

Rice

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7. Title Marker-Assisted Breeding and Genetic Improvement of Southern U.S. Rice			sent via BITNET/INTERNET electronic mail systems Date: 5-1-12
12. Investigator Name(s) (Last Name and Initials) Utomo, H. S.			
20. Termination Date 09/30/2012		40. Period Covered (mo/da/year): 10/01/2007 TO 09/30/2012	
Outputs: For the duration of this project, the molecular breeding lab generated the following outputs: 1) Advanced lines from marker-assisted breeding were evaluated in commercial advanced trials; 2) Marker-assisted elite lines were evaluated in preliminary yield trials, 3) 500 marker-assisted breeding lines were selected from introgression of various marker-directed traits; 4) A novel method was developed for rapid and economical SSR marker detection, 5) DNA markers were linked to two specific genomic regions that encode for high grain protein and were used for marker-assisted selections; and 6) Populations were mapped for grain chalkiness. In addition, this project has facilitated one book chapter, five refereed journal articles, one Louisiana Agriculture magazine article, 10 annual reports, 16 oral and poster presentations at national meetings and annual field days, and nine lab and teaching presentations to various groups of scientists, growers, administrators, future farmers, legislators, and university students.			
Outcomes/Impacts: DNA markers were used to advance rice breeding procedures and improve agronomic and production traits. Blast-resistant genes (Pi-ta2, Pib, Pi-z, Pi-kh, Pi-ks), aroma, and grain elongation were assembled using PCR-based markers during the development of breeding lines. Grain yield potential of advanced lines derived from marker-assisted breeding was very promising, and was higher than the commercial control. Marker-directed traits, including drought tolerance, cold tolerance (at seedling stage), salt tolerance, aroma (Jasmine), grain weight, and panicle blight resistance from outside the U.S. genetic pool, were introgressed into southern U.S. lines. The introgressed germplasms are available to other breeders, and will facilitate the development of future varieties carrying these novel traits. Markers were developed for two specific genomic regions that have been previously identified to encode high protein content. The availability of DNA markers for high grain protein content provides positive impacts on the development of high protein rice cultivars. Fine mapping provided detailed genetic functionality for each genomic segment surrounding the marked regions. Mapping populations for grain chalkiness allowed development of DNA markers. The markers can be used to pre-screen parental lines and allow breeders in the early stages of their breeding program to concentrate on lines that are not predisposed to the problem.			
Publications: Utomo, H.S., Linscombe, S.D., and Wenefrida, I. 2012. Comparative mutational site of high lysine rice lines and other crops. Proc. 34th Rice Technical Working Group (RTWG). Hot Springs, AR. Feb. 27-March 1, 2012 (Abstract). Wenefrida, I., Utomo, H.S., and Linscombe, S.D. 2012. Field performance and grain characteristics of high protein rice lines. Proc. 34th Rice Technical Working Group (RTWG). Hot Springs, AR. Feb. 27-March 1, 2012 (Abstract). Shrestha, B.K., Karki, H.S., Groth, D.E., Sha, X., Subudhi, P., Utomo, H.S. and Ham, J.M. 2012. Development of qualitative trait loci (QTL) mapping and breeding programs to improve rice resistance to bacterial panicle blight and sheath blight. Proc. 34th Rice Technical Working Group (RTWG). Hot Springs, AR. Feb. 27-March 1, 2012 (Abstract).			
Participants: Herry Utomo (PI), and Steve Linscombe, LSU AgCenter.			
Target Audiences: The target audience includes plant developers, extension agents, and farmers. Scientific information (peer-reviewed publications and annual report) were used to reach wider scientific and general audiences.			

Nothing significant to report during this reporting period.

Approved (Signature)	Title	Date
Boggs		