

## Pyroxasulfone (Sakura) resistance mechanism

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**Summary** Repeated herbicide field selection led to the evolution of a ryegrass (*Lolium rigidum* Gaudin) multiple-resistant (MR) population with complex pattern of resistance to the ACCase-inhibitor diclofop-methyl, the ALS inhibitor chlorsulfuron, the microtubule assembly-inhibitor trifluralin, and the very long chain fatty acid elongase (VLCFAE)-inhibiting herbicides S-metolachlor and triallate. Subsequent experimental evolutionary studies have selected, through recurrent pyroxasulfone selection, high-level pyroxasulfone resistance and cross-resistance to prosulfocarb + S-metolachlor and triallate. Recent RNA-Seq transcriptome analysis identified several putative genes (contigs) strongly associated with the resistance phenotype in ryegrass.

In this study we have attempted to explain and correlate the observed phenotypic resistance to pyroxasulfone evolved in the population MR against five individual annotated putative cytochrome P450 (P450s) resistance genes and five glutathione-S-transferase (GSTs) putative resistance genes.

We present the phenotypic characterization of pyroxasulfone resistance observed in the parental MR population versus the evolved pyroxasulfone resistance in the progeny P6, the relative increased expression of putative resistance GST genes assessed via q-PCR and thin-layer chromatography experimental data indicating that the pyroxasulfone metabolites formed in the pyroxasulfone-resistant ryegrass population P6 population are characteristic of the glutathione conjugation pathway.

This research emphasizes there are complexities associated to multiple-resistance due to enhanced herbicide metabolism. However, greater knowledge of resistance mechanism(s) can lead to improved management of metabolic herbicide resistance in the major weed ryegrass.

**Keywords** GST, herbicide detoxification, herbicide metabolism, herbicide resistance, metabolism, ryegrass, weed control, weed management.