

Molecular Mechanism of Resistance to ACCase-inhibiting Herbicide in Southern Crabgrass (*Digitaria ciliaris*) Biotypes

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Southern crabgrass (*Digitaria ciliaris* (Retz.) Koeler) is one of the most common and troublesome weeds infesting all major cropping systems including peanut throughout the southeastern United States. Acetyl-coenzyme A carboxylase (ACCase)-inhibiting herbicides are used for postemergence grass weed control in annual and perennial cropping systems. Recently, these herbicides failed to control southern crabgrass on the sod production field in Georgia. Two resistant R1 and R2 biotypes were collected from Georgia compared to a separate susceptible biotype (S) collected from Alabama. This study was aimed to determine the possible mechanism for resistance in these two resistant biotypes. Five seedlings of R1, R2, and S biotypes were transplanted onto agar media containing the discriminating doses (0-400 μ M) of sethoxydim herbicide for rapid screening of injury symptoms caused by the ACCase inhibitors. Both R1 and R2 biotypes showed low phytotoxicity to sethoxydim compared to the S.

The amplification of the carboxyl-transferase domain of the plastidic ACCase by standard PCR revealed a point mutation resulting in an amino acid substitution at position 1781 in the resistant R1 biotype. Cloning of PCR product surrounding the Ile-1781 region yielded two distinct ACCase gene sequences such as Ile-1781 and Leu-1781. Next-generation sequencing (NGS) using the Illumina platform was used for confirmation of the amino acid substitution in the resistant biotypes. Transcriptome profiling by RNA sequencing revealed a single nucleotide variation of adenine to cytosine resulted in an Ile-1781-Leu substitution in both resistant biotypes. Research, therefore, confirms that the amino acid substitution is the possible mechanism of action for resistance to ACCase-inhibiting herbicides in the resistant biotypes.