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First Report on Rhizome Rot Disease of *Curcuma longa* Caused by *Fusarium solani* in Bangladesh

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Abstract

Turmeric (Curcuma longa L.) is a valuable medicinal plant as well as spice crop in Bangladesh. The rhizome rot disease is a severe danger to turmeric cultivation. The current study sought to identify the fungal pathogen linked to turmeric rhizome rot disease. Rhizome of turmeric with distinct rotted symptoms was collected from the experimental site of the Botanical Garden, Jahangirnagar University, Bangladesh. The sample was screened to isolate the causative fungal pathogen through the tissue planting technique. Macro and micro-morphological characterization based on colony appearance, mycelial and conidial characteristics primarily identified the fungus as Fusarium sp. The ITS sequence of rDNA of the fungus exhibited 99 to 100 percent similarity with the other F. solani species formerly deposited in the NCBI database which confirmed the fungal identity as F. solani. An in vitro pathogenicity test validated the pathogenic nature of the fungus. Growth behaviors of the fungus were evaluated on different solid culture media viz., Potato dextrose agar, Potato sucrose agar, Sabouraud dextrose agar and Hansen's agar; temperature conditions (10°C, 15°C, 20°C, 25°C, 30°C and 35°C) and pH levels (pH 4, pH 5, pH 6, pH 7 and pH 8). Maximum mycelial growth was obtained on PSA medium at 30°C temperature and pH 7 conditions. Current findings also conclude that F. solani favors a wide range of temperature and pH levels. To the best of our search, the present investigation revealed the relationship of F. solani with the rhizome rot disease of turmeric for the first time in Bangladesh.

Keywords

Turmeric, Fungal Disease, Molecular Identification, Culture Media, Temperature, pH

1. Introduction

Turmeric *(Curcuma longa* L.) is a perennial, cylindrical, cross-pollinated rhizomatous herb belonging to the family Zingiberaceae [1] [2]. It has about 40 different genera and 400 species and the most common varieties are *Curcuma longa, Curcuma aromatic, Curcuma amada, Curcuma algustifolia, Curcuma zidoria.* Turmeric is distributed throughout the subtropical and tropical regions of the world, such as India, South-East Asian countries, and North Australia [3]. India is the world's biggest producer of turmeric, accounting for 75 - 80 percent of global output, followed by China, Myanmar, Nigeria, and Bangladesh [4]. In Bangladesh, Turmeric cultivation is a promising source of livelihood for hilly people and about 150 turmeric farms are located in the Khagrachari district of Bangladesh [5].

Curcumin, the active ingredient, is thought to have antimicrobial and anti-inflammatory properties and appears as an effective cure for several diseases [6] [7] [8]. *C. longa* contains carbohydrates (69.4%), minerals (3.5%), protein (6.3%), fat (5.1%), fiber (2.6%), and moisture (13.2%) [9]. It has an extremely important role in Hindu and Buddhist culture. It is also an essential spice and has become an inseparable part of some special dishes. For its wonderful dietary properties and acrimonious taste, this plant is referred to as the "Queen of Spices". The Bangladeshi people usually use turmeric in all curry preparation like fish, meat, vegetables, pulse, etc. for its typical color and bitter flavor [5]. Dried rhizomes of turmeric are used as condiments, dye, drugs, and cosmetics. It is also said to cleanse the liver, lower cholesterol, treat allergies, improve digestion, promote immunity, and improve appearance [10]. *Curcuma* sp. has been used as a medicinal herb due to its diverse superior characteristics such as antioxidant [11], anti-inflammatory [12], antimicrobial [13] and several therapeutic properties [14].

Although having so many therapeutic and antimicrobial properties turmeric is vulnerable to several fungal pathogens of both soil and air borne nature that reduce the quality as well as quantity of the crop production. The incidence of rhizome rot disease was surveyed and the causal organism of diseases was isolated in major turmeric growing tracts of South India [10]. In India, Fusarium solani and Pythium aphanidermatum have been reported to cause rhizome rot disease of turmeric [15] [16] [17] [18] [19]. The occurrence of rhizome rot disease of turmeric caused by Pythium aphanidermatum (Edson) Fitzp. has been recorded in Karnatak, Kerala, Tamilnadu, Andhra Pradesh states of India [6]. Another study has also been conducted in Tamil Nadu, India, and found the association of Fusarium solani and some other pathogens to cause rhizome rot infection [20]. In Bangladesh, numerous endophytic fungi were reviewed to associate with the rhizome of turmeric [21]. But there is still no published article on the rhizome rot disease of turmeric in Bangladesh. Hence, the present investigation was designed to detect and identify the causal fungal agent of rhizome rot disease of turmeric through morphological and molecular characterization and to study the effect of different physical factors (media, temperature and pH) on the growth pattern of the fungal pathogen.

