Marker–Trait Association Analysis Reveals ABA Signaling–Related Genes Associated with Root System Architecture in Rice under PEG-Induced Osmotic Stress

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Abstract

Rice (*Oryza sativa* L.) productivity is severely threatened by drought. Root system architecture (RSA), specifically root depth and branching (root tip number), is a primary component of drought avoidance by facilitating water acquisition from deep soil profiles. In this study, a Marker–Trait Association (MTA) analysis was conducted using an F_2 population derived from a cross between the high-yielding low land variety Pathum Thani 1 and the traditional upland variety Khao Pong Khrai under polyethylene glycol (PEG)-induced osmotic stress. Under 20% PEG-induced osmotic stress, significant phenotypic variation was observed in root tip number and root depth. MTA analysis revealed basic leucine zipper transcription factor 23 (*OsbZIP23*), Heme Activator Protein 5F (*OsHAP5F*), and zeaxanthin epoxidase (*OsZEP*) as key candidate genes. The coefficient of determination indicated that *OsbZIP23* and *OsHAP5F* were significantly associated with the number of root tips, while *OsZEP* and *OsHAP5F* were associated with root depth, explaining 10.43–21.38% of phenotypic variation with low positive correlations ($r = 0.3–0.5$, $p < 0.05$). Favorable alleles from the Khao Pong Khrai parent were significantly associated with increased root branching and vertical elongation. These genes have been previously reported to be involved in abiotic stress responses, especially drought tolerance and abscisic acid (ABA) signaling. Therefore, these genes represent valuable targets for marker assisted selection in aromatic rice breeding programs.

Keyword: Rice, Root system architecture, Drought avoidance, Marker–Trait Association analysis, ABA signaling