RESEARCH NOTE

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Occurrence of Soybean Sleeping Blight Caused by *Septogloeum sojae* in Korea

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Sleeping blight was observed on soybean plants grown in Yanggu, Suwon and Geumsan from 2005 to 2011. Symptoms developed on stems and pods of affected soybean plants. Five fungal isolates were obtained from the diseased plants and identified as *Septogloeum sojae* based on their morphological, cultural and molecular characteristics. Pathogenicity of the fungus was confirmed on soybean plants by artificial inoculation. This is the first report of *S. sojae* causing sleeping blight in soybean plants in Korea.

KEYWORDS : *Septogloeum sojae*, Sleeping blight, Soybean

Soybean (*Glycine max* Merr.) is an important global crop that provides oil and protein worldwide. In Korea, soybean is widely grown and used as a primary material for different kinds of Korean traditional foods such as tofu, soy sauce and soybean paste. Thirty two soybean diseases have been recorded in Korea [1]; however, an emerging disease showing sleeping blight occurred on soybean plants in late August to early September in Yanggu, Suwon and Geumsan from 2005 to 2011. The disease incidence ranged from 5% in Suwon in 2005 to as high as 90% in some fields at Punchbowl village in Yangu in 2005 and at Seodaesan in Geumsan, 2011. Symptoms of the disease were highly visible on young, weak and tender upper portion of affected stems, which were bent and had an inverted L shape (Fig. 1A) and had surfaces that became covered with masses of yellowish white powder (Fig. 1B). As the disease progressed, leaves attached to the infected stem gradually turned yellowish brown and dropped prematurely. Pod infection appeared during the pod-filling stage. Specifically, the infected pods first produced small dark brown spots and then became covered with masses of yellowish white powder (Fig. 1C) with age. Heavily infected pods were usually shriveled, deformed, and contained undeveloped and flattened seeds (Fig. 1D).

The morphology of the causal fungus was examined by light microscopy. Sporodochia on symptomatic stems and pods were yellowish white, powdered, subepidermal, and separate or confluent. Conidiophores (Fig. 1E) were hyaline to pale brown, 3 to 6 septate and 12.7~24.1 × 3.6~5.8 μm (mean, 20.4 × 4.3 μm). Conidia (Fig. 1F) were hyaline, clavate to long fusiform, straight or slightly curved, 3~7 septate, tapering at both ends and 31.1~49.0 × 4.1~5.4 μm (mean, 39.8 × 4.7 μm). Five fungal isolates were obtained from sporodochial masses on the stems and pods of the diseased soybean. Colonies on potato dextrose agar (PDA) plates were slow-growing, compact, rugged, somewhat raised, dark gray to black and produced reddish brown diffuse pigment (Fig. 1G). When the cultures were about 3-wk-old, many sporodochial masses with conidia (Fig. 1G) and spherical chlamydospores in chains (Fig. 1H) were formed on PDA plates. All isolates were identified as *Septogloeum sojae* Yoshii & Nishiz. based on their morphological and cultural characteristics. The morphological characteristics of *S. sojae* were similar to those described previously [2].

To confirm the results of morphological identification, comprehensive internal transcribed spacers (ITS1, 5.8S and ITS2) of ribosomal DNA of the *S. sojae* isolates, NAAS1187 and NAAS1192, were amplified using primers ITS1/ITS4 [3] and the resulting products were purified, sequenced and deposited in GenBank (accession Nos. JX853747 and JX853748). The sequences were then compared with those available in the GenBank database and through a culture catalogue search of the Biological Resource Center (NBRC), National Institute of Technology

