USE OF GGE BIPLOT TO EVALUATE VARIETY PERFORMANCE IN THE MID-SOUTH AND SOUTHEAST Mustafa McPherson Joe Johnson John Pellow Dru Rush Phytogen Seed Company, LLC Leland, MS

<u>Abstract</u>

Cottonseed companies routinely conduct multi-environment trials to evaluate the performance of experimental lines relative to that of commercial checks to determine which lines are to be advanced towards commercialization. The interaction of genotypes with environments (GxE) in these trials is almost always significant; however, due to the difficulty in understanding these interactions, the over-location means are most often the primary criteria for advancement decisions. GGE Biplot (GGE) is a graphical tool that is useful in gaining some understanding of complex GxE interactions.

In 2010, Phytogen Seed Company evaluated a 48-entry trial at 21 test environments across the Mid-South and Southeast. Both the entry (G) and entry by location interaction (GxE) terms were highly significant. GGE was used to evaluate the 48x21 matrix of means for patterns in the GxE interaction. As an illustration of the ability of GGE to identify pattern in the data, the 'Mean vs. Stability' view of GGE grouped three locations as being different from the others with a preponderance of transgenic entries falling on the same side of the 'Average Tester Axis' (ATA) to indicate a positive interaction between these three locations and transgenic entries. Conventional, non-Bt entries at these three locations were observed to have received significant Lepidopteran pest injury during the season. After these three locations were removed from the analysis, a more scattered distribution of transgenic entries was observed. This new GGE graph explained 50.9% of the GxE interaction and plotted a preponderance of early/mid entries on the same side of the ATA as the North Delta locations. The criterion of being above or below the ATA was used to classify locations, regardless of their geographical position, as 'GGE North' or 'GGE South' for averaging purposes to identify genotypes best adapted to those regions.