

Thida 2014: Molecular Breeding of Improved Sin-Thwe-Latt for Submergence Tolerance, Bacterial Leaf Blight Resistance, Grain Aroma and Salt Tolerance. Doctor of Philosophy (Tropical Agriculture), Major Field: Tropical Agriculture, Faculty of Agriculture at Kamphaeng Saen. Thesis Advisor: Mr. Theerayut Toojinda, Ph.D. 165 pages.

Sin-Thwe-Latt-108 (STL108), an improved line of Sin-Thwe-Latt showed intermediate salt tolerance when tested in salt prone areas in Myanmar. It posses the *Saltol* inherited from Pokkali (PK). Molecular breeding of improved STL108 with *Sub1*, *Xa21* and *badh2* was carried out at Rice Gene Discovery Unit (RGDU) for four years. Twenty nine BC<sub>2</sub>F<sub>5</sub> (BILs) carrying the three target genes were successfully developed with similar cooking quality characters as recurrent parent STL108. All BC<sub>2</sub>F<sub>5</sub> lines showed submergence tolerant, bacterial blight resistant and grain aroma characters but varied for salinity tolerance. Genome scan and association analysis indicated that salt tolerance traits were not only controlled by the *Saltol* but also involved genetic factors located on other locations especially on a long arm of chromosome 1. The selected BILs with high level of submergence and salinity tolerance, bacterial blight resistance and grain aroma were selected and will be evaluated at salt affected and submergence areas in Myanmar in the future. Therefore, Quantitative trait loci (QTL) for salt tolerance related traits at seedling and reproductive stages was studied using F<sub>6</sub> recombinant inbred lines (RILs) derived from KDML105 and PK. Eighteen putative QTLs were identified on chromosomes 1, 6 and 11. QTLs for salt injury score (SIS), survival days after treatment (SvDAT), and percent plant survival (PPS), were mapped on a long arm of chromosome 1. It is different location from the *Saltol* locus that used for molecular breeding in our study. However, QTL associated with Na<sup>+</sup> and K<sup>+</sup> ion in the flag leaf of reproductive stage were detected on *Saltol* region, a short arm of chromosome 1. So it can be concluded that chromosome 1 is the most important for salt tolerance related traits and the salinity tolerance in rice may be controlled by several genes which correspond to different mechanisms contributing tolerance ability. We investigated the Myanmar germplasm for salinity tolerance. Two hundred and forty two accessions of Myanmar rice were screened with 100 mM NaCl at seedling stage. Five accessions collected from Ayeyarwaddy and Rakhine region showed high level of salt tolerance at seedling stage as the same SIS with standard check PK. The selected accessions are prospective for future salt tolerant breeding programs in Myanmar.

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Thesis Advisor's signature