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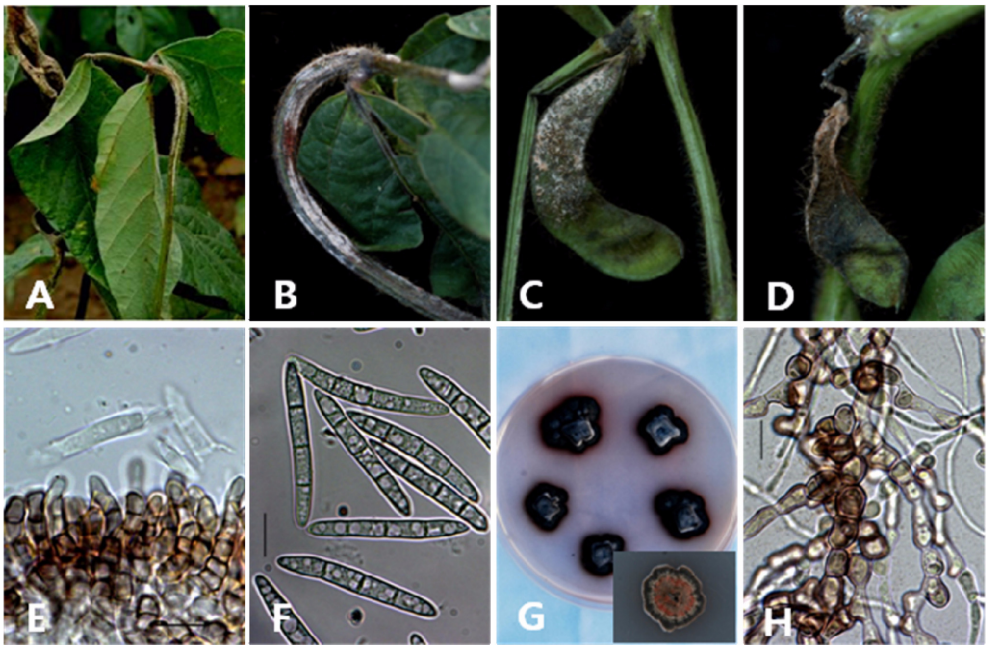

Fig. 1. Symptoms of soybean sleeping blight (A~D), conidiophores on lesions (E), conidia (F), colonies on potato dextrose agar (G) and chlamydospores (H) of *Septogloeum sojae* (scale bars: E, F, H = 10 μm).

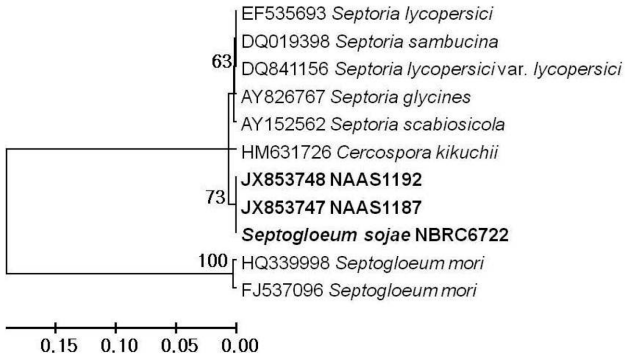

Fig. 2. Neighbor-joining tree based on internal transcribed spacer region sequences showing relationships among *Septogloeum sojae* and allied species. The numbers above each branch indicate bootstrap values of distance. The bootstrap values were obtained after a bootstrap test with 1,000 replications. The bar represents 0.05 substitutions per site.

and Evaluation. A phylogenetic tree was subsequently constructed by the neighbor-joining method with Kimura's two-parameter distance model [4] using MEGA version 4.0 [5]. An ITS-based phylogenetic analysis showed that the present isolates were clustered together with *S. sojae* isolate NBRC6722, but differentiated from the other genera and species with relatively high bootstrap support (Fig. 2).

A pathogenicity test was conducted by spray-inoculating soybean plants with conidial suspension (5×10^5 conidia/mL). The inoculated plants were kept in a growth chamber with relative humidity greater than 90% at 23°C for 20 days and then moved to a greenhouse at 23 ± 3°C. Symptoms were observed on the plants about 2 mon after artificial inoculation and were found to be similar to those resulting from the natural infections. However, no symptoms developed on control plants inoculated with sterilized distilled water. The pathogen was then reisolated from inoculated leaves.

Soybean sleeping blight caused by *S. sojae* was first described as soybean blast by Nishizawa *et al*. [2] in 1955 in Japan and has also been recorded in China [6]. It is likely that cooler temperature and more frequent rainfall in summer in locations with high-altitude such as Yangu and Geumsan have contributed to the outbreak of sleeping blight in Korea. Accordingly, the disease may cause significant damage to soybean crops when environmental conditions are favorable for its development. This is the first report of *S. sojae* causing sleeping blight in soybean plants in Korea.

Acknowledgements

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