

## MOLECULAR DIFFERENTIATION OF WILD OAT AND WILD RADISH SPECIES AND BIOTYPES

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**Abstract** Genetic diversity is an important factor contributing to the success and persistence of weeds. However, the bounds of how polymorphism contributes to weediness have hitherto been little studied, especially in Australia.

In this work, DNA technology is being utilized to distinguish between species and biotypes of wild oats, comprising ostensibly self-pollinating species, and wild radish which is predominantly an out-crossing species. Samples, including resistant biotypes from the north, south and western grain regions are being analysed.

Molecular techniques including restriction fragment length polymorphism (RFLP) and sequence analyses of nuclear ribosomal DNA, PCR with single random oligonucleotide primers of arbitrary sequence and microsatellites analysis are being utilised to differentiate the species and biotypes of the two groups of weeds. The molecular data will provide indicators of where objective boundaries might be drawn between species, biotypes and genotypes within each of the two weeds. Numerical methods including parsimony, distance matrix and maximum likelihood techniques will be employed to infer phylogenetic relationships in each of the two weed systems.

Work will also be directed to identifying polymorphisms in the various populations for correlation to phenotypic and physiological characters (in particular herbicide resistance). More recently, developments in molecular biology have provided information about herbicide action at the genetic level. Herbicide targets included disruption of photosynthesis, inhibition of amino acid biosynthesis, disruption of cell division and microtubule assembly and inhibition of fatty acid biosynthesis. The availability of molecular data on the targets of various herbicides will enable the use of molecular tools to screen herbicide resistant populations for mutations that have arisen and conferred herbicide resistance. The targets include the *psbA* gene, acetohydroxy acid synthase gene and the acetyl CoA carboxylase gene.

The investigation of patterns of genetic variability in different populations distributed throughout the north, south and western grain regions will provide important determinants of the evolutionary potential of the two weeds and hence have an important bearing on their control by herbicides or biological control agents. Just as herbicides have selected for particular biotypes, any weed control methodology imposes certain selection pressures and thus it is considered that these molecular tools will provide new opportunities for more precise and environmentally friendly management of weeds.

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