Short Notes

Fusarium annulatum causes Fusarium rot of cantaloupe melons in Spain

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Summary. During the summer of 2018, there was high incidence of fruit rots of cantaloupe melons (Cucumis melo var. cantalupensis) in Murcia province, south-eastern Spain. The fruits showed development of whitish mycelium and pulp softening. Morphological and molecular analysis of the internal transcribed spacer (ITS), translation elongation factor 1-α (TEF1-α) and the second largest subunit of RNA polymerase (RPB2) genes confirmed Fusarium annulatum as the causal agent of the disease. A phylogenetic study indicated that F. annulatum is in the Fusarium fujikuroi species complex (FFSC). Pathogenicity of the isolate was determined on healthy fruit verifying Koch’s postulates. The first symptoms of fruit rot were observed 3 d after inoculations at 28ºC. Fruit infections only occurred in artificially wounded melons, and F. annulatum was re-isolated from the wounds. This disease appeared after fruit harvesting, and could generate substantial economic losses mainly in fruit destined for foreign markets due to long transportation times. This is the first report of melon fruit rot caused by F. annulatum in Spain.

Keywords. Cucumis melo, fungal pathogen, pathogenicity test, first report, postharvest disease.

Regarding the *Fusarium* species affecting cucurbits in Spain, the following species have become particularly important: *F. oxysporum* (Martínez et al., 2003), and *F. solani* f. sp. *cucurbitae* Snyder & Hansen on watermelon grafted to pumpkin (Armengol et al., 2000), zucchini (Gómez et al., 2008) and melon (Gómez et al., 2014). In many studies only *Fusarium* rots caused by *Fusarium* sp. are mentioned, without specifying the pathogenic species, so that diagnostic information is lost. Thus, increasing knowledge of the diversity of species that cause melon rots through accurate diagnoses of the causal pathogens is relevant, because this would allow improvement of disease management practices.

Previous studies have not been carried out in Spain on the postharvest fruit rots of melons, caused by *Fusarium* sp., which can be favoured by the climatic conditions of the Mediterranean Basin. These diseases affect melon plantations and the subsequent marketing of melon fruits.

The present study aimed to identify the *Fusarium* species causing fruit rots in cantaloupe melons (*C. melo* var. *cantalupensis*) fruits. For this purpose, the organism associated with the symptomatology was isolated, its morphological characteristics were described, and the species was identified by molecular methods. Koch’s postulates were applied by means of pathogenicity tests of the percentage of infection in inoculated healthy fruit, as well as the severity of the resulting disease.

**MATERIALS AND METHODS**

**Sampling and fungal isolation**

Melon producers in Campo de Cartagena, Murcia province, Spain (37°36’18.4”N, 0°59’10.4”W), supplied cantaloupe fruits showing rot symptoms to the Phytopathology Laboratory of the Crop Protection Group of the Polytechnic University of Cartagena (UPCT) (Grupo de Protección de Cultivos de la Universidad Politécnica de Cartagena - UPCT). The fruits were harvested during July 2018, from different producing areas of Murcia province.

Fungus isolations were carried out using two different methods. Firstly, superficial mycelium developing on the skins of the fruits was transferred to Petri dishes containing Potato Dextrose Agar (PDA) (Scharlab), amended with 0.1 g L⁻¹ of streptomycin sulphate. In addition, diseased fruit tissues were disinfected with 1% NaOCl for 5 min, then sprayed with 96% ethanol, and subsequently rinsed with sterilized distilled water. Fragments of approx. 0.5 × 0.5 cm of the infected tissues were aseptically taken and placed onto PDA. The culture plates were incubated in darkness at constant 26°C for 7 d. After this period, tips of hyphae from emerging colonies were transferred to new PDA plates to obtain pure cultures.

