

Evolution or spread? The case of herbicide resistant *Lactuca serriola* L. in South Australia

Yi Qing Lu¹, Jeanine Baker^{1,2} and Christopher Preston^{1,2}

¹ School of Agriculture and Wine, University of Adelaide, PMB 1, Glen Osmond, South Australia 5064, Australia

² CRC for Australian Weed Management

Summary *Lactuca serriola* L. resistant to sulfonylurea herbicides first appeared near Snowtown in South Australia in 1995. Quickly thereafter, resistant populations were reported from several sites in an area of 40 km around Snowtown. *Lactuca serriola* produces flowers on the top of a tall stem and can grow up to 1.5 m high. The seeds are attached to a pappus and blow freely in the wind. These characteristics would allow herbicide-resistant seed to spread rapidly over a wide area. Such wind mediated seed movement will be difficult for land managers to prevent and the potential for the spread of herbicide resistant seed is investigated in this study.

Seeds were collected from plants growing in cropped fields or along roadsides in a 50 × 50 km area centred on Bute, South Australia. Seed was grown and seedlings treated with chlorsulfuron to determine which

of the populations tested contained resistant individuals. Survivors of chlorsulfuron treatment were grown to seed and seed collected. To determine the genetic relationship of resistant individuals from various sites, seedlings were germinated, leaf material collected and DNA extracted. ISSR primers based on anchored microsatellite core sequences were used to generate fingerprints for individuals in each population and the genotypes within and between the populations compared.

Resistant samples that have different banding patterns clearly arose from independent mutations. Where banding patterns are the same, resistance may have spread between sites. This research should assist in the development of management practices for controlling herbicide resistant *Lactuca serriola*.

Keywords *Lactuca serriola*, herbicide resistance, chlorsulfuron, ISSR, seed movement, gene flow.