

First Report of Basal Rot of Yellow Dragon Fruit (*Selenicereus megalanthus*)

Caused by *Fusarium oxysporum* in Peru

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Cultivation of yellow dragon fruit (*Selenicereus megalanthus*) in Peru has recently expanded (Verona-Ruiz et al. 2020). In August 2021, approximately 170 of 1,110 dragon

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fruit cuttings (15.3%) in the university's nursery (6°26'10" S; 77°31'25" W) showed basal rot symptoms. Initial symptoms included small brown spots on the base of stems, expanding towards the top that became soft and watery. All symptomatic plants eventually died, i.e., a severity of 100%. The disease was more prevalent on cuttings during the rooting phase than on well-established cuttings. We collected five symptomatic cuttings from throughout the nursery. Four sections of 1 × 1 cm² of tissue adjacent to the diseased area were excised from each cutting, immersed for 1 min in 2% NaClO, rinsed twice with sterile distilled water, placed on potato dextrose agar (PDA) medium (four sections per Petri plate, five plates), and incubated at 25°C for 7 days. Morphologically similar mycelia grew from all sections, and five monosporic isolates were obtained, one per plate. Colonies grew fast, reaching 60 to 64 mm in 7 days, and produced violet-white cottony aerial mycelia with orange sporodochia on PDA, and abundant macro- and microconidia on synthetic nutrient-poor agar. Macroconidia were straight to slightly curved, typically with 2 to 3 septa, 16.6 to 23.3 × 1.7 to 3.7 μm (*n* = 30); microconidia were oval or kidney-shaped, and commonly hyaline, 6.7 to 16.4 × 2.5 to 4.7 μm (*n* = 40). Genomic DNA was extracted from isolate AFHP-100, then the ITS region and the *TEF1* and *RPB2* partial genes were amplified and sequenced (Accession numbers PP977433, OR437358, PP537149) following Gardes and Bruns (1993) and O'Donnell et al. (1998). We conducted a BLASTn search of ITS sequence against the NCBI “nr” database and local ‘megablast’ searches of *TEF1* and *RPB2* sequences against FUSARIUM-ID v.3.0 (Torres-Cruz et al. 2022). We found 100%, 98.19 to 99.84%, and 98.81 to 99.76% identities in ITS, *TEF1*, and *RPB2* sequences, respectively, to the ex-epitype and other reference strains of *Fusarium oxysporum* (CBS 144134, NRRL26406, among others). A maximum likelihood phylogenetic analysis with a *TEF1*–*RPB2* concatenated dataset with FUSARIUM-ID sequences also showed isolate AFHP-100 was *F. oxysporum*. A

pathogenicity test was carried out by inoculating wounded healthy roots of three cuttings with submersion in a 5×10^6 conidia/ml suspension for 25 min. Then, the inoculated plants were planted in sterile soil. One cutting with wounded roots submerged in sterile water served as a control. In parallel, sterile soil was inoculated with 20 mL of the conidial suspension, and another three healthy cuttings were planted. A cutting planted in noninoculated soil also served as a control. Basal rot symptoms developed in all inoculated plants after 25 days. After re-isolation, the same fungus, corroborated based on micromorphology and *TEF1* sequence (PP335689), was recovered, fulfilling Koch's postulates. The isolate was deposited in the KUELAP Herbarium (voucher KUELAP-3214), located and administered by the National University Toribio Rodriguez de Mendoza de Amazonas, in Chachapoyas, Peru. *Fusarium oxysporum* has been reported to cause basal stem rot in Bangladesh and Argentina (Mahmud et al. 2021; Wright et al. 2007), and stem blight in Malaysia (Mohd Hafifi et al. 2019) on dragon fruit. This is the first report of *F. oxysporum* causing basal rot in *S. megalanthus* in Peru. This fungus is among the most destructive plant pathogens, and the rapid expansion of the crop in Peru requires a comprehensive knowledge of the biotic factors influencing production. Therefore, this report is foundational to implementing proper control strategies.

