UNDERSTANDING MOLECULAR MECHAISM OF HERBICIDE RESISTANCE IS A KEY FOR PROPER WEED MANAGEMENT DECISIONS IN RICE

Kassim AL-KHATIB* and Rafael M PEDROSO
University of California, Davis

Weeds are considered a serious problem in California rice fields. Decades of using a continuously-flooded rice cropping system in California have selected specific weed species that display similar ecological requirements and growing patterns to rice. Although effective preplanting weed control and proper cultural practices including water management is used in weed management program in rice, herbicides continue to be the most important component of any weed management program in rice. With the excessive reliance on a few herbicides and lack of crop rotation, however, several weeds in rice fields have evolved resistance to herbicides including California Arrowhead, Smallflower Umbrella Sedge, Ricefield Bulrush, Late Watergrass, Redstem, Barnyardgrass, Early Watergrass, and Junglerice. In California, rice has more herbicide-resistant weeds than any other crop or region in the United States which result in more complex and expensive weed management program. Understanding the molecular base for herbicide resistance is essential for any successful weed management program in California rice cropping system where the use of non-chemical weed control is not possible. Understanding resistance mechanisms including active site mutation, metabolic, over expression, and sequestration would help making the correct decision to manage resistant weeds. This is particularly important when resistance is a result of active site alternation. *Cyperus difformis* is major weeds of paddy rice in California (CA), where it evolved resistance to the acetolactate synthase (ALS)-inhibiting herbicide in the 1990's. More recently, applications of propanil and carfentrazone led to resistance to this important photosystem II (PSII)-inhibitor and PROTOX-inhibitor in a number of *Cyperus difformis* populations. Our research to elucidate the mechanism of resistance to propanil showed *Cyperus difformis* line studied displayed a 14-fold level of propanil resistance and be cross-resistant to the PSII-inhibitors bromoxynil, diuron and metribuzin. Strikingly, the resistant line displayed increased susceptibility to bentazon. Nucleotide sequence analysis of propanil binding site showed a change in amino acid Valine to Isoleucine at position 219 of the D1 protein. Such mutation, however, is shown to possess a novel attribute given that the psbA mutants displayed increased susceptibility to bentazon. Tank-mixing bentazon and propanil can thus be seen as an interesting option to manage and prevent the spread of the resistant phenotype.

Keywords: Bentazon, Cyperus difformis, diuron, propanil, rice