**Morphology and molecular characterization of isolated fungi**

The morphology of all isolates was similar, and the isolate MLFR-09 was used as a representative strain in for further study. Mycelium fragments (5 × 5 mm) were transferred to the centres of 90 mm diam. PDA plates (four replicates), which were incubated in darkness at 26°C to assess colony development. To allow the development of microscopic characteristics, the colonies were also grown on Spezieller Nährstoffarmer Agar (SNA) (Leslie and Summerell, 2006), incubated with a 12 h light/12 h darkness regime. Mycelium growth data, based on the perpendicular and horizontal diameters of colonies, were measured with a calliper. The average of both measurements was recorded after 4 d of incubation on PDA or 6 d on SNA. The colour of the colonies was evaluated after 14 d of growth. After 10 days of incubation on both media, samples were prepared for microscope observation. The criteria of Bugnicourt (1952), Nelson et al. (1983), and Yilmaz et al. (2021), taking into consideration presence of conidiophores and conidia on aerial mycelium, conidiogenous cells, and production of spore and chlamydospores. The average, maximum and minimum measurements were recorded for each identified structure (n = 30). Morphological features were observed using an Olympus BX50F optical microscope, and photomicrographs were taken of each observed fungal structure using an Olympus SC20 camera.

**Molecular identification and phylogenetic analysis**

To confirm the identity of isolate MLFR-09, partial gene fragments of the ITS region, translation elongation factor 1-α (*TEF1*-α), and the second largest subunit of RNA polymerase (*RPB2*) were analysed. Total genomic DNA was extracted from fresh mycelium using the Animal and Fungi DNA Preparation Kit (Jena Bioscience).

The ITS region was amplified with the primer pair ITS1 and ITS5 (White et al., 1990), the translation elon-
Pathogenicity test and evaluation of disease severity

For the pathogenicity test, healthy cantaloupe fruits at physiological maturity were used at 10 d after harvesting (≥ 10° Brix), and with diameters between 16 and 20 cm and approx. weight of 1–1.5 kg. The MLFR-09 isolate was first grown on PDA at 26°C to allow sporulation. The fruits were surface sterilized following the procedure described above. One group of fruits was wounded with a sterile needle and another group was left uninjured. A suspension of conidia (1 × 10⁶ conidia mL⁻¹) was prepared in sterile distilled water, and 50 µL were pipetted onto the wound/surface of each healthy melon, while the experimental controls were similarly treated with sterile distilled water. Ten fruits were used per inoculation treatment, and ten were used in the control treatment. The fruits were kept at 28 ± 2°C for 7 d. Relative humidity was maintained constant by covering the fruits with plastic bags, and the test was carried out twice. Development of any symptoms was checked and recorded daily from inoculation onwards. The percent-ages of melons that developed disease were determined. To assess the severity of any rot in each melon, a disease severity index (DSI; Promwee et al., 2017) was applied, and following the scale proposed by Wonglom and Sunpapao (2020):

\[
DSI (%) = \frac{\Sigma (\text{Score Amount of fruits})}{\text{Maximum score} \times \text{Total number of fruits}} \times 100
\]

The pathogen was re-isolated and re-identified with molecular methods to verify Koch’s postulates.

RESULTS

Disease description

The symptoms the disease comprised brownish areas (diam. up to 6 cm) of the melon skins, which were covered with white mycelium, on different areas of the exocarps, especially in the areas close to the stalks (Figure 1, a and b). These mycelium masses were surrounded by darkened and softened exocarps. The pathogen also colonised the inner tissues of the fruits, and internal lesions of the mesocarps reached a depth of approx. 4 cm, but which could also reach the fruit placental tissues, where sparse mycelium developed (Figure 1, c). The fruit pulp lost consistency, becoming watery as a result of cell degradation, even leading to internal browning in the areas near the skins.

Molecular and phylogenetic study of the isolated fungus

PCR amplification of ITS, TEF1-α and RPB2 genes provided fragments, respectively, of approx. lengths 582, 709 and 644 bases. The PCR amplifications of the three repetitions of isolate MLFR-09 were identical, so the sequences of this isolate were deposited in GenBank under the accession number MZ355136 for ITS, OL960473 for TEF1-α, and OL944300 for RPB2. A BLAST search in GenBank (NCBI) revealed the sequence of the ITS gene region to be 100% identical to F. annulatum (Accession No. MH862668, reference strain CBS 738.97). Translation elongation factor 1-α (TEF1-α) showed 99.30% sequence identity with sequence
MT010994, and the second largest subunit of RNA polymerase (RPB2) showed 99.69% sequence identity with sequence MT010983, both sequences corresponding to the CBS 258.54 type strain of *F. annulatum* (Table 1).

