First Report of Fusarium Wilt on Orange Coneflower (Rudbeckia fulgida) in Northern Italy

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DISEASE NOTES

A. Garibaldi, G. Gilardi, S. Matic, and M. L. Gullino, Centre of Competence for the Agro-Environmental Sector (AGROINNOVA) and DISAFA, University of Torino, 10095 Grugliasco, Italy.

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ABSTRACT

Orange coneflower (*Rudbeckia fulgida*) of the Asteraceae family is widely used as an ornamental plant in public and private gardens. At the end of the summer of 2016, in a garden in Biella Province (northern Italy, elevation 850 m, 45°36′00″ N, 8°03′00″ E), a previously unknown wilt was observed on 7-month-old plants. The disease affected 70% of about 30 plants grown in mixed borders and in pots. Affected plants were stunted and developed yellow leaves followed by wilting of basal leaves and stems. A continuous brown to black streak in the vascular tissue of roots, crown, and basal stem was observed. Tissues were excised from the vascular system of the crown and stem of 10 symptomatic plants, immersed in a solution containing 1% sodium hypochlorite for 1 min, rinsed in sterile water, then cultured on potato dextrose agar medium (PDA) amended with 25 mg/liter of streptomycin sulfate. After 6 days at 23°C, 80% of the obtained fungal colony were similar and developed a cottony mycelium with a purple pigmentation. The fungus was morphologically identified as *Fusarium* sp. (Leslie and Summerell 2006) by

combining the macroscopic observation on PDA, the type of high quality and quantity symptoms on diseased plants, and the part of the plants from which the strains were obtained using isolation protocols. One representative isolate (IT22) was subcultured onto PDA and a single-spore culture was obtained. On carnation leaf agar (CLA), these single-spore isolates produced 3-septate macroconidia of 23.1 to 33.9 × 2.9 to 4.5 (average 28.8 × 4.1) µm in orange sporodochia from monophialides (13.4 to 21.3 and 2.1 to 2.7) on branched conidiophores. Microconidia were elliptical or reniform (6.5 to 14.0 × 2.4 to 4.2, average 10.3 × 3.4 µm). Chlamydospores formed either terminally or intercalary and measured 7.1 to 9.6 (average 8.2 µm). DNA from isolate IT22 was obtained using E.Z.N.A. Fungal DNA Mini Kit (Omega Bio-Tek, Darmstadt, Germany), EF1/EF2 primers were used to amplify the elongation factor-1 alpha gene region from the extracted DNA (O'Donnell et al. 1998). The amplicon was sequenced (GenBank accession no. KY563701) at the BMR Genomics Centre (Padua, Italy). A BLASTn search of the 685 bp amplicon was 100% identical to that of the NRRL_52787 isolate of *Fusarium oxysporum* (JF740855.1). Pathogenicity tests were carried out on healthy, 60-day-old plants of *R. fulgida* inoculated by root immersion in conidial suspension (1×10^7 conidia/ml) of the IT22 isolate and transplanted into 2 liter pots filled with steam-sterilized soil. Noninoculated plants served as control. Plants (six per treatment) were kept in a glasshouse at an average temperature of 24°C (minimum 20, maximum 28°C). The pathogenicity test was carried out twice. Wilt symptoms and vascular discoloration in the roots, crown, and veins developed within 20 days on all inoculated plants, while noninoculated plants remained healthy. *F. oxysporum* was consistently reisolated from infected plants only. *F. oxysporum* has been reported on *R. hirta* in Florida (Alfieri et al. 1994). Marois and Norcini (2003) also isolated an *F. oxysporum* from seeds of wild plants of *R. hirta*, providing the evidence of the role of contaminated seed source in survival of the pathogen. This is the first report of *F. oxysporum* on *R. fulgida* in Italy, as well as in the world. Further studies are needed to identify the host range and the forma specialis of the Italian isolates.

***Reference*:** Section:

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