IDENTIFICATION OF HOMOLOG NRT2.1 GENE ON SHALLOT (*Allium cepa* L. Aggregatum group)

ABSTRACT

Crop rotation system of shallot cultivation on rice field causing farmers do not fertilize as recommendation that result in low available nitrogen in soil. Therefore, it is important to improve the activity of nitrate uptake of shallot because shallot prefers nitrate to ammonium. However, there were no reports about gene activities studies that related with nitrate transporter on shallot. In Arabidopsis, NRT2.1 has ability as a primary nitrate response, regulating lateral root development initiation, pathogen defense, and dominant gene on NRT2 family gene that operate to take up nitrate at low external nitrate concentration (HATS). This study aims to identify nitrate transporter gene using chlorate toxicity treatment and molecular method, to detect homolog NRT2.1 on 15 cultivars of shallot (Thailand, Probolinggo, Tuk-tuk, Vietnam, Trisula, Katumi, Mentes, Manjung, Pancasona, Sembrani, Sumenep, Bima, Biru, Crok and Tiron) and to amplify full length of homolog NRT2.1 gene on shallot used TAIL-PCR. The statistical analysis showed that there was interaction between nitrate and chlorate that cause changes in leaf color of shallot, indicating nitrate can be absorbed by shallot from external medium and shallot has nitrate transporter gene. Moreover, chlorate toxicity treatment can be used to identify nitrate transporter gene on shallot. Molecular method using degenerate primer can be used to amplify homolog NRT2.1 gene on shallot with length 310 bp (cDNA). Specific primer of NRT2.1 gene detect homolog NRT2.1 gene on 15 cultivars of shallot prove that TAIL-PCR can be used to extend homolog NRT2.1 fragment of shallot towards downstream region with length 388 bp.

Key words : *Allium cepa L.* Aggregatum group, homolog NRT 2.1, chlorate toxicity treatment, degenerate primer, TAIL-PCR