

Metabolic herbicide resistance gene discovery in wild oat

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Summary Weedy plant species that have evolved resistance to herbicides due to enhanced metabolic capacity to detoxify herbicides (metabolic herbicide resistance) are a major issue threatening herbicide sustainability and global crop production. Metabolic enzymes (e.g. cytochrome P450 monooxygenase (P450), glycosyl transferase (GT), glutathione S-transferase, GST) are major super families involved in herbicide metabolism. However, progress in biochemical and molecular understanding of these enzymes in endowing metabolic resistance has been very slow until recently, especially with rapid advance in next generation RNA-sequencing. Our recent work have identified a number of wild oat populations resistant to ACCase-inhibiting herbicides diclofop-methy, fenoxaprop and pinoxaden. We have isolated, characterised, and purified wild oat lines only possessing

metabolic resistance, and these are valuable materials for metabolic herbicide resistance gene discovery. The RNA samples have been prepared from individually phenotyped most resistant or susceptible plants, and RNA-sequencing will be performed using Illumina Hiseq4000 with PE 150 and total 35 M reads. Differentially expressed contigs relevant to herbicide metabolism (e.g. P450, GT, GST) and gene regulation (e.g. transcription factors) pathways will be identified and validated using RNA-seq samples and additional sample from the resistant (R) and susceptible (S) wild oat lines. Candidate genes will be amplified from the R and S plants, sequences compared for structural changes and expressed in *planta* for functional characterisation.

Keywords Diclofop, fenoxaprop, metabolic resistance, RNA-sequencing, wild oats.