Pranita Promsri 2012: Development for Screening Method of Corn Rust Disease Resistant Variety on Seedling. Master of Science (Agriculture), Major Field: Plant Pathology, Department of Plant Pathology. Thesis Advisor: Mrs. Jintana Unartngam, Ph.D. 84 pages.

Corn rust disease or southern rust in Thailand caused by *Puccinia polysora* is considered a major pathogen of corn production. Therefore, corn breeders have developed new verities which resistance to rust disease. Seedling inoculation studies are needed to develop reliable screening techniques that insure infection of susceptible variety seedling. Comparison of the inoculation method using filter paper (Whatman no.1) method and urediospores suspension dropping method on corn seedling was conducted. After inoculation 7-10 days, found that filter paper method was more effective than dropping method especially for the rate and timing of disease occurrence. Then, ten varieties of sweet corn (SC01 - SC10) were planted in the National Corn and Sorghum Research Center at Nakhon Ratchasima, Thailand. The rust disease severity on all varieties was evaluated. Then, all ten varieties seedling were inoculated using filter paper method in greenhouse condition. In the field observation, the disease severity of sweet corn 03, 04 and 05 varities were 84.66, 69.91 and 70.00% respectively, while the number of pustules on sweet corn seedling were 8 -16 pustules and increasing of pustules on the susceptible varieties. On the other hand, the resistant varieties in field test, the disease severity of sweet corn 02, 06, 07 and 09 varities were 38.41, 38.75, 36.41 and 38.33 % respectively, while the number of pustules on sweet corn seedling were 1-2 pustules and no development of pustules. The result indicated that inoculation method with filter paper was a suitable method for screening of resistant varieties. Moreover, sequencing analysis of internal transcribed spacer (ITS) region of ribosomal DNA was conducted. Twenty-one isolates of *P. polysora* were collected from various localities. All isolates DNA were amplified and sequenced using ITS1 and ITS4 universal primers. Twenty-one sequences were aligned and analyzed together with *P. polysora* and *P. sorghi* sequences obtained from GenBank (DDBJ) using the CLC Main workbench. The UPGMA clustering showed that the twenty-one sequences were in the same group with other sequences of *P. polysora* from Genbank and all sequences separated from *P. sorghi* supporting by 100% bootstrap value. The results suggested that DNA sequence of ITS region was sufficiently to distinguish *P. polysora* and *P. sorghi.* Furthermore, the screening of restriction enzymes for digestion of ITS region was conducted to distinguish the species of *P. polysora* and *P. sorghi* using CLC Main Workbench. The screening of 3 enzymes such as *Eco*RI, *Taq*I and *Sal*I enzymes could not distinguish *P. polysora* and *P. sorghi*.

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