

**First report of *Fusarium brachygibbosum* causing wilt and vascular necrosis in commercial potato crops in Sinaloa, Mexico.**

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In December 2021, symptoms of foliage wilting and vascular necrosis were observed in potato crops in the municipality of Ahome, Sinaloa (Mexico), with an incidence of 5 to 10 %. Samples with symptoms were collected and taken to the laboratory for analysis. Excised pieces of the stem and root were disinfected in 2% sodium hypochlorite and 70% ethanol, washed with sterile distilled water, placed in sterile cotton pads to remove moisture, and then plated on potato dextrose agar (PDA). After 5 days, typical colonies of *Fusarium* spp. (Leslie and Summerell 2006) were observed. From the isolated samples, 3 monosporic cultures were obtained by serial dilutions and selection of a single spore. On PDA, the colony developed white cottony mycelium that gradually turned cream-colored. Morphological characteristics were observed in 15-day-old cultures on carnation leaf agar (CLA). Microconidia (n=40) were pyriform, elliptical with a regular septum, also observed without septa, measuring 27.7-43.3 x 5.2-9.1  $\mu\text{m}$ . Macroconidia (n=50) were thin, almost straight and narrow, with 3 (predominantly) to 5 septa, measuring 46.7-115.2 x 4.9-11.3  $\mu\text{m}$ . Terminal spherical chlamydospores were observed. Molecular identification was performed by partial sequences of EF1- $\alpha$  gene (EF1 and EF2 primers) (O'Donnell et al. 2010) and rDNA-ITS (ITS1 and ITS4 primers) (White et al. 1990). The FBPA2CULSIN isolate selected for this purpose was registered in GenBank with the accession number OK641591 for EF1- $\alpha$  gene and the accession number PV139254 for rDNA-ITS. The sequences were used to perform maximum likelihood analysis with EF1- $\alpha$  and rDNA-ITS from species of the *Fusarium* genus. Phylogenetic analysis showed that the isolate was grouped with the sequences of *Fusarium brachygibbosum* (bootstrap 100%). The percentage similarity of the sequence of the isolate FBPA2CULSIN was 100% with the *Fusarium brachygibbosum* sequences registered in

GenBank (OM938022 and MT292640). Pathogenicity tests were carried out with the FBPA2CULSIN isolate on 12 healthy 1-month-old potato plants (cv. Fiana), contained in 0.5-liter containers with sterile substrate. A small wound was made in the stem of the plant with a sterile scalpel and a cotton ball moistened with 20 ml of the conidial suspension ( $(1 \times 10^6 \text{ CFU/ml})$ ) was placed on the wounded tissue (Freeman et al., 1999). Plants were maintained for 60 days under greenhouse conditions with a 12-h photoperiod at 22 to 26°C and 70% relative humidity. Wilting symptoms were observed 15 days after inoculation and vascular necrosis appeared 25 days after inoculation. Twelve plants used as a negative control were inoculated with sterile distilled water; no symptoms were observed within 3 months after inoculation. The test was performed twice. The pathogen was re-isolated from symptomatic plants and identified as *Fusarium brachygibbosum* based on morphological characteristics and sequencing of the EF-1 $\alpha$  gene, thus fulfilling Koch's postulates. In China, this species has been reported as the cause of tobacco root rot (Qui et al., 2021). *Fusarium equiseti* has been identified as the causal agent of vascular bundle wilt and necrosis in potato crops in China (Lingxiao et al., 2021). To our knowledge, this is the first report of potato vascular wilt and necrosis caused by *F. brachygibbosum* in Mexico.

#### References:

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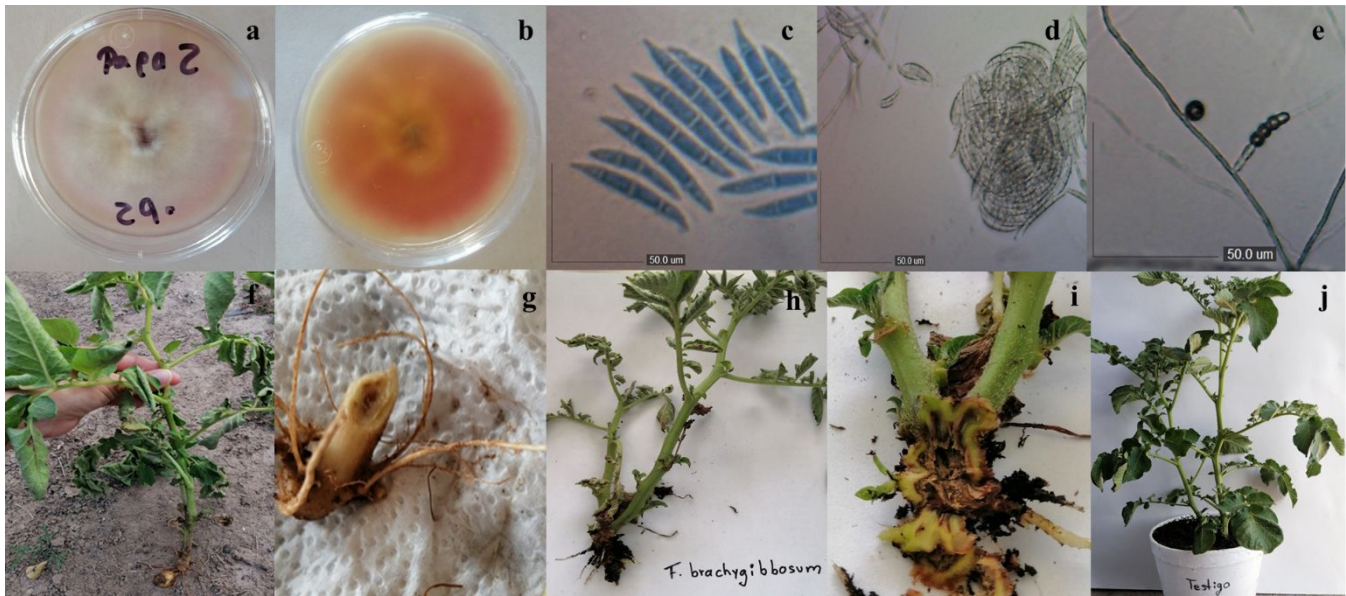


