

Pattama Janruang 2012: Study on Genetic Variability of Corn Rust Fungi on Kasetsart Inbred Line.
Master of Science (Agriculture), Major Field: Plant Pathology, Department of Plant Pathology.
Thesis Advisor: Mrs. Jintana Unartgram, Ph.D. 110 pages.

Corn rust disease caused by *Puccinia polysora* (southern rust), is considered as major pathogens in corn production of Thailand. *Puccinia polysora* is the air born pathogen widespread within and among corn field locations. Nowadays, many high yields and resistance varieties were developed and introduced to the farmers in order to increase the production. The objective of this study are 1) to estimate genetically variability of *P. polysora* populations from various location of corn plantation in Thailand and on Kasetsart inbred line (Ki1-Ki52) that were grown in different weather locations. 2) to estimate number of genotype patterns that *P. polysora* populations were grown in different weather locations. Genetic variation and differentiation of *P. polysora* in Thailand was analyzed using inter simple sequence repeat (ISSR) marker with five primers, including GAG(TCG)₅, GAG(CGA)₅, (CGA)₅, (GTC)₅ and (CAG)₅. Thirty-eight polymorphic bands were analyzed using the computer software by Nei's method. The results showed that the genetic differentiation occurred among populations ($G_{ST} = 0.5103$). However, the populations in the same geographical area, Tak and Phetchabun were closely related genetically more than another population base on Nei's genetic distance, indicating the movement of the fungus between these areas. Then, corn rust disease severity was evaluated on the Kasetsart inbred line (Ki1-Ki52) in Lampang, Nakhonratchasima, Songkhla and Kanchanaburi. The results showed that the rust symptom occurred on mostly of varieties in Lampang, Nakhonratchasima and Songkhla but not in Kanchanaburi. The Ki36 and Ki38 varieties showed that the rust disease free in all evaluated locations. While, the disease severity was found on Ki25 and Ki26 in Nakhon ratchasima and Songkhla. However, the disease severity level was different in each location. Genetic variability of *P. polysora* populations on Kasetsart inbred lines (Ki1-Ki52) was analyzed using ISSR marker with three primers, including (AGG)₅, GAG(TCG)₅ and (GTG)₅ primers. The results showed that there were high genetically differentiated within *P. polysora* populations ($G_{ST} = 0.1348$), the population of *P. polysora* in Nakhonratchasima was closely related to the population in Lampang. Moreover, the analysis of band pattern or genotype showed that there were thirty-nine genotypes occurred on the Kasetsart inbred line (Ki1-Ki52). There were five genotypes that found in more than one province such as Gen1 Gen14 Gen20 Gen27 and Gen37. However, there were two genotypes that occurred in three provinces as Gen20 and Gen27. The results supported that urediospores have to be migrated among these provinces.

Student's signature

Thesis Advisor's signature