A BLAST search of three sequences in the *Fusarium*-ID database (Geiser et al., 2004) showed that the MLFR-09 isolate belonged to the *Fusarium fujikuroi* species complex (FFSC).

Phylogenetic analysis supported the results obtained from the molecular analysis, confirming that isolate MLFR-09 was *F. annulatum*. The isolate was deposited in the culture collection (Microorganismos de la Agricultura, Poscosecha y Sostenibilidad (MAPYS), Escuela Técnica Superior de Ingeniería Agronómica (ETSIA), Universidad Politécnica de Cartagena (UPCT) (Microorganisms of Agriculture, Postharvest, and Sustainability, Higher Technical School of Agronomic Engineering, Polytechnic University of Cartagena (UPCT), Murcia, Spain).

**Figure 1.** External disease symptoms caused by *Fusarium annulatum* in cantaloupes after natural infections (a, b), and rot of the internal tissues (c). Colony of *F. annulatum* isolate MLFR-09 on potato dextrose agar after 14 d at 26°C, top view (d) and reverse view (e). Microconidial chains (f), polyphialide (g), monophialide (h), microconidia (i) and macroconidia (j). Scale bars: f = 20 µm, g, h, i and j = 10 µm.
Fusarium rot of cantaloupe melons in Spain

Fungus morphology

The mean diameter of the colonies of *F. annulatum* MLFR-09 grown on PDA was 54 ± 5 mm after 4 d of incubation in darkness. Development of the isolate was also assessed on SNA after 6 d incubation, where the average diameter of the colonies was 84 ± 2 mm. The aerial mycelium developed in SNA was sparse and whitish, extending over the entire medium surface in each culture plate.

*Fusarium annulatum* MLFR-09 culture had characteristic violet pigmentation on PDA (Figure 1, d). On the sides, the colour was deep purple (Figure 1, e). In general, the aerial mycelium had a cottony appearance, was initially white but gradually turned violet as it aged, and becoming grey in some areas. Deep purple sporodochia were occasionally observed. The scant macroconidia had straight, thin, partitioned arrangements (3–4 septa). Macroconidium sizes ranged from 20 to 55 μm length and from 3.7 to 5 μm width; the macroconidium apical cells were blunt, and the basal cells were foot-shaped (Figure 1, j). The abundant microconidia were observed in long chains (Figure 1, f) supported by monophialides (Figure 1, h) and polyphialides (Figure 1, g). No septa were detected in the microconidia, their shapes varied from obovoid or nearly oval with a truncate bases, to fusiform, while they ranged from 5.2 to 13.5 × 2.5 to 3.2 μm (Figure 1, i). No chlamydospores were observed.

The MLFR-09 isolate was morphologically compared with the first published description of *F. annulatum* in Bugnicourt (1952), and also referenced in Nelson *et al.*, (1983) and Yilmaz *et al.* (2021) (Table 2).

Pathogenicity

One week after inoculation, white mycelium covered the wounds of the fruits inoculated with *F. annulatum* MLFR-09 (Figure 2, b). No disease was detected in the uninjured melons or in the control treatment (Figure 2, a and c). Symptoms caused by *F. annulatum* MLFR-09 began to appear 3 d after inoculation. On the fruit surfaces, brown necrotic haloes initially appeared around the emerging mycelium, accompanied by the loss of structural rigidity and depression of the fruit exocarps in the same areas. The advance of the pathogen was also evident in the mesocarp of fruits, where there was a change in the colour of the pulp, which became soft with a woolly texture, reaching a depth of 3 cm after 7 d (Figure 2, d). Cross-sectioning of the fruits allowed the tissues between the mesocarp and exocarp to be analysed; the structure turned brown and oily as a result of the necrotic dehydration that had occurred.

