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First Report of *Fusarium proliferatum* Inciting Wilt of *Rumex acetosa* L. in Maharashtra, India

Udhav Narba Bhale1*, Vaishali Sidram Chatage1 and Mallama Gurunath Ambuse2

¹Research laboratory, Department of Botany, Arts, Science and Commerce College Naldurg, Dist. Osmanabad -413602 Maharashtra State, India ²Department of Botany, Shrikrishna College Gunjoti Tq. Omerga Dist Osmanabad- 413613 Maharashtra State, India.

Abstract

Wilt of sorrel is caused by *Fusarium proliferatum*. Symptoms included yellow discolorations and wilting of lower leaves. Internal transcribed spacer (ITS) region of rDNA was amplified using the ITS1 and ITS4 primers and resulted in a 569 bp which was utilized for identification of this fungus. This is the first report of wilt of sorrel from Maharashtra.

Keywords: *Rumex acetosa*; *Fusarium proliferatum*; Pathogenicity; Sequencing.

Rumex acetosa L. (sorrel) belongs to family Polygonaceae. It is an indigenous English plant, common, too in the greater part of Europe, in almost all soils and situations. The medicinal action of sorrel is refrigerant and diuretic, febrile disorders and in scurvy. In India it is cultivated as a medicinal and vegetable throughout the year. Both the root and the seed were formerly esteemed for their astringent properties, and were employed to stem haemorrhage [1]. During October 2009 to January 2011 an extensive surveys was conducted in sorrel growing areas of Marathwada region of Maharashtra, India where diseased plants were found with yellow discoloration of the vascular tissue in stems, wilting of the lower leaves & root rot (Figure 1). Roots from wilted plants were collected and cut into small pieces (2mm) and then surface sterilized with mercuric chloride (1% HgCl₂) for 1 min. The pieces were then washed with sterilized distilled water three times, blotted dry and plated on potato dextrose agar (PDA) medium and incubated at 27±2°C in BOD incubator. On PDA medium, Fusarium species with catenate microconidia and macroconidia borne on polyphialides was consistently isolated from the infected roots. Pathogenicity tests were conducted, using six healthy sorrel plants grown in the glasshouse. Two plants and a control were used for each of two replications. For each treated plants were sprayed with 5 ml conidia suspension (ca.1×10⁵ conidia/ml) in sterilized water (SDW) and maintained in a humid growth chamber for 24 h in room temperature. Five days after inoculation, white mycelial roots were infected and in control remained symptomless. The fungus was reisolated & was identical as Fusarium species. The fungal culture is deposited at CODON Life Sciences, Goa and Research laboratory, Department of Botany Arts, Science & Commerce College Naldurg Dist Osmanbad, Maharashtra State, India with Accession No.HQ332533.

Thirty isolates were identified as Fusarium proliferatum (Matsushima) Nirenberg [2,3].Cultural colonies were started from



Figure 1: Wilt of Rumex acetosa: A-Infected plant, B- Colony of Fusarium proliferatum, C-Conidia.

single conidium and grown on PDA at 27±2°C under fluorescent lights providing 12 hrs light period. The abundant aerial mycelium initially was white and later became purple violet. Colonies were fast growing, hyphae were septate and hyaline. Conidiophores were short, simple and branched. Microconidia were abundant and produced on mono and polyphialids, single celled, oval to club shaped size 7.0-22.5×3.5μm. Macroconidia were slightly sickle shaped to straight, with 2-5 septa and measured 43-65×3.3-5.0μm. Chlamydospores were absent (Figure 1).

The internal transcribed spacer (ITS) region of rDNA from the original isolate used for inoculation & re-isolated culture recovered from roots in the pathogenicity studies, were amplified with polymerase chain reaction (PCR) using primer ITS1 and ITS4 [4]. PCR amplicons of approximately 569 bp were obtained. Sequences of amplicons were identical and the sequence was submitted to GenBank (Accession No.JQ322969). The DNA sequences were 99% identical to telomorph of *G. intermedia* strains (EU364856.7; EU364846.5; EU364845.5).

Fusarium proliferatum is known to cause diseases like Fusarium crown and root rot of asparagus [5], leaf spot of cymbidium [6], and rot of garlic bulb [7]. To our knowledge this is the first report of Fusarium proliferatum causing wilting of sorrel in Maharashtra State, India.

Our further investigation will made to evaluate the management practices for controlling this disease.

Acknowledgement

Authors are thankful to UGC, New Delhi [F.No.38-19/2009 (SR)] for the financial assistance of major research project.

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*Corresponding author: Dr. Udhav Narba Bhale, Department of Botany, Arts, Science and Commerce College Naldurg, Dist. Osmanabad- 413602, Maharashtra State, India, Tel: 09890742997; Fax-02471-246042; E-mail: unbhale@rediffmail.com

Received January 16, 2012; Accepted February 29, 2012; Published March 02, 2012

Citation: Bhale UN, Chatage VS, Ambuse MG (2012) First Report of *Fusarium proliferatum* Inciting Wilt of *Rumex acetosa* L. in Maharashtra, India. J Plant Pathol Microbiol 3:116. doi:10.4172/2157-7471.1000116

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