertilisation of susceptible plants with pollen carrying alleles for herbicide resistance aids the spread of resistance (Maxwell and Mortimer 1994). This is clearly the case in plants which are mainly cross pollinated plants, such as *Medicago sativa* (alfalfa/lucerne), where the level of gene flow is greater when plants are closer together than when they are hundreds of metres apart (Fitzpatrick *et al*., 2003). However, gene flow in self pollinated plants is mainly by seed movement. Through knowledge of the major mechanisms of gene flow, management options can be manipulated to reduce the rate of resistance increase. For example, Walker *et al.,*  (2005a) advocate management strategies of spraying small seedlings and controlling late flushes of *S. oleraceus* in winter crops with selective herbicides instead of waiting for the first fallow spray after harvest. These strategies will kill the plants prior to flowering terminating the possibility of the resistance gene being transferred.

Davies and Sheley (2007) outline the fate of invasive plant seeds as either falling in the immediate vicinity of the parent plant or being dispersed by a number of vectors. In *S. oleraceus* seed is known to be widely dispersed by the wind, which consequently also disperses the resistance alleles. Understanding the mechanisms of gene flow can also be used in selecting the best weed control management methods. Likewise knowledge of the fitness between resistance and susceptible individuals can provide valuable insights as to the rate with which a resistant biotype could increase in frequency, with or without selection pressure.

# **2.3.2.3 Resistant biotype fitness**

Mutations conferring herbicide resistance in plants are expected to produce a fitness cost in individual progeny growing in an original stress free environment (Coustau *et al.,* 2000). The fitness cost is often difficult to measure and must be compared in light of a common genetic background (Neve 2007). The relative fitness of alleles dictates the frequency with which the different alleles will be present within the population. For the particular case of herbicide resistance, Holt and LeBaron (1990) concentrated on parameters such as growth rate and plant biomass as indicators of fitness. In the presence of herbicide, herbicide resistant plants have a fitness advantage over susceptible plants. However, in the absence of herbicide the opposite may occur. Herbicide resistance alleles are kept at low frequencies in populations in the absence of herbicide by the fitness penalty against the resistance allele (Jasieniuk *et al.,* 1996). Neve (2007) emphasises the need to have a good understanding of population differences that may have nothing to do with the presence or absence of the resistance allele.

Susceptible plants in the population are often classified as standard "fit" biotypes whereas resistant plants after herbicide has been applied may be classified in classes of fitness from 1, (the least fit) to 5, (the most fit) or equal to the non sprayed control. Widderick (2002) noted differences in *S. oleraceus* fitness traits and placed *S. oleraceus* plants, into 3 bands of fitness (after applying herbicide and measuring survival), as 1, 2 and 3, with 3 being the most fit. Other metric scales relating to the fitness level in resistance have included % R (% Resistant plants) and % Intermediate (% Intermediate resistant plants) (Hashem and Bowran 2001; Boutsalis and Powles 1995a). However, these classes do not allow for non-linear variations in the level of resistance or comparisons of total resistance equal to the fitness of the nonsprayed control. Two fundamental components of fitness are survival and reproduction (Silvertown 1987). Often the fitness of a weed is determined by its biomass production (Holt 1992), although this provides no indication of the ability to reproduce. In addition other genes in the plant can influence the fitness of the plant, such that an individual carrying a resistance allele may be more fit, as fit or less fit than any one individual carrying a susceptible allele.

#### **2.3.2.4 Inheritance of herbicide resistance**

In the majority of cases studied the inheritance of resistance is by a single partially dominant or dominant gene (Anderson and Gronwald 1987; Boutsalis and Powles 1995a; Betts *et al,.*  1992; Barr *et al,.* 1992; Mallory-Smith *et al.,* 1990b; Itoh and Miyahara 1984; Shaaltiel *et al.,* 1988; Islam and Powles 1988 and Purba *et al.,* 1993). An exception is the resistance to dinitroanaline herbicides in *Setaria viridis* where resistance is due to a single recessive gene (Jasieniuk *et al.,* 1994). Inheritance of resistance in all classes of herbicides except the triazines is by nuclear inheritance. In the majority of plants with resistance to triazine herbicides, resistance is inherited cytoplasmically through maternal inheritance (Jasieniuk *et al.,* 1996).

Mutations in ALS conferring herbicide resistance are at least partially dominant, and because the gene is nuclear inherited, it is transmitted by both seed and pollen (Saari *et al*., 1994; Tranel and Wright 2002). Boutsalis and Powles (1995a) crossed a chlorsulfuron resistant biotype of *S. oleraceus* with a susceptible biotype and followed the inheritance through  $F_1$ ,  $F_2$ , and  $F_3$  generations.  $F_1$  hybrids from this cross were uniformly resistant, but at an intermediate level compared to the resistant and susceptible parents. Following the application of chlorsulfuron herbicide to the  $F_2$  generation, three distinct phenotypes were identified, resistant, intermediate and susceptible. A segregation ratio of 1:2:1 was observed indicating a single, nuclear, incompletely dominant gene conferring resistance.  $F_3$  families also segregated in a 1:2:1 ratio. They concluded that resistance to herbicides inhibiting ALS in this biotype of *S. oleraceus* is due to the effect of a single gene coding for a resistant form of the target enzyme, ALS. Ashigh and Tardif (2007) conducted similar work investigating the genetics of resistance to ALS-inhibiting herbicide imazethapyr in the self-pollinated plant *Solanum ptychanthum* (eastern black nightshade). Their backcross progenies of the  $F_2$  families also segregated in the ratio of 1:2:1 (Resistant, Intermediate and Susceptible) agreeing with earlier work of Boutsalis and Powles (1995a).

#### **2.3.2.5 Cross resistance**

Cross resistance is said to exist in weed populations when the plants exhibit resistance to a herbicide that has never been applied to the population (Heap and Knight 1986; Holt *et al.,*  1993). In other words, the weed population or biotype has evolved resistance through a mechanism that allows resistance to another herbicide. Cross resistance has reported to be common within the sulfonylurea herbicide family. For example Holt *et al*., (1993) reported that chlorsulfuron resistance will also result in a population or biotype that is resistant to all the other sulfonylurea herbicides.

# **2.3.2.6 Multiple resistance**

Multiple resistance is said to exist in a weed population when it exhibits resistance to dissimilar herbicide modes of action through more than one resistance mechanism (Powles and Mathews 1991). In other words, multiple resistance refers to a weed biotype that has evolved mechanisms of resistance to more than one herbicide often brought about by separate selection processes. An example of this would be if an *S. oleraceus* biotype resistant to ALSinhibiting herbicide was found to also be resistant to inhibitors of photosynthesis at photosystem II, that is, resistant to chlorsulfuron and bromoxynil.

#### **2.3.2.7 The soil seed bank**

Liebman *et al*., (2007) reports that if cultural practices keep seed banks at negligible levels then a species may eventually be eliminated from a field, although this may take some time for species with highly persistent seed banks. The longevity of the seed within the seed bank and the size of the seed bank play important roles in population dynamics of herbicide resistant weeds (Holt and Thill 1994), because a long lived seed bank acts as a buffer against the rapid evolution of herbicide resistance. Repeated application of the same herbicide to a weed population will continuously enrich the seed bank with resistant seed (Gressel and Segel 1982). *S. oleraceus* emerges all year round, has low levels of seed dormancy and emergence is favoured by minimal tillage systems (Widderick 2002), so the genetic composition of the seed bank changes rapidly. Hence, it could be anticipated that there will be rapid selection for herbicide resistant biotypes with repeated applications of the same herbicide.

## **2.3.2.8 Herbicide resistance management**

Zollinger and Parker (1999) report that *Sonchus* spp. are pioneer species, invading natural habitats and disturbed sites, are long travelled by wind dispersion and their rapid germination allows establishment in diverse habitats. This produces a challenge for the management of a wind dispersed weed. Herbicide mode of action rotations and the use of herbicide mixtures are methods of reducing resistant population build up (Gressel 1991 and Slife 1986). Integrated Weed Management Strategies (IWMS) involve controlling weeds by using combinations of biological, physical or chemical methods (Powles 1993 and Mathews 1994). These include methods such as rotating herbicide mode of action, rotating crop varieties, utilising cultural weed control techniques, reducing weed seed contamination, crop and pasture topping and monitoring paddocks (CRC Australian Weed Management 2006). Neve (2007) calls for a greater integration of 'evolutionary-thinking' into herbicide resistance research with a need for weed scientists to become less focused on simply describing resistance and more driven towards a deeper understanding of the evolutionary forces that underpin resistance evolution. In addition Neve (2007) suggests that the major research effort should be towards the development of economically viable strategies to prevent and manage resistance. Research into the precise details of biochemical, genetic and molecular means by which plants evolve herbicide resistance will contribute to wiser use of herbicides, new innovations and better strategies for weed management (Powles and Yu 2010). It is hoped that the outcome of this research will provide strategies to prevent and manage resistance in a wind dispersed weed.

# **2.3.3 ACETOLACTATE SYNTHASE (ALS)-INHIBITING HERBICIDES**

#### **2.3.3.1 Acetolactate synthase–inhibiting herbicides**

In plants, acetolactate synthase (ALS) is the first enzyme in the biosynthetic pathway for the branched chain amino acids valine, leucine and isoleucine (DeFelice *et al.,* 1974). The enzyme acetolactate synthase is the target for the ALS-inhibiting herbicides. These herbicides are very potent, are applied at low rates, are selective in their action in plant species and have low mammalian toxicity (Beyer *et al.,* 1988 and Shaner *et al.,* 1982). These properties have ensured that ALS-inhibiting herbicides are widely used worldwide but the intensive use of these herbicides has resulted in the selection of resistance in weed populations.

# **2.3.3.2 ALS-inhibiting herbicide classification**

Mallory-Smith and Retzinger (2003) outlined a revised classification of herbicides by site of action for weed resistance management strategies following their original classification of 1997 (Retzinger and Mallory-Smith 1997). They classified the herbicides according to the primary site of action in the plant. Within the ALS-inhibiting herbicides there are 5 chemical families (Green *et al.,* 2009)

- 1. Sulfonylureas
- 2. Imidazolinones
- 3. Sulfonamides ( Triazolopyrimidines sulfonamides)
- 4. Pyrimidinylthiobenzoates
- 5. Sulfonylamino-carbonyl-triazolinones

### **2.3.3.3 The sulfonylurea chemical family**

The majority of the herbicide resistance work with ALS-inhibiting herbicides has been focused on herbicides within the sulfonylurea chemical family. Table 2.3 outlines the ALSinhibiting herbicides currently used in Australia, the weeds they control and the crops in which they are used.





Source: (Preston pers. comm. 2009)

# **2.3.4 RESISTANCE TO SULFONYLUREA HERBICIDES**

## **2.3.4.1 Background**

In 1987, Mallory-Smith *et al.,* (1990a) described resistance to ALS-inhibiting herbicides in prickly lettuce (*Lactuca serriola* L.), five years after the commercial introduction of chlorsulfuron.Since 1987 the number of weed species recorded as showing resistance to ALS-inhibiting herbicides has increased to 101 worldwide (Heap 2010). ALS-inhibiting herbicides have been widely adopted due to their low rates, broad spectrum of weed control, low mammalian toxicity and flexible application timing in a many crops (Mazur and Falco 1989; Duran-Prado *et al*., 2004; Saari *et al*., 1994).

#### **2.3.4.2 ALS genes and mutations**

Mutations in ALS conferring herbicide resistance are at least partially dominant, and because the gene is nuclear inherited, these mutations are transmitted by seed and pollen (Tranel and Wright 2002). Grula *et al.*, (1995) reported that all of the plant ALS genes sequenced to date lack introns. Genetic studies have shown the ALS gene to be encoded by a single copy in some species (Haughn and Sommerville 1986) and as two active ALS genes in tobacco (*Nicotiana tabacum*) (Lee *et al.,* 1988). The allotetraploid, *Brassica napus* has several ALS genes (Rutledge *et al.,* 1991). Work of Guttieri *et al.,* (1995) and Bernasconi *et al.,* (1995) found that amino acid substitutions exist at five sites (Alanine<sub>122</sub>, Proline<sub>197</sub>, Alanine<sub>205</sub>, Tryptophan<sub>574</sub> and Serine<sub>653</sub>) or domains (identified A to E) in the gene and that these domains are mutation sites. A sixth (Aspartate<sub>376</sub>,) and seventh (Glycine<sub>654</sub>,) site have since been identified (Whaley *et al*., 2007) and (Sales *et al*., 2008). In 2009 there were 22 resistance substitutions at seven sites across ALS (Powles and Yu 2010).

### **2.4 GENETICS AND EVOLUTION**

#### **2.4.1 INTRODUCTION**

The method of pollination in plants makes considerable difference to the genetic diversity of the progeny. Many plants are cross pollinated, which leads to increased genetic variation. However, some plants are self pollinated, which leads to more uniform progeny (Lawrence 1974). *S. oleraceus* is self pollinated and therefore produces more uniform progeny.

Stankiewicz *et al.*, (2001) stated that herbicide resistance in weeds is an example of microevolution in plant species caused by environmental changes brought about by human activity and is a result of selection for traits that allow a weed species to survive. Herbicide resistance in plants most often occurs as a single dominant allele, therefore phenotypic resistant plants will have the genotypes of either RR or Rr and susceptible plants will have the genotype of rr. The pattern of transmission of alleles to progeny will be affected by the method of pollination. Therefore, understanding the pollination biology of the target species can help in choosing an approach for a study of gene flow (Baker *et al.,* 2005).

# **2.4.2 POPULATION GENETICS**

Populations vary in their number or density per unit area depending on the level of availability of nutrients, water and environmental constraints such as temperature and light. Phenotypic variations in the population can exist or be caused by novel genetic mutations. Populations and the individuals within populations vary in both their genotype and phenotype and the frequency of alleles will vary depending on the selecting pressure applied (Russel 1980). Geographic isolation can result in significant genotypic divergence, although this will be influenced by the founding genotypes. For example, populations of one-leaf tulip (*Moraea flaccida*) collected in South Australia less than 136 km apart were found to be genetically similar, whereas populations in Western Australian and South Australian were genetically different (Blackman 2005).

# **2.4.2.1 Hardy-Weinberg equilibrium**

Within a defined geographical area and in the absence of genetic drift or significant immigration, but where mating is at random, a gene pool contains R alleles at a frequency of p and r alleles at a frequency of q. The gene pool will remain in equilibrium  $p^2 + 2pq + q^2 = 1$ as long as these conditions continue. This means that gene frequencies and genotype ratios in a randomly-breeding population remain constant from generation to generation, following what is known as the Hardy-Weinberg equilibrium. Selection processes affect the survival of individuals in the population and evolutionary changes, such as the development of herbicide resistance occur altering this equilibrium (Russel 1980).

#### **2.4.2.2 Selection Pressure**

The initial frequency of alleles can differ in populations. When no selection pressure is applied, the frequency of alleles for herbicide resistance is usually low (Neve and Powles 2005b). Herbicides provide a high level of selection pressure on a weed population (Jasieniuk *et al*., 1996) and the stronger the selection pressure, the faster the emergence of resistance (Gressel and Segel 1982). A ten times increase in the frequency of resistance alleles in the population is produced by a 90% kill with the use of a herbicide (Howat 1987). However, Preston and Roush (1998) point out that herbicides applied at a low rate may slow the rate of resistance evolution in weed populations because fewer susceptible weeds are killed.

#### **2.4.2.3 Genetic drift and genetic distance**

Genetic drift is a random change in allele frequency (Russel 1980). This drift can be small in large populations, but large in small populations because of the number of alleles present in the gene pool. That is, the level of original heterozygosity will remain high in large populations. Small populations respond differently as a result of random matings and the number of offspring from each successful mating over succeeding generations (Strickberger 1968). In the case of small populations, rare alleles are often lost purely by chance reducing the heterozygosity over time.

## **2.4.2.4** Inbreeding and fixation index  $(F_{ST})$

In individual plants, inbreeding redistributes alleles from the heterozygous to the homozygous state. Although the genotype frequencies may be changed under Hardy-Weinberg equilibrium, the allele frequencies are unaltered (Futuyma 1998). Fixation index  $(F_{ST})$  is

often used as a measure of the observed variation in allele frequencies among populations. Although it must be noted that the estimate obtained in one population cannot be compared with that of another, unless the breeding system is similar for the two populations (Nei 1973).  $F_{ST}$  can be interpreted as the averaged standardized variances of all allelic variants. The differences in the allele frequencies among populations allow us to infer the level of gene flow by assuming the more similar the allele frequencies the higher the rate of gene flow. However, two assumptions must also hold true: the alleles measured must be selectively neutral and the allele frequencies must have reached an equilibrium between genetic drift and gene flow. Although in general the magnitude of gene flow estimated from genetic data corresponds fairly well with what may be expected from the natural history of the species (Futuyma 1998).

# **2.4.2.5 Founder effect**

The founder effect commences from the initiation of a new population with new founding genes (Futuyma 1998). Essentially, without immigration and spontaneous mutations, those alleles present in the founding individuals will determine the alleles for the future population. Blackman (2005) found evidence of a founder effect in a closed population of one-leaved tulip in South Australia. The presence of different founder germplasm may provide support for multiple introductions of *S. oleraceus.* 

#### **2.4.2.6 Bottlenecks**

Bottlenecks in populations arise when the population is temporarily restricted in size, either by a new colonisation event or a natural disaster (Futuyma 1998). They occur when the size of a new population becomes so small that a genetic bottleneck is formed (Russel 1980). Under these conditions genetic drift may counteract natural selection and fix an allele purely by chance.

### **2.4.2.7 Seed bank characteristics**

The state of the seed bank can influence the rate of resistance evolution and the longer the seed life of susceptible biotypes the greater the buffering effects in the seed bank, resulting in a decreased rate of resistance evolution (Hidayat 2004). Since *S. oleraceus* has low seed dormancy (Widderick 2002) changes in the gene pool can move at a rapid rate.

#### **2.4.3 MOLECULAR GENETICS AND RESITANCE EVOLUTION**

### **2.4.3.1 Introduction**

Molecular genetics is the study of the regulation of genetic information at the level of DNA, RNA and protein molecules. The *in vitro* amplification of DNA by the Polymerase Chain Reaction (PCR) has proven to be a revolutionary technique in molecular biology (Phillips and Vasil 2001; Clark 2005). Molecular biotechnology emerged as a new research field in the late 1970s as the result of this fusion of recombinant DNA technology and traditional industrial microbiology (Glick and Pasternak 2003). In 1944, Avery, MacLeod and Mc Carthy demonstrated that DNA is the genetic material and in 1953, Watson and Crick determined the structure of DNA. From 1961 to 1966 the entire genetic code was deciphered. Through the 1970s there was the establishment of recombinant DNA technology. In the 1980s and 1990s further DNA, PCR technology and methods were established leading to genetically modified crops, the nuclear cloning of a sheep and more importantly the revolution in population studies as the methods provided the opportunity to rapidly assess genetic changes without extensive breeding programmes.

Molecular techniques are now widely used as a tool in herbicide resistance evolution, for example Prado *et al.*, (2004) outlined several mechanisms leading to resistance to ALSinhibiting herbicides, with the most important being the presence of nuclear–inherited dominant mutations in the DNA sequence coding for the ALS enzyme. In wild plants, these mutations are located in different conserved domains where the herbicide binds to the enzyme (Boutsalis *et al.,* 1999).

### **2.4.3.2 Molecular components, techniques and methods**

# *Molecular markers and polymorphism*

A polymorphism is a genetic variant that results in two or more clearly different phenotypes existing in the same population of a species. Phillips and Vasil (2001) outline some new methods for molecular maps in plants and point out that there are widespread polymorphisms in natural populations. Each plant has variations in DNA sequences in their genome and this variation can be detected using genetic markers (Sunnucks 2000).

## *PCR markers*

Polymerase Chain Reaction (PCR) is a laboratory test tube technique to amplify specific DNA sequences by the extension of primers on DNA strands (Taylor 1991). For example, Wagner *et al.,* (2001) discuss the adaptation of the PCR amplification of specific alleles (PASA) for detection of point mutations in *Amaranthus retroflexus* and *Amaranthus rudis* leading to ALS inhibitor resistance. The major advantages of the method include the fast and clear test of the young plants for mutations. This test is a valuable tool for the identification of ALS-inhibiting resistance mutations.

### *RFLP*

Restriction fragment length polymorphism (RFLP) uses a restriction endonuclease to digest genomic DNA to form different fragments of DNA as a result of variations in DNA sequence (Whitkus *et al*., 1994). This marker technique detects polymorphisms in the genome of individuals (Jones *et al.,* 1997*).*

# *AFLP*

Amplified Fragment Length Polymorphism (AFLP) is a fingerprinting technique increasingly used to study genetic variation in plants (Vos *et al*., 1995). As a molecular tool it is rapid and a relatively simple method that can be applied to give much information about the variation present within a population (Baker 2002).

### *RAPD*

Randomly amplified polymorphic DNAs (RAPDs) are DNA fragments generated by the polymerase chain reaction using primers (Williams *et al.,* 1990). RAPD analysis has been criticised due to user error, which makes results between different laboratories difficult to reproduce. However, they are simple and require no knowledge of the genome sequence (Baker *et al.,* 2005).

## *SSRs or microsatellites*

Microsatellites or simple sequence loci are mainly distributed in genomic DNA in all regions of the chromosomes (Lu 2005). SSRs and microsatellites are probably the marker of choice for marker-based genetic analysis and marker-assisted plant breeding (Akkaya *et al*., 1992). Akkaya *et al*., (1992) reports that acceptable numbers of polymorphisms are observed with SSRs in self pollinated plants, whereas the number of polymorphisms detected by RFLPs is prohibitively low.

#### *ISSR*

Inter simple sequence repeats (ISSRs) have been used in numerous plant research areas including genetic diversity, phylogenic studies, gene tagging, genome mapping and evolutionary biology of different plant species (Godwin *et al*., 1997). ISSRs are relatively simple repeatable and can handle a large number of samples (Blackman 2005).

34

## *Dominance issues*

McDonald and McDermott (1993) outline that molecular markers are either dominant or codominant. Dominant systems such as randomly amplified polymorphic DNAs (RAPDs) and amplified fragment length polymorphisms (AFLPs) are unable to differentiate between heterozygous (Rr) and homozygous (RR rr) individuals since the markers are identified as present or not present.

## **2.4.4 SUMMARY - ISSUES IN ECOLOGICAL EXPERIMENTS**

Issues such as genetic variation, environmental variation and changes in ecological characteristics will be considered in selecting the molecular method and statistical analysis method for interpreting genetic diversity and gene flow in this study. Differences in allele frequency detected between populations elucidate the reasons for these observed differences, based on all known information in each particular case (Baker 2002).

When collecting samples there is always the element of thought as to whether the number of samples collected will yield meaningful data relating to differences. If the alleles of interest are rare then large numbers of individuals are required to detect its presence (Roush and Miller 1986). However, these authors further found that to observe a band (allele) that occurs at a frequency of 0.1% with a confidence level of 60%, only 10 individuals are be required. Certainly sampling a large percentage of the population is logistically impossible and, if it is accepted that rare alleles may be missed, representative samples may give indications of the population's genetic makeup. This study is more concerned with genetic variability on a landscape scale than on the detection of rare alleles, therefore, collections of a small number of individuals have been made from a wide geographical area and will be used to establish the presence of herbicide resistance and the genetic similarity between the individuals.

In conclusion this literature review has outlined a broad spectrum of what is known of the biology and ecology of *S. oleraceus*, aspects of herbicide resistance, population genetics and molecular genetics. What is not known is the distribution of resistance alleles in *S. oleraceus* in Australia, how the genes move, the genetic diversity of *S. oleraceus* and the sensitivity of *S. oleraceus* to the ALS-inhibiting herbicide, chlorsulfuron. These unknowns are the basis of this investigation.

### **CHAPTER 3**

#### **3 GENERAL MATERIALS AND METHODS**

#### **3.1** *Sonchus oleraceus* **SEED COLLECTION IN AUSTRALIA**

Populations of *S. oleraceus* were collected from throughout Australia between 1997 and 2008 (Figure 4). The accessions collected are listed from So1 to So574 in Appendix 1. The list includes the collection date, location and whether tested for resistance or susceptibility to chlorsulfuron. So1 to So40 were collected in 1997 and 1998 (Widderick 2005). New collections for this study commenced with So101 from a railway line in Wasleys, South Australia. Subsequent collections of *S. oleraceus* were made in southern Queensland and northern New South Wales, in areas where the species was known to have evolved resistance to ALS-inhibiting herbicides, and in other areas in Australia (Figure 3.1) to find how widespread herbicide resistance was. Seed collection details are outlined in Section 3.2. The first recorded case of resistance to ALS-inhibiting herbicides in *S. oleraceus* was found in 1991 at Goondiwindi (Figure 3.1) (Boutsalis and Powles 1995a). Subsequent surveys from 1997 to 2008 collected more accessions from locations in Australia (Figures 3.2 to 3.7). A total of 274 accessions from across Australia were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide on a state by state basis.



**Figure 3.1** General location of seed collections of *S. oleraceus* made in Australia between 1997 and 2008. The collection site of the first *S. oleraceus* (sowthistle) resistant to ALSinhibiting herbicide found at Goondiwindi, Queensland in 1991 is also displayed.

# **3.1.1 QUEENSLAND**

Figure 3.2 shows the location of Goondiwindi, where the first recorded case of resistance to ALS-inhibiting herbicides in *S. oleraceus* was found in 1991 (Boutsalis and Powles 1995a). The location of collection sites in Queensland, north of Goondiwindi are also shown. Ninety eight accessions from Queensland were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide.



**Figure 3.2.** Distribution of *S. oleraceus* (sowthistle) collection sites in Queensland Australia.

## **3.1.2 NEW SOUTH WALES**

The location of collection sites south of Goondiwindi, in New South Wales (Figure 3.3). Thirty two accessions from New South Wales were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide.



