Identification of MicroRNAs as Biomarkers for Stress Conditions in Maize (*Zea mays*)

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Abstract. Over 2,000 microRNAs (miRNA) have been discovered in plants and animals, and these miRNAs regulate various biological processes. However, there is no definitive conclusion regarding the certain types of miRNAs expressed under different stress conditions in plants and animals. Although, one study has made efforts to construct artificial miRNA in potatoes (*Solanum tuberosum*) [7], adequate knowledge of miRNAs prevalent in drought stresses was lacking. This study aims to identify miRNAs expressed under different stress conditions in *Zea mays*. TotalRNA was isolated from *Zea mays* under different stress conditions, namely, darkness (etiolation), salinity, drought, and control (no stress). Isolated totalRNAs were reverse-transcribed (RT) into cDNA ends, using stem-loop pulsed RT protocol, and were tested using end-point PCR protocol for the presence of targeted zma-miRNA, using designed primer pairs. It was found that plants under stress conditions declined in average height (cm) and