Molecular (DNA) and Biochemical Investigations into Agricultural Weed Populations of the South Eastern United States

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Herbicides are chemicals for managing weeds, similar to antibiotics used in human health. The repeated use of herbicides has resulted in the evolution of herbicide resistant weed populations, comparable to antibiotic resistance. The purpose of the experiment is to determine the underlying molecular and/or biochemical processes responsible for endowing resistance to selected acetolactate synthase (ALS) enzyme inhibiting herbicides in pigweeds (Amaranthus spp.), a weed species that is extremely damaging to crops. In this experiment, two types of pigweed were used – red root pigweed and tall waterhemp. In the molecular analysis, plants are grown to a 10 cm height. Then, the leaves are harvested, and DNA extracted. Then, a polymerase chain reaction (PCR) was run using primers specific to the 574 loci of the ALS gene. Lastly, DNA was cloned and sequenced. In the biochemical analysis, similar plants were used. ALS enzyme was extracted and purified. Then, an enzyme assay was run by performing a color reaction by adding alpha-naphthol and creatine to acetoin. DNA sequencing results indicated a point mutation at the 574 loci of the ALS in redroot pigweed and tall waterhemp, two kinds of pigweeds. The mutation resulted in the alteration of “TGG” codon for tryptophan (susceptible) to “TTG” codon for leucine in the resistant plants. The above data supports the hypothesis that the herbicide resistance mechanism in the tested resistant pigweed species was target-site based. In other words, the point mutation prevented the herbicides from binding to the ALS enzyme in the resistant plants, thereby, preventing phytotoxicity from the herbicide. This knowledge will help in discovering sustainable pigweed management strategies, thus increasing the bottom line of Mississippi farmers.

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