**Figure 3.3** Distribution of *S. oleraceus* (sowthistle) collection sites in New South Wales Australia.

# **3.1.3 SOUTH AUSTRALIA**

The first sample collected in South Australia for this project was collected between railway lines at Wasleys (Figure 3.4) accession number So101. It was later screened and found to be resistant to the ALS-inhibiting sulfonylurea herbicide chlorsulfuron. The resistance is likely

to have evolved from the railway utilities continuous use of the sulfonylurea herbicide sulfometuron methyl. Other locations of collection sites in South Australia are shown. One hundred and nineteen accessions were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide.



**Figure 3.4** Distribution of *S. oleraceus* (sowthistle) collection sites in South Australia, Australia.

# **3.1.4 WESTERN AUSTRALIA**

The location of seed collected by Dr. Kathryn McCarren of CSIRO Entomology, Wembley,

W.A. whilst surveying for eriophyid mite on *Sonchus* (Figure 3.5). Twelve accessions from

this collection were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide.



**Figure 3.5** Distribution of *S. oleraceus* (sowthistle) collection sites in Western Australia, Australia.

# **3.1.5 TASMANIA**

Figure 3.6 shows the collection site at Roaches Beach, near Hobart where the only *S.* 

*oleraceus* plant was collected in Tasmania.



**Figure 3.6** *S. oleraceus* (sowthistle) collection site at Roaches Beach, 15 km east of Hobart in Tasmania, Australia.

# **3.1.6 VICTORIA**

Location of seed collected by Dr. Peter Boutsalis of the University of Adelaide whilst surveying herbicide resistant weeds in Victoria (Figure 3.7). Twelve accessions from Victoria were treated with the ALS-inhibiting herbicide, chlorsulfuron to determine the level of resistance to the herbicide.



**Figure 3.7** Distribution of *S. oleraceus* (sowthistle) collection sites in Victoria, Australia.

#### **3.2 SEED COLLECTION AND STORAGE**

#### **3.2.1 SEED COLLECTION AND DRYING**

Accessions were created by collecting seed from single plants. The number of seed heads collected from each plant varied from one to approximately 20. Seed was collected directly into a seed envelope. Envelopes were labelled with the *S. oleraceus* number, GPS coordinates and the date and time. Seed was allowed to dry naturally or if necessary dried in a fan forced dehydrator at  $35^{\circ}$ C for 24 hrs.

#### **3.2.2 SEED STORAGE**

Labelled envelopes of dry seed were placed in water proof plastic containers and stored in a cold room at  $3^{\circ}$ C until required.

# **3.3 GERMINATION, CULTIVATION AND PLANT TREATMENTS**

#### **3.3.1 GERMINATION**

Seeds were germinated on 0.6% (w/v) agar in a controlled environment cabinet with a 12 hour light period at 20 $^{\circ}$ C at 30 µmol m<sup>-2</sup>s<sup>-1</sup> during the day and 12 hours dark period at night for seven days. Seedlings of even size and vigour were transplanted at the cotyledon stage (Figure 3.8) to cell trays (30 mm x 30 mm cells with 9 rows and 22 columns, each cell being tapered to a depth of 50 mm) or  $0.55$  L MK12 MasracTaglok punnet pots  $(90 \times 80 \text{ mm})$ containing coco peat potting mix. Coco peat potting mix was produced by mixing 540 L of coco peat, 220 L of water and 60 L of sand prior to steaming for 1 hour. The following additives were then mixed to the pasteurised mix; 180 g Dolomite lime; 600 g Agricultural lime; 240 g Hydrated lime; 180 g Gypsum; 180 g superphosphate; 450 g iron sulphate; 30 g iron chelate; 180 g Micromax trace elements; 450 g Calcium nitrate and 1800 g of Osmocote mini 3-4m (16-3-9+te).

# **3.3.2 PLANT GROWTH CONDITIONS**

Cell trays or punnet pots were transferred to the temperature controlled  $(21^{\circ}C)$  glasshouse and watered with a mist spray as required.

## **3.3.3 LEAF SAMPLING FOR DNA EXTRACTION**

Leaf material for DNA extraction,  $1 \text{cm}^2$ , was cut with sterile scissors from plants and transferred to a sterile labelled 1.5 mL eppendorf tube on ice. DNA was extracted immediately as section 3.4.1. After leaf sampling, plants were treated with the herbicide, chlorsulfuron to determine whether they were resistant or susceptible to the herbicide (as section 3.3.4).

# **3.3.4 HERBICIDE TREATMENT AND MEASUREMENTS**

At the two-leaf stage (Figure 3.9), seedlings were treated with chlorsulfuron at varying rates. All herbicides were applied with 0.2% v/v BS1000 non-ionic surfactant (Wetter  $TX^{\circledast}$ NuFarm, South Australia). Herbicide treatments were applied in a laboratory cabinet (Plate 3.1) through two Fan Jet Nozzles F-110-01 (Hardi, Australia) placed 40 cm above the plants in a water volume of  $110 L$  ha<sup>-1</sup> at a pressure of 250 kPa. A moving belt carried the nozzles at a speed of 1 ms<sup>-1</sup> Control plants were treated with water and  $0.2\%$  v/v BS1000 non-ionic surfactant. After treatments plants were returned to the glasshouse. Thirty days after treatment each plant was recorded as dead or alive. Plant harvested for dry matter were cut at soil surface and dried at 80°C for 48 hours.



**Figure 3.8** *S. oleraceus* seed with a seedling 3 days after germination.



**Figure 3.9** Two leaf *S. oleraceus* seedling 21 days after germination. Note two cotyledon leaves, first unifoliate leaf and second true leaf emerging.



**Plate 3.1** *S. oleraceus* plants after treatment in spray cabinet, the boom with two yellow nozzles can be seen at the end of the spray run.

# **3.4 MOLECULAR METHODS**

# **3.4.1 DNA EXTRACTION**

# **3.4.1.1 CTAB extraction**

CTAB DNA extraction was used for preliminary primer set screening as in section 3.4.2. Subsequent to this QUIAGEN DNeasy DNA extraction was used as described in section 3.4.1.2. DNA was extracted from the collected 1  $\text{cm}^2$  samples of leaf material by the following method. To each 1.5 mL eppendorf tube containing the leaf sample, 8 µL of 0.2% (v/v) ß-mercaptoethanol was added to 4 mL of cetyltrimethylammonium bromide (CTAB) isolation buffer (2% CTAB in 0.1 M Tris pH 8.0, 0.05 M ethylenediaminetetra acetic acid disodium salt pH 8.0, 0.5 M sodium chloride, 1% polyvinyl pyrrolidone (vinylpyrrolidine homopolymer) Mw 40,000) in a 10 mL centrifuge tube. The tube was then capped, gently inverted to mix the mercaptoethanol and isolation buffer and then placed in a water bath at

60°C for 2 hrs. Isolation buffer (500  $\mu$ L) was added to the plant tissue and the tissue macerated with a sterile micro pestle till homogenised. The homogenised tissue and buffer was incubated at  $60^{\circ}$ C for 90 minutes with occasional swirling. Chloroform (500 µL) was added to the vial and gently inverted for 60 seconds prior to centrifuging in an Eppendorf 5417 C tabletop centrifuge (Eppendorf, Hamburg, Germany) for 4 minutes at 20,000 *g* (14,000 rpm). A portion of the supernatant (0.45 mL) was then transferred to a new 1.5 mL tube and 0.5 volume of 5M NaCl (0.225 mL) added. Isopropanol (0.45 mL) was then added to the tube and gently mixed to precipitate out the nucleic acids. The tube was spun for 5 minutes at 20,000 *g*, leaving a beige speck at the base of the centrifuge tube. The supernatant was carefully removed with a pipette leaving the pellet at the base of the tube. Wash buffer of 76% (v/v) ethanol and 10 mM ammonium acetate (0.5 mL) was added. The tube was gently inverted to help wash the pellet and then set aside for 20 minutes. The wash buffer was carefully removed with a clean pipette. This process was repeated twice. On the last wash the tube was then centrifuged at 20,000 *g* for 2 minutes before the liquid was removed leaving the pellet behind. A sterile cotton bud was used to remove the last remaining traces of liquid from around the pellet. The pellet was then resuspended with 50 µL of TE (10 mM Tris EDTA) buffer (pH 7.4 to 8.0) (Appendix 6) taking care not to shear or break the DNA. 4.5  $\mu$ L of 4 mg/mL RNase solution was added to the tube, which was then incubated at 37°C for 30 minutes. The DNA solution was then stored at - $20^{\circ}$ C until required.

#### **3.4.1.2** *QIAGEN DNeasy extraction* **of DNA**

DNA extraction was also performed using a QIAGEN<sup>®</sup> DNeasy Plant Mini kit. Steps were performed at room temperature  $(15^{\circ}C - 25^{\circ}C)$ . 1.5 mL eppendorf tubes (usually in groups of 10) were lined up in a lab rack with each tube containing a fresh 1 cm<sup>2</sup> piece of leaf tissue. 400 µL of buffer AP1 and 4 µL of RNase A were added to each tube and the tissue disrupted with a plastic pestle and a few sterile fine sand grains. After disruption, the tubes were sealed

and placed in a  $65^{\circ}$ C water bath for ten minutes to incubate. Tubes were inverted three times during incubation. After ten minutes 130 µL of buffer AP2 was added, gently mixed and incubated on ice for 5 minutes to precipitate detergents, proteins and polysaccharides. The tubes containing the lysates were then centrifuged for 5 minutes at 20,000 *g* (14,000 RPM) to remove the precipitates. After centrifugation the supernatant (typically 500 µL) was transferred to a QIA shredder mini spin column placed in a 2 mL collection tube and centrifuged for 2 minutes at 20,000 *g*. The top of the QIA shredder mini spin column was discarded and the liquid (typically  $450 \mu L$ ) in the 2 mL collection tube transferred into a new 1.5 mL eppendorf tube. To the solution 675 µL of AP3 buffer was added and mixed immediately. A volume of 650 µL was transferred to the top of the mini spin column and centrifuged at 11,430 *g* (8000 rpm) for 1 minute. The flow through liquid was discarded and the remaining 450 µL transferred to the top of the column and centrifuged at 11,430 *g* for 1 minute. The 2 mL collection tube and flow through was discarded and the top of the mini spin column transferred to a new 2 mL collection tube. 500 µL of Buffer AW was transferred to the top of the mini spin column and centrifuge at 11,430 *g* for 1 minute. The flow through liquid was discarded and a second 500 µL of Buffer AW added to the mini spin column and centrifuged at 20,000 *g* for 2 minutes. The flow through base liquid was discarded and the top of the column transferred to a new 1.5 mL eppendorf tube. 80 µL of Buffer AE was added directly onto the DNeasy membrane in the mini spin column and incubated at room temperature (15<sup>°</sup> to 25<sup>°</sup>C) for 5 minutes. This was then centrifuged at 11,430 *g* for 1 minute. The minispin column was then discarded and the 1.5 mL eppendorf tube closed and kept on ice while concentration tests were performed. The concentration of DNA in the extracted samples was measured using a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, Wilmington, DE, USA) at  $260$ nm before being labelled and stored at - $20^{\circ}$ C until required.

## **3.4.2.1 INTER SEQUENCE REPEATS PRIMER SETS**

Primers complementary to inter sequence repeats, with variable three-base anchors at the 5' end and random primers were screened in PCR analyses to select the most informative primers in terms of number of bands and polymorphisms. A set of 12 primers were screened (Table 3.1). This method was not proceeded with due to superior results found when using AFLPs (section 3.4.3).

#	Primer	Primer sequence
	888	BDB CA CA CA CA CA CA CA CA
	891	HVH TG TG TG TG TG TG TG
3	880	HVH GT GT GT GT GT GT GT
	811	GAG AGA GAG AGA GAG AC
	820	GTG TGT GTG TGT GTG TC
6	818	CAC ACA CAC ACA CAC AG
	889	DBD AC AC AC AC AC AC AC
8	1423	HVH TGT TGT TGT TGT TGT
9	<b>OPT</b> 16	GGT GAA CGC T
10	OPT <sub>18</sub>	GAT GCC AGA C
11	OPT <sub>4</sub>	CAC AGA GGG A
12	OPT <sub>5</sub>	GGG TTT GGC A

**Table 3.1** Set of primers screened with *S. oleraceus* DNA.

### **3.4.2.2 AMPLIFICATION REACTION**

The amplification reactions were performed in 20  $\mu$ L volumes containing 2  $\mu$ L of DNA of known concentration, 13.7 µL of nanopure water, 2 µL of buffer [10 mM Tris-HCl (pH 8.8 at 25<sup>o</sup>C), 50 mM KCl, 0.1 % Triton X-100], 1.2 µL of 25 mM MgCl<sub>2</sub>, 0.5 µL of 10 mM dNTPs, 0.4  $\mu$ L of 0.25  $\mu$ M primer and 0.2  $\mu$ L of Taq (5 U/ $\mu$ L) DNA polymerase (Promega, Australia). A negative control without DNA template was included in each amplification reaction. The mixture was gently agitated and transferred to a Programmable Thermal Controller (PTC-100<sup>TM</sup>, MJ Research, Inc). The machine was programmed with the following thermal profile: 2 minutes for denaturation at  $94^{\circ}$  C, followed by 35 cycles of: 30 seconds of denaturation at  $94^{\circ}$ C, 30 seconds for annealing at  $54^{\circ}$ C and 1 minute for extension at  $72^{\circ}$  C. At the end of 35 cycles a final extension was applied at  $72^{\circ}$  C for 2 minutes. The reactions were then held at  $4^{\circ}$ C until used.

## **3.4.2.3 PCR PRODUCT VISUALISATION**

Amplified DNA was separated on 1.5% agarose gel (GibcoBRL Ultrapure, Cat. # 15510-021) prepared in a 1 x tris-acetate-EDTA (TAE) buffer. Six µL of each amplified product was mixed with 1  $\mu$ L of blue/orange loading buffer (Promega G1881) and loaded into each well. A high molecular mass standard ladder (Invitrogen Life Technologies, Carlsbad, CA, USA) was run in one well to quantify the concentration of DNA in each sample. Gel running conditions were 80 volts D.C. for 45 minutes. On completion of electrophoresis, gels were removed from the TAE buffer, drained and stained in 1  $\mu$ g mL<sup>-1</sup> ethidium bromide (Invitrogen Life Technologies, Carlsbad, CA, USA) in TAE running buffer for 15 minutes. Gels were then drained and washed in reverse osmosis water, then visualised under Ultra Violet light.

## **3.4.3 AMPLIFIED FRAGMENT LENGTH POLYMORPHISMS (AFLP)**

AFLPs are used in population genetics for genetic variation analysis as they are rapid to develop, produce individual fingerprints and use low amounts of DNA for analysis (Vos *et al*. 1995). The AFLP technique described by Vos *et al*., (1995) was used with the following modifications: the DNA was cut using M*se*1 and P*st*1 restriction enzymes, consequently M*se*1 and P*st*1 adapters were used in the ligation step. Concentrations of nucleotides throughout were reduced to reflect the sensitivity of a fluorescent based technique compared to the original method outlined by Vos *et al*., (1995). Pre-amplification PCR used P*st*1+A and M*se*1+C with the selective PCR amplification using dimers of P*st*1+A and M*se*1+C sequences (M*se*1+CC and P*st*1+AC: M*se*1+CT and P*st*1+AG). The P*st*1+AC and P*st*1+AG dimer primers were fluorescently labelled (Figure 3.10).
PCR products were run on an Applied Biosystems 3730, fluorescence-based DNA analyzer at the Australian Genome Research Facility (AGRF) in Adelaide. All reactions were performed in 96 well PCR polypropylene plates (Labcon, Petaluma, U.S.A.). After the addition of all reagents the well plate was sealed with sealex-PP adhesive film (Adelab, Adelaide, South Australia). Plates were then transferred to a Programmable Thermal Controller (Gradient Mastercycler, Eppendorf, Germany) or incubator for temperature variation processing. Products were stored at  $-20^{\circ}$ C until required.

Genomic DNA



Electrophoretic separation

**Figure 3.10** Flow chart showing the generation and detection of AFLPs from the digestion of genomic DNA with the restriction enzymes P*st1* and M*se*1.

## **3.4.3.1 DNA SELECTION AND ANNEALING OF ADAPTERS**

The DNA of *S. oleraceus* biotypes for analysis was selected and their concentrations adjusted to a final concentration of around 150 ng/µL. M*se*I and P*st*I adapters were annealed by the method outlined in Appendix 5B and 5C. Stock solutions were prepared containing both M*se*1 adapters (Table 3.2) at 50 µL each and P*st*1 adapters (Table 3.2) at 5 µM. Stocks were heated at  $90^{\circ}$ C for 3 minutes and then come to room temperature for 30 minutes.



#### **3.4.3.2 RESTRICTION LIGATION OF DNA**

The amplification reactions were performed in a 60 µL volumes in a 96 well plate. 20 µL of isolated genomic DNA with a concentration of 120 ng was transferred to the 96 well plate and kept on ice. A new 2 mL tube containing a master mix of 28.3 µL nanopure water, 6.0 µL of buffer [100 mM Tris-HCl (pH 7.5 at  $25^{\circ}$ C), 100 mM MgAcetate, 500 mMKAcetate & 50 mMDTT] two restriction enzymes P*st*1 (10 units) and M*se*1 (5 units), 0.2 mM ATP Cofactor, 0.08 µM Pst1 and 0.83 µM Mse1 adapters, and 1 Unit of T4 DNA ligase. The isolated genomic DNA was then double digested and ligated to the restricted fragments with 40 µL of master mix in the 96 well plate incubated for 3 hrs at  $37^{\circ}$ C.

# *Fragment testing and quantification*

The cut DNA fragments were separated on 1% TAE agarose gels. Samples of  $5 \mu L$  of cut DNA were loaded with 1 µL of 6X loading buffer (10% glycerol, 2 mM EDTA, 0.1% xylene cyanol and 0.1% bromophenol blue). A negative control of 5  $\mu$ L nanopure water and 1  $\mu$ L of 6X loading buffer was run in one cell. DNA fragment sizes were estimated by comparison to fragments present in a molecular weight marker mix 2 µL of high DNA mass ladder (Invitrogen Cat.# 10496-016) and 1 µL of 6X loading buffer. A low molecular mass ladder was used in the sequencing steps in 6.3.3. The gel was run at 80 volts for 45 minutes and then stained in ethidium bromide (1 mg/ $\mu$ L) for 12 minutes. The gel was gently washed with distilled water then visualised and photographed under 260 nm UV light.

# **3.4.3.3 PREAMPLIFICATION OF DNA**

The amplification reactions were performed in a 185 µL volumes in a 96 well plate. Digested ligated DNA (5.3 µL) with a concentration of 10.6 ng was transferred to a new 96 well plate and kept on ice. A new 2 mL tube containing a master mix of 9.5  $\mu$ L nanopure water, 6.0  $\mu$ L of buffer (10 x Taq buffer Mg free),  $1.9 \text{ mM } MgCl_2$ ,  $0.254 \text{ mM } dNTPs$ ,  $75 \text{ ng } Pst1$  primer (5') – GAC TGC GTA CAT GCA GA – 3' 5' – GAT GAG TCC TGA GTA AC – 3' with an additional A at the 3' extreme acting as the basis for selection) (Table 3.3), 75 ng M*se*1 primer  $(5' - GAT GAG TCC TGA GTA AC - 3'$  with an additional C at the 3' extreme acting as the basis for selection) (Table 3.3), and 1 Unit T*aq* polymerase.

<b>Table 3.3</b> Dequences of primers ascular modified the Let analysis.		
Mse1 pre-selective primer		$M+1$ primer $C = 5' - GAT GAG TCC TGA GTA AC - 3'$
Pst1 pre-selective primer		P+1primerA $5'$ – GAC TGC GTA CAT GCA GA – 3'
Mse1 selective primer CC	M1 primer2	$5'$ – GAT GAG TCC TGA GTA CC – 3'
Pst1 selective primer AC Fluro	P1 primer1	$5'$ – 7GA CTG CGT ACA TGC AGA C – 3'
Mse1 selective primer CT	M <sub>2</sub> primer <sub>2</sub>	$5'$ – GAT GAG TCC TGA GTA – 3'
Pst1 selective primer AG Fluro	P <sub>2</sub> primer <sub>1</sub>	$5'$ – 5GA CTG CGT ACA TCC AGA G – 3'

**Table 3.3** Sequences of primers used in modified AFLP analysis.

The mixture was gently agitated and transferred to a Programmable Thermal Controller (PTC- $100<sup>TM</sup>$ , MJ Research, Inc). The machine was programmed with the following thermal profile: 30 seconds of denaturation at  $94^{\circ}$  C, 1 minute for annealing at  $54^{\circ}$  C and 1 minute for extension at  $72^{\circ}$  C. This was followed by a further 25 cycles of further denaturation, annealing and extension. At the end of 25 cycles a final extension was applied at  $72^{\circ}$ C for 4 minutes. The reactions were then held at  $4^{\circ}$ C for further processing.

After pre amplification in the thermocycler 160  $\mu$ L of nanopure water was added to each reaction well and the plate and shaken at a slow speed for 15 minutes. Pre amplification preparations (template DNA) were stored at -20 $\mathrm{^{\circ}C}$  for further processing.

### **3.4.3.4 SELECTIVE PCR**

The amplification reactions were performed in a 20 µL volumes in a 96 well plate. Template DNA (5.3 µL) with a concentration of 0.31 ng was transferred to a new 96 well plate and maintained on ice. This step was duplicated to accept two different master mixes containing different primers. Two new 1.5 mL tubes were used for two master mixes 1 and 2. Master mix 1 consisted of 6.65 µL nanopure water, 2.0 µL of buffer (10 x Taq buffer Mg free), 2.04 mM MgCl2, 0.27 mM dNTPs, 25 ng P*st*1 fluorescent primer 1 AC (5' – 7GA CTG CGT ACA TGC AGA C – 3'), 25 ng M*se*1 primer 2 CC (5' – GAT GAG TCC TGA GTA CC – 3'), and 0.25 Units of T*aq* polymerase. Master mix 2 consisted of 6.65 µL nanopure water, 2.0 µL of buffer (10X Taq buffer Mg free),  $2.04 \text{ mM } MgCl_2$ ,  $0.27 \text{ mM } dNTPs$ ,  $25 \text{ ng } Pst1$  fluorescent primer 1 AG (5' – 5GA CTG CGT ACA TCC AGA G – 3') (Table 6), 25 ng M*se*1 primer 2 CT (5' – GAT GAG TCC TGA GTA  $-3$ ) (Table 3.3), and 0.25 Unit Tag polymerase. In the 96 well plate one group was mixed with 14.7 µL master mix 1 primer set and the other with master mix 2 primer set.

The following thermal profile was initiated: 30 seconds denaturation at  $94^{\circ}$  C, 30 seconds annealing at  $65^\circ$  C and 1 minute extension at  $72^\circ$  C, followed by 9 cycles of further denaturation, annealing and extension in which each annealing cycle was reduced by  $1^{\circ}$ C. At

the end of this sequence a second cycle of denaturation for 30 seconds at  $94^{\circ}$ C, annealing 30 seconds at  $56^{\circ}$  C and extension 1 minute at  $72^{\circ}$  C for 25 cycles was initiated. The PCR product was held in the dark at  $4^{\circ}$ C for further processing.

### **3.4.3.5 SEQUENCE ANALYSIS**

Selective PCR product  $(5.3 \mu L)$   $(3.4.3.4)$  was transferred to a new 96 well PCR polypropylene plate with 64.7 µL of nanopure water in each receiving well. This transfer was carried out in two separate groups, one for each of the two master mixes (Figure 3.11). After addition of all reagents the plate was sealed with Sealex-PP adhesive film wrapped in alfoil and delivered to the Australian Genome Research Facility for capillary analysis on an Applied Biosystems 3730, fluorescence–based DNA analyser.

		2	3	4	5	6		8	9	10	11	12
	$DNA - 1$	DNA - 2	$DNA - 3$	$DNA - 4$	<b>DNA - 5</b>	$DNA - 6$	$DNA - 7$	<b>DNA - 8</b>	$DNA - 9$	<b>DNA - 10</b>	<b>DNA - 11</b>	<b>DNA - 12</b>
	<b>CC-ACflur</b>	<b>CC-ACflur</b>	<b>CC-ACflur</b>	<b>CC-ACflu</b>	<b>CC-ACflu</b>	<b>CC-ACflur</b>	<b>CC-ACflur</b>	<b>CC-ACflur</b>	<b>CC-ACflur</b>	<b>CC-ACflur</b>	CC-ACflu	<b>CC-ACflur</b>
B	DNA - 13	<b>DNA - 14</b>	<b>DNA - 15</b>	DNA - 16	DNA - 17	DNA - 18	<b>DNA - 19</b>	DNA - 20	<b>DNA - 21</b>	DNA - 22	DNA - 23	<b>DNA - 24</b>
	<b>CC-ACflur</b>	<b>CC-ACflu</b>	<b>CC-ACflur</b>	<b>CC-ACflu</b>	<b>CC-ACflur</b>							
	<b>DNA - 25</b>	<b>DNA - 26</b>	<b>DNA - 27</b>	<b>DNA - 28</b>	<b>DNA - 29</b>	<b>DNA - 30</b>	<b>DNA - 31</b>	<b>DNA - 32</b>	<b>DNA - 33</b>	<b>DNA - 34</b>	<b>DNA - 35</b>	<b>DNA - 36</b>
	<b>CC-ACflur</b>	<b>CC-ACflu</b>	<b>CC-ACflur</b>									
	<b>DNA - 37</b>	<b>DNA - 38</b>	<b>DNA - 39</b>	<b>DNA - 40</b>	DNA - 41 I	DNA - 42	<b>DNA - 43</b>	DNA - 44	<b>DNA - 45</b>	DNA - 46	DNA - 47	<b>DNA - 48</b>
	<b>CC-ACflur</b>	<b>CC-ACflu</b>	<b>CC-ACflur</b>									
E	<b>DNA - 1</b>	<b>DNA - 2</b>	$DNA - 3$	$DNA - 4$	$DNA - 5$	<b>DNA - 6</b>	<b>DNA - 7</b>	$DNA - 8$	$DNA - 9$	DNA - 10	<b>DNA - 11</b>	DNA - 12
	CT-AGflur	CT-AGflur	<b>CT-AGflur</b>	<b>CT-AGflur</b>	CT-AGflur	<b>CT-AGflur</b>	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur	<b>CT-AGflur</b>
F	DNA - 13	<b>DNA - 14</b>	<b>DNA - 15</b>	<b>DNA - 16</b>	<b>DNA - 17</b>	<b>DNA - 18</b>	<b>DNA - 19</b>	<b>DNA - 20</b>	<b>DNA - 21</b>	<b>DNA - 22</b>	<b>DNA - 23</b>	<b>DNA - 24</b>
	CT-AGflur	<b>CT-AGflur</b>	CT-AGflur	CT-AGflur								
G	<b>DNA - 25</b>	DNA - 26	<b>DNA - 27</b>	<b>DNA - 28</b>	<b>DNA - 29</b>	<b>DNA - 30</b>	<b>DNA - 31</b>	<b>DNA - 32</b>	<b>DNA - 33</b>	<b>DNA - 34</b>	<b>DNA - 35</b>	<b>DNA - 36</b>
	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur	<b>CT-AGflur</b>	<b>CT-AGflur</b>	<b>CT-AGflur</b>	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur
Н	DNA - 37	DNA - 38	<b>DNA - 39</b>	$DNA - B$	<b>DNA - 41</b>	DNA - 42 I	<b>DNA - 43</b>	DNA - 44	<b>DNA - 45</b>	DNA - 46	<b>DNA - 47</b>	<b>DNA - 48</b>
	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGf40	CT-AGflur	<b>CT-AGflur</b>	<b>CT-AGflur</b>	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur	CT-AGflur

**Figure 3.11** Ninety six well plate for capillary analysis on an Applied Biosystems 3730 fluorescence based DNA analyser. Final volume 70 µL process of 5.3 µL selective PCR product plus 64.7 µL of nanopure water. This plate has 48 duplicated DNA samples with 2 master mixes (CC-AC and CT-AG).

