Waranya Ariyasura 2007: Determination of *Ustilago scitaminea* Sydow on the Infection of Sugarcane at the Early Stage. Master of Science (Agriculture), Major Field: Plant Pathology, Department of Plant Pathology. Thesis Advisor: Assistant Professor Chalida Leksomboon, Ph.D. 72 pages.
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Study on the inoculation procedure in sugarcane to smut disease, caused by *Ustilago scitaminea* Sydow was conducted in the greenhouse condition. The main treatments were the immersion of seed cane and injection of young seedling on K84-200, UT1 , H59-3775 and KPS 94-13, Both seed cane and young seedlings were inoculated with sporidia and teliospore of pathogen. The inoculation on the seedlings with teliospore by the injection method developed disease symptom rapidly and relatively easy to apply than the immersion method. By 2 months of age, smut whips began to emerge from injected seedlings of UT1 and H59-3775.

A detection of *U. scitaminea* Sydow in UT1, K84-200, H59-3775 and KPS94-13 was performed with Polymerase Chain Reaction (PCR) and microscopy after inoculation with sporidia by injection method at 1, 3, 5, 7, 14, 21 and 28 days. Primers *b*E4 and *b*E8 amplified a DNA fragment of 450 bp in KPS 94-13 and UT1 at 4 weeks post-inoculation. Under identical PCR condition, no amplification product was observed in K84-200 and H59-3775. In microscopic sections, hyphae were seen all in inoculated plants as early as 24 hr after inoculation. While the microscopy may be used to detect the smut pathogen in plantlets not exhibiting symptoms, there was no relationship between the presence of the pathogen and plant resistance.

Variation among 43 isolates of *U. scitaminea* Sydow in size of teliospore and diameter of mycelial colony were assessed. The results demonstrated that the isolates could divided into 2 and 3 groups, respectively. DNA primers corresponding variable number of tandom repeate (VNTR) and internal transcribed spacer (ITS) were employed to generate DNA fingerprint pathogens of 43 isolates by PCR technique. These results showed 2 DNA band and grouped into 1 and 3 DNA fingerprint patterns from primer VNTR and ITS, respectively. There was no correlation among clusters to geographic location in considering PCR data.

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