

NATIONAL PEANUT BOARD/SOUTHEAST PEANUT
RESEARCH INITIATIVE
REPORT FOR WORK
DONE UNDER RESEARCH AGREEMENT

Final Report 9/14/2010
Summary

290

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2009

INSTITUTION: University of Georgia

PROJECT TITLE: Evaluating an enhanced tilling resource for peanut

RES. AGR. NO.: #290

PROJECT LEADER: P. Ozias-Akins

GACCP Control NO.:

EXPIRATION DATE: June 30, 2010

NPB CONTACT: Marie Fenn or M Mehok

NPB Control NO.: 290

REPORT OF PROGRESS:

The method of EMS mutagenesis followed by TILLING (targeting induced local lesions in genomes) has successfully identified mutations in *ara h 2.01*, *ara h 2.02*, and two *ara h 1* genes in cultivated peanut. Populations consisting of 3420 M2 lines have been screened. The sequences of twenty of these mutants have been verified. Most are silent or conservative amino acid changes, although one mutation in *ara h 1 β* introduces a premature stop codon in the first exon, which should result in a significantly truncated protein. M4 seeds from a homozygous plant were harvested and cotyledon tissues were analyzed for protein changes using 2-dimensional difference gel electrophoresis (2-D DIGE). Since the two genes of *Ara h 1* encode similarly sized proteins, separation is not absolute; however, 2-D DIGE shows quantitative changes in several protein spots attributable to *Ara h 1*. Some of the isoforms are decreased in quantity while others are increased, probably as a compensation mechanism. An interesting mutation that alters the start codon of *Ara h 2.02* also was recovered. Plants homozygous for this mutation have one of the two *Ara h 2* proteins eliminated from their seed protein. The missing protein is clearly evident by both 1-D and 2-D protein gel analysis. *Ara h 2*, the most serious peanut allergen, could be eliminated from peanut seeds if a mutation were also discovered in *Ara h 2.01* and the two were combined by traditional breeding.