# **3.4.3.6 GENOMIC DATA ANALYSIS**

Genomic data was viewed with Genemapper<sup>®</sup> software for the presence and absence of peaks at each loci. Judgements were made on peak profiles at each loci and a binary score of one for a peak (cut off 200 relative fluorescence units) and zero for no peak (less than 200 relative

fluorescence units) was assigned for each sample at each loci. A total of x loci (about 200) were scored for selective primer pair M*se*1+CC and P*st*1+AC and a total of y loci (about 200) were scored for selective primer pair M*se*1+CT and P*st*1+AG, giving a maximum of x+y loci (about 400). Data for each sample were stored on an excel file prior to transfer to a text file for analysis with PopGene<sup>®</sup> software to determine genetic relationships. Popgene<sup>®</sup> is freeware for analysis of genetic variation among and within populations using co-dominant and dominant markers, such as AFLP's. The software generated dendrograms for each population analysis, based on Nei's regular and unbiased genetic distance measures. It was used to compute genetic distance.

#### **CHAPTER 4**

#### **4 ALS-INHIBITING HERBICIDE RESISTANCE**

### **4.1 INTRODUCTION**

There are 4 chemical families within the ALS-inhibiting herbicides that have been commercialised in Australia. These are the sulfonylureas, imidazolinones, sulfonamides and the pyrimidinylthiobenzoates. Resistance to each of these families are known and different mutations can result in different patterns of resistance (Tranel and Wright 2002). The first ALS inhibiting herbicide to be used in Australia was chlorsulfuron (a sulfonylurea), which was widely used in the cereal growing regions in the early 1980s (Boutsalis 1996). Since the discovery of the first biotype of *S. oleraceus* resistant to ALS inhibiting herbicides in Australia (Boutsalis and Powles 1995a), others have confirmed additional populations of *S. oleraceus* with resistance to ALS-inhibiting herbicides in Queensland and New South Wales (Adkins *et al*., 1997, Widderick 2002 and Walker *et al.,* 2005b).

As previously reviewed in 2.3.2.5, cross resistance to a number of different herbicides in the same group (for example sulfonylureas) can be found to exist in a single plant accession. However, the patterns of resistance produced by a dose rate experiment can vary. Acknowledging that exceptions exist, resistance caused by altered ALS can be classified into 3 groups of cross resistance: 1. Sulfonylurea and Sulfonamides; 2. Imidazolinones and Pyrimidinylthiobenzoates; and 3. Sulfonylurea, Sulfonamides, Imidazolinones and Pyrimidinylthiobenzoates (Tranel and Wright 2002).

Since it is known that in the last two decades, numerous populations of *S. oleraceus* in southern Queensland have evolved resistance to ALS-inhibiting herbicides (Widderick 2002), it follows that this resistance may be evolving in other locations in Australia. To ascertain the extent of ALS-inhibiting herbicide resistant *S. oleraceus* in Australia, seed was collected (with GPS locations) and tested to determine whether resistance exists or not. In 2005 the first seed collection from *S. oleraceus* plants was from a bulk of approximately 10 plants in a field at Roseworthy, South Australia. On treatment with a sulfonylurea herbicide it was discovered that there was a mixture of susceptible and resistant plants. Since *S. oleraceus* is self pollinated (Barber 1941), it was suspected that individual plants either did or did not have the mutation for resistance. However, some rare cross pollination has been reported (Stebbins *et al.*, 1953; Lewin (1975) and Boutsalis and Powles (1995b). Preliminary work found that seed from individual plants produced either 100% resistant or susceptible progeny.

All seed in the collection from 2005 to 2008 were from individual single plants (accessions). From this seed, resistance screening was conducted. In section 4.2 the sensitivity of *S. oleraceus* germplasm collected from across Australia to chlorsulfuron was tested. In addition, the distribution of resistance in *S. oleraceus* across Australia is tabulated. From these results populations were selected for studies to understand the spread of ALS-inhibitor resistance in this species.

Since resistance to sulfonylureas and imidazolinones is known to be caused by different mutations (Sathasivan *et al*., 1991) there is a need to screen some sulfonylurea resistant populations against imidazolinones to ascertain whether the resistant *S. oleraceus* plants are cross resistant to these herbicides. In section 4.3 the treatment of 22 *S. oleraceus* lines (resistant to chlorsulfuron) with an imidazolinone herbicide (imazethapyr) were assessed.

Dose rate experiments are conducted to determine the plants sensitivity when treated with a herbicide (White 2002) and they are an important tool in weed science (Seefeldt *et al*., 1995). Here I report on the sensitivity of 9 *S. oleraceus* biotypes to chlorsulfuron to test the hypothesis that *S. oleraceus* populations throughout Australia vary in their sensitivity to different dose rates of chlorsulfuron.

### **4.2 MATERIALS AND METHODS**

#### **4.2.1** *S. oleraceus* **seed collection**

A collection of seed was compiled from past collections maintained at the Waite Institute since 1991, Queensland Primary Industry and Fisheries (1997-1998) and recent collections between 2005 and 2008 were from southern Queensland, northern New South Wales, South Australia, Western Australia, Victoria and Tasmania. Seed was collected from single plant accessions. Dry seed was stored in labelled envelopes placed in sealed boxes and refrigerated at  $3^{\circ}$ C until required for further tests.

# **4.2.2 Seed and seedling treatment - chlorsulfuron**

Seeds from each of the accessions were germinated on 0.6% (w/v) agar as section 3.3. After 7 days seedlings were transplanted to 22 x 9 individual cell trays containing pasteurised commercial premium potting mix with 9 seedlings planted on a column per accession. At the two to three leaf stage 28 days after germination the trays were treated with chlorsulfuron at 15g a.i. ha<sup>-1</sup> + 0.2% (v/v) non-ionic surfactant. Herbicide treatment was applied in a laboratory cabinet sprayer as section 3.3. After treatment labelled trays were held in the spray treatment laboratory for one day to allow the spray treatment to dry before being allocated to space in the glasshouse. Plants were watered as required to maintain the soil at field capacity.

### **4.2.3 Seed and seedling treatment - imidazolinone**

Seed for imidazolinone (imazethapyr) screening was selected from 15 lines resistant to the chlorsulfuron from field south 4 at Roseworthy, South Australia (Table 4.3.2.4). Seed and seedling treatment is as 3.3 but at the two to three leaf stage 28 days after germination the trays were treated with imazethapyr at 75g a.i. ha<sup>-1</sup> + 0.2% (v/v) non-ionic surfactant.

# **4.2.4 Seed and seedling treatment – dose rate experiment**

# **4.2.4.1 Plant material selected for treatment**

From preliminary experiments using a single chlorsulfuron rate of 15 g a. i. ha<sup>-1</sup> conducted in late 2005 and early 2006 with *S. oleraceus* biotypes, five resistant and four susceptible populations (Table 4.1) were selected for dose response experiments. Accessions were randomly selected with approximately half resistant and half susceptible.

Sonchus number	Location	Latitude/Longitude	Response to chlorsulfuron <sup>a.</sup>	
So 56	Paradise, South Australia	34° 52′ 24.81″ S	$138^{\circ} 40' 08.01"$ E	Susceptible
So 57	<sup>b</sup> :Goondiwindi, Queensland	28° 32′ 49.33″ S	$150^{\circ}$ 18' 26.66" E	Resistant
So 101	Wasleys, South Australia	34° 28′ 51.65″ S	138°41′12.81″E	Resistant
So 102	Roseworthy, South Australia	34° 29′ 52.75″ S	$138^{\circ}41'18.12''$ E	Resistant
So 103A	Nairne, South Australia	$35^{\circ}$ 02' 42.44" S	$138^{\circ}$ 54' 43.40" E	Susceptible
So 103B	Nairne, South Australia	35° 02′ 42.44″ S	$138^{\circ}$ 54' 43.40" E	Susceptible
So 125	Dalby, Queensland	$27^{\circ}$ 08' 93.00" S	$151^{\circ}$ 17' 11.00" E	Resistant
So 220	Wasleys, South Australia	34° 28′ 41.38″ S	138° 40' 51.99" E	Resistant
So 234	Roseworthy, South Australia	34° 30′ 10.20″ S	138°41′24.22″E	Susceptible

**Table 4.1** Geographic location of *S.oleraceus* plants selected for inclusion in the dose rate experiment and their response to chlorsulfuron 15 g a. i. ha<sup>-1</sup> (20 g ha<sup>-1</sup> Glean<sup>®</sup>).

<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

<sup>b</sup> Goondiwindi, Queensland. First ALS-inhibiting herbicide resistant plant found in Australia in 1991.

## **4.2.4.2 Treatment methodology**

The experiment was conducted in a glasshouse at the University of Adelaide, Waite Campus in South Australia. It was a randomised complete block design with 4 replicates where 9 factor biotypes (So56, So57, So101, So102, So103A, So103B, So125, So220 and So234) were randomly assigned to the experiment and the 8 treatments  $(0, 1.875 \text{ g}, 3.75 \text{ g}, 7.5 \text{ g}, 15 \text{ g},$ 30 g, 60 g and 120 g ha<sup>-1</sup> chlorsulfuron) were also randomly allocated. On 24 March 2006 120 seeds from each of the 9 biotypes were sown on 0.6% agar in individual containers. The seeds were germinated and treated as general methods section 3.3. On 3 April 2006, 32 even seedlings (8 treatments by 4 replicates) were transplanted to 12 x 12 cm pots containing pasteurised, commercial, premium potting mix (3.3.1). All pots were labelled and randomly allocated in the glasshouse. At the two to three-leaf stage, on the 21 April 2006, 4 replicates of each of the 9 biotypes were separated into 8 treatment groups. One group of 32 plants was not treated with chlorsulfuron and retained as a control. The seven remaining groups were treated with 1.875 g, 3.75 g, 7.5 g, 15 g, 30 g, 60 g and 120 g ha<sup>-1</sup> chlorsulfuron + 0.2% (v/v) non-ionic surfactant. Herbicide treatments were applied in a laboratory cabinet sprayer (as section 3.3.5). After treatment plants were returned to the glasshouse. Plants were watered as required to field capacity until the end of the experiment.

#### **4.2.4.3 Measurements**

To assess the response of individual plants to chlorsulfuron, dry matter biomass was measured and an assessment of plant status (dead or alive) was made 30 days after treatment. When assessing dry matter biomass, plants were carefully cut at soil level, ensuring all above ground plant material was sampled. Plant material was dried at 80°C for 2 days prior to weighing.

#### **4.2.4.4 Data analysis**

Statistical analysis of the dose response curves followed the procedure detailed by Seefeldt *et al.* (1995). Data were fitted to the log-logistic model:  $Y = C + (D - C)/(1 + exp(b(\ln(x) - \ln(x)))$  $(GR_{50}))$ )) where Y = shoot weight (% of untreated control), x = herbicide dose (g ha<sup>-1</sup>; a value of 1.0 was added to each dose to calculate natural logarithms, In),  $C =$  lower limit of the response curve, D = upper limit, b = slope and  $GR_{50}$  = dose (g ha<sup>-1</sup>) of herbicide that reduced shoot weight by 50% relative to the untreated control. Data were fitted to the model using Prism  $5^{\circledR}$ .

### **4.3 RESULTS AND DISCUSSION**

The results of this experiment (Tables 4.2 and 4.7) indicate a varying frequency in the level of resistance between individual states in Australia and that resistance to chlorsulfuron is now widespread in Australia as summarized in Table 4.8 Specific detail of the location of resistant and susceptible plants, state by state are presented in Tables 4.2 to 4.7. From these lists, plants were selected for use in the dose rate experiment, gene flow experiment and for AFLP analysis.

# **4.3.1 Queensland** *S. oleraceus* **chlorsulfuron treatment**

The results from the Queensland accessions tested (Table 4.2) show varying sensitivity to chlorsulfuron with 58 accessions being resistant and 40 susceptible. The progeny from the seed of 23 accessions taken from a field at Warra produced 11 resistant and 12 susceptible populations (Table 4.2, footnote <sup>c</sup>). Similarly the progeny from the seed of 11 individual plants taken from a field in the Condamine produced 10 resistant and 1 susceptible accessions (Table 4.2, footnote  $\mathrm{d}$ ).

	Location	Latitude/Longitude	Response to	
Sonchus				chlorsulfuron <sup>a.</sup>
number				
$\mathbf{1}$ So	Billa Billa, Queensland	$28^{\rm o}\,10'$ 00.00" S	150° 16' 00.00" E	Resistant
$\overline{7}$ So	Billa Billa, Queensland	28° 10' 00.00" S	150° 16' 00.00" E	Susceptible
14 So	Dalby, Queensland	27° 08′ 93.00″ S	151° 17' 11.00" E	Resistant
16 So	Jackson, Queensland	26° 38' 29.49" S	149° 41' 51.19" E	Resistant
17A So	Gatton, Queensland	27° 33' 34.00" S	152° 16' 46.00" E	Susceptible
17B So	Gatton, Queensland	27° 33' 34.00" S	152° 16' 46.00" E	Susceptible
34 So	Roma, Queensland	26° 34′ 51.54″ S	148° 57' 27.02" E	Susceptible
57 So	<sup>b.</sup> Goondiwindi, Queensland	28° 32' 49.33" S	150° 18' 26.66" E	Resistant
So 123	Oakey, Queensland	27° 24′ 57.00" S	151° 39' 70.00" E	Susceptible
So 124	Dalby, Queensland	27° 18' 20.00" S	151° 26' 32.00" E	Susceptible
So 125	Dalby, Queensland	27° 08′ 93.00″ S	151° 17' 11.00" E	Resistant
So 126	Dalby, Queensland	27° 08′ 93.00″ S	151° 17' 11.00" E	Susceptible
So 127	Dalby, Queensland	27° 08' 93.00" S	$151^{\circ}$ 17' 11.00" E	Susceptible
So 128	<sup>c.</sup> Warra, Queensland	26° 53' 82.00" S	150° 51' 08.00" E	Susceptible
So 129	<sup>c.</sup> Warra, Queensland	26° 53′ 15.00" S	150° 51' 48.00" E	Susceptible
So 130	<sup>c.</sup> Warra, Queensland	26° 53' 17.00" S	150° 51' 47.00" E	Resistant
So 131	<sup>c.</sup> Warra, Queensland	26° 53' 18.00" S	150° 51' 45.00" E	Resistant
So 132	<sup>c.</sup> Warra, Queensland	26° 53' 19.00" S	150° 51' 44.00" E	Resistant
So 133	<sup>c.</sup> Warra, Queensland	26° 53' 20.00" S	150° 51' 43.00" E	Resistant
So 134	<sup>c.</sup> Warra, Queensland	26° 53' 18.00" S	150° 51' 43.00" E	Resistant
So 135	<sup>c.</sup> Warra, Queensland	26° 53' 16.00" S	150° 51' 44.00" E	Susceptible
So 136	<sup>c.</sup> Warra, Queensland	26° 53' 14.00" S	150° 51' 44.00" E	Susceptible
So 137	<sup>c.</sup> Warra, Queensland	26° 53' 12.00" S	150° 51' 44.00" E	Susceptible
So 138	<sup>c.</sup> Warra, Queensland	26° 53' 12.00" S	150° 51' 42.00" E	Susceptible
So 139	<sup>c.</sup> Warra, Queensland	26° 53' 13.00" S	150° 51' 42.00" E	Susceptible
	<sup>c.</sup> Warra, Queensland	26° 53' 14.00" S	150° 51' 40.00" E	Susceptible
So 140	<sup>c.</sup> Warra, Queensland	26° 53′ 15.00" S	150° 51' 40.00" E	
So 141		26° 53' 16.00" S	150° 51' 37.00" E	Susceptible
So 142	<sup>c.</sup> Warra, Queensland	26° 53' 14.00" S	150° 51′ 37.00" E	Susceptible
So 143	<sup>c</sup> Warra, Queensland			Resistant
So 144	<sup>c.</sup> Warra, Queensland	26° 53' 12.00" S	150° 51' 37.00" E 150° 51' 38.00" E	Susceptible
So 145	<sup>c.</sup> Warra, Queensland	26° 53' 10.00" S		Resistant
So 146	<sup>c.</sup> Warra, Queensland	26° 53' 07.00" S	150° 51' 40.00" E	<b>Resistant</b>
So 147	<sup>c.</sup> Warra, Queensland	26° 53' 07.00" S	150° 51′ 38.00" E	Resistant
So 148	<sup>c.</sup> Warra, Queensland	26° 53′ 09.00" S	150° 51′ 37.00" E	Resistant
So 149	<sup>c.</sup> Warra, Queensland	26° 53' 10.00" S	150° 51' 36.00" E	Resistant
So 150	<sup>c.</sup> Warra, Queensland	26° 53' 12.00" S	150° 51' 34.00" E	Susceptible
So 151	Condamine, Queensland	26° 55' 35.00" S	$150^{\rm o}$ 04' 64.00" E	Resistant
So 152	Condamine, Queensland	27° 06' 12.00" S	149° 56' 44.00" E	Susceptible
So 153	Condamine, Queensland	27° 06' 12.00" S	149° 58' 17.00" E	Susceptible
So 154	Meandarra, Queensland	27° 22′ 00.00" S	150° 04' 71.00" E	Resistant
So 155	Dalby, Queensland	27° 16' 00.00" S	150° 05' 69.00" E	Resistant
So 156	Brookstead, Queensland	27° 47' 00.00" S	151° 24' 51.00" E	Resistant
So 157	Millmeran, Queensland	28° 00' 53.00" S	150° 53' 99.00" E	Susceptible
So 158	Goondiwindi, Queensland	28° 09' 97.00" S	150° 25' 79.00" E	Susceptible
So 159	Billa Billa, Queensland	28° 10' 00.00" S	150° 27' 00.00" E	Resistant
So 160	Billa Billa, Queensland	28° 07' 61.00" S	150° 15' 29.00" E	Susceptible
So 161	Billa Billa, Queensland	28° 07' 00.00" S	150° 15' 29.00" E	Resistant
So 162	Billa Billa, Queensland	28° 05' 00.00" S	150° 15' 08.00" E	Resistant
So 163	Moonie, Queensland	27° 44' 00.00" S	150° 19' 80.00" E	Resistant
So 164	Moonie, Queensland	27° 44' 00.00" S	$150^{\circ}$ 15' 96.00" E	Resistant
So 165	Bungunya, Queensland	28° 01' 43.00" S	149° 41' 93.00" E	Susceptible
So 168	Bungunya, Queensland	28° 25' 00.00" S	149° 42′ 05.00" E	Resistant

**Table 4.2** The collection locations of *S. oleraceus* accessions from Queensland and the response of their progeny to the ALS-inhibiting herbicide, chlorsulfuron (15 g a. i. ha<sup>-1</sup>).



<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

<sup>b</sup> Goondiwindi, Queensland. First ALS-inhibiting herbicide resistant plant found in Australia in 1991.

<sup>c</sup> Warra, Queensland. Plants from a single field.

<sup>d</sup> Condamine, Queensland. Plants from a single field.

<sup>e</sup> Goondiwindi, Queensland. Plants from a single field.

f Toowoomba, Queensland. Plant from town centre.

## **4.3.2 South Australian** *S. oleraceus* **chlorsulfuron treatment**

The results from the South Australian accessions tested (Table 4.3), show varying sensitivity to chlorsulfuron with 35 accessions being resistant and 84 susceptible. The progeny from the seed of 37 accessions taken from a single field at Roseworthy produced 15 resistant and 22 susceptible populations (Table 4.3, footnote  $\frac{g}{g}$ ). Detailed studies of plants from this field are covered in Chapter 7. Plants from the roadside adjacent to this field proved to be a mixture of resistant and susceptible individuals. However, a collection of 9 plants from a different field on the same farm all proved to be susceptible. A single resistant plant was found at Stirling in the Adelaide Hills, where few ALS-inhibiting herbicides are used. It is possible this seed arrived by wind from elsewhere and shows the mobile nature of the wind blown seeds. At one site in metropolitan Adelaide, 4 resistant plants were found growing close together. This may have been caused by evolution of resistance from council roadside spraying over numerous years.

Sonchus	Location		Latitude/Longitude	Response to
number				chlorsulfuron <sup>a</sup>
56 So	Paradise, South Australia	34° 52′ 24.81" S	138° 40' 08.01" E	Susceptible
So 101	Wasleys, South Australia	34° 28′ 51.65″ S	138°41′12.81″E	Resistant
So 102	Roseworthy, South Australia	34° 29' 52.75" S	138°41′18.12″E	Resistant
So 103	Nairne, South Australia	35° 02′ 42.44″ S	138° 54' 43.40" E	Susceptible
So 104	St. Kilda, South Australia	34° 42′ 54.57″ S	138° 34' 35.13" E	Susceptible
So 106	Virginia, South Australia	34° 38' 56.29" S	138° 34′ 21.94″ E	Resistant
So 107	Roseworthy, South Australia	34° 34' 15.74" S	138° 40' 06.32" E	Susceptible
So 108	Wasleys, South Australia	34° 33' 09.35" S	138° 41' 32.88" E	Resistant
So 114	Adelaide, South Australia	34° 56' 35.35" S	138° 34' 53.29" E	Susceptible
So 115	Adelaide, South Australia	34° 56' 35.35" S	138° 34' 53.29" E	Susceptible
	Urrbrae, South Australia	34° 58' 06.99" S	138° 38' 02.95" E	Susceptible
So 120		34° 28' 20.95" S	138° 41' 10.44" E	
So 121	Wasleys, South Australia			Susceptible
So 122	Wasleys, South Australia	34° 28' 20.95" S	138° 41' 10.44" E	Susceptible
So 178	Adelaide, South Australia	34° 56' 05.22" S	138° 36' 45.92" E	Susceptible
So 179	Myrtle Bank, South Australia	34° 57' 44.93" S	138° 38' 17.55" E	Susceptible
So 196	Myrtle Bank, South Australia	34° 57' 44.93" S	138° 38' 17.55" E	Susceptible
So 197	Glenunga, South Australia	34° 57' 33.23" S	138° 38' 58.08" E	Resistant
So 198	Urrbrae, South Australia	34° 58′ 13.55″ S	138° 38' 22.89" E	Susceptible
So 199	Myrtle Bank, South Australia	34° 57′ 44.80″ S	138°38′17.60″E	Resistant
So 200	Myrtle Bank, South Australia	34° 57' 44.94" S	138° 38' 17.55" E	Susceptible
So 201	Myrtle Bank, South Australia	34° 57' 44.95" S	138° 38' 17.55" E	Susceptible
So 215	Myrtle Bank, South Australia	34° 57' 44.96" S	138° 38' 17.55" E	Susceptible
So 216	Myrtle Bank, South Australia	34° 57' 43.01" S	138° 38' 25.85" E	Susceptible
So 217	Urrbrae, South Australia	34° 58' 06.99" S	138° 38' 02.95" E	Susceptible
So 220	Wasleys, South Australia	34° 28′ 41.38" S	138° 40' 51.99" E	Resistant
So 230	Eden Hills, South Australia	35° 00' 53.33" S	138° 34' 54.77" E	Susceptible
So 234	Roseworthy, South Australia	34° 30' 10.20" S	138° 41' 24.22" E	Susceptible
So 239	Port Lincoln, South Australia	34° 44′ 46.01" S	135° 52′ 45.74″ E	Susceptible
So 240	Port Lincoln, South Australia	34° 44′ 46.02″ S	135° 52' 45.74" E	Susceptible
So 241	Port Lincoln, South Australia	34° 44' 46.03" S	135° 52' 45.74" E	Susceptible
So 242	Port Lincoln, South Australia	34° 44′ 46.04″ S	135° 52' 45.74" E	Susceptible
So 266	Roseworthy, South Australia	34° 30' 43.38" S	138° 41' 20.06" E	Susceptible
So 267	Roseworthy, South Australia	$34^{\circ}30'$ 43.39" S	138°41′20.06″E	Susceptible
So 268	Roseworthy, South Australia	34° 30' 43.40" S	138° 41' 20.06" E	Susceptible
So 269	Roseworthy, South Australia	34° 32′ 24.31″ S	138° 41' 29.26" E	Susceptible
So 270	Wasleys, South Australia	34° 28′ 40.00" S	138° 40' 51.00" E	Resistant
So 271	Wasleys, South Australia	34° 28′ 16.00" S	138° 40' 41.00" E	Resistant
So 272	Gawler, South Australia	34° 34′ 02.62″ S	138° 43' 37.17" E	Susceptible
So 273	Roseworthy, South Australia	34° 30' 54.50" S	138° 41' 55.00" E	Resistant
So 274	Roseworthy, South Australia	34° 30' 58.11" S	138° 42′ 34.10″ E	Susceptible
So 275	Nairne, South Australia	35° 02′ 42.54″ S	138° 54' 42.98" E	Susceptible
So 276	Semaphore, South Australia	35° 50' 22.22" S	138° 28' 52.11" E	Susceptible
So 277	<sup>h</sup> Roseworthy, South Australia	34° 30' 47.65" S	138° 41' 22.10" E	Susceptible
So 278	<sup>h</sup> Roseworthy, South Australia	34° 30' 46.82" S	138° 41' 21.89" E	Susceptible
So 279	<sup>h</sup> Roseworthy, South Australia	34° 30' 47.72" S	138° 41' 21.70" E	Susceptible
So 280	<sup>h</sup> Roseworthy, South Australia	34° 30' 44.35" S	138° 41' 21.77" E	Susceptible
So 281	<sup>h</sup> Roseworthy, South Australia	34° 30' 43.24" S	138° 41' 21.53" E	Susceptible
So 282	<sup>h</sup> Roseworthy, South Australia	34° 30' 42.32" S	138° 41' 21.46" E	Susceptible
So 283	h.Roseworthy, South Australia	34° 30' 41.04" S	138° 41' 21.87" E	Susceptible
So 284	<sup>h</sup> Roseworthy, South Australia	34° 30' 39.84" S	138° 41' 21.89" E	Susceptible
So 285	Baratta, South Australia	31° 56' 09.54" S	139° 05' 44.64" E	Susceptible
So 286	<sup>g</sup> Roseworthy, South Australia	34° 33' 05.00" S	138° 41' 32.00" E	Susceptible
	<sup>g</sup> Roseworthy, South Australia	34° 33' 02.50" S	138° 41' 30.00" E	Susceptible
So 287				

**Table 4.3** The collection locations of *S. oleraceus* accessions from South Australia and the response of their progeny to the ALS-inhibiting herbicide, chlorsulfuron (15 g a. i. ha<sup>-1</sup>).





