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Overexpression of OsNAC17 enhances drought tolerance in rice

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Abstract

Drought conditions during cultivation reduce agricultural production yield less than a theoretical maximum yield under normal condition. Plant specific NAC transcription factors in rice are known to play an essential roles in stress resistance transcriptional regulation. In this study, we report the rice (*Oryza sativa L japonica*) NAM, AFTF and CUC transcription factor Os*NAC17*, which is predominantly induced by abiotic stress in leaf, was contribute to the drought tolerance mediated reactive oxygen species (ROS) in transgenic rice plants. Constitutive (*PGD1*) promoter was introduced to overexpress *OsNAC17* and produced the transgenic *PDG1:OsNAC17*. Overexpression of *OsNAC17* throughout the whole plant improved drought resistance phenotype at the vegetative stage. Morphological characteristics such as grain yield, grain filling rate, and total grain weight improved by 22~64% over wild type plants under drought conditions during the reproductive stage. The improved drought tolerance in transgenic rice was involved in reducing stomatal density up to 15% than in wild type plants and in increasing reactive oxygen species-scavenging enzyme. DEG profiling experiment identified 119 up-regulated genes by more than twofold ($P<0.01$). These genes included UDP-glycosyltransferase family protein, similar to 2-alkenal reductase (NADPH-dependent oxireductase), similar to retinol dehydrogenase 12, Lipoxygenase, and NB-ARC domain containing protein related in cell death. Furthermore, OsNAC17 was act as a transcriptional activator, which has an activation domain in C-terminal region. These result demonstrate that the overexpression of *OsNAC17* improve drought tolerance by regulating ROS scavenging enzymes and by reducing stomatal density.

Keywords: NAC transcription factors, Drought tolerance, ROS, Transcriptional activation, Stomatal density

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