References

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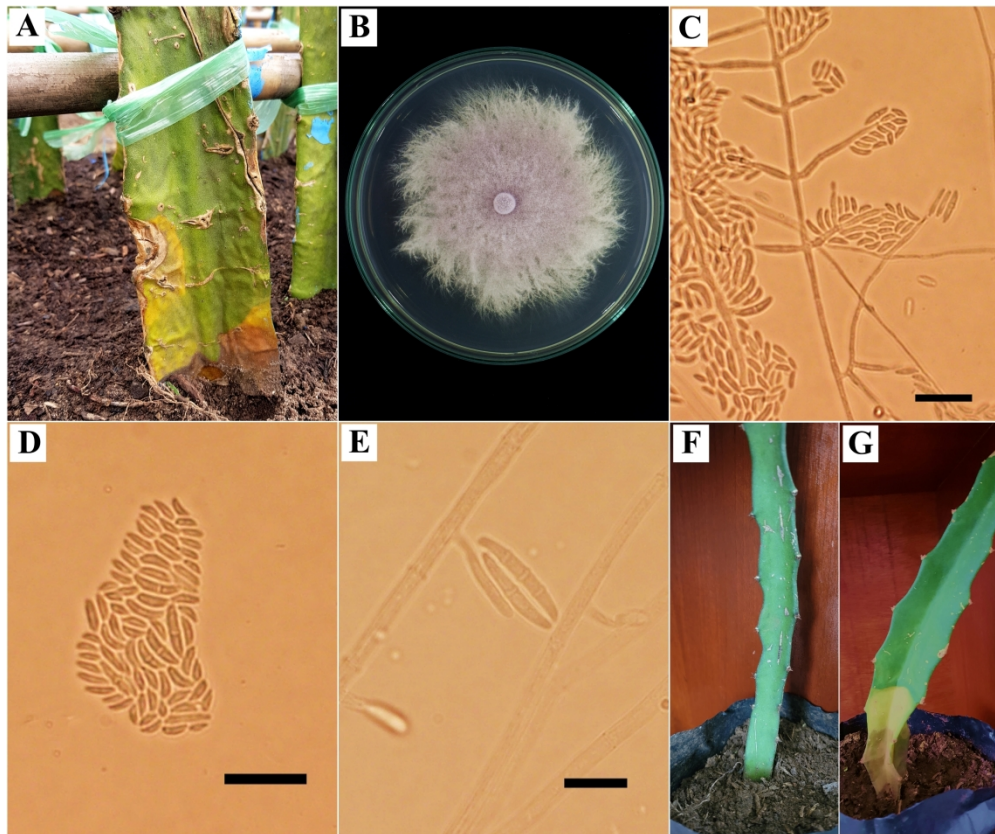
Verona-Ruiz, A., et al. 2020. Sci. Agropecu. 11:439.

Wright, E. R., et al. 2007. Plant Dis. 91:323.