<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination.

 $g<sup>g</sup>$  Roseworthy, South Australia. Plants from one field (S4)

<sup>h</sup> Roseworthy, South Australia. Plants from one field.

<sup>i</sup> Holden Hill, South Australia. Plants from metropolitan Adelaide street side.

<sup>j</sup> Roseworthy, South Australia. Plants from roadside adjoining single field South 4.

### **4.3.3 New South Wales** *S. oleraceus* **chlorsulfuron treatment**

The results from the New South Wales accessions tested (Table 4.4) show varying sensitivity to chlorsulfuron with 25 accessions being resistant and 7 susceptible. The results further show varying numbers of resistant and susceptible plants from the same field. DNA from these plants was used later in the study. Seed of multiple plants were collected from 4 different fields at North Star in New South Wales. In one field six plants were collected of which three plants were resistant and three plants were susceptible. In the other three fields all plants were resistant. This highlights the need to collect at least 5 plants from any location to draw a reasonable conclusion as to the true resistance status at that location.

Sonchus	Location		Latitude/Longitude	Response to
number				chlorsulfuron <sup>a</sup>
5 So	Croppa Ck, New South Wales	27° 07' 32.00" S	150° 18' 26.00" E	Resistant
10 So	Yallaroi, New South Wales	29° 09' 00.05" S	$150^{\rm o}\,28'$ 20.00" E	Susceptible
So 172	North Star, New South Wales	28° 52' 76.00" S	150° 23' 96.00" E	Resistant
So 173	Yallaroi, New South Wales	28° 08' 03.00" S	150° 22' 27.00" E	Resistant
So 174	Warialda, New South Wales	29° 29' 93.00" S	150° 34' 77.00" E	Resistant
So 175	Yetman, New South Wales	28° 55' 50.00" S	150° 46' 12.00" E	Susceptible
So 176	Yetman, New South Wales	28° 55' 50.00" S	150° 46' 12.00" E	Resistant
So 249	Narabri, New South Wales	30° 00' 13.26" S	149° 38' 33.26" E	Susceptible
So 391	North Star, New South Wales	28° 48' 49.00" S	150° 25' 03.00" E	Resistant
So 397	North Star, New South Wales	28° 52′ 14.00" S	150° 24' 07.00" E	Susceptible
So 401	<sup>k</sup> North Star, New South Wales	28° 53' 01.00" S	150° 23' 59.00" E	Resistant
So 402	<sup>k</sup> North Star, New South Wales	28° 53' 02.00" S	150° 23' 58.00" E	Resistant
So 403	<sup>k</sup> North Star, New South Wales	28° 53' 03.00" S	150° 23' 58.00" E	Resistant
So 404	<sup>k</sup> North Star, New South Wales	28° 53' 04.00" S	150° 23' 58.00" E	Resistant
So 405	<sup>k</sup> North Star, New South Wales	28° 53' 04.00" S	150° 23' 58.00" E	Resistant
So 406	<sup>1</sup> North Star, New South Wales	28° 54' 47.00" S	150° 23' 40.00" E	Resistant
So 407	<sup>1</sup> North Star, New South Wales	28° 54' 48.00" S	150° 23' 40.00" E	Resistant
So 408	<sup>1</sup> North Star, New South Wales	28° 54' 49.00" S	150° 23' 40.00" E	Resistant
So 409	<sup>1</sup> North Star, New South Wales	28° 54' 50.00" S	150° 23' 40.00" E	Resistant
So 410	<sup>1</sup> North Star, New South Wales	28° 54' 50.00" S	150° 23' 40.00" E	Resistant
So 411	m. North Star, New South Wales	28° 56' 36.00" S	150° 24' 03.00" E	Resistant
So 412	mNorth Star, New South Wales	28° 56' 28.00" S	150° 24' 05.00" E	Resistant
So 413	mNorth Star, New South Wales	28° 56' 27.00" S	150° 24' 05.00" E	Susceptible
So 414	m. North Star, New South Wales	28° 56' 26.00" S	150° 24' 05.00" E	Susceptible
So 415	mNorth Star, New South Wales	28° 56' 25.00" S	150° 24′ 05.00" E	Susceptible
So 416	m North Star, New South Wales	28° 56' 23.00" S	150° 24' 05.00" E	Resistant
So 417	<sup>n</sup> . North Star, New South Wales	28° 53' 53.00" S	150° 22' 50.00" E	Resistant
So 418	<sup>n</sup> :North Star, New South Wales	28° 55' 54.00" S	150° 22' 49.00" E	Resistant
So 419	<sup>n</sup> :North Star, New South Wales	28° 55' 54.00" S	150° 22' 49.00" E	Resistant
So 420	<sup>n</sup> North Star, New South Wales	28° 55' 53.00" S	150° 22' 48.00" E	Resistant
So 421	<sup>n</sup> North Star, New South Wales	28° 55' 53.00" S	150° 22' 49.00" E	Resistant
So 422	<sup>n</sup> North Star, New South Wales	28° 55' 53.00" S	150° 22' 49.00" E	Resistant

**Table 4.4** The collection locations of *S. oleraceus* accessions from New South Wales and the response of their progeny to the ALS-inhibiting herbicide, chlorsulfuron (15 g a. i. ha<sup>-1</sup>).

<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

<sup>k</sup> North Star, New South Wales. Collection from close proximity in one field.

<sup>1</sup> North Star, New South Wales. Collection from close proximity in one field.

<sup>m</sup> North Star, New South Wales. Collection from close proximity in one field.

<sup>n</sup> North Star, New South Wales. Collection from close proximity in one field.

# **4.3.4 Western Australian** *S. oleraceus* **chlorsulfuron treatment**

In Western Australian, 12 accessions were tested (Table 4.5) and showed varying sensitivity

to chlorsulfuron with 2 accessions being resistant and 10 susceptible.

Sonchus number	Location	Latitude/Longitude	Response to chlorsulfuron a	
So 505	Busselton, Western Australia	33° 39 24.40" S	$115^{\circ}24'00.00''$ E	Susceptible
So 506	Myalup, Western Australia	33° 06' 35.42" S	$115^{\circ}42'$ 28.23" E	Resistant
So 509	Busselton, Western Australia	33°39′24.40″S	$115^{\circ}$ 24' 42.32" E	Resistant
So 516	Cowaramup, Western Australia	33°48′24.40″S	$115^{\circ}07'00.00''$ E	Susceptible
So 523	Witchcliffe, Western Australia	$34^{\circ}01'21.14"$ S	115° 05' 56.53" E	Susceptible
So 524	Witchcliffe, Western Australia	34° 01′ 21.14″ S	115° 05' 56.53" E	Susceptible
So 527	Pemberton, Western Australia	$34^{\circ}$ 26' 39.50" S	$115^{\circ} 54' 03.14''$ E	Susceptible
So 529	Nanarup, Western Australia	34° 59′ 37.41″ S	$118^{\circ}$ 03' 48.00" E	Susceptible
So 530	Porongurup, Western Australia	34° 39′ 24.00″ S	117° 53' 21.22" E	Susceptible
So 532	Mt Barker, Western Australia	34° 38′ 02.53″ S	117° 39' 59.02" E	Susceptible
So 534	Arthur River, Western Australia	33° 20′ 07.59″ S	$117^{\circ}$ 02' 00.22" E	Susceptible
So 541	Bannister, Western Australia	$32^{\circ}40'$ 45.14" S	116°31′ 10.08" E	Susceptible

**Table 4.5** The collection locations of *S. oleraceus* accessions from Western Australia and the response of their progeny to the ALS-inhibiting herbicide, chlorsulfuron (15 g a. i. ha<sup>-1</sup>).

<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

# **4.3.5 Victorian** *S. oleraceus* **chlorsulfuron treatment**

In Victoria, 12 accessions were tested (Table 4.6) shows varying sensitivity to chlorsulfuron

with 1 accession being resistant and 11 susceptible.

Sonchus number	Location	Latitude/Longitude		Response to chlorsulfuron <sup>a</sup>
So 254	Horsham, Victoria	$36^{\circ}$ 42' 45.67" S	$142^{\circ}$ 12' 04.41" E	Susceptible
$So$ 255	Edenhope, Victoria	$36^{\circ} 53' 56.86'' S$	141° 30' 59.96" E	Susceptible
$So$ 256	Edenhope, Victoria	36° 55' 38.37" S	141° 27' 16.56" E	Susceptible
So 257	Murtoa, Victoria	$36^{\circ}34'$ 57.52" S	$142^{\circ}28'14.64''$ E	Susceptible
So 258	Murtoa, Victoria	$36^{\circ}33'$ 15.99" S	$142^{\circ}$ 28' 36.35" E	Susceptible
$So$ 259	Murtoa, Victoria	$36^{\circ}33'$ 05.62" S	142° 29' 37.37" E	Susceptible
So 260	Murtoa, Victoria	$36^{\circ}33'$ 65.64" S	142° 29′ 37.35″ E	Susceptible
So 261	Rupanyup, Victoria	36° 37′ 31.40″ S	142° 42′ 00.88" E	Susceptible
So 262	Rupanyup, Victoria	$36^{\circ}36'51.16''$ S	142° 44′ 28.25″ E	Susceptible
So.263	Banyena, Victoria	$36^{\circ}34'$ 17.56" S	142° 48' 52.82" E	Susceptible
So 264	Sea Lake, Victoria	36° 29′ 37.89″ S	142° 50' 18.47" E	Susceptible
So 265	Sea Lake, Victoria	$35^{\circ}$ 28' 45.64" S	$142^{\circ}48'$ 22.65" E	Resistant

**Table 4.6** The collection locations of *S. oleraceus* accessions from Victoria and the response of their progeny to the ALS-inhibiting herbicide, chlorsulfuron  $(15 \text{ g a. i. ha}^{-1})$ .

 $a<sup>a</sup>$  Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

# **4.3.6 Tasmanian** *S. oleraceus* **chlorsulfuron treatment**

A single accession from Tasmanian was tested (Table 4.7) and was susceptible to chlorsulfuron.

**Table 4.7** The collection location of *S. oleraceus* accession from Tasmania and the response of its progeny to the ALS-inhibiting herbicide, chlorsulfuron  $(15 \text{ g a. i. ha}^{-1})$ .

Sonchus	Location	Latitude/Longitude	Response to
number			chlorsulfuron
So 238	Roaches Beach, Tasmania	$147^{\circ}$ 29' 49.23" E $42^{\circ}$ 54' 03.12" S	Susceptible

 $a<sup>a</sup>$  Response to chlorsulfuron - resistant: 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

The results of testing for resistance are summarised in Table 4.8. In total 274 accessions were tested for resistance to chlorsulfuron, with 44% being resistant to the herbicide. Resistance to chlorsulfuron was discovered in every state of Australia except Tasmania. One accession came from Tasmania and was used for DNA fingerprinting rather than an indication of the level of resitance in the state. The frequency of accessions with resistance to chlorsulfuron varied across states, being most prevalent in Queensland and New South Wales. Relatively high levels of resistance to chlorsulfuron were found in South Australia. The germplasm collection and the DNA extracted from it formed the basis for population relationship studies conducted and discussed in further chapters of this work.

**Table 4.8** Susceptibility and resistance of 274 *S. oleraceus* plants treated with the ALSinhibiting herbicide, chlorsulfuron.

Australian states	Total	Susceptible	Resistant	% Resistant
New South Wales	32		25	78%
Queensland	98	40	58	59%
South Australia	119	84	35	29%
Western Australia	12	10		17%
Victoria	12			8%
Tasmania				0%
<b>Grand Total</b>	274	153	121	44%

It should be noted that one accession from Tasmania is not sufficient to provide meaningful data on the resistance level in Tasmania however it was sufficient to provide DNA for genetic comparison purposes.

### **4.3.7** *S. oleraceus* **imazethapyr treatment**

Cross resistance between sulfonylurea and imidazolinone herbicides can occur (Tranel and Wright 2002). To identify whether cross-resistance to imidazolinone herbicides was common in *S. oleraceus*, a sample of 15 chlorsulfuron resistant accessions from a single field at Roseworthy in South Australia were treated with 75 g ha<sup>-1</sup> imazethapyr. All 15 chlorsulfuron resistant plants from a field at Roseworthy, South Australia were found to be susceptible to imidazolinone (Table 4.9).





<sup>a</sup> Response to imazethapyr - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination.

 $g<sup>g</sup>$  Roseworthy, South Australia. Plants from one field (S4).

Often weeds resistant to one sulfonylurea herbicide have cross resistance to other different sulfonylurea herbicides (Powles and Holtum 1994). They may also have resistance to imidazolinone herbicides, depending on the mutation present (Tranel and Wright 2002). In this study all the chlorsulfuron resistant *S. oleraceus* biotypes were found to be susceptible to imazethapyr and this is consistant with the findings of Tranel and Wright (2002) that point mutations in the ALS gene at proline 197 are claimed to result in high levels of sulfonylurea resistance, but little to no imidazolinone resistance.

### **4.3.8** *S. oleraceus* **dose rate experiment**

*S. oleraceus* was found to be very sensitive to chlorsulfuron with adequate control at 1.875 g ha<sup>-1</sup> well below the recommended rate of 15 g ha<sup>-1</sup> (Plate 4.1). This high level of sensitivity has been also found in related *Lactuca serriola* (Preston *et al*., 2006).



**Plate 4.1** *S. oleraceus* 30 days after treatment with 1.875 g a. i. ha<sup>-1</sup> chlorsulfuron. Resistant plants on the left and susceptible plants on the right.

Different dose rates produced different responses between *S. oleraceus* populations when treated with chlorsulfuron (Figure 4.1). Susceptible biotypes (103A, 103B, 234 and 56) were completely controlled when treated with and above the normal recommended rate of chlorsulfuron (15 g ha<sup>-1</sup>) or higher rates. All susceptible biotypes were also controlled at rates of chlorsulfuron well below the recommended rate. This shows that *S. oleraceus* is normally very sensitive to chlorsulfuron. Adequate control was not achieved with biotypes 101, 102, 220, 57 and 125 with the recommended rate of chlorsulfuron. These resistant biotypes survived at rates of up to 120 g  $ha^{-1}$  chlorsulfuron (8 times the recommended rate). This finding highlights the fact that increasing herbicide rates will have no benefit in increasing weed kill once resistance has evolved or is present in a field. Seedlings of germplasm 220 were from a single parent and showed consistent high levels of resistance, greater than 80% of the control through to 120 g ha<sup>-1</sup> chlorsulfuron. Seedlings from germplasm 101, 102, 57 and 125 were from early collections where seed of a number of plants were collected at a location and represent population responses. Because these latter collections were mixed populations, the diminishing dry weights of these latter seedlings when treated with high rates of chlorsulfuron compared with population 220 (Figure 4.1) could be due to a mix of resistant and susceptible plants in the populations tested. However, survival data do not support this hypothesis, because no plants in these populations were killed at the recommended rate of chlorsulfuron (data not shown). Therefore, it is more likely the differences could be explained by different point mutations within ALS in the different populations.



**Figure 4.1** Response of *S. oleraceus* treated with chlorsulfuron at different rates. Measurements were made 30 days after treatment. Curves are 103:  $Y=4+96/(1+e^{((-1.297-10g)}))$ dose)\*-1.490), 101: Y=4+96/(1+e<sup>((-1.811-log dose)\*-0.9781)</sup>), 102: Y=4+96/(1+e<sup>((-1.092-log dose)\*-0.9168)</sup>), 220: Y=4+96/(1+e<sup>((-3.030-log dose)\*-0.83)</sup>), 234: Y=4+96/(1+e<sup>((-53.12-log dose)\*-0.05626)</sup>), 56 (Function unable to be fitted to these data), 57:  $Y=4+96/(1+e^{((-1.577-\log dose)^{*}-1.484)})$  and 125:  $Y=4+96/(1+e^{((-1.424-\log \text{dose})*-1.335)}).$ 

### **4.4 CONCLUSIONS**

ALS-inhibiting herbicide resistance to chlorsulfuron in *S. oleraceus* is now widespread in Australia. From the areas tested there is a much greater frequency of resistance in populations of *S. oleraceus* from southern Queensland and northern New South Wales than in South Australia. *S. oleraceus* plants resistant to the ALS-inhibiting herbicide, chlorsulfuron from a single field in South Australia were all found to be susceptible to the ALS-inhibiting herbicide, imazethapyr. Susceptible *S. oleraceus* populations from a single plant can be very sensitive to the herbicide chlorsulfuron, being controlled by rates as low as 10% of the recommended field rate of this herbicide. Typically, resistant plants can withstand chlorsulfuron treatment of 8 times the recommended rate. Therefore, increasing herbicide rate will not control resistant plants so land managers will need to use alternate strategies to control resistant *S. oleraceus*.

#### **CHAPTER 5**

#### **5 GENE MOVEMENT**

### **5.1 INTRODUCTION**

Herbicide resistance gene flow may occur through pollen or by seed. Levels of gene flow are known to vary. For example, herbicide tolerant canola has been shown to pollinate susceptible individuals at 2.6 km from the source (Reiger *et al*., 2002). Levels of resistance gene flow of greater than 80% of both glyphosate and glufosinate in resistant roadside canola populations which had escaped from canola field crops have been reported (Knispel *et al*. 2008). In *Medicago sativa* L. (alfalfa or lucerne), which is predominately cross-pollinated, Fitzpatrick (2003) reported gene flow of 1.39% at 500 feet plant separation and a reduction to 0.08% at greater than 1500 feet of separation. Messeguer *et al*., (2001) reported that gene flow due to pollen movement in *Oryza sativa* L. (rice), which is self-pollinated, to be less than 0.1% in plants 5 meters apart however this increased to 0.53% in plants in line with the direction of wind movement. Since *S. oleraceus* is self pollinated it is expected that little if any gene flow will occur by cross pollination. Gene flow introduces new alleles into a population and in this study the interest is the movement of the resistant allele into a plant that is susceptible to ALS-inhibiting herbicides.

Seed set in self-pollinated plants is known to be enhanced by insect visits, as reported by Lu *et al*., (2008) to occur in *Eupatorium adenophorum* (crofton weed). Bees were observed visiting the flowers of *S. oleraceus* in the current study (Plate 5.1); however, it is not known whether any cross pollinated seed was produced by the bee visits. Boda Slotta (2006) noted that suppressing flowering and seed set could achieve the greatest effect in prevention of continued spread and the formation of novel genotypes through pollen and seed dispersal.



**Plate 5.1** *S. oleraceus* being visited by a bee.

Davies (2007) outlines the potential fates of a seed via 16 pathways. These pathways and fates included movement to the immediate vicinity of the parent plant, special dispersion, multiple vector dispersal, death and establishment; and suggested wind breaks to reduce wind dispersal. Gene flow in weeds can be due to the movement of farm equipment, contamination of seeds or transport by wildlife or animals, insects, wind or ballistic spread (Ashigh and Tardiff 2007; Davies 2007; St.John-Sweeting and Morris 1991). Shields (2006) using remote piloted model planes with attached seed collection mesh bags collected wind dispersed *Conyza canadensis* (horseweed) seeds at levels of up to 140 meters above the ground and further concluded that seed dispersal can easily exceed 500 km in a single dispersal event. This movement also contributes to the movement of the gene. Management strategy plays an important role in the immigration and extinction level of the genes contained within plant seeds (Liebman 2007).

In this experiment two plants, one resistant and another susceptible to ALS-inhibiting herbicides, were placed side by side in the field and allowed to flower and produce seed heads. By testing the seed from the susceptible plants for resistance to ALS-inhibiting herbicide the frequency of gene flow can be determined. If gene flow does occur, self pollination of the resistant progeny can be used to see if segregation has occurred and if so determine level of cross pollination. The aim of this experiment was to ascertain whether any gene flow occurred through pollen movement.

#### **5.2 MATERIALS AND METHODS**

### **5.2.1 Experimental site of field experiment**

The experiment was conducted in a field at Urrbrae, South Australia,  $(34^{\circ} 58' 14'' S 138^{\circ} 38'$ 23'' E), in late spring and early summer 2006 during a period were the plant naturally flowers and natural pollination is maximised.

### **5.2.2 Germination, seedling and plant treatment**

Plants selected for inclusion in the gene flow experiment are listed in Table 5.1. Seed from these accessions was germinated as described in section 3.3.1. Black pots were used for susceptible plants and pink pots for resistant plants to reduce the risk of inadvertently harvesting a resistant head by mistake when harvesting susceptible heads. Seedlings from So115 (Table 5.1) were transplanted to 10 black pots (80 X 80 mm diameter and 180 mm tall) labelled S01 to S10, as described in section 3.3.2. Similarly resistant seedlings from field pair numbers R01 to R10 as listed in Table 5.1 were transplanted to 10 pink pots. All pots were kept in the glasshouse and watered to field capacity for 9 days prior to movement to a bird proof enclosure outside for a further 26 days to acclimatise and reach the point of flowering.

After outside acclimatisation, plants were then placed in the field as shown in Plate 5.2 with a resistant and susceptible plant placed 100 mm apart in a container to hold 50 mm of water for plants to absorb by capillary rise. Each of the ten plant pairs (Table 5.1) were set up as field stations located 10 to 20 m apart in the field. The plants were placed 100 mm apart to maximise the potential for cross pollination and 10 to 20 m apart to minimise the potential. The flow chart (Figure 5.1) shows the proposed general methodology of the gene flow experiment.



**Plate 5.2** Resistant plant (in pink pot) and susceptible plant (in black pot) placed side by side in the field.

**Table 5.1.** Geographic origin of resistant *S. oleraceus* plants selected for inclusion in the gene flow experiment paired with susceptible plants So1 to So10 which were progeny from *Sonchus oleraceus* accession (So115) from the Adelaide parklands.

Field station pair <sup>a</sup>	<i>Sonchus</i> resistant parent identification	Resistant parent collection location
$S01 - R01$	So 57	Goondiwindi, Queensland
$S_{02} - R_{02}$	So 101	Wasleys, South Australia
$S$ 03 - R03	So 102	Roseworthy, South Australia
$S04 - R04$	So 106	Virginia, South Australia
$S_{05} - R_{05}$	So 108	Wasleys, South Australia
$S06 - R06$	So 125	Dalby, Queensland
$S_{07} - R_{07}$	So 145	Warra, Queensland
$S08 - R08$	So 149	Warra, Queensland
$S09 - R09$	So 154	Meandarra, Queensland
$S10 - R10$	So 155	Dalby, Queensland

 $a<sup>a</sup>$  Field pairs consist of two pots with a susceptible plant in one (black) and resistant plant in the other (pink).



**Figure 5.1** Flow chart showing the cultivation and treatment of *S. oleraceus* plants and seedlings within the gene flow experiment.

# **5.2.3 Measurements**

Over a six week period (February and March 2007) flowering heads were tagged daily and the seed heads from both plants were harvested about 10 days after flowering. Seed heads were air dried and stored. All seed from susceptible heads were then germinated as identified lots into Mk12 pots containing coco peat as described in section 3.3.2. Seed from resistant plants was sown into the centre row of the Mk12 pots as a control (Plate 5.3) then treated with chlorsulfuron as section 3.3.5 and measurements made as section 3.3.6.



**Plate 5.3** Resistant plants in the centre four pots and susceptible plants sown in the outside four pots to the right and left of the centre column.

### **5.2.4 Segregation test**

Any resistant plants identified in the chlorsulfuron treated progeny from susceptible parents were transplanted to fresh pots and grown to produce self seed. Flowering seed heads were bagged (Plate 5.4) to reduce the chance of insect cross pollination and the subsequent seed produced was harvested, dried and sown in pots as section 3.3.2., for treatment with chlorsulfuron and determination of level of resistance or susceptibility. Eleven progeny were

allowed to self with heads bagged individually, and the progeny of these selfed plants were grown and treated with chlorsulfuron to determine the proportion of resistant and susceptible progeny. A  $\chi^2$  test was used to determine whether the segregation of the progeny fitted a 3:1 ratio.



