

Structural Characterization of Waterlogging Responsive Aerenchyma Formation and Reactive Oxygen Species Signaling Genes in Maize

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Abstract—Reactive oxygen species (ROS) are the free radicals that induce cellular damage under low oxygen conditions. During oxidative stress, ROS promotes the breakdown of cellular components in roots leading to the formation of a new tissue called aerenchymous tissue that unblocks the oxygen transfer from roots to shoots. ROS signaling transductions involve ROS generation and scavenging that induce the transcription of cell wall modification (CWM) genes that breakdown and then form new cellular components such as aerenchyma. Our study revealed the structural characterization of waterlogging responsive ROS and CWM genes in tolerant maize inbred line. Predicted protein structures of ROS genes shared complete secondary structures (SS) to the PDB submitted structures: ZmNADPH oxidases shared SS to regulatory domain of NADPH oxidases in rice; ZmPhospholipase D shared SS to phospholipase D in streptomyces. Predicted protein structures of CWM genes shared complete SS to the PDB submitted structures: Zmpolygalacturonases shared SS to an endo xylogalacturonan hydrolase from *Aspergillus*; Zmexpansins shared SS to β -expansins in maize. NADPH oxidases, phospholipase D, polygalacturonases, and expansins were investigated for their differential expression under waterlogging stress in maize. These genes were differentially expressed and upregulated in the waterlogging tolerant genotype (SKV239) of maize and downregulated in the waterlogging susceptible genotype (CML22) of maize. These stress responsive genes will be used as candidate genes for breeding waterlogging tolerant genotypes in maize.