Pathogenicity of *F. annulatum* MLFR-09 to cantaloupe fruit was confirmed, as shown in Table 3. The infection rate was 100% when the fruits were artificially wounded and 0% in the non-wounded and inoculated fruit. The mean IDS was 89.75% for wounded and 0% for non-wounded and inoculated fruit. Symptoms of fruits in which the disease developed was compared with the control treatment in which no disease appeared (Figure 2). The severity of the damage was similar to that caused to the fruits by natural infections at the time of isolation of the pathogen (Figure 1).

Microscopic analysis of the pathogen present in the wounds showed that *F. annulatum* that had been inocu-

<table>
<thead>
<tr>
<th>GenBank accession No. (MLFR-09)</th>
<th>DNA target</th>
<th>BLAST match sequence</th>
<th>Reference accession No.</th>
<th>Type material</th>
<th>Coverage (%)</th>
<th>Identity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MZ355136</td>
<td>ITS, rRNA*</td>
<td><em>Fusarium annulatum</em> MH862668</td>
<td>CBS 738.97</td>
<td>98</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Fusarium concentricum</em> MH862659</td>
<td>CBS 450.97</td>
<td>96</td>
<td>99.82</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Fusarium fujikuroi</em> NR_111889</td>
<td>CBS 221.76</td>
<td>95</td>
<td>99.82</td>
<td></td>
</tr>
<tr>
<td>OL960473</td>
<td>TEF1-αb</td>
<td><em>Fusarium annulatum</em> MT010994</td>
<td>CBS 258.54</td>
<td>100</td>
<td>99.30</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Fusarium globosum</em> MT010993</td>
<td>CBS 428.97</td>
<td>100</td>
<td>98.31</td>
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<tr>
<td></td>
<td></td>
<td><em>Fusarium fujikuroi</em> AB725605</td>
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<td>93</td>
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<td>OL944300</td>
<td>RPB2c</td>
<td><em>Fusarium annulatum</em> MT010983</td>
<td>CBS 258.54</td>
<td>100</td>
<td>99.69</td>
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<td></td>
<td></td>
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<td>CBS 450.97</td>
<td>100</td>
<td>97.52</td>
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<tr>
<td></td>
<td></td>
<td><em>Fusarium proliferatum</em> MN534272</td>
<td>CBS 480.96</td>
<td>92</td>
<td>97.32</td>
<td></td>
</tr>
</tbody>
</table>

*ITS, internal transcribed spacer; rRNA, ribosomal gene.
*TEF-α, translation elongation factor 1-α gene.
*RPB2, second largest subunit of RNA polymerase gene.
lated in the pathogenicity tests was also recovered from the fruits with symptoms (data not presented). The morphological and molecular characteristics of the inoculated isolate were maintained, verifying Koch’s postulates.

**DISCUSSION**

This research completed a morphological, molecular, and pathogenicity characterization of *F. annulatum* as a fruit rot pathogen of cantaloupe melons collected from different producing areas of Murcia province of Spain.

*Fusarium annulatum* is a pathogen found in tropical and temperate climates, affecting a variety of crops (Yilmaz et al., 2021). According to Nelson et al. (1992), this fungus is considered an uncommon species, partially because *F. annulatum* has often been misidentified as *F. proliferatum* (Yilmaz et al., 2021). In Spain, *F. proliferatum* has been reported as a frequent pathogen in the production of garlic, causing rots during storage (Gálvez et al., 2017), while it has also been detected in strawberry crops, where it causes vascular wilt (Borrero et al., 2019). In Mexico, Rivas-García et al. (2018) found *F. annulatum* causing rot in muskmelon, where affected fruits showed tissue darkening and thickening, with dehydrated and pinkish white exocarps. In the present case, the pink-violet colouration was not detected in the mycelium that developed in the fruit, but was detected during subsequent isolation of the pathogen on synthetic culture medium.

*Fusarium annulatum* was described by Bugnicourt (1952) as producing ring-shaped macroconidia. Based on this original description, Nelson et al. (1983) indicated that *F. annulatum* was basically a *F. proliferatum* with strongly curved macroconidia. However, Yilmaz et al. (2021) noted that this feature is atypical of the species because most isolates of *F. annulatum* tend to produce straight macroconidia (Figure 1, g).