**Plate 5.4** A bagged resistant plant which is the progeny from a susceptible plant. The plant is bagged to exclude large insects and reduce the already low chance of cross pollination.

# **5.3 RESULTS AND DISCUSSION**

### **5.3.1 Field experiment**

The results of chlorsulfuron treated seedlings from the seed heads collected from the 10 field station pairs listed in Table 5.1 are displayed in Appendix 2 (S1&R1 to S10&R10). One example from Appendix 2, S1 is displayed in Table 5.2 and shows the 11 head harvested numbers (in the second column) over the flowering period (February and March 2007). Column three shows the number of heads harvested and column five the number of emerged seedlings treated with chlorsulfuron. The last two columns show the results of the chlorsulfuron treatment with a total of 329 dead and zero living seedlings. The totals from S01 in Table 5.2 appear in the first row of Table 5.3. Table 5.3 displays the results from all 10 stations, with the first line being the totals from the first field pair from Table 5.2. Table 5.3 shows no cross pollination has occurred from the proximate resistant plant So57. Seed from selected resistant plants (R1 to R10, in Appendix 2) were used to confirm parental resistance, with all being confirmed resistant. Seeds collected from the heads of susceptible parent plants of each of the 10 field stations are displayed in Table 5.3 with the level of resistance found in the progeny from the maternal susceptible parent. The 14,144 seeds collected from susceptible parent plants produced 3795 seedlings and of these 10.34% were found to be resistant. This figure is higher than expected, but is biased by results from one plant (S03) as displayed in Table 5.3. By excluding this outlier the cross pollination rate is less than 4%.

**Table 5.2** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So057 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron 15g ai  $ha^{-1}$ and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Susceptible S. oleraceus</b>		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#$ <sup>a</sup>		heads harvested	$#$ sown	# treated $b$	<b>Susceptible</b>	<b>Resistant</b>
S01So115	H <sub>0</sub> 33		80	38	38	
S01So115	H <sub>0</sub> 37		100	76	76	
S01So115	H <sub>079</sub>			0		
S01So115	H <sub>091</sub>		30	24	24	
S01So115	H <sub>136</sub>		140	102	102	
S01So115	H <sub>168</sub>		160	31	31	
S01So115	H189		100	6	6	
S01So115	H <sub>207</sub>	6	<b>200</b>	6	6	
S01So115	H <sub>222</sub>		100	17	17	
S01So115	H <sub>235</sub>	4	100	28	28	
S01So115	H <sub>251</sub>	3	30			
Totals		35	1040	329	329	

<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table 5.3** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So057 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron 15g ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

$\mathbf{r}$			Result 30 days after treatment			
<i>S. oleraceus</i> susceptible	Seed	Seedling	# Dead	# Alive	$\frac{0}{0}$	
and resistant pair <sup>a</sup>	$#$ sown	# treated $b$	<b>Susceptible</b>	<b>Resistant</b>	<b>Resistant</b>	
S01So115 & R01So057	1040	329	329	$\theta$	0	
S02So115 & R02So101	1678	407	383	24	5.90	
S03So115 & R03So102	570	191	46	145	75.92	
S04So115 & R04So106	700	77	77	$\theta$	0	
S05So115 & R05So108	2120	640	629	11	1.72	
S06So115 & R06So125	2485	530	465	65	12.26	
S07So115 & R07So145	2240	657	638	19	2.89	
S08So115 & R08So149	1440	91	91	0		
S09So115 & R09So154	900	382	374	8	2.09	
S10So115 & R10So155	995	491	478	13	2.65	
sum	14168	3795	3510	285	103.43	
Mean	1417	380	351	29	10.34	

<sup>a</sup> Pair of plants (susceptible and resistant) flowering in the field 100 mm apart.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

#### **5.3.2 Segregation test**

Table 5.4 displays the outcome of the selfed segregation test. Segregation of 3:1 (R:S) was expected for a single dominant gene. The progeny of 7 of the selfed plants were composed entirely of resistant individuals (8, 18, 8, 32, 12, 19 and 21) suggesting these were not from the susceptible parent but possibly harvested by error from the resistant plant. Self 1 is most likely to have been progeny of a susceptible plant surviving spraying with herbicide. For the other three selfs, the segregation of the progeny was not significantly different to a 3:1 ratio (Table 5.4)

Selfed parent			Result 30 days after treatment		$\chi^2$	P
Self number	Parent progeny name	Seedlings	# Dead	# Alive		
		treated	<b>Susceptible</b>	<b>Resistant</b>		
Self 1	S02So115H015A	45	45	0		
Self 2	S02So115H032A	8	0	8		
Self 3	S02So115H032B	18	0	18		
Self 4	S05So115H150	16	4	12	0	
Self 5	S05So115H185	8	0	8		
Self 6	S06So115H184A	32		32		
Self 7	S06So115H184B	38		33	2.84	0.09
Self 8	S07So115H047	22		15	0.55	0.46
Self 9	S07So115H111	12	0	12		
Self 10	S07So115H131	19		19		
Self 11	S07So115H217	21		21		

**Table 5.4** The table displays the number of seeds sown from each selfed parent, the number of 2 leaf emerged seedlings treated with chlorsulfuron 15 g a. i. ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

The movement of weed germplasm by seed is widely known, (Shields *et al.,* 2006, Lu 2005, Sheldon and Burrows 1973 and Davies and Sheley 2007) and gene flow in numerous weeds through pollen is also known (Maxwell and Mortimer 1994). Specific knowledge as the gene movement in *S. oleraceus* up to now has not been clear.

#### **5.4 CONCLUSION**

In this study, field pollination in *S. oleraceus* is shown to have resistance cross pollination movement of less than 10% and is more likely to be less than 4% and gene flow of ALSinhibiting herbicide resistance in *S. oleraceus* is likely to be predominately by seed movement. This supports the premise that gene flow in *S. oleraceus* is predominately by wind-bourne seed movement. However, this study shows that field pollination does occur and even a small proportion of pollen movement from resistant to susceptible plants is notable as it has the potential to increase the level of resistant seed in the seed bank.
#### **CHAPTER 6**

### **6 GENETIC DIVERSITY IN INDIVIDUAL FIELDS**

#### **6.1 INTRODUCTION**

Resistance to ALS-inhibiting herbicides is complex and evolves as a result of selection for individuals within plant species that can survive the normal rate of herbicide application. Resistance can be attributed to an enhanced ability of plants to metabolize the herbicide (Christopher *et al*., 1992), but most commonly involves an altered form of the target ALS enzyme (Saari *et al*., 1990, 1992 and 1994). Resistant alleles occur at low frequencies within natural populations (Preston and Powles 2002), but the alleles increase in frequency with frequent use of herbicides with the same mode of action. It is also possible that resistance alleles may enter populations from outside. Such gene flow may be a particular issue where resistance alleles are infrequent or absent from a population and may greatly increase the speed of resistance selection. *S. oleraceus* is self pollinated, so any gene flow would most likely occur through seed movement. Rapid dispersal of wind blown seed over large distances has been reported in *Lactuca serriola* L. (Lu 2005). *S. oleraceus* has similar wind borne seed and therefore could also be transported over large distances.

Managing gene flow under such conditions can be difficult. For example, Walker *et al.*  (2005b) advocate spraying small seedlings and controlling late flushes of *S. oleraceus* in winter crops with effective selective herbicide groups instead of waiting for the first fallow spray after harvest. These strategies will kill plants prior to flowering, reducing the possibility of resistance allele movement. This may not be the only successful method of controlling resistance allele movement and understanding the major mechanisms of gene flow will assist in selecting and manipulating management options to reduce the rate of resistance increase.

In October 2005 whilst collecting seed heads from individual *S. oleraceus* plants from fields in Queensland, a field of barley was found with a high infestation of mature *S. oleraceus*. From this 25 ha field, seed heads from 23 individual plants were sampled to determine whether there was any variation in the frequency of resistance. After treating emerged seedlings from these plants with chlorsulfuron it was found that 40% of the sampled plants in the field were resistant to the herbicide chlorsulfuron and 60% were susceptible.

Following the finding of mixed susceptible and resistant plants in an individual Queensland field, a second field in South Australia containing *S. oleraceus* that could be readily sampled and monitored was identified. In November 2006 a field of faba beans (*Vicia faba*) containing S. *oleraceus*, at approximately 1 plant per m<sup>2</sup>, was found 60 km north of Adelaide at Roseworthy. This field was used to investigate the frequency of resistance, and the genetic plus spatial relationship between plants in this population. This field was selected as it was on the Roseworthy Agricultural College farm where detailed field records had been preserved and was readily accessable. DNA was extracted from the 37 individual plants collected in the Roseworthy field and AFLPs were used to determine the relationship of the 37 genotypes. From the extracted DNA of the 15 resitant plants and one susceptible plan sequence analysis was conducted to identify points of mutation.

### **6.2 MATERIALS AND METHODS**

#### **6.2.1 Site of Queensland individual field experiment and seed collection**

In 2005, seed from single *S. oleraceus* plants were sampled from a 25 ha field 30 km south east of Chinchilla and 6 km north west of Warra in southern Queensland  $(26^{\circ} 53' 54.00'' S$ 150 $^{\circ}$  52' 14.00" E). This field contained a population of *S. oleraceus* at about 1 plant per m<sup>2</sup> within a crop of barley. One to five seed heads per plant were collected from 23 individual plants. After collection, seed was dried in a dehydrator at 40°C for 24 hrs. Seed was stored at 3°C until required.

### **6.2.2 Site of Roseworthy individual field experiment and seed collection**

This survey was conducted in a 22 ha field (South 4) located at Roseworthy Agricultural College 60 km north of Adelaide, South Australia (34° 32′ 50" S, 138° 41′ 25" E). This field was selected due to the high numbers of *S. oleraceus* found in the crop and the availability of an accurate paddock history. The soil in the field is a calcareous loamy mallee with a mean annual rainfall of 440 mm (predominantly of winter incidence). The past use of ALSinhibiting herbicides within the field is outlined in Table 6.1. Seed was collected from 37 individual *S. oleraceus* plants in November 2006. After collection seed was dried in a dehydrator at 40°C for 24 hrs, and then stored at  $3^{\circ}$ C until required.

Year	Crop or Pasture	ALS Inhibiting herbicide	Herbicide
			application rate
1982	Wheat	Glean	20g/ha
1983	Pasture Medic		
1984	Barley		
1985	Pasture Medic		
1986	Wheat	Glean	20g/ha
1987	Pasture Medic		
1988	Pasture Medic seed		
1989	Oat Medic Vetch		
1990	Pasture Medic		
1991	Pasture Medic seed		
1992	Barley	Ally	7g/ha
1993	Pasture Medic		
1994	Triticale		
1995	Pasture Medic		
1996	Wheat	Ally	7g/ha
1997	Pasture Medic		
1998	<b>Barley</b>	Ally	7g/ha
1999	Oats		
2000	Pasture Medic		
2001	Pasture Medic		
2002	Canola		
2003	Wheat	Ally	5g/ha
2004	Wheat		
2005	<b>Barley</b>		
2006	Faba Beans		

**Table 6.1** Paddock history collected from farm records of field South 4 at Roseworthy Agricultural College, South Australia (34° 32' 45" S 138° 41' 20" E).

### **6.2.3 Seedling treatment and measurements**

Seeds were germinated, transplanted, cultivated and treated as general methods 3.3.1, 3.3.2 and 3.3.3. Seedlings were treated with 15 g a. i. ha<sup>-1</sup> chlorsulfuron as method in section 3.3.4. After 30 days, treated seedlings were scored as either dead or alive.

# **6.2.4 Genomic DNA extraction and AFLP analysis**

DNA was extracted (as method in section 3.4.1.2) from the 37 plants collected. AFLP analysis was performed (as method in section 3.4.3) using the extracted DNA.

### **6.2.5 Primer Design for ALS Gene Sequencing**

DNA from a single susceptible (So115) and 2 resistant plants (So302 and So 313) were used to determine which primer pairs would be used to test all plants. Four reactions were performed So115, So302, So313 with a nanopure water control. The reactions were performed with 4 sets of forward and reverse primers as Table 6.2. Each PCR reaction contained approximately 40 ng genomic DNA, 10µM of each forward and reverse primer, 10mM deoxynucleotide triphosphates (dNTPs), ), 50mM MgSO4, 1µL (5U/µL) Platinum HiFI Taq and 1X HiFi PCR buffer in a final volume of 25.5µL. PCR reactions were (after preheating to  $90^{\circ}$ C) subjected to initial 3 minutes denaturation at  $94^{\circ}$ C; 34 cycles of (30 seconds at 94°C, annealing for 30 seconds at  $54^{\circ}$ C and extension for 1 minute at 68°C); then a final 7 minutes at  $68^{\circ}$ C prior to holding at  $4^{\circ}$ C. After fragment testing and quantification (as section 3.4.3.2) PCR product was sent to the Australian Genome Research Facility (AGRF) in Adelaide for sequence analysis. Primer pair 2-F05: 2R04A gave the most distinct bands and these primers were used throughout.

**Table 6.2** Primer sequences used to select a suitable set of forward and reverse primers in the study of the ALS gene mutations in *S. oleraceus.* The shaded text identifies the selected primers used for ALS gene sequencing.



### **6.2.6 DNA Amplification and Sequencing**

#### **Source of DNA**

Extracted DNA from 21 individual plants was used in this experiment. The DNA of 15 resistant plants and 6 susceptible plants (So293, So294, So297, So317, So321 and So322) came from field South 4 at Roseworthy as listed in Table 6.4. The DNA of a single susceptible plant (So115) from the Adelaide plains was also included as a standard control.

# **Sequencing**

The ALS gene was sequenced to determine the molecular basis for resistance. The two polymerase chain reaction (PCR) forward and reverse primers as highlighted in Table 6.2 were used to amplify a section of the ALS gene known to contain the region where mutations conferring chlorsulfuron resistance occur from each of the 21 *S. oleraceus* biotypes. A susceptible control was included to confirm the CCC mutation. PCR reactions containing 40ng of genomic DNA were set up as described in section 6.2.6 and sent to the AGRF for sequencing.

AFLP data was viewed with Genemapper  $^{\circledR}$  (as method in section 3.4.3.7) for the presence and absence of peaks at each loci, and Popgene  $^{\circledR}$  was then used for analysis of genetic variation. Sequence data were analysed using Invitrogen Vector NTI ® bioinformatics software package.

## **6.3 RESULTS AND DISCUSSION**

### **6.3.1 Queensland individual field**

Table 6.3 shows the response of the 23 *S. oleraceus* plants to chlorsulfuron treatment within a single field at Warra, Queensland. The field location of the resistant and susceptible plants shown in Figure 6.1. The finding that 48% of the plants were resistant prompted further investigation about the spatial evolution of resistance in a single field.

	2003 from a field north of warra, Queensland and their response to chlorsuffuron treatment.			
Sonchus	Location		Latitude/Longitude	
number				a chlorsulfuron
So 128	Warra, Queensland	26° 53' 47.59" S	150° 52' 01.49" E	Susceptible
So 129	Warra, Queensland	$26^{\circ}$ 53' 49.99" S	150° 52′ 01.76″ E	Susceptible
So 130	Warra, Queensland	$26^{\circ}$ 53' 52.97" S	150° 52' 01.77" E	Resistant
So 131	Warra, Queensland	$26^{\circ}$ 53' 53.24" S	$150^{\circ}$ 52' 04.10" E	Resistant
So 132	Warra, Queensland	$26^{\circ} 53' 53.26'' S$	$150^{\circ}$ 52' 06.66" E	Resistant
So 133	Warra, Queensland	26° 53' 53.14" S	$150^{\circ}$ 52' 09.01" E	Resistant
So 134	Warra, Queensland	26° 53' 56.34" S	$150^{\circ}$ 52' 09.43" E	Resistant
So 135	Warra, Queensland	$26^{\circ}$ 53' 59.90" S	150° 52′ 11.46″ E	Susceptible
So 136	Warra, Queensland	$26^{\circ}$ 53' 59.56" S	150° 52′ 13.53″ E	Susceptible
So 137	Warra, Queensland	26° 53' 59.08" S	150° 52′ 16.02″ E	Susceptible
So 138	Warra, Queensland	26° 54' 01.92" S	150° 52′ 16.63″ E	Susceptible
So 139	Warra, Queensland	26° 54' 04.49" S	150° 52′ 20.89″ E	Susceptible
So 140	Warra, Queensland	26° 54' 01.89" S	150° 52′ 22.90″ E	Susceptible
So 141	Warra, Queensland	26° 53' 59.16" S	150° 52′ 24.64″ E	Susceptible
So 142	Warra, Queensland	$26^{\circ}$ 53' 56.43" S	150° 52' 24.19" E	Susceptible
So 143	Warra, Queensland	$26^{\circ} 53' 56.63'' S$	$150^{\circ}$ 52' 20.68" E	Resistant
So 144	Warra, Queensland	$26^{\circ} 53' 53.64'' S$	$150^{\circ}$ 52' 18.46" E	Susceptible
So 145	Warra, Queensland	26° 53' 54.76" S	$150^{\circ}$ 52' 14.65" E	Resistant
So 146	Warra, Queensland	$26^{\circ} 53' 51.49'' S$	150° 52′ 13.99″ E	Resistant
So 147	Warra, Queensland	26° 53' 47.63" S	150° 52′ 12.90″ E	Resistant
So 148	Warra, Queensland	$26^{\circ}$ 53' 47.04" S	150° 52' 07.95" E	Resistant
So 149	Warra, Queensland	26° 53' 45.71" S	150° 52′ 04.74″ E	Resistant
So 150	Warra, Queensland	26° 53' 45.49" S	150° 52' 00.04" E	Susceptible

**Table 6.3** Geographic location of 23 plants of *S. oleraceus* collected on the 18<sup>th</sup> October 2005 from a field north of Warra, Queensland and their response to chlorsulfuron treatment.

<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination.



**Figure 6.1** Map of a field at Warra, Queensland showing the locations of the 11 resistant plants (pink) and the 12 susceptible plants (yellow).

The finding showed that the hypothesis that *S. oleraceus* plants in an individual field will either be all resistant or all susceptible was unfounded. It is likely that the frequency of resistance will vary in an individual field and this suggests that, because there is a high level of selfing in *S. oleraceus*, populations within fields are founded by more than one parent.

# **6.3.2 South Australian individual field survey**

Resistance to chlorsulfuron was found in the progeny of 15 plants within the S4 field at Roseworthy, South Australia with the other 22 being susceptible (Table 6.4). Resistant and susceptible plant locations within the field are listed in Table 6.4 and displayed in Figure 6.2.

Sonchus	Location		Latitude/Longitude	Response to
number				chlorsulfuron <sup>a</sup>
So 286	S4, Roseworthy, South Australia	34° 33' 05.00" S	138°41′32.00" E	Susceptible
So 287	S4, Roseworthy, South Australia	34° 33' 02.50" S	138°41′30.00" E	Susceptible
So 288	S4, Roseworthy, South Australia	34° 33' 02.50" S	138° 41' 32.50" E	Resistant
So 289	S4, Roseworthy, South Australia	34° 33' 00.00" S	138° 41' 32.50" E	Resistant
So 290	S4, Roseworthy, South Australia	34° 33' 00.00" S	138° 41' 30.00" E	Susceptible
So 291	S4, Roseworthy, South Australia	34° 33' 00.00" S	138° 41' 27.50" E	Resistant
So 292	S4, Roseworthy, South Australia	34° 32' 57.50" S	138°41′27.50″E	Susceptible
So 293	S4, Roseworthy, South Australia	34° 32′ 57.50" S	138°41′30.00" E	Susceptible
So 294	S4, Roseworthy, South Australia	34° 32' 57.50" S	138°41′32.50" E	Susceptible
So 295	S4, Roseworthy, South Australia	34° 33' 55.00" S	138° 41' 32.50" E	Resistant
So 296	S4, Roseworthy, South Australia	34° 32′ 55.00" S	138° 41' 30.00" E	Susceptible
So 297	S4, Roseworthy, South Australia	34° 32′ 55.00" S	138°41′27.50" E	Susceptible
So 298	S4, Roseworthy, South Australia	34° 32′ 55.00" S	138° 41' 25.00" E	Susceptible
So 299	S4, Roseworthy, South Australia	34° 32′ 52.50" S	138° 41' 22.50" E	Susceptible
So 300	S4, Roseworthy, South Australia	34° 32′ 52.50" S	138° 41′ 25.00" E	Susceptible
So 301	S4, Roseworthy, South Australia	34° 32' 52.50" S	138° 41' 27.50" E	Susceptible
So 302	S4, Roseworthy, South Australia	34° 33' 52.50" S	138° 41' 30.00" E	Resistant
So 303	S4, Roseworthy, South Australia	34° 32' 52.50" S	138° 41' 32.50" E	Resistant
So 304	S4, Roseworthy, South Australia	34° 33' 50.00" S	138° 41' 32.50" E	Resistant
So 305	S4, Roseworthy, South Australia	34° 32' 50.00" S	138°41′30.00" E	Susceptible
So 306	S4, Roseworthy, South Australia	34° 32' 50.00" S	138°41′27.50" E	Susceptible
So 307	S4, Roseworthy, South Australia	34° 32' 50.00" S	138° 41' 25.00" E	Susceptible
So 308	S4, Roseworthy, South Australia	34° 32' 50.00" S	138°41′22.50" E	Resistant
So 309	S4, Roseworthy, South Australia	34° 32′ 50.00" S	138° 41' 20.00" E	Resistant
So 310	S4, Roseworthy, South Australia	34° 32' 47.50" S	138°41′17.50" E	Resistant
So 311	S4, Roseworthy, South Australia	34° 32' 47.50" S	138° 41' 20.00" E	Resistant
So 312	S4, Roseworthy, South Australia	34° 32' 47.50" S	138° 41' 22.50" E	Susceptible
So 313	S4, Roseworthy, South Australia	34° 32' 47.50" S	138°41′25.00" E	Resistant
So 314	S4, Roseworthy, South Australia	34° 32' 47.50" S	138° 41' 27.50" E	Resistant
So 315	S4, Roseworthy, South Australia	34° 32' 47.50" S	138°41′30.00" E	Susceptible
So 316	S4, Roseworthy, South Australia	34° 32' 45.00" S	138° 41' 30.00" E	Susceptible
So 317	S4, Roseworthy, South Australia	34° 32' 45.00" S	138° 41' 27.50" E	Susceptible
So 318	S4, Roseworthy, South Australia	34° 32' 45.00" S	138° 41' 25.00" E	Susceptible
So 319	S4, Roseworthy, South Australia	34° 32' 45.00" S	138°41′22.50" E	Resistant
So 320	S4, Roseworthy, South Australia	34° 32' 45.00" S	138°41′20.00" E	Resistant
So 321	S4, Roseworthy, South Australia	34° 32' 45.00" S	138°41′17.50″E	Susceptible
$S_0$ 322	S4. Roseworthy. South Australia	34° 32′ 45.00″ S	138°41′15.00″E	<b>Susceptible</b>

**Table 6.4** The geographic location of 37 plants of *S. oleraceus* collected from a single field (South 4) at Roseworthy, South Australia in November 2006 and their response to treatment with the ALS-inhibiting herbicide, chlorsulfuron.

So 322 S4, Roseworthy, South Australia  $34^{\circ}32'$  45.00" S  $138^{\circ}41'$  15.00" E Susceptible a Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination.



**Figure 6.2** Map of field (south 4) at Roseworthy, South Australia showing the locations of the 15 resistant plants  $(R)$  and the 22 susceptible plants  $(S)$ .

Of the plants collected from the single field at Roseworthy, South Australia 59% were found to be susceptible to the ALS-inhibiting herbicide, chlorsulfuron and 41% were found to be resistant. This was slightly lower level of resistance to the findings of the single field at Warra in Queensland (section 6.3.1), where 52% were found to be susceptible and 48% resistant. These findings show that it is important to sample multiple plants from across a field to determine an estimate of the frequency of the resistance allele.

AFLP analysis produced the dendrogram (Figure 6.3), which shows the 15 resistant plants from the field at Roseworthy, South Australia fall into 4 separate genetic groups or clusters. The four groups of resistant genotypes (R1, R2, R3 and R4) determined from the AFLP analysis tended to cluster together within the field (Figure 6.4), but some were distributed more widely. This suggests independent evolution of resistance has occurred in several

individuals from a number of mutation events. This could have occurred in situ, but may also have resulted from wind blown seed successfully colonizing patches in the field. The location of the resistant individuals within the field suggests wind blown seed has probably played a role in the spread of chlorsulfuron resistant *S. oleraceus*, as related biotypes are dispersed within the field.



**Figure 6.3** Dendrogram showing four separate genetic groups (biotypes) of resistant plants (R1 (aqua), R2 (blue), R3 (red) and R4 (white)) and 22 susceptible plants (yellow).



**Figure 6.4** Map of the field (south 4) at Roseworthy, South Australia showing the locations of the 15 resistant plants with different genotypes indicated (**R1**, **R2**, **R3** and **R4**).

Given that *S. oleraceus* is primarily a self-pollinated species, the presence of resistant and susceptible plants in a field emphasizes the need for farmers to continue to maintain a zerotolerance approach to localized infestations and use alternate control methods if a resistant population is detected. This new knowledge provides opportunities for improving current management practices.

As *S. oleraceus* is self pollinated with wind dispersed seed, information from other similar species can be used to increase the understanding of the genetic relationships. Genetic relationships were investigated in a similar wind dispersed self pollinating plant, *L serriola* (Lu *et al*., 2007). Lu *et al*., 2007 found that 25 *L. serriola* plants collected over less than 5 km were identical and collections over a larger area had greater genetic variance. Seed movement as far as 43 km was also reported. This study from a single field shows different genotypes growing together, which may reflect a larger genetic variation in the founder population or a level of outcrossing. The potential for outcrossing is supported by the finding from section 5.3 which showed outcrossing levels of between 0 to 10% can occur.

