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First Report of *Rhizopus oryzae* as a Postharvest Pathogen of Sweet Potato in Korea

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Sweet potato (*Ipomoea batatas* Lam.), an important root vegetable, is cultivated widely in Korea because of its starchy, dietary fiber, beta carotene, and sweet tasting tuberous roots. The most common and serious postharvest diseases of sweet potatoes are soft rots, caused by *Rhizopus* spp. (Agrios, 2005). During November 2010, sweet potatoes were collected from commercial markets in Jinju, Korea. After 1 month storage at room temperature and high humidity, morphologically distinct *Rhizopus* sp. was observed on soft rot symptoms of sweet potato (Fig. 1A and B). The pathogen was isolated on potato dextrose agar (PDA). The colonies of fungus grown on PDA were white and cottony at first, then became heavily speckled with the appearance of sporangia and finally became brownish-grey to blackish-grey and spread rapidly with stolons fired at various points to the substrate by rhizoids (Fig. 1C). The optimum temperature for mycelial growth was 30ºC, with good growth still apparent at 37ºC. Mycological characteristics of the causal fungal pathogen coincided with *Rhizopus oryzae* (Lunn, 1977) (Fig. 1D-G).

For pathogenicity test, 12 sweet potatoes were artificially inoculated with a representative fungus. After surface sterilization, air-dried sweet potatoes were soaked into the conidial suspension (3×10^4 conidia/ml) of the causal fungus for 15 min. The inoculated sweet potatoes were kept in a moist chamber with 100% relative humidity at 30ºC. After 7 days of incubation, the same fungal symptoms were reproduced (Fig. 1H). The causal pathogen was re-isolated from the lesions to prove Koch's postulates.

To confirm the identity of the causal fungus, the complete internal transcribed spacer (ITS) rDNA was amplified using the primers ITS1 and ITS4, as described by White et al. (1990), and was sequenced. The resulting sequence of 627-bp was deposited in GenBank (Accession No. HQ908275). A comparison of ITS rDNA sequences showed 100% similarity with sequences from *R. oryzae*. Phylogenetic analysis was performed using MEGA4 with neighbor-joining method and Tajima-Nei distance model. Previously published ITS sequences from *R. oryzae* strains were included for reference, and *Mucor miehei* (Accession No. AF198253) was used as an out-group (Abe et al., 2006). In the phylogenetic tree, the present isolate was placed within a clade comprising references isolates of *R. oryzae* (Fig. 2). The representative culture of the causal fungus has been deposited with the Korean Agricultural Culture Collection (KACC 45814), National Academy of Agricultural Science, Suwon, Korea. On the basis of the mycological characters, molecular data, and pathogenicity test, the causal fungus was identified as *Rhizopus oryzae* Went & Prisen Geerligs. To our knowledge, this is the first report of *R. oryzae* as a postharvest pathogen on sweet potato in Korea.

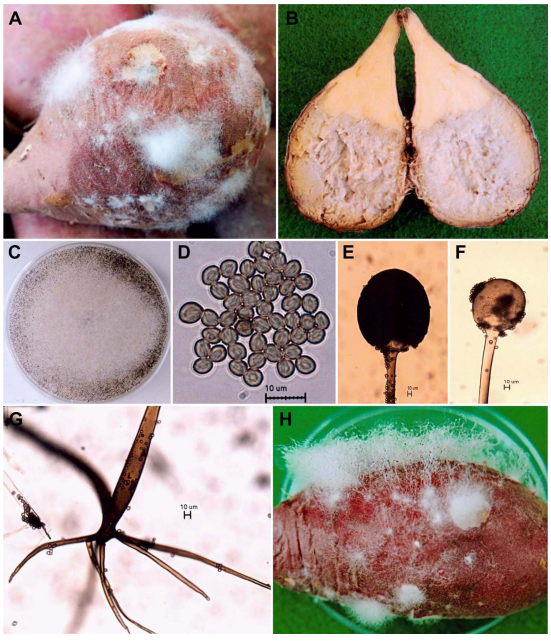

Fig. 1. Symptoms and morphological characteristics of *Rhizopus oryzae*. A: Soft rot symptoms. B: Longitudinal section. C: Colony on PDA. D: Sporangiospores. E: Sporangium and sporangiophore. F: Columellum. G: Rhizoid. H: Symptoms induced by artificial inoculation. Bar = 10 μm.

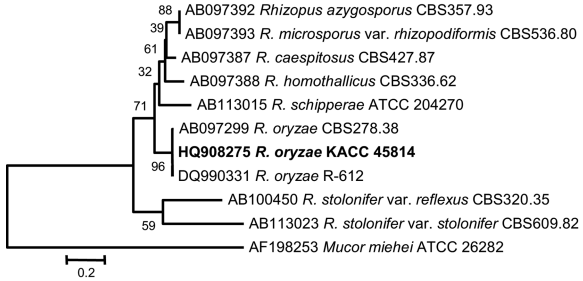

Fig. 2. Phylogenetic tree using ITS sequences showing closest known relatives of *Rhizopus oryzae*. Numbers above the branches indicate the bootstrap values. Bars indicate number of nucleotide substitutions per site. The present isolate infecting *Ipomoea batatas* Lam. was marked in bold font.

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References

Abe, A., Oda, Y., Asano, K. and Sone, T. 2006. The molecular phylogeny of the genus *Rhizpus* based on rDNA sequences. *Biosci. Biotechnol. Biochem.* 70:2387–2393.

Agrios, G. N. 2005. Plant Pathology. 5th ed. Academic Press. New York. 922 pp.

Lunn, J. A. 1977. *Rhizopus oryzae.* CMI descriptions of pathogenic fungi and bacteria. No. 525. Commonwealth Mycological Institute, Ferry Lane, Kew, Surrey, England.

White, T. J., Bruns, T., Lee, S. and Taylor, J. W. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: *PCR Protocols: A guide to methods and applications*, ed. by M. A. Innis, D. H. Gelfand, J. J. Sninsky, and T. J. White, pp. 315–322. Academic Press, New York.

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