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First Report of *Neofusicoccum parvum* associated with Bark Dieback of **Blueberry in Korea**

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Highbush blueberry (Vaccinium corymbosum L.), a woody plant native to North America, belongs to the family Ericaceae. Blueberry grows abundantly in Canada and the United States and has become a popular commercial crop in Korea. Blueberry, has been widely cultivated in Korea because of its health benefits including anti-cancer, anti-oxidant, macular degeneration etc. More than 15% of blueberry was produced in Gochang and Sunchang of Korea. In September, 2009, bark dieback disease of blueberry was first observed in Sunchang (<5%), Jeollabuk-do, Korea. The typical symptoms of the disease are blight and dieback of the stems, with lesions extending along the entire branches (Fig. 1A). The cross section of the stem, in the process of dieback, appeared brown and water-soaked (Fig. 1B). Perithecia were globose type, 25% emergent from the surface with dimensions of 145-245 µm (Fig. 1C). Ascospores were spindle or barrel shaped, smooth hyaline, brown in color, biseptate with darker middle cells, and had a length and width of 15–27 \times 6–11 μm with a L/W ratio 2.2 \pm 0.5 (Fig. 1D). Diseased plants were collected from orchards in Sunchang, and surface sterilized with 1% NaOCl. The surface-sterilized tissues were then rinsed with sterile distilled water, and plated on potato dextrose agar (PDA). The fungal isolates produced white mycelium at 25 °C and became light gray within a week. Conidia were hyaline, thin walled, smooth, non septate, ellipsoidal to fusiform, 12.4–18.1 \times 5.6–8.1 µm (L/W ratio of 2.4 \pm 0.1). The morphological characteristics of the isolates were coincided with those of Neofusicoccum parvum (Wright and Harmon, 2010). To confirm the identities of the fungal isolates, the internal transcribed space regions (ITS) were amplified with primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3')/İTS4 (5'-TCCTCCGCTTATTGATATGC-3') and sequenced. The ITS rDNA sequences of Sunchang isolate P1 and P5 were 99.8% similar, and P3 was 100% similar to those of the GenBank

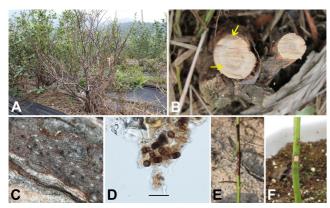


Fig. 1. Symptoms of bark dieback on highbush blueberry (cv. Duke) caused by Neofusicoccum parvum. A, dead stems of blueberry; B, infected stem cutting- arrows showing a damaged region inside the stem; C, perithecia on bark of a dead tree (bar $100~\mu m$); D, ascospores from nature (bar 100 μ m); E & F, results of pathogenicity test of N. parvum on blueberry plants; E, necrotic lesions on the stem after 1-month of inoculation; F, symptomless control plant.

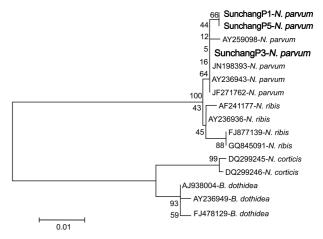


Fig. 2. Phylogenetic comparison of sequences with MEGA (ver. 4.0) of the ITS region and 5.8S rDNA of the Neofusicoccum parvum isolates with closely related strains and other species of Botryosphaeria. The tree was constructed based on the neighbor-joining analysis and the confidence intervals in tree topology were estimated by bootstrap analysis with 1,000 replicates.

accession numbers AY259098, JN198393, AY236943 and JF271762, that were similar to the deposited sequence of N. parvum isolates (Fig. 2). Therefore, both the morphological and ITS sequences confirmed this species to be N. parvum (Javier-Alva et al., 2009, Wright and Harmon, 2010). Pathogenicity tests were carried out on 2-year old blueberry plants. Ten plants of cv. Duke were stem wounded with a 5-mm cork borer up to skin depth. Inoculation consisted of inserting 5-mm mycelium plugs of the pathogen into the wounds and rapping with parafilm. Sterile PDA plugs applied to a similar number of plants with the same method served as the control treatment. After 1-month, all inoculated plants showed necrotic lesions with a mean length of 12.0 cm, whereas no lesion was observed on the control plants (Fig. 1E & F). To complete Koch's postulates, the fungus was re-isolated from the lesions and confirmed to be N. parvum. Shen et al. (2010) reported that N. parvum can also cause dieback in a wide range of fruit trees, including pears.

References

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