To elucidate this sequencing was conducted as described in section 6.3.3 to determine if the mutations occurring within the field were identical, evolved independently from similar genotypes already present or if incoming seed, with different genotypes and mutations, established the resistant patches.

# **6.3.3 ALS SEQUENCING**

The four primer sets tested from Table 6.2 are shown in the Gel Plate (Figure 6.5) with a water control (W). The second set in the top three wells lanes 4, 5 and 6 (Figure 6.5) were selected for use in further sequencing analysis. Low molecular DNA mass ladder bands (M) from top down are 2000bp, 1200bp, 800bp, 400bp, 200bp and 100bp. Prominent distinct bands in the second primer pair are at 483 bp (Reverse 4A [532bp] minus Forward 5 [49bp] = 483bp).

Primer pair 2 (F05 & R04A) as shown (grey background) in Table 6.2 and Lanes 4, 5 and 6 in Gel (Figure 6.5) was selected to sequence 21 individual plants in Section 6.2.6 due to its clear distinct banding pattern.



**Figure 6.5** Four primer pairs tested with a water control (W) first set in top wells 1, 2 & 3, second set in top wells 4, 5 & 6, third set in bottom wells 7, 8 &9 and fourth set in bottom wells 10, 11 & 12. Susceptible DNA (So115) in lanes 1 and 4 in the top wells and lanes 7 and 10 in the bottom well columns, resistant DNA (So302) in lanes 2, 5, 8 and 11 and resistant DNA (So313) in lanes 3, 6, 9 and 12.

The results of the sequencing show that resistant AFLP clusters R1 (Aqua) and R2 (Blue) (Figure 6.4) had the same mutation (Table 6.5) Proline to Threonine. These clusters are spatially close in the field despite being grouped distantly in the AFLP analysis (Figure 6.3): R3 (Red) and R4 (White/Black) were also close in the field (Figure 6.4) and had one different mutation, proline to leucine (Table 6.5). In five plants no mutation within the part of the ALS gene sequenced was identified. These plants may have had a mutation elsewhere within the ALS gene or may have a different mechanism of resistance, but like R1 (Aqua) and R3 (Blue) appeared as distinct clusters in the AFLP analysis.

	South4 Field Cluster	Phenotype	Proline 197	
S. oleraceus	from AFLP	(resistance profile)	<b>CCC</b>	
Plant number	See Dendrogram Fig 19	Chlorsulfuron	sequence	
		$(20g \text{ ha}^{-1})$		
So320	$R1$ (Aqua)	Resistant	$ACCa$ Threonine	Resistant
So319	R1	Resistant	$ACCa$ Threonine	Resistant
So314	R1	Resistant	CCC Proline	Susceptible
So310	R1	Resistant	$ACCa$ Threonine	<b>Resistant</b>
So304	R1	Resistant	$ACCa$ Threonine	Resistant
So302	R1	Resistant	$ACCa$ Threonine	Resistant
So309	$R2$ ( <b>Blue</b> )	Resistant	$ACCa$ Threonine	Resistant
So311	R <sub>2</sub>	Resistant	$ACCa$ Threonine	<b>Resistant</b>
So313	R <sub>2</sub>	Resistant	$ACCa$ Threonine	Resistant
So289	$R3$ ( <b>Red</b> )	Resistant	CCC Proline	Susceptible
So291	R <sub>3</sub>	Resistant	CCC Proline	Susceptible
So308	R <sub>3</sub>	Resistant	CCC Proline	Susceptible
So288	R <sub>4</sub> (White)	Resistant	CTC Leucine	Resistant
So295	R <sub>4</sub>	<b>Resistant</b>	CCC Proline	Susceptible
So303	R4	Resistant	CCC Proline	Susceptible
So115	S (Yellow)	Susceptible	CCC Proline	
So293	S (Yellow)	Susceptible	CCC Proline	
So294	S (Yellow)	Susceptible	CCC Proline	
So297	S (Yellow)	Susceptible	CCC Proline	
So317	S (Yellow)	Susceptible	CCC Proline	
So322	S (Yellow)	Susceptible	CCC Proline	

**Table 6.5** Resistant plants from field South 4 with their response to chlorsulfuron and sequence outcome. Also shown are five susceptible plants from South 4 and one from the Adelaide parklands as a standard control.

<sup>a</sup> Mutant resistant alleles are in bold.

# **6.4 CONCLUSION**

*S. oleraceus* plants resistant to ALS-inhibiting herbicides in a single field have evolved resitance from more than one mutation or mechanism. Although AFLP analysis was helpful in determining the presence of distinct clusters further sequencing analysis found at least 2 different mutations, plus 1 unidentified or different resistance mechanism conferring resistance in the 4 resistant clusters identified in the AFLP analysis.

### **CHAPTER 7**

#### **7 GENETIC DIVERSITY IN AUSTRALIA**

### **7.1 INTRODUCTION**

Rapid and less expensive molecular marker systems linked with easy to use software to analyse molecular data has increased the number of published studies examining genetic structure in weed populations (Ward and Jasieniuk 2009). However, Ward and Jasieniuk (2009) noted that in 39 molecular technique and genetic diversity studies published, researchers paid scant attention to sampling design. As discussed earlier, all seed accession collected in this study were from single individuals. Seed from each individual plant may have been collected from one or a number of seed heads. Since *S. oleraceus* is self pollinated, all progeny from this seed is expected to have the same genetic makeup. This was shown to be true in Chapter 4 in that rarely were plants grown from a single parent not either all resistant or susceptible to chlorsulfuron. This high level of self pollination means that seed movement is the most likely avenue for resistance alleles to enter a population or colonise new areas.

Seed dispersal also influences how rapidly resistance spreads. For example, wind blown *Lactuca serriola* L. seed has been associated with its rapid dispersal over large distances (Lu 2005). *S. oleraceus* is a wind dispersed weed having achenes with a pappus enhancing dispersal, so may also be readily dispersed across large areas by wind movement. *S. oleraceus*  seed has little dormancy and readily germinates (Widderick 2002), so the gene pool changes rapidly within sites, enhancing the evolution of resistant populations when selective pressure is present.

Little is known about wind dispersal of the ALS-inhibiting resistance alleles through seed movement. An understanding of the evolution and dispersal of these alleles is likely to be helpful in not only in managing resistant *S. oleraceus*, but also in understanding resistance to other herbicides in self pollinated and wind dispersed weeds.

*S. oleraceus* is a weed of major importance in the northern Australian cropping regions and the evolution of ALS-inhibiting herbicide resistance complicates management of this weed. This work researched the gene flow of *S. oleraceus* with a view to develop improved management strategies to minimise adaptation to herbicides and subsequent spread of resistant genotypes. The aim of this work was to determine how widespread resistance was in Australia and to use AFLPs to elucidate the relationship of resistant genotypes in Australian states and provide an opportunity for improving current management practices.

### **7.2 MATERIALS AND METHODS**

### **7.2.1 Seed collections and treatment**

Seed from individual plant accessions were collected throughout Australia between 1997 and 2008. Plants were collected from 50 m diameter patches within fields or along roadsides. At least 5 plant samples were taken from a sampling patch or location. One to five capitulum seed heads per plant were collected with each location recorded using a Global Positioning System (GPS). Plant seed collection and storage method is detailed in section 3.2. Seedlings were germinated from the collected seed. Leaf material was collected from one seedling from each of the seed samples and used for DNA extraction. Seedlings were then treated with 15 g a. i.  $ha^{-1}$  chlorsulfuron. The herbicide was applied in a custom-built spray cabinet through two flat-fan nozzles on a moving boom 40 cm above the plants. The nozzle output was  $103$  L ha<sup>-1</sup> at a pressure of 240 kPa with a boom speed of 1 m  $s^{-1}$ . Thirty days after treatment plants were scored as alive (resistant) or dead (susceptible).

## **7.2.2 DNA extraction and Amplified Fragment Length Polymorphisms**

A selection of 34 plants from across the country, including some from within the same field were used for AFLP analysis. DNA was extracted using a DNeasy® Plant Mini Kit (QIAGEN, cat#69106) and used for AFLP analysis. The AFLP technique described by Vos *et al*., (1995) was modified for use with fluorescent detection. The DNA was cut using M*se*1 and P*st*1 restriction enzymes, consequently M*se*1 and P*st*1 adapters were used in the ligation step. Pre-amplification PCR used P*st*1+A and M*se*1+C with the selective PCR amplification using dimers of P*st*1+A and M*se*1+C sequences (M*se*1+CC and P*st*1+AC: M*se*1+CT and P*st*1+AG). P*st*1+AC and P*st*1+AG dimer primers were fluorescently labeled. PCR products were run on an Applied Biosystems 3730, fluorescence-based DNA analyser at the Australian Genome Research Facility (AGRF) in Adelaide. AFLPs are used in population genetics for genetic variation analysis as they are rapid to develop, produce individual fingerprints and use low amounts of DNA for analysis (Vos *et al*., 1995).

#### **7.2.3 Population analysis**

Genomic data was viewed with GeneMapper® software for the presence or absence of peaks which were analysed using PopGene® software to determine genetic relationships. The method is detailed in section 3.4.3.6 under genetic data analysis.

### **7.3 RESULTS AND DISCUSSION**

A key aspect of this study is that each *S. oleraceus* accession is from an individual plant. This is a critical point of note as it allows a clear understanding of expected outcomes from the seed without the complications of mixed sampling techniques as discussed by Ward and Jasieniuk (2009).

A study of 34 susceptible and resistant individuals (Table 7.1) sourced from several populations across Australia were selected for AFLP analysis. Despite some evidence of geographic clustering a dendrogram produced from these individuals (Figure 7.1) using 255 scored loci shows large genetic diversity present in Australia. It also shows the presence of several different resistant genotypes. For example genotypes from South Australia cluster with those from Queensland (Clusters A1 and A2) and also include both resistant and susceptible plants. The geographic distance from the Western Australian cluster B1a1a2 and the South Australian cluster B1a1a1 was 2100 km, however the genetic distance between these two clusters was were small. Geographic distances between South Australian and Queensland, South Australian and New South Wales, South Australian and Victorian and Tasmanian and Queensland clusters were 1400 km, 1200 km, 400 km and 1600 km respectively and there was a close genetic relationship in some populations over these large distances.

Although seed can be moved great distances via wind-dispersal, it is unlikely that resistant genotypes would be moved between Queensland and Victoria over a relatively short time period. Therefore, it is most likely that resistance has evolved, or been selected for, in several different genotypes across the continent at different times through the persistent use of ALSinhibiting herbicides. Subsequent work, not reported here, looked at whether resistant populations had the same mutations reported by Ashigh and Tardif (2007) and whether there was a geographical correlation in identified mutations in Australian plants. Different mutations, some occurring in the same location, were identified, supporting the supposition that *S. oleraceus* has evolved resistance to ALS-inhibiting herbicides as a result of independent mutation events on multiple occasions in Australia (Section 6.3.3).

Sonchus	Location		Latitude/Longitude	Response to
number				chlorsulfuron <sup>a.</sup>
14 So	Dalby, Queensland	27° 08′ 93.00″ S	151° 17' 11.00" E	Resistant
17 So	Gatton, Queensland	27° 33' 34.00" S	152°16' 46.00" E	Susceptible
57 So	<sup>b.</sup> Goondiwindi, Queensland	28° 32' 49.33" S	150° 18' 26.66" E	Resistant
So 101	Wasleys, South Australia	34° 28′ 51.65" S	138°41′12.81″E	Resistant
So 103	Nairne, South Australia	35° 02′ 42.44″ S	138° 54' 43.40" E	Susceptible
So 115	Adelaide, South Australia	34° 56' 35.35" S	138°34′53.29″E	Susceptible
So 125	Dalby, Queensland	27° 08' 93.00" S	151° 17' 11.00" E	Resistant
So 142	Warra, Queensland	26° 53' 16.00" S	150° 51' 37.00" E	Susceptible
So 154	Meandarra, Queensland	27° 22′ 00.00" S	150° 04' 71.00" E	Resistant
So 159	Billa Billa, Queensland	28° 10' 00.00" S	150° 27' 00.00" E	Resistant
So 172	North Star, New South Wales	28° 52' 76.00" S	150° 23' 96.00" E	Resistant
So 173	Yallaroi, New South Wales	28° 08' 03.00" S	150° 22' 27.00" E	Resistant
So 176	Yetman, New South Wales	28° 55' 50.00" S	150° 46' 12.00" E	Resistant
So 238	Roaches Beach, Tasmania	42° 54' 03.12" S	147° 29' 49.23" E	Susceptible
So 241	Port Lincoln, South Australia	34° 44′ 46.03" S	135° 52' 45.74" E	Susceptible
So 254	Horsham, Victoria	36°42′45.67″S	142° 12' 04.41" E	Susceptible
So 256	Edenhope, Victoria	36° 55' 38.37" S	141° 27' 16.56" E	Susceptible
So 257	Murtoa, Victoria	36° 34′ 57.52″ S	142° 28' 14.64" E	Susceptible
So 265	Sea Lake, Victoria	35° 28′ 45.64" S	142° 48' 22.65" E	Resistant
So 285	Baratta, South Australia	31° 56' 09.54" S	139° 05' 44.64" E	Susceptible
So 289	Roseworthy, South Australia	34° 33' 00.00" S	138°41′32.50" E	Resistant
So 299	Roseworthy, South Australia	34° 32′ 52.50" S	138°41′22.50" E	Susceptible
So 401	North Star, New South Wales	28° 53' 01.00" S	150° 23' 59.00" E	Resistant
So 402	North Star, New South Wales	28° 53' 02.00" S	150° 23' 58.00" E	Resistant
So 408A	North Star, New South Wales	28° 54' 49.00" S	150° 23' 40.00" E	Resistant
So 408B	North Star, New South Wales	28° 54' 49.00" S	150° 23' 40.00" E	Resistant
So 413	North Star, New South Wales	28° 56' 27.00" S	150° 24' 05.00" E	Susceptible
So 431	Toowoomba, Queensland	27° 35' 18.00" S	151° 56' 54.00" E	Susceptible
So 509	Busselton, Western Australia	33° 39' 24.40" S	115° 24' 42.32" E	Resistant
So 523	Witchcliffe, Western Australia	34° 01′ 21.14″ S	115° 05' 56.53" E	Susceptible
So 530	Porongurup, Western Australia	34° 39' 24.00" S	117° 53' 21.22" E	Susceptible
So 534	Arthur River, Western Australia	33° 20' 07.59" S	117° 02' 00.22" E	Susceptible
So 555	Adelaide, South Australia	34° 55' 57.52" S	138° 35' 47.11" E	Susceptible
So 562	Roseworthy, South Australia	34° 32' 59.28" S	138°41'32.87" E	Susceptible

**Table 7.1** Geographic location of *S. oleraceus* plant accessions collected throughout Australia selected for inclusion in the genetic diversity study and their response to the recommended field rate of chlorsulfuron 15g ai ha<sup>-1</sup>

<sup>a</sup> Response to chlorsulfuron - resistant:- 100% survival and no biomass reduction, susceptible: 0% survival and biomass elimination

b Goondiwindi, Queensland. First ALS-inhibiting herbicide resistant plant found in Australia in 1991.



**Figure 7.1** Dendrogram of 34 individuals produced from 255 scored loci using Popgene ® software. Resistant (Res) and Susceptible (Sus) plants were from South Australia (SA), Queensland (Qu), Victoria (Vic), New South Wales (NSW) Western Australia (WA) and Tasmania (Tas).

ALS-herbicide resistance in *S. oleraceus* is now present in a number of states in Australia with the resistance evolving from a number of independent mutation events. This information coupled with knowledge of weed biology and ecology further enhances the development of integrated weed management strategies. For example, *S. oleraceus* is a self-pollinated species and this study emphasizes the need for farmers to have a zero tolerance approach to localized herbicide resistant infestations and use alternate control methods if a resistant population is detected or suspected.

# **7.4 CONCLUSION**

There is large genetic diversity in *S. oleraceus* in Australia and seed has been dispersed across large distances. This has facilitated the movement of the resistant gene in addition to numerous independent mutation events. The results presented here show that field pollination does occur and could result in pollen movement from resistant to susceptible plants. While this does have the potential to increase the level of resitant seed in the seed bank the predominant movement of R alleles is through seed dispersal, most likely wind or human mediated.

#### **8 GENERAL DISCUSSION**

Worldwide, weeds are evolving resistance to many herbicides, which poses a great challenge to herbicide sustainability in world agriculture (Powles and Yu 2010). The evolution of herbicide resistance demonstrates that over-reliance on any single weed management tool will cause that tool to fail (Powles and Shaner 2001). For example, the widespread adoption of sulfonylurea herbicides across farming areas from the 1980s has resulted in selection within weed populations for resistance to ALS-inhibiting herbicides (Preston *et al*., 2006). Herbicide resistance reduces the economic viability of farming due to the high cost of herbicides, which are ineffective in controlling resistant weeds and the costs of alternate weed control strategies. Once resistance has evolved, the movement of seed from that resistant plant can spread the problem across the landscape. For example, when weather conditions are conducive to the dispersal of *S. oleraceus* seed, the pappus bearing seed is dispersed by wind over both short distances (within metres) and long distances (hundreds of kilometres) Lu *et al*., (2007).

This study has investigated how resistance alleles might move in a plant with wind dispersed seeds. Little was known about how widespread ALS-inhibiting herbicide resistance in *S. oleraceus* is in Australia. In addition, it was not known how frequently resistance to ALSinhibiting herbicides was evolving, what the likely impact of dispersal of resistance alleles has on the spread of resistance once evolved and how far migration of seed could occur. This work is important as it provides knowledge to make informed decisions as to the best management strategies particularly for wind dispersed weeds.

In this study a dose rate experiment, treating resistant and susceptible biotypes of *S. oleraceus* with different rates of chlorsulfuron, found the susceptible *S. oleraceus* could be controlled with as little as 10% of the recommended field rate of this herbicide. This experiment also found that resistant *S. oleraceus* plants could withstand 8 times the recommended field rate of chlorsulfuron. This result highlights the high levels of resistance to this herbicide that can occur in *S. oleraceus* and the likely problems controlling this weed.

Seed of *S. oleraceus* was collected from plants across Australia as a basis for this study. Plants grown from this seed were treated with the ALS-inhibiting herbicide, chlorsulfuron at the recommended field rate to ascertain the level of resistance. The Australia wide survey found that 44% of the 274 accessions treated were resistant to chlorsulfuron and resistance was particularly prevalent in Queensland (59%) and New South Wales (78%), states with intensive summer fallow programs (Chapter 4). Similar findings have been found in surveys with other weed species such as *Lactuca serriola* (Mallory-Smith *et al*., 1990a) and numerous other weed species (Heap 2010). This finding is consistent with world wide research findings (Powles and Yu 2010), although the frequency of resistant populations in *S. oleraceus* is particularly high in comparison with other plant species (Powles pers. comm. 2011). The high frequency of resistance found in this study is of concern and will need to be addressed to reverse the trend of increasing resistance and to control the weed. The problem with *S. oleraceus* illustrates the greater problems of resistance with wind blown seed. Wind blown seed is known to disperse widely across the landscape. In contrast, dispersal of resistance pollen is likely to occur over small distances due to pollen viability decaying rapidly and the need for a recipient plant, although it is known that wind borne pollen can travel long distances, with 20 km being recorded (Watrud *et al*., 2004). The collection of seed from individual plant accessions in this study proved to be a very valuable method as more detailed and accurate conclusions were able to be drawn from the results; this was particularly valuable in the gene flow experiment as variations could be precisely explained.

Weed spread can occur by numerous methods, such as wind, in manure, through equipment and contamination in seed (Thill and Mallory-Smith 1997, Llewellyn and Allen 2006, Boyd and White 2009). Gene flow in a plant population is capable of causing evolutionary change through emigration or immigration (Radosevich *et al*., 1991). Therefore, an increased knowledge of gene flow in a specific plant species is beneficial in formulating strategies to combat the problem of herbicide resistance. Gene flow of ALS-inhibiting herbicide resistance in *S. oleraceus* is clearly by seed movement with field pollination in *S. oleraceus* being shown in this study as less than 10% and is more likely to be less than 4% after removing an outlyer (Chapter 5). These findings are consistent with low levels of cross pollination in most self pollinated plants, rice < 1% (Messeguer *et al*., 2001), barley grass (Baker *et al*., 2005) and eastern black nightshade (Ashigh *et al*., 2008).

*Hordeum glaucum* (barley grass) is an obligate self pollinator, with different gene profiles indicating independent mutations causing the evolution of resistance (Baker *et al*., 2005). Similarly, because *S. oleraceus* is self pollinated any gene flow would most likely occur through seed movement. This means it would be possible to track individual plants to determine genetic diversity on a close (field) and large landscape scale (Australia).

Although genomic technologies have a proven record in advancing plant biological knowledge, they are not without their difficulties such as software with numerous shortcomings including lack of user-friendly functionality (Stewart *et al.,* 2009). The use of molecular markers to investigate herbicide resistance in weed populations has the potential to influence weed management strategies by providing a clearer understanding of resistance mechanisms (Boda Slotta 2008). Molecular methods can be used to explain the potential for gene flow in herbicide resistant or genetically modified organisms.

The individual field work in this study utilised genomic molecular technologies and found that a number of different *S. oleraceus* genotype clusters resistant to ALS-inhibiting herbicides and different mutations can exist within a single field (Chapter 6). Mutations within the ALS protein sequence resulting in resistance to herbicides are known at seven different sites in plants (Powles and Yu 2010). One of the most common of these mutations is at Proline 197 and it appears that any amino acid substitutions at this proline residue will result in an active enzyme that is resistant to chlorsulfuron (Preston *et al*., 2006). The threonine to proline 197 substitution found in this study have also been observed in *Lactuca serriola* (Preston *et al*., 2006), *Kochia scoparia* (Guittieri *et al*., 1995, Warwick *et al*., 2008) and *Papaver rhoeas* (Scarabel *et al*., 2004). In a single field in this present study it was found that 2 different mutations occurred plus an unidentified mutation or mechanism.

There is large genetic diversity in *S. oleraceus* in Australia and seed has been dispersed across large distances, which has facilitated the movement of resistance alleles in addition to independent mutation events. Increasing the chlorsulfuron herbicide rate will not control resistant plants and land managers will need to use alternate control strategies for resistant *S. oleraceus*. It is important to know the genetic diversity of *S. oleraceus* in Australia, as this knowledge gives an insight into the plant's ability to cope with environmental variability. Genetic diversity is the primary basis from which *S. oleraceus* can adapt to changes in the environment over time, such as differing herbicide exposures (Tranel and Wright 2002). From the geographic diversity analysis of plants (34) collected from different states in Australia a large genetic diversity of *S. oleraceus* was found to be present in Australia. Close genetic relationships found in populations that were large distances apart (1000 to 2000 km) suggests that seed movement has occurred, which might have been by either wind or animal transport.

Lu *et al*., (2007) working with the self pollinated wind dispersed weed *Lactuca serriola* found that the genotypes of samples collected in the Adelaide region were different to samples collected on the Yorke peninsula, 100 km to the west. Lu et al., (2007) found variation in *L. serriola* genotypes at close distances (<100 km) and that ALS resistant *Lactuca* had moved from the field to the roadside as ALS-inhibiting herbicides were not used on the roadsides. This study found that, although there was evidence of high genetic diversity in *S. oleraceus*, there were similar genotypes separated by large distances (>1200 km). Human mediated movement may have assisted movement of *S. oleraceus* genotypes over large distances, but it is also possible that, unlike *L. serriola*, with its smaller less sophisticated seed and pappus structure, the larger seed and pappus structure of *S. oleraceus* contributes to a greater freedom of movement in the wind. The seed and pappus structure of *S. oleraceus* may contribute to it being picked up by updrafts and carried to high altitude wind currents. Although the actual dispersal method has not been investigated in this study, the results presented here suggest seed movement plays a significant role in the spread of resistance in *S. oleraceus* populations (Chapter 7). Given the ability of *S. oleraceus* seed to spread, resistant seed from adjoining fields, roadsides or railway lines, plants could easily migrate to resistance-free fields.

ALS-inhibiting herbicide resistance to chlorsulfuron in *S. oleraceus* is widespread in Australia. This knowledge in the extent and structure of genetic variation in *S. oleraceus* allows for a greater understanding of the potential for wind dispersed weed populations to disperse. Although human mediated movement can be managed through a variety of practices, such as increased hygiene related to animal and fodder transport, a plant with wind dispersed seed that can be widely dispersed across the landscape will exacerbate managing resistant seed in the landscape. Gene flow of ALS-inhibiting herbicide resistance in *S. oleraceus* is in the main by seed movement and management strategies aimed at reducing the weed seed bank will reduce the level resistant plants.

The finding that a number of different resistant *S. oleraceus* genotypes clusters with distinct specific mutations can exist in a single field provides knowledge for a close understanding of the nature of mutation existence and proliferation by further utilisation of molecular technologies. This finding is shown in chapter 6 with the existence of 2 different known mutations and one unknown mutation or mechanism being found in an individual field. The extinction of resistant genes in a typical field in the southern Australian cropping zone is unlikely to be a practical option (Weersink *et al*., 2005). This is important as management strategies will need to be aimed at the best economic outcome of reducing the levels of herbicide resistance to a realistic level, given that it is unlikely that total extinction of the resistance allele will occur. Simply zero tolerance may be preferred, but it is unlikely to be economically viable. Farmers will make their compromises to manage at the best economic threshold and future research to understand how the density of *S. oleraceus* impact on productivity would assist these decisions.

Information obtained from research into herbicide resistance can have profound benefits due to the low levels of diversity in Australian crop production and herbicide controls. These aspects have been elucidated by Powles and Shaner (2001), with the authors stating there was a need to educate legislators and farmers about the importance of herbicide mixtures as a strategy to prevent herbicide resistance because once resistant populations spread and increase in density across the Australian landscape eradication is often not economically feasible.

