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Genetic interaction of *Sub1A* and *Pup1* in rice

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Abstract

Rice is one of the major staple food in Asia, covering around half of the world population. More than 40% of rice cultivation area are subject to abiotic stresses such as drought, submergence and phosphate deficiency. Pyramiding useful genes into elite variety is a promising strategy to develop tolerance varieties to multiple abiotic stresses. However, some genes are not functionally compatible when they are introgressed into the same elite variety. Here, we tested the functional compatibility of *Sub1* and *Pup1*, major QTLs for tolerance to submergence and phosphate (P)-deficiency conditions, respectively. Phenotypic analysis revealed that IR64-*Sub1 Pup1*(SP1) plants harboring both *Sub1* and *Pup1* QTLs showed significant tolerance to submerged conditions, similarly in IR64-*Sub1* (Sub1) plant, while SP1 plants failed to tolerate to P-deficiency conditions; only IR64-*Pup1* (Pup1) showed strong P-deficiency tolerance phenotype. In submerged conditions, the expression levels of *Sub1A* and *PSTOL1*, major genes for *Sub1* and *Pup1* QTLs, respectively, were not significantly different in between Pup1 and SP1 plants. On the other hand, the expression of both *Sup1A* and *PSTOL1* was significantly downregulated in P-deficiency conditions, suggesting that *Sub1* and *Pup1* repressed gene expression each other in P-deficiency conditions. These results suggest *Pup1* does not compromise the *Sub1* function in submerged conditions while *Sub1* suppresses the function of *Pup1* in (P)-deficient condition, possibly by regulating transcript level of *Pup1*. In conclusion, *Sub1* and *Pup1* are functionally compatible in terms of submergence tolerance but not in P-deficiency conditions. Further analysis need to be performed to elucidate how *Sup1* suppresses the function of *Pup1* in P-deficiency conditions.

Keywords: rice, *Sub1*, *Pup1*, submergence tolerance, P-deficiency tolerance, interaction

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