2. Materials and Methods

2.1. Isolation and Identification of the Pathogen

Infected rhizome of turmeric with characteristic symptoms was collected in a sterilized zipper polybag from the experimental site of the Botanical Garden, Jahangirnagar University, Savar, Dhaka, Bangladesh. The diseased sample was washed with distilled water followed by surface sterilization with 5% NaOCl for 3 minutes. The sample was then rinsed with distilled water 3 - 4 times and subsequently air-dried into the laminar airflow cabinet until the surface water was disappeared. The diseased sample was cut into pieces and inoculated into a Potato dextrose agar (PDA) medium following the tissue planting method and incubated at room temperature ($25^{\circ}C \pm 2^{\circ}C$) to isolate the fungal pathogen associated with the rhizome rot disease [22].

The isolated fungal pathogen was identified through morphological and molecular techniques. Morphological identification was carried out by observing macro and microscopic characteristics of the colony, mycelial and conidia such as colony appearance, mycelial color, branching pattern of mycelium, shape, size and pigmentation of the conidia etc. In the molecular approach, the fungal isolate was identified using the internal transcribed spacer (ITS) sequence of the rDNA region. DNA was extracted using a DNA extraction kit (Promega, USA). PCR amplification of the target region of DNA was performed using ITS4 and ITS5 primers [23]. The PCR cycles were performed with Taq polymerase activation at 94°C for 5 minutes, 35 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 5 minutes followed by a 10-minute step at 72°C [24]. The Maxwell[®] 16 LEV Plant DNA Kit (Promega, USA) was used to purify the PCR product. The PCR product was sent to First BASE Laboratories (Sdn Bhd, Malaysia) for sequencing. The sequenced data were then submitted to NCBI to assign an accession number to the work.

2.2. Pathogenicity Test

A healthy rhizome of turmeric was detached from the susceptible cultivar and surface sterilized with 5% NaOCl and then cleaned with distilled water after being washed with flowing tap water. The artificial wound was made by using a sterilized needle and inoculated with a 2 mm diameter agar block containing tested fungal pathogen [25]. Artificially inoculated rhizome was kept at 25° C ± 2°C in a desiccator with moistened cotton to preserve humidity. After 35 - 40 days of incubation, a typical symptom was reproduced and the pathogen was re-isolated from the artificially inoculated plant part to corroborate Koch's postulates.

2.3. Growth Response of the Fungus to Culture Media, Temperature and pH

Culture media, temperature and pH play a vital role in fungal growth and de-

velopment. Four different fungal culture media, Potato sucrose agar (PSA), Sabouraud dextrose agar (SDA), Potato dextrose agar (PDA), and Hansen's agar (HA); six different temperature regimes (10°C, 15°C, 20°C, 25°C, 30°C, and 35°C) and five different pH levels (4.0, 5.0, 6.0, 7.0, and 8.0) were employed and observed to evaluate the effects on the growth and development of the fungus. A 2 mm diameter agar plug was removed from 7 days old culture of the pathogen grown on PDA medium and inoculated on the center of each plate containing culture medium. The effects of temperature and pH were observed on the PDA medium. The experiment was conducted in controlled environmental conditions and mycelial growth was recorded at 7 days post-incubation (dpi) [24] [26].

2.4. Statistical Analysis

Statistical analysis of the data generated during the experiments was analyzed using standard statistical analyzing tools *viz*; MS Excel, SPSS 16.0, MEGA 6 software and BLAST tool, etc.

3. Result and Discussion

3.1. Identification of the Fungus

Rhizome rot disease symptom of turmeric was observed light brown color in the margin with deep brown rotted center. The diseased tissues were inoculated into the Potato dextrose agar (PDA) medium and found a cottony white-colored fungal colony after 3 days of incubation. The upper surface of the colony was white, wooly with a slightly elevated center and the lower surface of the colony was off-white color. Under the compound microscope, the mycelium of the fungus was found hyaline, septate, and branched. Macroconidia were hyaline, 2 - 4 celled with thick wall, slightly curved, and blunt-ended. Microconidia are ab-undant and oval to kidney-shaped. Chlamydospores were also formed in the fungal mycelia (Figure 1). *Fusarium solani* (Mart.) Sacc causing wilt disease of bitter gourd in India was identified through cultural and morphological characterization [27].

The molecular identification of the fungus was carried out by analyzing the ITS sequence of rDNA region of the fungus. Data were submitted to NCBI and received an accession number OL691079.1. The sequenced data were compared with the database previously deposited to NCBI through BLAST search. Our organism OL691079.1 showed 100% similarity with *Fusarium solani* (KY949606.1 and MN653247.1) followed by above 99% similarity with *Fusarium solani* (MK-174970.1, KY013237.1, OL314780.1 and MK174971.1). The phylogenetic tree was produced to reveal the closest matching taxa. This analysis involved 30 nucleotide sequences. In the maximum likelihood tree (**Figure 2**), current studied fungus (OL691079.1) form cluster with other species of *Fusarium solani* which revealed that the fungus is *Fusarium solani*. *F. solani* species complex were also identified through phylogenetic analysis in Malaysia [28].