e-Xtra Figure Captions

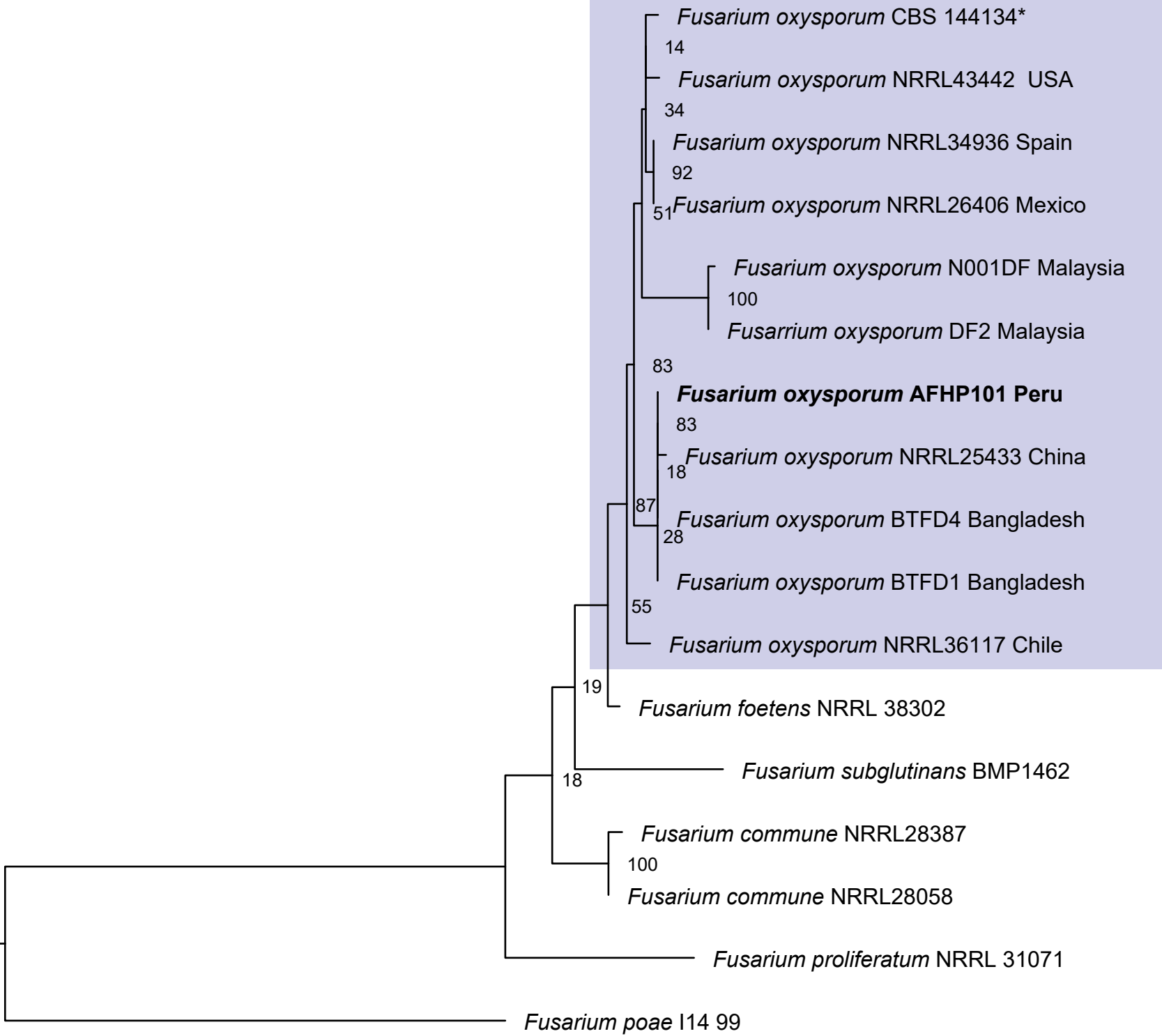
e-Xtra Figure 1. Basal rot of dragon fruit (*Selenicereus megalanthus*) caused by *Fusarium oxysporum* in Peru. **A.** Symptoms observed in the nursery. **B.** Seven-day old colony on potato dextrose agar. **C.** Conidiophores. **D.** Microconidia. **E.** Macroconidia. **F, G.** Pathogenicity test on healthy seedlings of dragon fruit: Control plant and inoculated plants showing basal rot symptoms. Scale bars = 20 μm (C–D), = 10 μm .

e-Xtra Figure 2. Mid-point rooted maximum likelihood phylogenetic tree built with a concatenated dataset of the partial sequences of the translation elongation factor (*TEF1*) and the second largest subunit of RNA polymerase II (RPB2) genes of *Fusarium oxysporum* AFHP-100, obtained in this study (in bold), and other *F. oxysporum* isolates and closely related taxa from other relevant studies (ex-epitype of *F. oxysporum* is marked with an asterisk).



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