Supoch Lueangpraplut 2011: Genetic Diversity of *Pseudoplagiostoma eucalypti* Causing Leaf Spots and Leaf Blight Disease on Eucalyptus. Master of Science (Agricultural Biotechnology), Major Field: Agricultural Biotechnology, Interdisciplinary Graduate Program. Thesis Advisor: Mrs. Jintana Unartngam, Ph.D. 88 pages.

Leaf spot and leaf blight disease is a main problem for eucalyptus forest plantations. The disease had been reported causing by fungi *Cryptosporiopsis eucalypti*. However, at present the fungi are re-identified as *Pseudoplagiostoma eucalypti* using molecular and morphological data. This study aims to identify and evaluate the genetic diversity of the fungi causing leaf spot and leaf blight disease on eucalyptus in Thailand. The data earned from the study will be useful for breeding improvement of eucalyptus resistance to leaf spot and leaf blight disease. The disease samples were surveyed and collected from eucalyptus plantations in 10 Provinces of Thailand. Fungal species were isolated and identified using morphological characteristics and colony growth measurements on synthetic media. The fungal isolates were identified as *Ps. eucalypti* which were of diverse morphologies especially for colony characteristics. The DNA fingerprint analysis of *Ps. eucalypti* was conducted using AFLP technique with 4 primer combinations. The results showed that there were 77 polymorphic bands and 178 total bands. All polymorphic bands were analyzed using NTSYS pc ver. 2.02. Program. The similarity coefficient was obtained using Dice's method. The phenogram was then generated by UPGMA method. The results showed that fungal isolates could be categorized into ten groups with cophenetic correlation of 0.955. The results also indicated that there was genetic diversity among *Ps. eucalypti* isolates. Moreover, these groups were not correlated to the localities and morphological characteristics. Sequencing analysis of internal transcribed spacer (ITS) region of ribosomal DNA was conducted. Eight isolates of *Ps. eucalypti* were amplified and sequenced using ITS1 and ITS4 universal primers. Eight sequences were aligned and analyzed together with the sequences obtained from GenBank (DDBJ) using the CLC Main workbench. The UPGMA clustering showed that the eight sequences were in the same group as other sequences of *Ps. eucalypti* recorded in the database supporting by 100% bootstrap value. The results indicated that the eight isolates could be identified as *Ps. eucalypti* based on ITS region analyses, which corresponding to the morphological based identification. In addition, the screening of restriction enzymes for digestion of ITS region was conducted to distinguish between *Ps. eucalypti* and other closed related species using CLC Main Workbench. The screening of 10 enzymes showed that *Alu*I and *Hin*CII enzymes could differentiate *Ps. eucalypti* and *Ps. oldii* from *Ps. variabile*. While, *Ctr*10I *Eco*RI *Hae*II *Hae*III *Hin*CII *Mse*I *Stu*I and *Taq*I enzymes could not distinguish *Ps. eucalypti, Ps. oldii and Ps. variabile*.

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