

Genome sequencing of glyphosate resistant fleabane (*Conyza bonariensis*) and sowthistle (*Sonchus oleraceus*)

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Summary Genome sequencing is the process of digitising the complete set of genetic instructions for an organism. The cost of sequencing has been dropping steadily, but until very recently it has still been expensive and difficult to assemble (piece together) the genome of a species that has not been previously characterised. Some weeds present additional challenges because they have large genomes and polyploidy. New technologies promise to reduce this challenge to one that can be accomplished within a single project at a

reasonable cost. This talk will discuss the progress made to date in genome sequencing projects initiated for flaxleaf fleabane (*Conyza bonariensis*) and sowthistle (*Sonchus oleraceus*). Both of these species have evolved glyphosate resistance in Australia. A genome sequence is like a map for any genetic studies, and a well-resolved assembly will enable the component genomes in these polyploid species to be disentangled.

Keywords Genome sequencing, assembly, sowthistle, fleabane.