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A Cytogenomic Analysis Reveals a New *Fusarium fujikuroi* Species Associated with Lemongrass (*Cymbopogon citratus*)†

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Abstract: *Fusarium* is one of the most prominent genera of plant pathogens due to its wide range of hosts and mycotoxin production. The *Fusarium fujikuroi* species complex (FFSC) encompasses several threatening known plant pathogens. *Cymbopogon citratus* is a broadly distributed aromatic and medicinal plant rich in bioactive volatiles, which have relevance for several industries. In the present study, a preliminary first report of *C. citratus* wilt caused by a FFSC species in Portugal is described. Symptomatologic, cultural, morphologic, genetic, and cytogenomic characteristics associated with this pathogen and disease are displayed. The cultural features included flat, white-colored colonies with filiform margins and abundant cottony aerial mycelia at the upper surface and orange-violet colored at the lower surface. On Carnation Leaf-Piece Agar, septate fusoid macroconidia were present, displaying a flattened tapering toward the basal part and a number of septa ranging from one to four. The comparison of amplified and aligned ITS sequences revealed a 100% similarity between the isolated fungus and the FFSC. Finally, a flow cytometry assay revealed an estimated genome size of 29.9 Mbp, contrasting with other FFSC-known pathogens. Ultimately, by examining these various aspects, this work aims to comprehensively understand the wilt and its causal agent.

Keywords: Cytogenomics; lemongrass; fungal pathogen; *Fusarium fujikuroi* species complex; plant pathology

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1. Introduction

The *Fusarium* genus (Ascomycota: Hypocreales) is composed of ubiquitous filamentous fungi, comprising 20 species complexes [1]. These ascomycetes are among the most economically relevant fungal plant pathogens, therefore being a threat to crop health and farmers' financial sustainability [2]. Furthermore, *Fusarium* spp. has secondary biosynthetic pathways capable of producing harmful mycotoxins, which lessens food safety worldwide [3]. The *Fusarium fujikuroi* species complex (FFSC) is divided into three distinct clades (American, African, and Asian), encompassing more than 50 different species [4]. Several causal agents of plant diseases belong to the FFSC, such as *Fusarium circinatum*, *F. fujikuroi*, *F. sacchari*, and *F. verticillioides*.

Cymbopogon citratus (DC.) Stapf (lemongrass) is a perennial widely distributed aromatic and medicinal plant of the Poaceae family rich in secondary metabolites [5]. Most of *C. citratus* cultivation is related to essential oil (EO) extraction since their volatiles have

applications in the food, fragrance, and pharmaceutical industries [6]. The EO bioactivity is related to their usual main compounds, namely the monoterpene isomeric aldehyde mixture of neral and geranial, the monoterpene alcohol geraniol, and less frequently the monoterpene hydrocarbon β-myrcene [7]. This biological activity is greatly diversified, including bactericidal, insecticidal, fungicidal, and nematicidal activities [8–11]. Thus, *C. citratus* EO can be a great source of new biochemical biopesticides which can justify an increasing demand for this crop.

In the present study, a preliminary first report of *C. citratus* wilt caused by a FFSC species in Portugal is described. Symptomatologic, cultural, morphologic, genetic, and cytogenomic characteristics associated with this pathogen and disease are displayed. Ultimately, by examining these various aspects, this work aims to gain a comprehensive understanding of the wilt and its causal agent.

2. Materials and Methods

2.1. Infected Plant Material and Isolation

The infected plants were observed and collected in a small organic garden (10 x 20 m) at Instituto Superior de Agronomia, Tapada da Ajuda, Portugal (38°42′46°N 9°11′04°W). The fungus was isolated from plant-infected tissues by cutting 5 pieces, each with approximately 2 cm^2, from the plant´s collar in the transition zone between diseased and healthy tissue. Tissue pieces were then disinfected by immersing them in a NaClO solution (2% *v*/*v*) for 30 seconds followed by double-rinsing in sterile distilled water to remove the disinfectant for 30 seconds each. After being washed and dried with sterile filter paper, the pieces were plated on potato dextrose agar (PDA, BD-Difco Laboratories, Detroit, MI, USA) supplemented with 250 mg/L chloramphenicol (BioChemica, AppiChem, Germany). Inoculated Petri dishes were incubated at an inverted position at 25 °C and regularly checked (3-5 days) for the development of *Fusarium*-like fungi, based on the cultural characteristics of colonies. After incubation, one isolate was selected and single-spored to obtain a monosporic culture. For that purpose, spores were diluted in sterile distilled water and a drop of the suspension was spread on an agar medium using a platinum loop. Small agar blocks containing a single spore were cut under a microscope and transferred to new Petri dishes with PDA or malt extract agar (MEA, Oxoid, England). Four replicates of this process were performed, two for each medium. Petri dishes were incubated for 7 days with a 12-hour cycle of light or in complete darkness at 25 °C.

