MODELING THE EVOLUTION OF BARNYARDGRASS (*Echinochloa crus-galli* L.) RESISTANCE TO GLYPHOSATE IN COTTON AND ITS MANAGEMENT IMPLICATIONS Muthukumar V. Bagavathiannan Jason K. Norsworthy University of Arkansas Fayetteville, AR Kenneth L. Smith University of Arkansas - Monticello Monticello, AR Paul Neve Warwick HRI Wellesbourne, UK

Abstract

Barnyardgrass is an important weed in the cotton production systems of the Midsouth. In this region, cotton is mostly grown as a monoculture crop, and three to five applications of glyphosate within a cropping season are common. Roundup Ready Flex technology has allowed farmers to apply glyphosate in later stages of cotton growth. Coupled with this, there is a substantial reduction in the use of cultural weed control, leading to heavy reliance on glyphosate for weed control in cotton. Although herbicide-resistant barnyardgrass has been widespread in rice production systems for major rice herbicides, glyphosate resistance has not yet been confirmed in this species. Nevertheless, there exist a body of evidence indicating that barnyardgrass is a potential candidate for evolution of resistance to herbicides. Additionally, the widespread occurrence of glyphosate-resistant horseweed (Conyza canadensis) and Palmer amaranth (Amaranthus palmeri) in Midsouth cotton fields suggests that glyphosate resistance in barnyardgrass is not a question of if but when. Given this situation, proactive measures that slow the evolution of resistance will be highly valuable, and herbicide resistance simulation models are useful in this regard. A mathematical model is being developed for simulating glyphosate resistance in barnyardgrass in cotton. The general framework of the model has been adapted from the Palmer amaranth model developed for cotton in Arkansas (Neve et al. 2010). The model was utilized to simulate the risks of barnyardgrass resistance to glyphosate under current management regimes and to explore the effectiveness of some alternative strategies in slowing the rate of evolution of resistance. Future research will continue to refine the model, incorporating new mutation, seed immigration, and crop rotation. The biological, genetic, and management assumptions for the model are presented in a separate poster presentation.