Section 2:

Executive Summary of the Project

Shortage of water (i.e. drought) is one of the principal constraints to increase rice production in Sri Lanka, especially in view of the increased frequency of drought due to long-term climate change. Therefore, identification of drought-resistant rice varieties from Sri Lankan rice germplasm and elucidation of candidate genes that are responsible drought tolerance is extremely important. The present project consisted of two major activities: (1) Screening of a selected set of Sri Lankan rice varieties for drought tolerance during the vegetative and reproductive stages and identification of a drought tolerant variety to be used in molecular analysis of drought tolerance; (2) Identification of candidate genes that are responsible for drought tolerance of the selected drought tolerant Sri Lankan rice variety. Activity 1 was completed successfully. After overcoming considerable difficulties and delays initially, Activity 2 was progressing successfully when the project was terminated despite a request for extension by the investigators.

Screening of rice germplasm for drought tolerance in the vegetative and reproductive stages (i.e. Activity 1) was carried out in a rain-sheltered plant house using 30 selected rice varieties, which also included germplasm from International Rice Research Institute's Drought Screening Nurseries. Based on relative vegetative growth under induced drought at the vegetative stage (i.e. for 10 days before panicle initiation), varieties Bg300, DSN43, Bg358 and A14 were identified as drought tolerant at the vegetative stage. Based on relative yield under induced drought during the reproductive stage (i.e. for 10 days from panicle initiation), varieties Bg301, Bw302, A46, Bg358 and H10 were identified as drought tolerant at the reproductive stage. As Bg358 showed tolerance at both stages, it was selected for molecular analysis of drought tolerance to detect candidate genes.

For molecular analysis, shoot tissues of drought-stressed Bg358 were obtained from plants grown in the rain-shelter. In order to detect the expressed genes in response to drought stress, total RNA and mRNA were extracted. A cDNA library containing the expressed genes in Bg358 under drought stress was constructed from mRNA. At this point, the project had to be terminated on the directive of the NSF.

However, the investigators continued the project until November 2012 and carried out screening of the cDNA library.

During this period, the previously prepared cDNA library of the rice variety Bg 358, was further screened for drought responsive genes. The cDNA library was subjected to differential hybridization using cDNA probes prepared from drought stressed and unstressed rice leaves. Differential hybridization of 192 cDNA clones identified six up-regulated and 18 down-regulated genes, respectively due to drought stress. Out of the 24 cDNA clones identified by differential hybridization, six up- regulated and five down-regulated cDNA clones were subjected to DNA sequencing. Subsequent DNA/protein homology search identified ten putative gene products namely ubiquitin conjugating

enzyme E2, hypothetical protein, phosphoprotein phosphatase, stress-associated protein 8 and putative heat shock protein 82 as up regulated genes due to drought stress and serine/threonine protein kinase, putative transaldolase, MRG family protein and protein phosphatase 1 as down regulated genes due to drought stress in rice leaves of Bg 358.

These genes could be categorized in to the functional groups of growth and development (10% of the genes), protection and repair (10% of the genes), energy and metabolism (10% of the genes), protein synthesis, folding and stabilizing (60% of the genes) and hypothetical proteins (10% of the genes).