2.2. Cultural and Morphological Characterization

The isolate was characterized based on their cultural and morphological characteristics. Colony morphology, pigmentation, and type of aerial mycelium were determined on PDA and photographed using a Leica MZ12.5 stereomicroscope (Stuttgart, Germany) coupled with a Leica MC170 HD digital camera using the software Leica Application Suite (LAS) version 4.12.0. Morphological observations included the presence and characteristics of sporodochia, size of sporodochial macroconidia and aerial microconidia, shape, and degree of septation of conidia, disposition of the microconidia conidiophore branching patterns, and presence or absence of chlamydospores, as previously described by Kamali-Sarvestani et al. [12]. These observations were done using a Leica DM 2500 microscope (Stuttgart, Germany) with differential interference contrast illumination, and the images were captured using a Leica DFC295 digital camera using the software Leica Application Suite (LAS) version 3.3.0. To induce the formation of sporodochia, agar blocks from single-spore cultures were placed in Petri dishes on Carnation Leaf-Piece Agar (CLA) following the method of the Fusarium Laboratory Manual [13].

2.3. DNA Extraction, PCR Amplification and Sequencing

Total genomic DNA was extracted from mycelium grown in PDA plates adapting the Cenis protocol [14]. A 1.5 mL Eppendorf tube was filled with 500 µL of an Extraction Buffer (200 mM Tris HCl pH 8.5, 250 mM NaCl, 25 mM EDTA, 0.5% SDS) containing an abrasive agent (glass beads 100 µm) and a collected piece of mycelium was suspended. After macerating with a micro pestle and incubate 10 min at 65 °C, the mycelial mat was pelleted by centrifugation for 1 min at 12000 rpm, and collected the supernatant to a new tube, measuring the collected volume was an equal volume of isopropanol was added, after mixing by inverting the tubes, precipitated DNA was pelleted by centrifugation for 3 min at 12000 rpm. After a wash with 300 µL of 70% ethanol and centrifuge for 1 min at 12000 rpm, the pellet was vacuum dried and resuspended in 50 µL of an Elution Buffer (10 mM Tris HCl pH 8.0, 1 mM EDTA). The primers V9G [15] and ITS4 [16] were used to amplify part of the nuclear rRNA operon (ITS) spanning the 3' end of 18S rRNA gene, the first internal transcribed spacer, the 5.8S rRNA gene, the second ITS region and the 5' end of the 28S rRNA gene. PCR amplifications were performed using NZYTaq 2x Green Master Mix (Lisbon, Portugal), 1 µL of each primer (10 µM stock), and 1 µL of gDNA in a final volume of 20 µL. The cycle conditions in a T-gradient (Biometra, Göttingen, Germany) were 94 °C for 5 min, followed by 30 cycles at 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 30 s, and final elongation at 72 °C for 5 min. Verification of amplification was followed by performing agarose gel 1% electrophoresis, with DNA stained using GreenSafe (3 µL/100 mL gel) and visualized under UV light. Sequencing was performed by StabVida (Caparica, Portugal) using ITS4 primer. The sequence was edited using the UGENE program (Unipro, Novosibirsk, Russia) to remove ambiguous regions, and contigs assigned to the isolate were compared to the information available in NCBI non-redundant nucleotide database.

2.4. Cytogenomic Analysis

Nuclear DNA content was estimated using flow cytometry. The preparation of suspensions of intact nuclei for analysis was performed following the method of Galbraith et al. [17]. The mycelium grown in PDA was chopped with a razor blade in a Petri dish containing 1 mL of a buffer (WPB 0.2 M Tris–HCl, 4 mM $MgCl_2$, 1% Triton X-100, Na_2EDTA 2 mM, NaCl 86 mM, sodium metabisulfite 20 mM, 1% PVP-10, pH 7.5; Loureiro et al. [18]). The nuclear suspension was sieved using a nylon mesh with 30 µm to remove large debris. Then, nuclei were stained with 25 µg mL^{-1} and a volume of 50 µL of propidium iodide (PI; Sigma-Aldrich, USA). To estimate the nuclear DNA content, DNA from *Colletotrichum acutatum* (C = 0.0689 pg; [19]) was used as the reference standard. The isolate´s genome size was estimated by flow cytometry using a Partec CyFlow Space flow cytometer (Partec GmbH, Görlitz, Germany). The acquisition of numeric data and fluorescence graphs was made by Sysmex FloMax software v2.4d (Sysmex, Görlitz, Germany), as described by Guilengue et al. [20]. The histograms for each sample were recorded and the C-values were calculated with the following formula:

