



The Spread of Herbicide Resistance in *Lactuca serriola* at a Landscape Scale

Yi Qing Lu

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School of Agriculture and Wine

Faculty of Sciences

University of Adelaide

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Abstract

Several populations of *Lactuca serriola* have appeared with resistance to ALS-inhibiting herbicides within a small area of the northern Yorke Peninsula of South Australia. Resistance appeared quickly at a number of sites following the first initial report of resistance near Snowtown in 1994. One explanation for the widespread and rapid appearance of herbicide-resistant *L. serriola* in the area around Snowtown could be movement of resistant seed from the original field where resistance evolved. An alternative explanation is that resistance has evolved multiple times in the area. The aim of the study is to determine which of these two factors is more important for the spread of herbicide resistance in this area.

In this research, seeds were collected from various sites along roadsides and adjacent fields in 1999 and again in 2004. In 1999, seeds were collected in a 60 by 60 km area centred on Bute, South Australia. Seed were germinated and the seedlings tested for resistance to the ALS-inhibiting herbicide chlorsulfuron. As *L. serriola* is a self-pollinated plant, resistance in the progeny will indicate resistance in the parent plant. Of the samples tested for resistance, 75.0% of field sites and 58.8% of roadside sites contained resistant individuals. In the second collection, seedlings were collected from a smaller number of sites within the area. Seedlings were treated with chlorsulfuron and assessed for resistance. In this collection all field sites and 81.8% of roadside sites contained resistant individuals.

DNA was extracted from the leaves of plants and inter simple sequence repeat analysis (ISSR) was used to generate fingerprints for individuals in each population. A single

individual from 25 populations from the 1999 collection and two control samples was genotyped. A total of four different primers were used and 179 bands scored. Of these bands 49.7% were polymorphic across the samples tested. UPGMA analysis indicated the samples could be organised into 20 different clades. Only a small number of samples had identity. One group of three susceptible samples collected from 66 km apart had identical banding patterns to each other. A separate group of three resistant samples from 43 km apart had identical bands and a third group of four resistant samples from 48 km apart had identical bands. Among the resistant individuals in this collection, 13 different genotypes were identified.

From the 2004 samples, up to eight individuals from each population were genotyped. Within sites, many individuals shared the same genotype. However, some sites contained multiple genotypes. The same resistant genotype was identified in four different collecting points, two fields and two adjacent roadsides, within a 5 km radius. Within the samples tested, nine different resistant genotypes were identified.

This research has provided evidence for multiple independent evolutionary events resulting in the selection of chlorsulfuron resistance in *L. serriola* in South Australia. It is also likely that *L. serriola* can move from site to site, with the same genotype present across 66 km. Lastly, there are indications from the research that populations of *L. serriola* become locally extinct and sites are recolonised at a rapid frequency. This has probably contributed to the rapid spread of herbicide resistance in roadside populations of *L. serriola* in South Australia.

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 and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

I give consent to this copy of my thesis, when deposited in the University Library, being available for loan and photocopying.

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