Identification of Single Nucleotide Polymorphism Markers Associated with Northern Corn Leaf Blight Resistance in Sweet Corn

Kedsadaporn Junta[1, 5], Orapin Saritnum[2, 5*], Ruangchai Juwattanasamran[1], Prawit Puddhanon[1, 5], Darush Struss[3], Jumrearn Puttarach[5], and Seksan Songchanthuek[4]

[1]*Department of Agronomy, Faculty of Agricultural Production, Maejo University, Chiang Mai 50290, Thailand*
[2]*Department of Horticulture, Faculty of Agricultural Production, Maejo University, Chiang Mai 50290, Thailand*
[3]*Department of Biotechnology, East West Seed Company, Chiang Mai 50290, Thailand*
[4]*The office of Agricultural Research and Extension, Maejo University, Chiang Mai 50290, Thailand*
[5]*Center of Excellence on Agricultural Biotechnology: (AG-BIO/PERDO-CHE), Bangkok 10900, Thailand*

*****Corresponding author. E-mail: orapins343@hotmail.com*
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ABSTRACT

Northern corn leaf blight disease (NCLB) is a foliar disease of corn (Zea mays L.) caused by Exserohilum turcicum (Pass.). The Ht1, Ht2 and HtN1 genes in corn were found to control NCLB resistant traits. There has been an ongoing effort to identify various types of molecular markers associated with these genes in order to use them in marker-assisted selections. The objective of this study was to identify Single Nucleotide Polymorphism (SNP) markers which are associated with the Ht1 resistant gene. Ninety-three SNP markers were found in Ht1 regions, which are located on chromosome 2. Five SNP primers (MZSNP-0055106, MZSNP-0065744, MZSNP-0070164, MZSNP-0063922, MZSNP-0073150) showed polymorphism between susceptible and resistant lines. The Chi-square test of genotypic data of 184 F_2 plants (NT58WS$_6$#4 x ChallengerS$_6$-1) amplified by five markers fit a 1:2:1 ratio with Chi-square values of 0.82, 1.08, 1.08, 0.64 and 0.64 respectively. These 5 SNP primers may be useful as molecular markers for NCLB resistance in sweet corn.

Keywords: Northern corn leaf blight, Sweet corn, SNP markers, Resistance

INTRODUCTION

Northern corn leaf blight disease (NCLB), previously called *Helminthosporium turcicum* (Pass.), is a foliar disease of corn (*Zea* mays L.) which is caused by *Exserohilum turcicum* (Pass.) (Leonard et al., 1989). The most economically important host of *E. turcicum* is corn, especially in susceptible corn varieties. It could result in a yield loss of up to 30%. Optimal conditions for the disease infection include relatively low temperatures, such as 18-27 °C at night, and a humidity level of about 90-100% which is conducive to the growth of fungus (Ogliari et al., 2005). The disease symptoms appear as narrow lesions on leaves, expand to an elliptical shape and finally cause blight. Furthermore, symptoms may be found on the husks or leaf sheaths of susceptible corn hybrids. On the other hand, these lesions tend to be smaller due to reduced spore formation in resistant cultivars. In highly resistant hybrids, the only visible disease symptoms may be yellow spots.

Resistant cultivars have been widely used to control NCLB. E28 contains the gene *Ht1*, which confers resistance to *E. turcicum*, and was derived from a cross of Lv-9kuan with A619*Ht1*, followed by three backcrosses with Lv-9kuan and by gradual selection through self-pollination (Wu et al., 1996). There have been great efforts to explore the disease resistance of widely used maize lines in China, and 87.3-94.4% of these lines were found to be moderately sensitive or highly sensitive to this disease (Gao et al., 1997; Zhao, 2000). The *HtNB* dominant gene on chromosome 8 confers a non-lesion resistance at the flowering stage in an Indonesian landrace called 'Bramadi'. *HtNB* has an independent hereditary pattern similar to *Ht1*, *Ht2*, and *Ht3*, and has a dominant epistatic effect, which establishes that the non-lesion resistance could be inhibiting the appearance of the chlorotic-lesion phenotype (Xu et al., 1987).

The resistant cultivars were used to provide an effective way to control NCLB. The identification of markers linked to resistance genes for sweet corn germplasm will facilitate the breeding of resistant sweet corn in Thailand. Currently, many researchers use molecular markers to assist with selection. One of the Thai sweet corn MAS studies, conducted by Puttarach et al. (2016), studied marker-assisted selections for resistance to NCLB. One highly susceptible line and three highly resistant lines were identified and used for population development. One hundred and fifty-seven F_2 plants ($NT58WS_6$#4 x $ChallengerS_6$-1) were used to determine the linkage between traits and markers. Only two, SSR bnlg 1721 and umc1042 primers about 6.7 cM on chromosome 2, were closely linked to the resistant gene *Ht1*. Based on this result, these two SSR primers may be useful as molecular markers for NCLB resistance in sweet corn.

With the influence of PCR technology, primers that flank microsatellite loci are simple and fast to use, but the development of correctly functioning