*Fusarium annulatum* belongs to the *Fusarium fujikuroi* species complex (FFSC) (Yilmaz et al., 2021), formerly designated as the *Gibberella fujikuroi* (GFC) species complex (Wigmann et al., 2019). Three clades form

**Table 2.** Morphological characteristics of *Fusarium annulatum* isolate MLFR-09, causing fruit rot in cantaloupes, compared with previous descriptions of *F. annulatum* by Bugnicourt (1952), Nelson et al. (1983), and Yilmaz et al. (2021).

<table>
<thead>
<tr>
<th>Morphological characteristics</th>
<th><em>Fusarium annulatum</em> grown on Corn Meal Agar (CMA) Isolate MLFR-09 grown on Potato Dextrose Agar (PDA)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony top view</td>
<td>Aerial mycelium absent or late-developed, very light, powdery, slightly dispersed, white in colour. Blackish-purple pigments are normally formed in synthetic cultures</td>
</tr>
<tr>
<td>Colony reverse view</td>
<td>ND</td>
</tr>
<tr>
<td>Macroconidia</td>
<td>Thin-walled, strongly curved and sickle-shaped, with the basal cell clearly foot-shaped</td>
</tr>
<tr>
<td>Shape</td>
<td>Cylindrical or claviform with a truncate tip</td>
</tr>
<tr>
<td>Length (µm)</td>
<td>13-58</td>
</tr>
<tr>
<td>Wide (µm)</td>
<td>1.9-3.3</td>
</tr>
<tr>
<td>Number of septa</td>
<td>3-6</td>
</tr>
<tr>
<td>Microconidia</td>
<td></td>
</tr>
<tr>
<td>Shape</td>
<td></td>
</tr>
<tr>
<td>Length (µm)</td>
<td>4.7-14.4</td>
</tr>
<tr>
<td>Wide (µm)</td>
<td>1.7-2.3</td>
</tr>
<tr>
<td>Number of septa</td>
<td>0-1</td>
</tr>
<tr>
<td>Chlamydospores</td>
<td>Absent</td>
</tr>
</tbody>
</table>

*ND* = not described.

**Table 3.** Pathogenicity test and disease severity index (DSI) of caused by *Fusarium annulatum* isolate MLFR-09 on *Cucumis melo* var. *cantalupensis* fruits.

<table>
<thead>
<tr>
<th>Inoculum</th>
<th>Percentage infection</th>
<th>Average DSI (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Wounded</td>
<td>Not wounded</td>
</tr>
<tr>
<td>Spore suspension (MLFR-09)</td>
<td>100</td>
<td>0</td>
</tr>
<tr>
<td>Sterile distilled water</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
the GFC complex, with *F. annulatum* belonging to the Asian clade (O’Donnell et al., 1998).

The pathogenicity test in the present study confirmed that melon fruits must be naturally wounded (mechanical injury) for the pathogen inoculations to be effective (Figure 2), as was also noted by Wonglom and Sunpapao (2020). Nuangmek et al. (2019) suggested that cutting the fruit peduncles during harvesting...
could be the source of infections in the field. Another determining factor could be the texture of the surface tissues of some commercial melon varieties, with natural cracking facilitating pathogen infections. Fruit cracking disorders and open netting areas due to a defective synthesis of lignin and suberin are considered natural infection pathways for pathogens (Martínez et al., 2009). However, Champaco et al. (1993) commented on the possible association between the root rot caused by *Fusarium* species and fruit rot, since melons grow on the soil surface which would act as an inoculum reservoir. If pathogen penetration occurs prior to, or during, harvesting procedures, *Fusarium* survival in the soil and in the plant debris from previous crops is likely to be important.

This is the first report of *F. annulatum* causing rot in cantaloupe fruits in Spain. The results presented here provide the basis for new disease management strategies, based on the precise identification of the causal agent of this disease.

**ACKNOWLEDGEMENTS**

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**LITERATURE CITED**


