Figure 3.5

(a) Graphical representation could not be shown since gene expression in respective controls was not detectable.

(b) Legend

*Graphical representation could not be shown since gene expression in respective controls was not detectable.
Figure 3.3 Phylogenetic analysis of 1000 bases upstream region of ABF genes from sorghum and rice. The dendrogram was constructed using maximum parsimony algorithm with 1,000 bootstrap replicates (**MEGA** version 4). A bZIP protein coding gene (**AtGBF2**) not belonging to ABFs was used as an out group.
Figure 2.1 Phylogenetic analysis of Arabidopsis GROUP A bZIP proteins with their orthologs from sorghum and rice. The dendrogram was constructed using maximum parsimony algorithm with 1,000 bootstrap replicates (MEGA version 4). A bZIP protein coding gene (AtGBF2) not belonging to Group A was used as an out group.
Figure 3.2 Quantitative expression of four SbABF genes showing differential expression in response to 3 h of desiccation stress (hatched bars), in response to ABA application (black bars) and cold stress (unfilled bars), in sorghum seedlings. The mRNA levels in controls were considered to be 1. Error bars represent standard deviations of 3 technical replicates.
Figure 2.2

Figure 2.2 Localization of conserved motifs on the ABF proteins classified into 4 subgroups based on their clustering using MEME software. Subgroup 4 showed the presence of an additional 14-3-3 protein binding motif*.