Herbicide Resistance relevant DNA sequences for Johnsongrass and Pigweeds ecotypes in Tennessee

Resistance to one or more types of herbicides in weeds remains the primary and current issue especially for Johnsongrass and those within the Amaranthus genus threatening the safety of the world's food supply. DNA based identification of different ecotypes showing resistance from these two types of weeds can prove the way for finding effective controls. This study provided interesting details regarding herbicide resistance related DNA-sequences in Johnsongrass and Amaranthus weeds based on the eight selected quantitative trait loci (QTLs) associated with the resistance mechanisms. The NCBI Blast website identified the precise locations of the chosen QTLs for DNA sequences related to herbicide-resistance in the genomes of the Johnsongrass and Amaranthus weeds. The use of such bioinformatics tools would facilitate the lab-based validation for herbicide resistance in both the weeds. The bioinformatics-based search provided a way to approach the effective genotyping tools that can detect the specific genetic mutations linked to herbicide resistance. The density plots across the selected sequences helped to understand the spatial distribution of the many genetic variants in the weed populations. The recorded genetic variations and density data directly relates to the endeavors towards development of effective controls for the weeds. Identifying the genetic markers associated with the herbicide resistance leads to targeted management strategies, which might reduce the risk posed by such weeds to the world's food production. This research would be continuing to further investigation towards developing sustainable and reliable identification tools for weed herbicide- resistance.