Concerns already exist among weed scientists and agronomists that the current level of adoption of practices that reduce herbicide reliance is sub optimal and that farmers may be unaware of the benefits from preventing herbicide resistance (Weersink 2005). If herbicide resistance is highly mobile between fields and farms there is likely to be less incentive for farmers to invest in preventing resistance (Llewellyn and Allen 2006). Management strategies to mitigate resistance increasing have been proposed such as using a greater diversity of crops (Broster and Pratley 2008). Diversifying agro-ecosystems and using different herbicide modes of action are being used (Powles and Preston 2006, Powles 2008). This work provides scientific understanding of key aspects of this problem as there is a need to move in this direction in research in addition to crop agronomic relationships (Neve *et al.,* 2009).

Gressel (1982) points out that the pattern of herbicide use by farmers is a significant factor in the evolution of herbicide resistance. The knowledge gained from research is likely to improve the use of herbicides and other management strategies to reduce the increasing problem of herbicide resistance. It is virtually impossible to stop weed seeds migrating by wind into fields however it is possible to rotate herbicide groups, manage rotations and use alternative integrated weed management practices.

#### **FUTURE WORK**

The results of this study indicate that ALS-inhibiting herbicide resistance to chlorsulfuron in *S. oleraceus* is now widespread in Australia. The movement of the resistance gene within populations is low (<4%), however, population dendrograms indicate seed has been dispersed across large distances in Australia facilitating the movement of the resistance gene. In addition sequence analysis indicates numerous independent mutation events. Further surveys will enhance the picture of chlorsulfuron resistance levels in *S. oleraceus* in Australia. This study found that collecting individual plant accessions which produced mainly all resistant or all susceptible progeny, elucidates how the frequency of resistance varies in individual fields. More comprehensive individual field collections over a wider area will enhance the picture of the frequency of resistance. Future work could focus on the change in proportion of resistance and susceptible plants over time under different management practices, given we know that gene movement is via seed. Further work may also focus on determining whether populations of *S. oleraceus* go locally extinct and are then re-populated from neighbouring fields or roadsides and how high density *S. oleraceus* populations affect production levels.

In a broader sphere there are three key events in the environment to study, firstly the selection of resistance, secondly the movement of resistance and finally the extinction of the resistance gene. From this study we now know that *S. oleraceus* has a large genetic diversity and, due to this, it is likely that *S. oleraceus* will readily evolve resistance to many if not all of the herbicide groups known to control it. Managers will therefore need to incorporate numerous integrated management strategies to keep *S. oleraceus* under economical control. For example, since *S. oleraceus* plants resistant to chlorsulfuron were found to be susceptible to imidazolinones then utilizing this herbicide in a farming system will lead to reduced chlorsulfuron resistant plant levels.

Furthermore, utilising the existing seed collection for treatment with other groups of herbicides such as the inhibitors of photosynthesis at photosystem II, inhibitors of tubulin formation, inhibitors of carotenoid biosynthesis and inhibitors of EPSP synthase will clarify the cross resistance picture. Extending the work on the sequence of mutants found in the single field (South 4) in South Australia will identify mutation sites in the unknown resistant plants. Future work to determine changes in the resistance frequency under various management regimes will enhance the improvement of best practice management methods.

- Adkins, S.W., Wills, D., Boersma, M., Walker, S.R., Robinson, G., McLeod, R.J. and Einam, J.P. (1997) Weeds resistant to chlorsulfuron and atrazine from the north-east grain region of Australia. *Weed Research.* **37**: 343-349.
- Akkaya, M.S., Bhagwat, A.A. and Cregan, P.B. (1992) Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics.* **132**: 1131-1139.
- Alemseged, Y., Jones, R.E. and Medd, R.W. (2001) A farmer survey of weed management and herbicide resistance problems of winter crops in Australia. *Plant Protection Quarterly*. **16**: 21 - 24.
- Alex, J.F., Cayouette, R. and Mulligan, G.A. (1980) Common and botanical names of weeds in Canada. Canadian Department of Agriculture Publication, 1397. Revised. Ottawa. Ontario. p 132.
- Anderson, M.P. and Gronwald, J.W. (1987) Noncytoplasmic inheritance of atrazine tolerance in velvetleaf (*Abutilon theophrasti*). *Weed Science*. **35**: 496-498.
- Andersson, S. (1991) Geographical variation and genetic analysis of leaf shape in *Crepis tectorum* (*Asteraceae*). *Plant System. and Evolution*. **178**: 247-258.
- Anonymous (2004) Herbicide synopsis a chronological listing of all herbicide, safener and PGR compounds to 1995. From the Global Herbicide Dictionary,  $2<sup>nd</sup>$  Edition (2001)
- Ashigh, J. and Tardif, F.J. (2007) An Ala<sub>205</sub> Val substitution in acetolactate synthase of eastern black nightshade (*Solanum ptychanthum*) reduces sensitivity to herbicides and feedback inhibition. *Weed Science*. **55**: 558-565.
- Ashigh, J., Rajcan, I. and Tardif, F.J. (2008) Genetics of resistance to acetolactate synthase inhibitors in populations of eastern black nightshade (*Solanum ptychanthum*) from Ontario. *Weed Science*. **56**: 210-215.
- Auld, B.A. and Medd, R.W. (1987) *Weeds- An Illustrated Botanical Guide to the weeds of Australia.* Inkata Press. p 117.
- Australian Virtual Herbarium 2009, Council of Heads of Australasian herbaria, viewed 20 May, 2009, <http://www. anbg.gov.au>
- Baker, J. (2002) Factors affecting the establishment of a classical biological control agent, the horehound plume moth (*Wheeleria spilodactylus*) in South Australia. PhD. Thesis. University of Adelaide, Australia.
- Baker, J., Hidayat, I. and Preston, C. (2005) Molecular tools for understanding distribution and spread of weed genotypes. *Crop Protection.* **26**: 198-205
- Barber, H.N. (1941) Spontaneous hybrids between *Sonchus asper* and *Sonchus. oleraceus*. *Annals of Botany.* **18**: 375-377.
- Barr, A.R., Mansooji, A.M., Holtum, J.A.M. and Powles, S.B. (1992) The inheritance of herbicide resistance in *Avena sterilis* spp. *Ludoviciana*, biotype SAS 1. Proceedings of the 1st International Weed Congress, Melbourne, Australia, pp. 70-75.
- Bernasconi, P., Woodworth, A.R., Rosen, B.A., Subramanian, M.V. and Siehl, D.L. (1995) A naturally occurring point mutation confers broad range tolerance to herbicides that target acetolactate synthase. *Journal of Biological Chemistry.* **270**: 17381-17385.
- Berube, D.E. (1978) The basis for host plant specificity in *Tepritis dilacerate* and *T. Formosa*  [Dipt: Tephritidae]. *Entomophaga.* **23**: 331-337.
- Betts, K.J., Ehlke, N.J., Wyse, D.L., Gronwalde, J.W. and Somers, D.A. (1992) Mechanisms of inheritance of diclofop resistance in Italian ryegrass (*Lolium multiflorum*). *Weed Science.* **40**: 184-189.
- Beyer, E.M., Duffy, M.J., Hay, J.V. and Schulueter, D.D. (1988) Sulfonylurea herbicides. In '*Herbicides: Chemistry, Degradation and Mode of Action, eds.'* P.C. Kearney and D.D. Kaufman. **3**: 117-189. (Marcel Dekker Inc., New York).
- Black, J.M. (1986) Flora of South Australia III South Australian Government. Printers Division.
- Blackman, D.M. (2005) What does genetic variation in one-leaf Cape tulip (*Moraea flaccida*) populations in Australia tell us: implications for classical biocontrol? Honours Thesis. University of Adelaide, Australia.
- Bodo Slotta, T. A. (2008) What we know about weeds: Insights from genetic markers. *Weed Science.* **56**: 322-326.
- Bodo Slotta, T. A., Rothhouse, J.M., Horvath, D.P. and Foley, M.E. (2006) Genetic diversity of Canada thistle (*Circusium arvense*) in North Dakota. *Weed Science.* **54**: 1080- 1085.
- Boulos, L. (1972) *Botany* Notis. **125**: 287-319.
- Boutsalis, P. (1996) Resistance to acetolactate synthase-inhibiting herbicides in *Sonchus oleraceus*, *Sisymbrium orientale* and *Brassica tournefortii*. PhD Thesis. University of Adelaide, Australia.
- Boutsalis, P. and Powles, S. B. (1995a) Resistance of dicotyledon weeds to acetolactate synthase (ALS)-inhibiting herbicides in Australia. *Weed Research.* **35**: 149-155.
- Boutsalis, P. and Powles, S. B. (1995b) Inheritance mechanism of resistance to herbicide inhibiting acetolactate synthase in *Sonchus oleraceus* L. *Theoretical Applied Genetics.* **91**: 242-247.
- Boutsalis, P., Karotam, J. and Powles, S. B. (1999) Molecular basis for resistance to acetolactate synthase – inhibiting herbicide in *Sisymbrium orientale* and *Brassica tournefortii. Pest Science.* **55**: 507-516.
- Boyd, N.S. and White, S. (2009) Impact of wild blueberry harvest on weed seed dispersal within and between fields. *Weed Science.* **57**: 541-546.
- Broster, J.C. and Pratley, J.E. (2008) Incidence of herbicide resistance in relation to cropping practices of south eastern Australia. Proceedings of the  $16<sup>th</sup>$  Australian Weeds Conference, eds. R.D. van Klinken, V.A. Osten, F.D. Panetta and J.C. Scanlan, pp. 84-86. (Weed Society of Queensland, Cairns).
- Christopher, J.T., Powles, S.B. and Holtum, J.A.M. (1992) Resistance to acetolactate synthase-inhibiting herbicides in annual ryegrass (*Lolium rigidum*) involves at least two mechanisms. *Plant Physiology*. **100**: 1909-1913.
- Clapham, A.R., Tutin, T.G. and Moore, D.M. (1987) *Flora of the British Isles.* Third Edition. Cambridge University Press. pp.490-498.
- Clark, D.P. (2005) *Molecular Biology* Elsevier Academic Press. Oxford. United Kingdom.
- Cooper, D.C. and Mahony, K.L. (1935) Cytological observations on certain compositae. *American Journal of Botany*. **12**: 843.
- Corbett, C.A. and Tardif, F.J. (2006) Detection of resistance to acetolactate synthase inhibitors in weeds with emphasis on DNA-based techniques: a review. *Pest Management Science.* **62**: 584-597.
- Coustau, C., Chevillon, C. and Ffrench-Constant, R. (2000) Resistance to xenobiotics and parasites: can we count the cost? *Trends in Ecology and Evolution.* **15**: 378-383.
- CRC Australian Weed Management. (2006) University of Adelaide, Glen-Osmond, South Australia, viewed 1 February, 2006, <http://www.weeds.crc.org.au/publications/scientific-papers.html
- Darmency, H. (1994) Genetics of herbicide resistance in weeds and crops, in *Herbicide Resistance in Plants; Biology and Biochemistry.* Powles, S.B. and Holtum, J.A.M., Eds. Lewis Publishers, Florida. pp. 263-298.
- Davies, K.W. and Sheley, R.L. (2007) A conceptual framework for preventing the spatial dispersal of invasive plants. *Weed Science.* **55**: 178-184.
- DeFelice, M., Guardiola, J., Esposito, B. and Iaccarino, M. (1974) Structural genes for a newly recognised acetolactate synthase in *Escherichia coli* K-12. *Journal of Bacteriology.* **120**: 1068-1077
- Dorph-Peterson, K. (1924) Examinations of the occurrence and vitality of various weed seed species under different conditions, made at the Danish State Seed Testing Station during the years 1896-1923. Fourth International Seed Testing Conference, Cambridge, U.K. pp.124-138.
- Duran-Prado, M., Osuna, M.D., De Prado, R. and Franco, A.R. (2004) Molecular basis of resistance to sulfonylureas in *Papaver rhoeas*. *Pesticide Biochemistry and Physiology*. **42**: 110-118.
- Fitzpatrick, S., Riesen, P. and McCaslin, M. (2003) Pollen mediated gene flow in alfalfa: A three year summary of field research. From: Proceedings of the 2003 central alfalfa improvement conference, virtual meeting July 21-25, 2003.
- Futuyma, D.J. (1998) *Evolutionary Biology.* 3rd Ed. Sinauer Associates, Incorporated. Publishers, Sunderland, Massachusetts.
- Ghersa, C.M., Martinez-Ghersa, M.A., Brewer, T.G. and Roush, M.L. (1994) Use of gene flow to control diclofop-methyl resistance in Italian ryegrass (*Lolium multiflorum*). *Weed Technology.* **8**: 139-147.
- Gilbey, D.J. (1974) Estimating yield losses in wheat resulting from infestations by doublegee (*Emex australis*). *Australian Journal of Experimental Agriculture.* **14**: 656-657.
- Glick, B.R. and Pasternak, J.J. (2003) *Molecular Biotechnology Principles and applications of recombinant DNA.* ASM Press. Washington.
- Godwin, I.D., Aitken, E.A.B. and Smith, L.W. (1997) Application of inter simple sequence repeat (ISSR) markers to plant genetics. *Electrophoresis.* **18**: 1545-1558.

Google Earth. (2009) Viewed 9 February 2009. <http://www.google.com

- Green, J.M., Hale, T., Pagano, M.A., Andreassi, J.L. and Gutteridge, S.A. (2009) Response of 98140 corn with *gat4621* and *hra* transgenes to glyphosate and ALS-inhibiting herbicides. *Weed Science*. **57**: 142-148.
- Gressel, J. and Segel, L.A. (1982) Interelating factors controlling the rate of appearance of resistance: the outlook for the future, in *Herbicide Resistance in Plants.* LeBaron, H.M. and Gressel, J. Eds. John Wiley and Son. New York. pp. 325-347.
- Gressel, J. (1991) Why get resistance? It can be prevented or delayed, *In. Herbicide resistance in weeds and crops.* J.C. Caseley, G.W. Cussans and R.K. Atkin, Eds. Butterworth-Heineman. Oxford. pp. 1-26.
- Groves, R.H. (1991) Status of environmental weed control in Australia. *Plant Protection Quarterly*. **6**: 95-98.
- Grula, J.W., Hudspeth, R.L., Hobbs, S.L. and Anderson, D.M. (1995) Organisation, inheritance and expression of acetohydroxyacid synthase genes in the cotton allotetraploid *Gossypium hirsutum. Plant Molecular Biology.* **28**: 837-846.
- Guertin, P. and Halvorson, W.L. (2003) Factsheet for *Sonchus* L. spp. USGS Weeds in the West project: Status of Introduced Plants in southern Arizona Parks. University of Arizona. U.S.A.
- Guttieri, M.J., Eberlein, C.V. and Thill, D.C. (1995) Diverse mutations in the acetolactate synthase gene confer chlorsulfuron resistance in kochia (*Kochia scoparia*) biotypes. *Weed Science.* **43**: 175-178.
- Haughn, G.W. and Sommerville, C. (1986) Sulfonylurea-resistant mutants of *Arabidopsis thaliana*. *Molecular and General Genetics.* **204**: 430-434.
- Hall, J.C., Van Eeerd, L.L., Miller, S.D., Owen, M.D.K., Prather, T.S., Shaner, D.L., Singh, M., Vaughn, K.C. and Weller, S.C. (2000) Future research directions for weed science. *Weed Technology*. **14**: 647-658.
- Harper, J.L. (1956) The evolution of weeds in relation to resistance to herbicide, in *Proceedings of the 3rd British Weed Control Conference.* pp. 179-188.
- Harper, J.L. (1977) *Population Biology in Plants.* Academic Press. San Fransisco p. 892
- Hashem, A. and Bowran, D. (2001) Resistance of wild radish (*Raphanus raphanistrum*) to acetolactate synthase inhibiting herbicides in the Western Australian wheat belt. *Weed Technology*. **15**: 68-74.
- Heap, I. (2010) Weed Science, International survey of herbicide resistant weeds, Weed Science Society of America, viewed 12 November, 2010, <http://www.weedscience.org/in.asp>
- Heap, J. and Knight, R. (1982) A population of ryegrass tolerant to the herbicide diclofopmethyl. *Journal of Australian Institute of Agricultural Science.* **48**: 156-157.
- Heap, J. and Knight, R. (1986) The occurrence of herbicide cross-resistance in a population of annual ryegrass, *Lolium rigidum*, resistant to diclofop-methyl. *Journal of Australian Institute of Agricultural Science.* **37**: 149-156.
- Hidayat, I. (2004) Evolution and spread of paraquat resistant barley grasses (*Hordeum glaucum* Stead. and *H. leporinum* Link. ) PhD. Thesis. University of Adelaide, Australia.
- Holm, L.G., Plucknett, D.l., Pancho, J.V. and Herberger, J.P. (1977) *The world's worst weed: Distribution and Biology*. The University Press of Hawaii, Honolulu. pp. 436-439.
- Holt, J.S. (1992) History of identification of herbicide resistant weeds. *Weed Technology.* **6**: 615-620.
- Holt, J.S. and LeBaron, H.M. (1990) Significance and distribution of herbicide resistance. *Weed Technology.* **4**: 141-149.
- Holt, J.S., Powles, S.B. and Holtum, J.A.M. (1993) Mechanisms and agronomic aspects of herbicide resistance. *Annual Revelations in Plant Physiology. Plant Molecular Biology.* **44**: 203-229.
- Holt, J.S. and Thill, D.C. (1994) Growth and productivity of resistant plants, *In. Herbicide Resistance in Plants; Biology and Biochemistry.* S.B. Powles and J.A.M. Holtum, Eds. Lewis Publishers, Florida. pp. 299-316.
- Hsieh, T.A., Schooler, A.B., Bell, A. and Nalewaja, J.D. (1972) Cytotaxonomy of three *Sonchus* species. *American Journal of Botany*. **59**: 789-796.
- Howat, P.D. (1987) Weeds resistant to herbicides in Australia and contributing factors leading to their appearance. *Plant Protection Quarterly.* **2**: 82-85.
- Hutchinson, I., Colosi, J. and Lewin, R.A. (1984) The biology of Canadian weeds. 63. *Sonchus asper* (L.) Hill and *S. oleraceus* L. *Canadian Journal of Plant Science*. **64**: 731-744.
- Islam, A.K.M.R. and Powles, S.B. (1988) Inheritance of resistance to paraquat in barley grass *Hordeum glaucum* Steud. *Weed Research.* **28**: 393-397.
- Itoh, K. and Miyahara, M. (1984) Inheritance of paraquat resistance in *Erigeron philadelphicus* L. *Weed Research* (Japan). **29**: 301-307.
- Jasieniuk, M., Brule-Babel, A.L. and Morrison, I.N. (1994) Inheritance of trifluralin resistance in green foxtail (*Setaria viridis*). *Weed Science*. **42**: 123-127.
- Jasieniuk, M., Brule-Babel, A.L. and Morrison, I.N. (1996) The evolution and genetics of herbicide resistance in weeds. *Weed Science*. **44**: 176-193.
- Jones, N., Ougham, H., Thomas, H. and Farrar, J. (1997) Markers and mapping: we are all genetists now. *Proceedings of the 2nd New Phytologist Symposium.* **137**: 165-177.
- Judd, W.S., Campbell, C.S., Kellogg, E.A. and Stevens, P.F. (1999) *Plant systemics: a phylogenic approach*. Sinauer Associates, Sunderland, MA.
- Julien, M.H. (1982) Biological control of weeds. A World Catalogue of Agents and their Target Weeds. 108. (Commonwealth Agricultural Bureau, Slough, UK.).
- King, M. (1993) Species evolution: the role of chromosome change. Cambridge University Press, Cambridge, UK.
- Knispel, A.L., McLachlan, S.M., Van Acker, R.C. and Frierson, L.F. (2008) Gene flow and multiple herbicide resistance in escaped canola populations. *Weed Science.* **56**: 72- 80.
- Lamego, F.P., Charlson, D., Delatorre, C.A., Burgos, N.R. and Vidal, R.A. (2009) Molecular basis of resistance to ALS-inhibitor herbicides in greater beggarticks. *Weed Science*. **72**: 474-481.

Lawrence, W.J.C. (1974) *Plant Breeding.* Unwin Publishers, New York.

- LeBaron, H.M. (1991) Distribution and seriousness of herbicide resistant weed infestations worldwide, in *Herbicide Resistance in Weeds and Crops.* Casley, J.C., Cussans, G.W. and Atkin, R.K. Eds. Butterworth-Heineman. Oxford. pp.27-44.
- Lebeda, A., Dolezalova, I and Astley, D. (2004) Representation of wild *Lactuca* spp. (Asteraceae, Lactuceae) in world genebank collections. *Genetic Resources and Crop Evolution.* **51**: 167-174.
- Lee, K.Y., Townsend, J., Tepperman, J., Black, M., Chui, C.F., Mazur, B., Dunsmuir, P. and Bedbrook, J. (1988) The molecular basis of sulfonylurea herbicide resistance in tobacco. *EMBO Journal*. **7**: 1241-1248.
- Lewin, R.A. (1948) Biological Flora of the British Isles. *Sonchus* L. (*Sonchus oleraceus* L. and *S. asper* (L.) Hill). The *Journal of Ecology*. **36**: 203-223.
- Lewin, R.A. (1975) *Sonchus* L. *in* Stace, C.A. ed. Hybridization and the flora of the British Isles. Academic Press, London, U.K, pp 432-433.
- Liebman, M., Mohler, C.L. and Staver, C.P. (2007) Ecological Management of Agricultural weeds. Cambridge University Press, Cambridge, UK, p 446.
- Llewellyn, R.S. and Allen, D.M. (2006) Expected mobility of herbicide resistance via weed seeds and pollen in Western Australian cropping region. *Crop Protection*. **25**: 520- 526.
- Lovett, J.V. and Knights, S.E. (1996) Where in the world is weed science going? Proceedings of the 11<sup>th</sup> Australian Weed Conference, University of Melbourne, pp. 3-13.
- Lu, Y.Q. (2005) The spread of herbicide resistance in *Lactuca serriola* at a landscape scale. M.Sc. Thesis, Discipline of Plant and Pest Sciences, University of Adelaide, South Australia.
- Lu, Y.Q., Baker, J. and Preston, C. (2007) The spread of resistance to acetolactate synthase inhibiting herbicides in wind borne, self-pollinated weed species, *Lactuca serriola* L. *Theoretical Applied Genetics.* **115**: 443-450.
- Lu, H., Shen, J., Sang, W., Zhang, X. and Lin, J. (2008) Pollen viability, pollination, seed set and germination of croftonweed (*Eupatorium adenophorum*) in China. *Weed Science.* **56**: 42-51.
- Mallory-Smith, C.A., Thill, D.C. and Dial, M.J. (1990a) Identification of sulfonylurea herbicide resistant prickly lettuce (*Lactuca serriola*). *Weed Technology*. **4**: 163-168.
- Mallory-Smith, C.A., Thill, D.C., Dial, M.J. and Zemetra, R.S. (1990b) Inheritance of sulfonylurea herbicide resistance in *Lactuca* spp. *Weed Technology*. **4**: 787-790.
- Mallory-Smith, C.A. and Retzinger, E.J. (2003) Revised Classification of herbicides by site of action for weed resistance management strategies. *Weed Technology*. **17**: 605-619.
- Maneechote, C. (1995) Mechanisms of herbicide resistance in wild oats (*Avena* spp.). PhD Thesis. University of Adelaide, Australia.
- Marchal, E. (1920) Recherches sur les variations numeriques des chromosomes dan la série végétale. *Memorandum Academy of Belgium*. **4**: 3-108.
- Martin, R.J., McMillan, M.G. (1988) Survey of farm management practices of the northern wheat belt of New South Wales. *Australian Journal of Experimental Agriculture.*  **28**: 499-509.
- Mathews, J.M. (1994) Management of herbicide resistant weed populations. *In. Herbicide Resistance in Plants. Biology and Biochemistry.* S.B. Powles and J.A.M. Holtum, Eds. Lewis Publishers. Florida. pp. 317-335.
- Maxwell, B.D. and Mortimer, A.M. (1994) Selection for herbicide resistance. In: *Herbicide Resistance in Plants: Biology and Biochemistry.* (Eds. S.B. Powles and J.A.M. Holtum). Lewis Publishers. Florida. pp. 1-26.
- Maxwell, B.D., Roush, M.L. and Radosevich, S.R. (1990) Population genetics of plant pathogenic fungi. *BioScience*. **43**: 311-319.
- Mazure, B.J. and Falco, S.C. (1989) The development of herbicide resistant crops. *Annual Review of Plant Physiology and Molecular Biology*. **40**: 441-470.
- McDonald, B.A. and McDermott, J.M. (1993) Gene flow in plant pathosystems. *Annual Review of Phytopathology.* **31**: 353-373.
- McDonald, B.A. and Linde, C. (2002) Pathogen population genetics, evolutionary potential and durable resistance. *Annual Review of Phytopathology.* **40**: 349-379.
- Messeguer, J., Fogher, C., Guiderdoni, E., Marfà, V., Català, M. M., Baldi, G. and Melé, E. (2001) Field assessments of gene flow from transgenic to cultivated rice (*Oryza sativa* L.) using a herbicide resistance gene as tracer marker. *Theoretical Applied Genetics*. **103**: 1151-1159.
- Mitich, L.M. (1998) Thistles II: *Sonchus* and *Centaurea. Weed Technology*. **2**: 380-381.
- Nei, M. (1973) Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences of the USA.* **70**: 3321-3323.
- Neve, P. Vila-Aiub. M.and Roux, F. (2009) Research Review. Ev. *New Phytologist.* **184**: 783-793.
- Neve, P. and Powles, S. (2005a) Recurrent selection with reduced herbicide rates result in the rapid evolution of herbicide resistance in *Lolium rigidum*. *Theoretical Applied Genetics.* **110**: 1154-1166.
- Neve, P. and Powles, S. (2005b) High survival frequencies at low herbicide use rates in populations of *Lolium rigidum* result in rapid evolution of herbicide resistance. *Heredity.* **95**: 485-492.
- Neve, P. (2007) Challenges for herbicide resistance evolution and management: 50 years after Harper. European Weed Research Society. *Weed Research*. **47**: 365-369.
- O'Hanlon, P.C., Peakall, R. and Briese, D.T. (2000) A review of new PCR-based genetic markers and their utility to weed ecology. *Weed Research.* **40**: 239-254.
- O'Loughlin, G.T. and Chambers, T.C. (1969) The feeding sites in *Sonchus oleraceus* of *Hyperomyzus lactucae*, the aphid vector of lettuce necrotic yellows. *The Australian Journal of Biological Sciences.* **20**: 629-637.
- Percival M.S. (1955) The presentation of pollen in certain angiosperms and its collection by *Apis mellifera*. *New Phytologist*. **54**: 353-368.
- Peschken, D.P. (1982) Host specificity and biology of *Cystiphora sonchi* [*Dip.: Cecidomyiidae*], a candidate for the biological control of *Sonchus* species. *Entomophaga.* **27**: 405-416.
- PestGenie 2010, Pest Genie data base of plant protection and animal health products, viewed 17 November, 2010,

