### Results (Cont’d.)

#### QTL for Seed Isoflavones Contents

Seven QTL for seed isoflavones contents were identified on 5 different linkage groups (LGs) or chromosomes (Chr) from the seeds grown in 2010 season at FSU campus, Fayetteville, NC (Table 3). Nine additional QTL for seed isoflavones content was identified on nine different LGs/Chr from the seeds grown in 2011 season at Saint Pauls, NC (Table 3). The LOD scores of all QTL in 2010 and 2011 ranged from 3.5 and 2.5 to 8.0 and 2.7 respectively (Table 3). In the seeds of 2010 growing period, two QTL were identified each for daidzein (Chr 2LG D1b), genistein (Chr 17LG D2), and five QTLs for glycitein (Chr 8LG A2; Chr 17LG G, Chr 16LG B) in the seeds of the 2011 growing season. Genes located within QTL confidence intervals were retrieved and gene ontology (GO) terms were used to identify those related to the flavonoid biosynthesis process. Twenty six candidate genes were identified that may be involved in isoflavones accumulation in soybean seeds.

### Analysis of QTL Regions for Candidate Genes

Twenty eight genes involved in flavonoid biosynthesis pathways (Table 4) which would influence isoflavones were found on seven different chromosomes. One gene encoded in Chr_8 (LG A2; glycitein), three genes in Chr_12 (LG H, genistein) and two genes in Chr_17A (LG D2, daidzein) were within the (from data) QTL intervals. The second group of QTL (from 2011) contained ten genes likely to encode genistein synthesis (Chr 3LG and Chr 6LG, two genes for daidzein (Chr 17LG D2) and Chr 13bLG F) and one gene encoding (Chr 17LG D C). The analysis of QTL regions for candidate genes was performed using MapQTL 5.0 and the candidate genes with the highest LOD scores for each QTL were identified.

### References