First report of *Fusarium proliferatum* causing wilt and root rot disease on wild accessions of pigeonpea from India

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Pigeonpea (*Cajanus cajan* L.) is the sixth most important legume crop in the world. India is the largest producer and consumer. Approximately 15–20% wild pigeonpea plants from three distinct genera (*Cajanus* spp., *Rhynchosia* spp. and *Flemingia* spp.) in the Research Farm of ICAR-IIPR, Kanpur, India, during 2019–20 were visually affected by wilt and root rot symptoms at flowering and fruiting stage. Initial symptoms of the disease showed chlorosis and drooping of leaves. Infected plants showed browning to blackening discoloration with a gradual drying and eventually death of the plant. Symptomatic plants were sampled from experimental field. Then, 5.0 mm size pieces of stem tissues surface-sterilized with 1% sodium hypochlorite for 2 min were transferred to 90 mm Petri dishes containing *Fusarium* Specific Medium (FSM) and incubated at 27 °C. After 48 h white to light orange mycelial growth was observed. Fungus was further purified by single spore technique. Macro conidia had 3–4 septa, hyaline and slightly curved at apex, ranged from 18.0–22.0 × 3.0–5.0 µm. Microconidia were clavate, hyaline, smooth, 4.0–10.4 × 2.2–3.1 µm. No clamydospores were observed. Morphological characteristics of isolates were consistent with the description reported by Leslie and Summerell (2006) of *F. proliferatum*. Pathogenicity test was conducted on 15-day healthy seedlings of wild pigeonpea (ICP-15882) using ‘root dip inoculation’ and ‘soil inoculation’ technique. Disease symptoms observed on inoculated plants after 10 days of inoculation were similar to those observed in fields. The same fungus was re-isolated from the inoculated plants. The identity

of the fungal cultures were confirmed by analyzing the ITS region of rDNA, FUMS gene 1, TEF-1 and Beta-tubulin gene (Nosratabadi et al. 2018; Stepień et al. 2011). All the sequences, ITS (MG859733, MG859731), Tef1 (MN175178, MN175177), FUMS 1 (MN175180, MN175179) and Beta-tubulin (MK357892, MN205564) showed 99–100% identity with *F. proliferatum* available at NCBI (KM459007). Phylogenetic analysis clustered isolates readily and consistently with *F. proliferatum* reference strains. To the best of our knowledge, this is the first report of wilt and root rot disease of wild accession of pigeonpea caused by *F. proliferatum* in India.

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Declarations

Conflict of interest Authors declare that they have no conflict of interest.

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