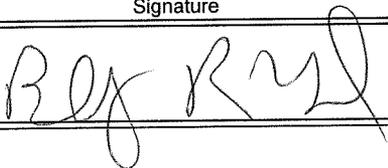


U.S. Department of Agriculture Work Unit Description AD-416 U.S. Dept. of Agriculture, State Agricultural Experiment Stations and Other Institutions			Date (Month/Day/Year) 08/06/2012	
1. Accession No.	Agency Identifiers		5. Work Unit/Project No.	6. Status
	2. NIFA	3. LA.B	LAB94143	A = New Project
7. Title Reducing Aflatoxin Contamination of Maize through Understanding its Interactions with Aspergillus Flavus				
8. Performing Organization 0647 - 2010 Plant Pathology & Crop Physiol Agricultural Experiment Sta, Louisiana State Univ			9. Cooperating Departments within State Performing Institution	
10. Multistate Project No.			11. Cooperating States <small>sent via BITNET/INTERNET electronic mail systems</small>	
12. Investigator Name(s) Last Name and Initials)				Date: <u>8/7/12</u>
1. Chen, Z.				POSTED
13. Project Contact Last Name and Initials: Chen, Z.		Phone: 225-578-7850 Fax: 225-578-1415		
E-Mail: zchen@agcenter.lsu.edu URL:				
14. Project Type Hatch	15. Contract/Grant/Agreement No.	16. Amount	17. FY	
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Goals/Objectives/Expected Outputs				
<p>The specific objectives are to: (a) understand the regulation of previously identified maize aflatoxin resistance related proteins; (b) examine the potential role of WRKY transcription factors in enhancing maize aflatoxin resistance; and (c) develop a new strategy to control A. flavus infection in maize through host induced gene silencing. Our long-term goal is to enhance host resistance in maize through up-regulation of key resistance-related regulatory gene(s) to reduce A. flavus infection and aflatoxin contamination in food and feed.</p>				
Methods				
<p>For objective one, the focus is to determine whether the previously identified RAP proteins are regulated by a common regulatory protein through performing promoter analysis and DNA-protein interaction studies. Identification of a common regulatory protein can significantly accelerate the development of maize germplasm with enhanced resistance compared to the current method to pyramid multiple resistance genes after genetic engineering. For objective two, the main focus is to determine whether WRKY transcription factors are involved in the regulation of maize host aflatoxin resistance associated protein expressions and whether any WRKY TF can be used to enhance maize resistance to A. flavus infection and aflatoxin contamination. Here, we propose to select a subset of possible candidate WRKY genes based on existing microarray data. Then, the expression of these candidate WRKY genes will be analyzed in kernels of resistant and susceptible maize germplasm in response to A. flavus inoculation under field conditions using real-time/quantitative polymerase chain reaction (qPCR) techniques to determine which WRKY genes might be involved in resistance to A. flavus colonization of maize kernels. For objective three, the main goal of this part of the study is to test the possibility that genes from A. flavus can be used as a new source to reduce infection and/or aflatoxin production in maize through HIGS or trans-silencing.</p>				
23. Non-Technical Summary				
<p>The proposed HATCH project tries to better understanding the interaction between Aspergillus flavus and corn including to determine what WRKY genes , and to seek possible new approaches to control aflatoxin contamination in corn.</p>				
24. Keywords				

corn; maize; Aspergillus flavus; aflatoxin; contamination; food safety; crop loss

**** The Original signed document is on file at this institution. ****

Signature	Title	Date
Dept:  Admin:	Associate Director	8-6-12