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**Development of Molecular Stress Response Markers in *Halodule wrightii***

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*Halodule wrightii* is the most common seagrass along the Texas Gulf Coast, but some populations are in decline presumably due to anthropogenic influences. Measurements of biomass are commonly used to gauge the physiological status of seagrass meadows, but these are “lagging indicators” of the underlying causal event(s) and have not answered questions about why, despite attempts to correlate with environmental parameters. Thus, there is a need to understand the molecular response of *H. wrightii* to stresses. We propose RT-PCR measurements of gene expression to assess relative stress levels between impacted and nonimpacted seagrass beds. Stress-related genes were first identified by literature search using rice (*Oryza sativa*) genome as a model. Candidate stress-response genes identified in rice include *APX1*, non-symbiotic *Hb1*, and *PAL1*. Multiple amino acid sequence alignments of rice and other plants were performed to identify conserved regions in these stress-related proteins. Nucleotide sequences from these conserved regions were used to develop degenerate PCR primers for cloning. A putative actin gene (1124 bp corresponding to exons 2-4) was cloned and sequenced from *H. wrightii* to serve as a housekeeping standard in gene-expression assays. BLASTN results show 92%-94% similarity of *H. wrightii* actin to monocot sequences from *Zea mays*, *Oryza sativa*, *Sorghum bicolor*, and *Avena nuda*. Cloning and sequencing of the aforementioned stress genes is underway. Amplification of *APX1* has been completed, while clones with the expected insert sizes for *Hb1* and *PAL1* are being sequenced.