$$\text{Nuclear DNA Content (pg)} = (\text{Sample G1 Peak Mean} \times \text{GS of Reference Standard}) / \text{Reference Standard G1 Peak Mean} \quad (1)$$

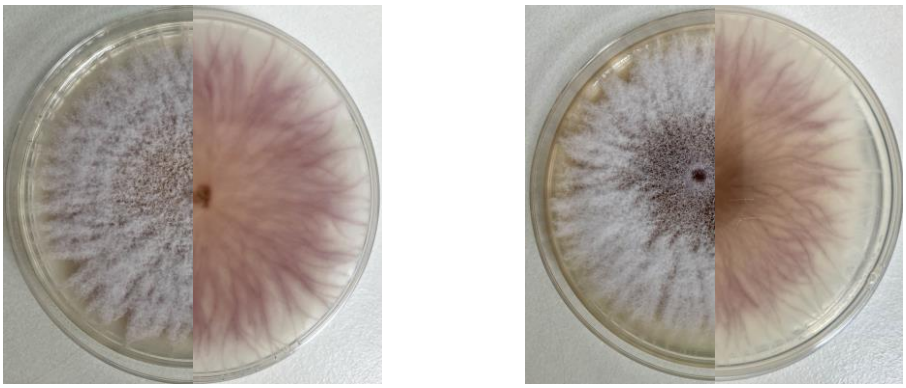
3. Results

3.1. Symptomatological Characteristics

Chlorotic spots on the leaves are the first symptoms of this disease that rapidly evolve into necrosis. Then, the collar region of the plant starts to necrose followed by rot and wilt. Finally, the collar region is colonized by the pathogen mycelium, externally visible. Ultimately, generalized wilt affects the plant, and the collar region is severally rotted.

3.2. Cultural Characteristics

The cultural features in PDA included flat, white-colored colonies with filiform margins and abundant cottony aerial mycelia at the upper surface and orange-violet colored at the lower surface. Colonies appearance presented slight differences when incubated with a 12-hour cycle of light or in darkness, becoming dark brown at the center with age in the last case. Additionally, isolates grew slightly less in dark conditions. (Figure 1).

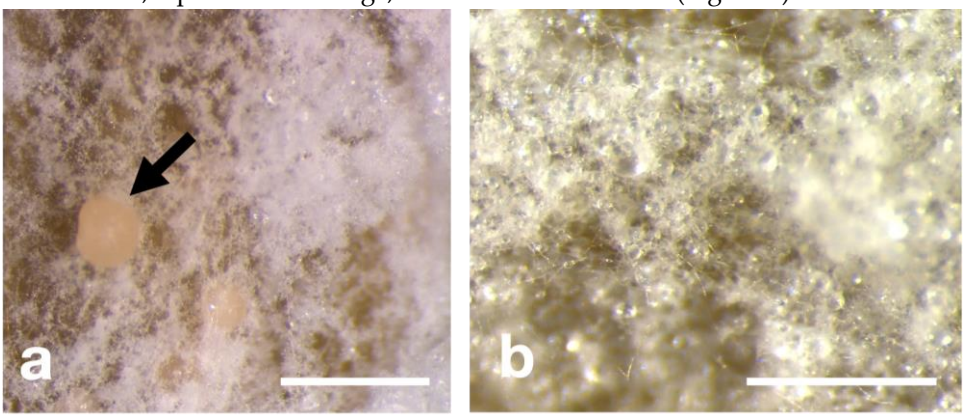


(**a**) (**b**)

Figure 1. Isolate growth on PDA after seven days of incubation; (**a**) upper and reverse sides (from left to right) of a culture incubated with a 12-hour cycle of light; (**b)** upper and reverse sides (from left to right) of a culture incubated in darkness.