Figure S1. Morphological characteristics of *Fusarium brachygibbosum*. **A-B)** culture in PDA; **C)** Microconidia and macroconidia (50µm bar); **D)** Sporodochia (50µm bar); **E)** Terminal chlamydospores (50µm bar); **F-G)** Symptoms observed in the field; **H-I)** Wilt symptoms and vascular necrosis in inoculated potato plants; **J)** Healthy potato plant.

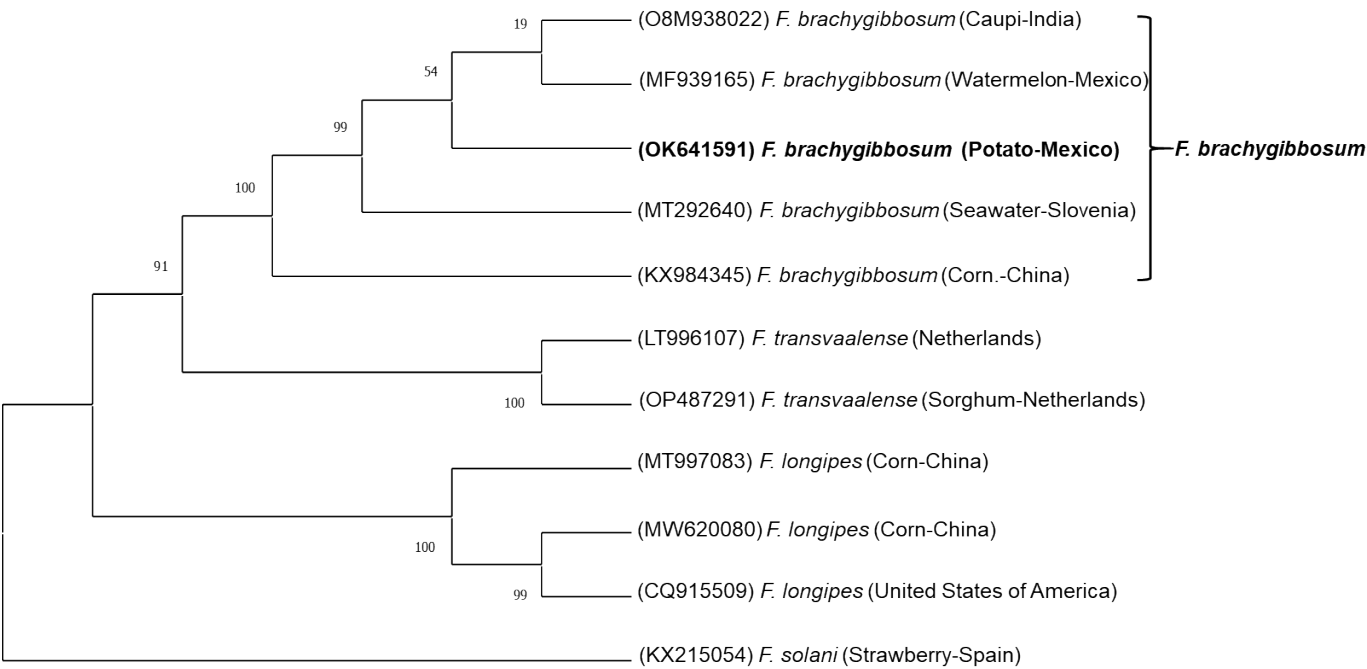


Figure S2. Cladogram inferred by Neighbor Joining for partial EF-1a sequences from *Fusarium* species. Values at the nodes represent the bootstrap scores based on 1000 replicates. Sequence OK641591 (isolate FBPA2CULSIN ) is from this study.