<http://www.pestgenie.com.au>

- Phillips, R.L. and Vasil, I.K. (2001) *DNA-Markers in plants.* Kluwer Academic Publishers. Dordrecht.
- Powles, S.B. and Mathews, J.A.M. (1991) Multiple herbicide resistance in annual ryegrass (*Lolium rigidum*): a driving force for adoption of integrated weed management, *In. Resistance 91: Achievments and Developments in Combating Pesticide Resistance.* I. Denholm, A.L. Devonshire and D.W. Hollomon, Eds. Elsevier Applied Science. London. pp. 75-87.
- Powles, S.B. (1993) Multiple herbicide resistance in annual ryegrass (*Lolium rigidum*): a driving force for adoption of integrated weed management. *Proceedings of the International Symposium of the Indian Society of Weed Science.* **1**: 189-194.
- Powles, S.B. and Holtum, J.A.M. (1994) Herbicide resistant plants. Biology and biochemistry. CRC Press. Boca Raton, London, New York and Washington, D.C.
- Powles, S.B., Preston, C., Bryan, I.B. and Jutsum, A.R. (1997) Herbicide resistance: Impact and management. *Advances in Agronomy.* **58**: 57-93.
- Powles, S.B. and Shaner, D.L. (2001) Herbicide resistance and world grains. CRC Press. Boca Raton, London, New York and Washington, D.C.
- Powles, S.B. and Preston, C. (2006) Evolved glyphosate resistance in plants: Biochemical and genetic basis of resistance. *Weed Technology.* **20**: 282-289.
- Powles, S.B. (2008) Evolved glyphosate-resistant weeds around the world: lessons to be learnt. *Pest Management Science.* **64**: 360-365.
- Powles, S.B. and Yu, Q. (2010) Evolution in Action: Plants Resistant to Herbicides. *Annual Review of Plant Biology.* **61**: 317-347.
- Prado, M.D., De Prado, R.D. and Franco, A.R. (2004) Design and optimisation of degenerated universal primers for the cloning of the plant acetolactate synthase conserved domains. *Weed Science*. **52**: 487-491.
- Pratley, J.E., Broster, J.C. and Michael, P. (2008) Evaluation of barnyard grass (Echinochloa spp) in Australian rice crops. *Australian Journal of Agricultural Research*. (In Press).
- Preston, C. and Roush, R. (1998) Variation in herbicide dose rates: risks associated with herbicide resistance, pp. 128-137, In R.W. Medd and J.E. Pratley, eds. *Precision Weed Management in Crops and Pastures* CRC for Weed Management Systems, Adelaide.
- Preston, C. and Powles, S.B. (2002) Evolution of herbicide resistance in weeds: initial frequency of target site-based resistance to acetolactate synthase-inhibiting herbicides in *Lolium rigidum. Heredity.* **88**: 8-13.
- Preston, C., Stone, L.M., Rieger, M.A. and Baker, J. (2006) Multiple effects of a naturally occurring proline to threonine substitution within acetolactate synthase in two herbicide-resistant populations of *Lactuca serriola*. *Pesticide Biochemistry and Physiology.* **84**: 227-235.
- Pubcris 2010, Australian Government Public Chemical Registration Information System, viewed 17 November 2010, <http://services.apvma.gov.au>
- Pupilli, F., Martinez, E.J., Busti, A., Calderini, O., Quarin, C.L. and Arcioni, S. (2004) Comparative mapping reveals partial conservation of synteny at the apomixis locus in *Paspalum* spp. *Molecular Genetic Genomics.* **270**: 539-548.
- Purba, E., Preston, C. and Powles, S.B. (1993) Inheritance of bipyridyle herbicide resistance in *Arctotheca calendula* and *Hordeum leporinum*. *Theoretical Applied Genetics*. **87**: 598-602.
- Radosevich, S.R., Maxwell, B.D. and Roush, M.C. (1991) Managing herbicide resistance through fitness and gene flow, in *Herbicide Resistance in Weeds and Crops.* Caselet, J.C., Cussans, G.W. and Atkin, R.K. Eds. Butterworth-Heineman. Oxford. pp. 129- 143.
- Retzinger, E.J. and Mallory-Smith, C.A. (1997) Classification of herbicides by site of action for weed resistance management strategies. *Weed Technology*. **11**: 605-619.
- Rieger, M. A., Lamond, M., Preston, C., Powles, S.B. and Roush, R.T. (2002) Pollen mediated movement of herbicide resistance between commercial canola fields. *Science.* **296**: 2386- 2388.
- Rieseberg, L.H. (2001) Chromosomal rearrangements and speciation. *Trends in Ecology and Evolution.* **16**: 351-358.
- Roush, R.T. and Miller, J. (1986) Resistance monitoring. *Journal of Economic Entomology*. **79**: 293-297.
- Russel, P.J. (1980) *Essential Genetics*. Blackwell Scientific Publications. London.
- Rutledge, R.G., Ouellet, T., Hattori, J. and Miki, B.L. (1991) Molecular characterization and genetic origin of the *Brassica napus* acetohydroxyacid synthase multigene family. *Molecular and General Genetics*. **229**: 31-40.
- Saari, L.L., Cotterman, J.C. and Primiani, M.M.. (1990) Mechanisms of sulfonylurea herbicide resistance in the broadleaf weed, *Kochia scoparia*, *Plant Physiology*. **93**: 55-61.
- Saari, L.L., Cotterman, J.C., Smith, W.F. and Primiani, M.M.. (1992) Sulfonylurea herbicide resistance in common chickweed, perennial ryegrass and Russian thistle. *Pesticide Biochemistry and Physiology*. **42**: 110-118.
- Saari, L.L., Cotterman, J.C. and Thill, D.C. (1994) Resistance to acetolactate synthaseinhibiting herbicides. Pages 83-139 *in* Powles, S.B. and Holtum, J.A.M., eds. Herbicide resistance in plants: Biology and Biochemistry. Boca Raton, Florida: Lewis Publishers.
- Sales, M.A., Shivrain, V.K., Burgos, N.R. and Kuk, Y.I. (2008) Amino acid substitutions in the acetolactate synthase gene of red rice (*Oryza sativa*) confer resistance to imazethapyr. *Weed Science*. **56**: 484-489.

Salisbury, E.J. (1964) *Weeds and aliens*. Collins Press, London, United Kingdom.

- Sathasivan, K., Haughn, G.W. and Murai, N. (1991) Molecular basis of imidazolinone herbicide resistance in *Arabidopsis thaliana* var. Columbia. *Plant Physiology*. **97**: 1044-1050.
- Sanyal, D., Bhowmik, P.C., Anderson, R.L. and Shrestha, A. (2008) Revisiting the perspective and progress of integrated weed management. *Weed Science*. **56**: 161- 167.
- Scarabel, L., Carraro, N., Sattin, M. and Varotto, S. (2004) Molecular basis and genetic characterisation of evolved resistance to ALS-inhibitors in *Papaver rhoeas*. *Plant Science.* **166**: 703-709.
- Seefeldt, S.S., Jensen, J.E. and Fuerst, E.P. (1995) Log-logistic analysis of herbicide doseresponse relationships. *Weed Technology.* **9**: 218-227.
- Shaaltiel, Y., Chua, N.H., Gepatein, S. and Gressel, J. (1988) Dominant pleiotropy controls enzymes co-segregating with paraquat resistance in *Conyza bonariensis*. *Theoretical Applied Genetics.* **75**: 850-856.
- Shaner, D.L., Umeda, K., Ciarlante, D.R. and Los, M. (1982) AC 222-293 a new postemergent herbicide for cereals: Greenhouse studies. *Proceedings British Crop Protection Conference-Weeds*. **1**: 25-31.
- Sheldon, J.C. and Burrows, F.M. (1973) The dispersal effectiveness of the achene-pappus units of selected *Compositae* in steady winds with convection. *New phytology*. **72**: 665-675
- Shields, E.J., Dauer, J.T., VanGessel, M.J. and Neumann, G. (2006) Horseweed (*Conyza candensis*) seed collected in the planetary boundary layer. *Weed Science*. **54**: 1063- 1067.

Silvertown, J.W. (1987) *Introduction to Plant Ecology*. 2<sup>nd</sup> Edn. Longman, New York, USA.

- Slife, F.W. (1986) Resistance in weeds. *In. Pesticide Resistance: Strategies and Tactics for Management.* National Academy Press. Washington DC. pp. 317-334.
- Stankiewicz, M., Gadamski, G. and Gawronski, S.W. (2001) Genetic variation and phylogenic relationships of triazine-resistant and triazine–susceptible biotypes of *Solanum nigrum* analysis using RAPD markers. *Weed Research*. **41**: 287-300.
- Stebbins, G.L., Jenkins, J.A. and Walters, M.S. (1953) Chromosomes and phylogeny in the compositae, tribe Cichoriaeae. University of California. *Publication Botany*. **26**: 401- 430.
- Stewart, C.N., Tranel, P.J., Horvath, D.P., Andreson, J.V., Rieseberg, L.H., Westwood, J.H., Mallory-Smith, C.A., Zapiola, M.L. and Dlugosch, K.M. (2009) Evolution of weediness and invasiveness: charting the course for weed genomics. *Weed Science*. **57**: 451-462.
- St. John-Sweeting, R.S. and Morris, K.A. (1990). Seed transmission through the digestive tract of the horse. Proceedings of the 9th Australian Weeds Conference, Adelaide, South Australia. pp. 137-139.
- Strickberger, M.W. (1968) *Genetics.* Macmillan, New York.
- Sunnucks, P. (2000) Efficient genetic markers for population biology. *Trends in Ecology and Evolution*. **15**: 199-203.
- Taylor, G.R. (1991) Polymerase chain reaction: basic principles and automation. *In.* M.J. McPherson, P. Quirke and G.R. Taylor, eds. *PCR: A Practical Approach*. Oxford University Press, New York. pp. 1-14.
- Thill, D.C. and Mallory-Smith, C.A. (1997) The nature and consequences of weed spread in cropping systems. *Weed Science.* **45**: 337-342.
- Tranel, P.J. and Wright, T.R. (2002) Resistance of weeds to ALS-inhibiting herbicides: what have we learned? *Weed Science.* **50**: 700-712.
- Tucker, E.S. and Powles, S.B. (1988) Occurrence and distribution in southern Australia of barley grass (*Hordeum glaucum* Steud. ) resistant to paraquat. *Plant Protection Quarterly* **3**: 19-21.
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., Van de Lee, T.V.D., Hornes, M., Frijters, A., Pot, J., Peleman, J., Kuiper, M., Zabeau, M. and Van de Lee, T. (1995) AFLP: a new technique for DNA fingerprinting. *Nucleic Acid Research*. **23**: 4407-4414.
- Walker, S.R., Taylor, I.N., Milne, G., Osten, V.A., Hoque, Z. and Farquharson, R.J. (2005a) A survey of management and economic impact of weeds in dryland cotton cropping systems of subtropical Australia. *Australian Journal of Experimental Agriculture.*  **45**: 79-91.
- Walker, S.R., Widderick, M. J. and Galea, K. (2005b) Stopping Herbicide Resistance in southern Queensland. Queensland Government. Department of Primary Industries and Fisheries publication.
- Ward, S.M., and Jasieniuk, M. (2009) Review: Sampling weedy and invasive plant populations for genetic diversity analysis. *Weed Science.* **57**: 593-602.
- Warwick, S.I., Xu, R., Sauder, C. and Beckie, H.J. (2008) Acetolactate synthase target site mutations and single nucleotide polymorphism genotyping in ALS-resistant Kochia (*Kochia scoparia*) *Weed Science.* **56**: 796-806.
- Watrud, L.S., Lee, E.H., Fairbrother, A., Burdick, C., Reichman, J.R., Bollman, M., Storm, M., King, G. and Van de Water, P.K. (2004) Evidence for landscape-level, pollenmediated gene flow from genetically modified creeping bent grass with CP4 EPSPS as a marker. *Proceedings of the Natural Academy of Science* USA **101**: 14533-14538
- Weersink, A., Llewellyn, R.S. and Pannell, D.J. (2005) Economics of pre-emptive management to avoid weed resistance to glyphosate in Australia. *Crop Protection.* **24**: 659-665.
- Whaley, C.M., Wilson, H.P. and Westwood, J.H. (2007) A new mutation in plant ALS confers resistance to five classes of ALS-inhibiting herbicides. *Weed Science*. **55**: 83- 90.
- White, A.D., Owen, M.D.K., Hartzler, R.G. and Cardina, J. (2002) Common sunflower resistance to acetolactate synthase-inhibiting herbicides. *Weed Science*. **50**: 432-437.
- White, M.J.D. (1978) Modes of speciation. W.H.Freeman, New York, USA.
- Whitkus, R., Doebley, J. and Wendel, J.F. (1994) Nuclear DNA markers in systemics and evolution. *In.* R.L. Phillips and I.K. Vasil, eds. *DNA-based markers in plants.* Kluwer Academic Publishers, Dordrecht, The Netherlands. pp. 116-141.
- Widderick, M.J. (2002) Ecology and management of the weed common sowthistle (*Sonchus oleraceus* L.) Ph.D Thesis. University of New England, Armidale, NSW.
- Williams, J.G.K., Kubelik, A.R., Livak, K.J., Rafalski, J.A. and Tingey, S.V. (1990) "DNA polymorphisms amplified by arbitrary primers are useful as genetic markers." *Nucleic Acid Research.* **18**: 6531-6535.
- Zollinger, R.K. and Parker, R. (1999) Sowthistles. *In*: Sheley, R.L. and Petroff, J.K. (eds.). *Biology and management of noxious rangeland weeds.* Oregan State University Press, Corvallis, Oregon. p 438.

## **APPENDICES**

- 1. *Sonchus oleraceus* germplasm collection
- 2. Gene flow experiment data
- 3. Source of chemicals
- 4. Source of equipment
- 5. Oglionucleotides
- 6. Gels, Buffers and media

## **Appendix 1.** *Sonchus oleraceus* **Germplasm**

































## **Appendix 2. GENE FLOW DATA**

Table 18 or S1. Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So057 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Susceptible</b> S. oleraceus		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#$ <sup>a</sup>		heads harvested	$#$ sown	# treated $b$	<b>Susceptible</b>	<b>Resistant</b>
S01So115	H <sub>0</sub> 33		80	38	38	
S01So115	H <sub>0</sub> 37		100	76	76	
S01So115	H <sub>079</sub>			0		
S01So115	H <sub>091</sub>		30	24	24	
S01So115	H <sub>136</sub>		140	102	102	
S01So115	H168		160	31	31	
S01So115	H189		100	6	6	
S01So115	H <sub>207</sub>	h	200	6	6	
S01So115	H <sub>222</sub>		100	17	17	
S01So115	H <sub>235</sub>		100	28	28	
S01So115	H <sub>251</sub>	3	30			
Totals		35	1040	329	329	

 $a^{a}$  Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

Table 18B or R1. Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So057 grown within 100mm of an individual susceptible *S. oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So057 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

**Table S2.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So101 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



 $a$  Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R2.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So101 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So101 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

**Table S3.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So102 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Susceptible</b> S. <i>oleraceus</i>		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#$ <sup>a</sup>		heads harvested	$#$ sown	# treated $\degree$	<b>Susceptible</b>	<b>Resistant</b>
S03So115	H <sub>134</sub>		60	60		60
S03So115	H <sub>151</sub>		150	70		70
S03So115	H <sub>167</sub>		100	18	18	
S03So115	H <sub>187</sub>	2	60			
S03So115	H <sub>205</sub>	2	120	27	27	
S03So115	H <sub>245</sub>		80	15		15
Totals				191	46	145

 $a^{a}$  Capitulum heads harvested as mature from mid February 2007 to late March 2007.

b Number of established 2 leaf seedlings treated with chlorsulfuron.

Table R3. Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So102 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So102 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

**Table S4.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So106 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

b Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R4.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So106 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So106 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.<br><sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table S5.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So108 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Susceptible</b> S. oleraceus		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#$ <sup>a</sup>		heads harvested	$#$ sown	# treated $\degree$	<b>Susceptible</b>	<b>Resistant</b>
S05So115	H <sub>150</sub>		120	60	50	$10^{S4}$
S05So115	H <sub>185</sub>	8	600	120	159	$1^{S5}$
S05So115	H <sub>204</sub>		<b>200</b>	30	30	0
S05So115	H <sub>2</sub> 19		500	160	160	
S05So115	H <sub>237</sub>		400	150	150	
S05So115	H <sub>249</sub>	6	300	80	80	
<b>Totals</b>		33	2120	600	629	

<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R5.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So108 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So108 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



 $a^{a}$  Capitulum heads harvested as mature from mid February 2007 to late March 2007.

**Table S6.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So125 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R6.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So125 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So125 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

**Table S7.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So145 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R7.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So145 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So145 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.
**Table S8.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So149 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R8.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So149 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So149 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table S9.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So154 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Susceptible</b> S. <i>oleraceus</i>		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#$ <sup>a</sup>		heads harvested	$#$ sown	# treated $\degree$	<b>Susceptible</b>	<b>Resistant</b>
S09So115	H <sub>0</sub> 14		150	56	56	
S09So115	H <sub>046</sub>		150	102	101	
S09So115	H <sub>060</sub>		150	80	76	4
S09So115	H <sub>144</sub>		100	20	20	
S09So115	H <sub>163</sub>		100	11	11	
S09So115	H <sub>200</sub>		100	28	28	0
S09So115	H <sub>215</sub>		150	85	82	
Totals			900	382	374	8

<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

b Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R9.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So154 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So154 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.

					Result 30 days after treatment	
<b>Resistant</b> S. <i>oleraceus</i>		# of capitulum	Seed	Seedling	# Dead	# Alive
line and head harvest $\#^a$		heads harvested	$#$ sown	# treated $b$	<b>Susceptible</b>	<b>Resistant</b>
R09So154	H <sub>0</sub> 14		60	27		25
R09So154	H <sub>0</sub> 15		50			
R09So154	H <sub>170</sub>		100	44		44
Totals			210	71		69

<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table S10.** Number of capitulum seed heads harvested from an individual plant of susceptible *S. oleraceus* line So115 grown within 100mm of an individual resistant *S. oleraceus* line So155 over a six week period. The table also displays the number of seed progeny from So115 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



 $a$  Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

**Table R10.** Number of capitulum seed heads harvested from an individual plant of resistant *S. oleraceus* line So155 grown within 100mm of an individual susceptible *S .oleraceus* line So115 over a six week period. The table also displays the number of seed progeny from selected capitulum heads of So155 sown, the number of 2 leaf emerged seedlings treated with chlorsulfuron  $15g$  ai ha<sup>-1</sup> and the number of plants that were either dead or alive 30 days after treatment.



<sup>a</sup> Capitulum heads harvested as mature from mid February 2007 to late March 2007.

<sup>b</sup> Number of established 2 leaf seedlings treated with chlorsulfuron.

# **Appendix 3. SOURCE OF CHEMICALS**



# **Appendix 4. SOURCE OF EQUIPMENT**



# **Appendix 5. OGLIONUCLEOTIDES**

All oglionucleotide primers and their application are shown in the table below

## Sequencing Primers



## **Appendix 5B. OGLIGONUCLEOTIDES**

Annealing of M*se*I adapters

#### **ADAPTER 1**

Supplier is Geneworks

M*se*I Adapter 1 (16 mer)

MW=4946.3

387.0 µg

 $TM=46.0^{\circ}C$ 

78.2 n mol

5' GAC GAT GAG TCC TGA G

Concentration of 200µM

### **ADAPTER 2**

Supplier is Geneworks M*se*I Adapter 2 (14 mer) MW=4222.8 189.5 µg  $TM=40.0^{\circ}C$ 44.9 n mol 5' TAC TCA GGA CTC AT Concentration of 200µM

#### **PROCEDURE**

Add 50µL of Adapter 1 and 50µL of Adapter 2 to a PCR tube. Add 100µL of MQ water (nanopure sterile water) to the tube. This gives 200µL at a concentration of 5µM. In a thermocycler machine heat to  $90^{\circ}$ C for 3 minutes then remove from thermocycler and Store at  $-20^{\circ}$ C. allow to settle at room temperature for 30 minutes.

## **Appendix 5C. OGLIGONUCLEOTIDES**

Annealing of P*st*I adapters

### **ADAPTER 1**

Supplier is Geneworks

P*st*I Adapter 1 (21 mer)

MW=6406.2

494.3 µg

 $TM = 54.0$ <sup>o</sup>C

77.2 n mol

5' CTC GTA GAC TGC GTA CAT GCA

Concentration of 200µM

### **ADAPTER 2**

Supplier is Geneworks P*st*I Adapter 2 (14 mer) MW=4238.8 229.3 µg  $TM=42.0$ <sup>o</sup>C 54.1 n mol 5' TGT ACG CAG TCT AC Concentration of 200µM

### **PROCEDURE**

Add 5µL of Adapter 1 and 5µL of Adapter 2 to a PCR tube. Add 190µL of MQ water (nanopure sterile water) to the tube. This gives 200µL at a concentration of 5µM. In a thermocycler machine heat to  $90^{\circ}$ C for 3 minutes then remove from thermocycler and Store at  $-20^{\circ}$ C. allow to settle at room temperature for 30 minutes.

## **Appendix 5D. OGLIGONUCLEOTIDES**

M*se*1 + 1 primer C Supplier is Geneworks M*se*I C (17 mer) MW=5234.5 195.1 µg  $TM = 44.0$ <sup>o</sup>C 37.0 n mol 5' - GAT GAG TCC TGA GTA AC- 3' Concentration of 50µM

### **PROCEDURE**

Dilute to 75ng/µL

10µL of 1µg/µL PstI A + 123µL of nanopure water.

## **Appendix 5E. OGLIGONUCLEOTIDES**

 $Pst1 + 1$  primer A Supplier is Geneworks PstI A (17 mer) MW=5219.4 320.2 µg  $TM=47.0$ <sup>o</sup>C 61.4 n mol 5' – GAC TGC GTA CAT GCA GA- 3' Concentration of 50µM

### **PROCEDURE**

Dilute to 75ng/µL

10µL of 1µg/µL PstI A + 123µL of nanopure water.

## **Appendix 5F. OGLIGONUCLEOTIDES**

M*se*1 CC Supplier is Geneworks Mse1 CC (17 mer) MW=5210.4 273.9 µg  $TM=47.0$ <sup>o</sup>C 56.6 n mol 5' – GAT GAG TCC TGA GTA CC- 3' Concentration of 1µg/µL ie 1000ng/µL

### **PROCEDURE**

10µL of 1µg/µL M*se*1 CC + 390µL of nanopure water.=400µL of 25ng/µL

## **Appendix 5G. OGLIGONUCLEOTIDES**

P*st*1 AC Fluorescent hex green Supplier is Geneworks P*st*1 AC (17 mer) MW=6253.8 101.9 µg  $TM = 50.0$ <sup>o</sup>C 16.3 n mol 5' – 7GA CTG CGT ACA TGC AGA C- 3' Concentration of 1µg/µL ie 1000ng/µL

### **PROCEDURE**

5µL of 1µg/µL P*st*1 AC + 195µL of nanopure water.=200µL of 25ng/µL

## **Appendix 5H. OGLIGONUCLEOTIDES**

M*se*1 CT Supplier is Geneworks Mse1 CC (18 mer) MW=5538.7 240.4 µg  $TM=46.0^{\circ}C$ 43.3 n mol 5' – GAT GAG TCC TGA GTA ACT- 3' Concentration of 1µg/µL ie 1000ng/µL

## **PROCEDURE**

10µL of 1µg/µL M*se*1 CC + 390µL of nanopure water.=400µL of 25ng/µL

## **Appendix 5I. OGLIGONUCLEOTIDES**

P*st*1 AG Fluorescent hex green Supplier is Geneworks P*st*1 AG (18 mer) MW=6225.0 83.8 µg  $TM = 50.0$ <sup>o</sup>C 13.5 n mol 5' – 5GA CTG CGT ACA TGC AGA G- 3' Concentration of 1µg/µL ie 1000ng/µL

### **PROCEDURE**

10µL of 1µg/µL M*se*1 CC + 390µL of nanopure water.=400µL of 25ng/µL

## **Appendix 5J. OGLIGONUCLEOTIDES**

1.25mM dNTP's PCR nucleotide mix Supplier is Bioline (Australia) Contents and concentration 500µLof 25mM

### **PROCEDURE**

Dilute to 75ng/µL

5µL of 25mM + 95µL of nanopure water = 100µL of 1.25mM dNTP's

## **Appendix 6. GELS, BUFFERS and MEDIA**

#### **1. Agarose gel**

1.0 -1.5g of agarose was dissolved by heating in a microwave oven in 100mL of TAE buffer to make  $1-1.5\%$  (w/v) agarose.

Ethidium bromide was added to 0.5µg/mL

#### **2. Miscellaneous buffers**

6X Loading Buffer:

1 X TAE: 40mM Tris-HCl, 20 mM sodium acetate, 2 mM EDTA, adjusted to pH 7.8 with glacial acetic acid