3.3. Morphological Characteristics

On CLA, septate fusoid macroconidia were present, displaying a flattened tapering toward the basal part and a number of septa ranging from one to four; 1-septate conidia: (12.3–)15.9–19.1(–22.7) × (3.0–)3.2–3.6(–3.8) µm (av. 17.5 × 3.4) µm; 2-septate conidia: (18.4–)22.7–25.0(–28.2) × (3.0–)3.6–3.8(–4.4) µm (av. 23.8 × 3.7) µm; 3-septate conidia: (26.2–)28.0–31.7(–38.1) × (3.3–)3.4–3.8(–4.2) µm (av. 30.3 × 3.7) µm; 4-septate conidia: (35.3–)36.6–40.5(–45.4) × (3.5–)3.8–4.3(–4.6) µm (av. 39.1 × 4.1) µm. Microconidia were oval-shaped with a flattened basal and 0-septate or rarely 1-septate. They were formed on aerial conidiophores from monophialides which may occur in V-shaped pairs to give a *rabbit ear* appearance or were sometimes grouped in *false heads* but not found in chains. Aseptate microconidia: (5.4–)7.5–10.7(–12.1) × (2.2–)2.4–3.2(–3.8) µm (av. 8.9 × 2.8) µm. Chlamydospores were absent. Other morphological features were found, such as *loop hyphae* and anastomosis, a parasexual bridge, between macroconidia (Figure 2).



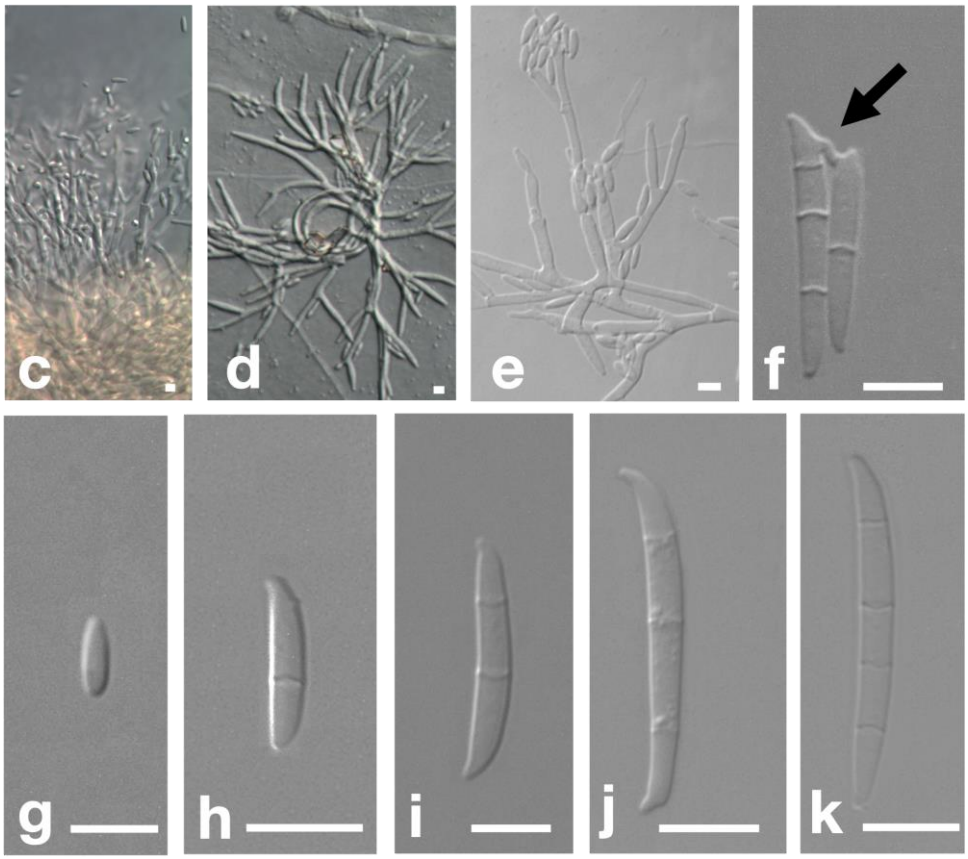


Figure 2. Morphological characteristics of the isolated *Fusarium* sp.; (a) sporodochia formed in CLA, after 15 days of inoculation at 25 °C; (b) mycelium of a colonized leaf; (c) sporodochial conidiophore on CLA; (d) loop hyphae; (e) conidiophores with V-shaped pairs on aerial mycelium with aseptate microconidia; (f) anastomosis between macroconidia; (g-k) conidia with different septa number. Scale bars 1 mm (a and b), 10 μm (c - k).

3.4. Genetic Characteristics

Comparison of amplified and aligned sequences to the nucleotide NCBI database yielded 1157 hits. Using the BLAST similarity search (performed on March 15th, 2023), the ITS region of the ribosomal DNA region of the strain showed 100% (626/626 bp) similarity (with 0% gaps) to the FFSC. It was possible to infer about fungus phylogeny and identify it as an Ascomycete, belonging to the Pezizomycotina subdivision, Sordariomycetes class, Hypocreales order, Nectriaceae family, and the FFSC.

3.5. Cytogemonic Characteristics

The genome size reference used, *Colletotrichum acutatum*, has a nuclear DNA content of approximately 0.0689 pg [19]. Considering the output data from flow cytometry, displayed in Figure 3, the FFSC isolate has an estimated nuclear DNA content of about 0.0307 pg, which roughly corresponds to a genome size of 29.9 Mbp (Figure 3).

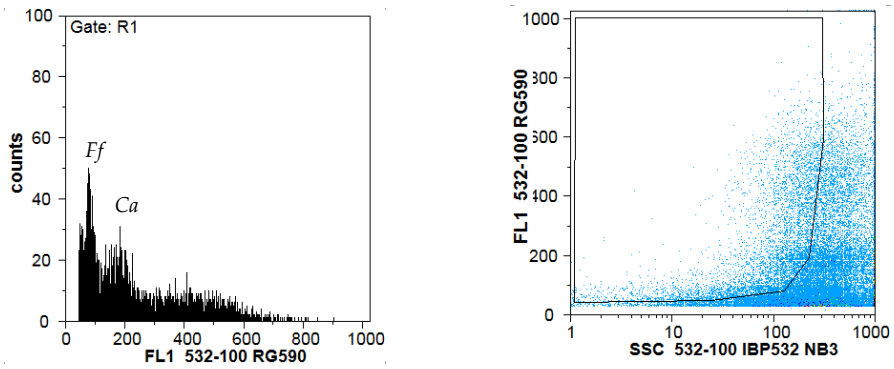


Figure 3. Genome size measurement of the isolated fungus using flow cytometry; (**a**) histogram of relative fluorescence intensities of propidium iodide-stained nuclei simultaneously isolated from mycelium of FFSC isolate (*Ff*) and the DNA reference standard, *Colletotrichum acutatum* (*Ca*); (**b**) dot-plot of side light scatter (SSC) vs. fluorescence pulse integral in linear scale applying a gating region to exclude as much as possible partial nuclei and other debris to improve the quality of the histogram.

4. Discussion

Several diseases of C. citratus have a fungal aetiology, comprising species from several genera such as Botrydiplodia, Curvularia, Fusarium, Helminthosporium, Pestalotiopsis, Puccinia, Rhyzoctonia, Tolyposporium, and Ustilago [21,22]. Only Fusarium equiseti and F. verticillium have been associated with causing leaf spot and clump rot on C. citratus [21]. Neither of these species belongs to the FFSC, leading to the conclusion that the isolated pathogen cannot be one of these species, according to the nucleotide sequences of the ITS region. However, collar rot and wilt of Cymbopogon winterianus, java citronella, have been associated with Fusarium verticillioides, formerly known as F. moniliforme, which belongs to the FFSC [23,24]. Nevertheless, despite morphological similarities as monophialides in V-shaped pairs, F. verticillioides in CLA present numerous microconidial chains [24] which weren´t observed in the isolate. In addition, considering the cytogenomic data which indicates that the isolated pathogen has a genome size of approximately 29.9 Mbp, it is clear that the causal agent is not Fusarium verticillioides, which has a genome size of 42.4 Mbp [24]. Furthermore, C. citratus EO is capable of inhibiting the growth of F. verticillioides at in vitro assays, reinforcing the different aetiology [25].

To the best of our knowledge, this is the first time that a fusariosis affecting *C. citratus* caused by a FFSC species is described. A preliminary comprehensive characterization of the fungal causal agent was conducted, although some traits may be further studied.

In future research, others isolates will be collected and more genome regions of this pathogen will be sequenced such as TEF and RPB2 gene sequences. Furthermore, the sequencing will include both forward and reverse directions using ITS1F or V9G and ITS4 primers, to unveil the full identity of this *Fusarium* isolate. Additionally, Koch's postulates must be fulfilled to be sure of the pathogenicity of the isolate.

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