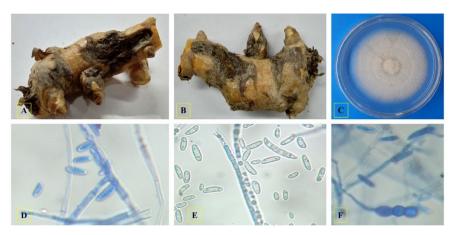


Figure 1. Morphological characterization of *Fusarium solani* causing rhizome rot disease of Turmeric (A—Rhizome rot symptom in the primary stage; B—Symptom in advanced stage; C—Mycelial growth of the fungus on PDA medium; D—Branched, septate mycelia with conidia (40X); E—Macro and microconidia (40X); F—Chlamydospore).

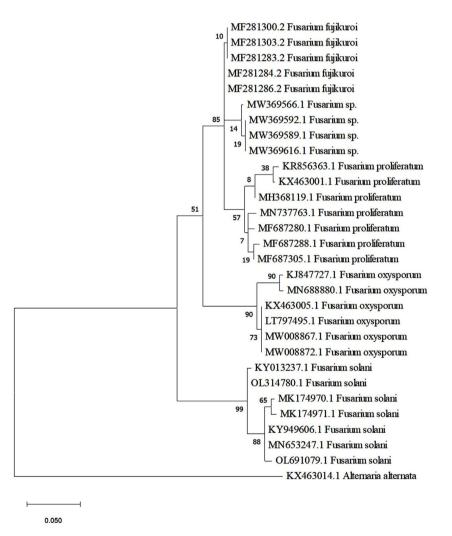


Figure 2. Maximum Likelihood (ML) tree derived from analysis of ITS sequence dataset of the studied fungus with bootstrap value (Bootstrap replication = 1000). The accession number of our organism is OL691079.1.

3.2. Pathogenicity Test

The healthy susceptible rhizome of turmeric (*C. longa*) was artificially inoculated with respective fungal isolate under *in vitro* condition in a desiccator following the modified "detached leaf technique" (Figure 3). Typical symptom with a light brown margin and dark brown center was reproduced after 35 - 40 days of inoculation (Figure 3). The fungus was reisolated and characterized and found identical with the primarily isolated organism which proved the pathogenic nature of *Fusarium solani* causing rhizome rot disease of turmeric (Figure 3). An experiment has been conducted to test the pathogenicity of *Fusarium langsethiae* towards oats and wheat in *in vitro* conditions using the detached leaf technique in the UK [29].

3.3. Growth Rresponse of Fusarium solani to Culture Media

The growth and development of fungi are largely dependent on the media where they grow. In the current investigation, four different solid culture media such as PDA, SDA, PSA and HA were used and the results revealed that the highest mycelial growth of F. solani was obtained on PSA medium followed by PDA, SDA and HA at 7 days post-incubation (dpi) in room temperature (25°C ± 2°C) (Figure 4). These findings showed analogies with the previous study. Mean mycelial growth of Fusarium spp. (47.58 mm) and F. solani (61.94 mm) was observed on PDA and PSA media respectively [30]. The best growth of F. solani was obtained on the Sabouraud dextrose agar (SDA) medium [31]. In India, the influence of physiological variables on the growth of Fusarium sp was studied using eight different solid culture media viz., Corn meal agar (CMA), Potato carrot agar (PCA), Potato dextrose agar (PDA), Richards' agar (RA), Host extract agar (HEA), Oatmeal agar (OMA), Sabouraud maltose agar (SMA) and V-8 juice agar (V8JA) to identify the best medium for growth and development of F. solani and highest radial growth was found on PDA medium (90 mm) and lowest on RA medium (63 mm) [32].

3.4. Growth Response of *F. solani* to Temperature

During the present investigation, six different temperature regimes were tested *viz.*, 10°C, 15°C, 20°C, 25°C, 30°C, and 35°C on PDA medium. The highest mycelial growth of *F. solani* was found at 30°C followed by 25°C and 35°C. The mycelial growth almost ceased at 10°C (**Figure 5**). According to the data, *F. solani* prefers a temperature range of 25°C - 35°C for normal growth and development, however, at low temperatures, its growth is halted. Previous experiments showed similarities with the current result. In India, the growth characteristics of *Fusarium* spp. were studied and 28°C was recorded as the optimum temperature for the growth and development of *F. solani* [33]. The effect of temperature on *F. solani* causing disease in soybean was investigated and 29.3°C was estimated as the optimum temperature for the proliferation of the fungal pathogen [34]. *F. solani* revealed the highest growth performance at 25°C [31].

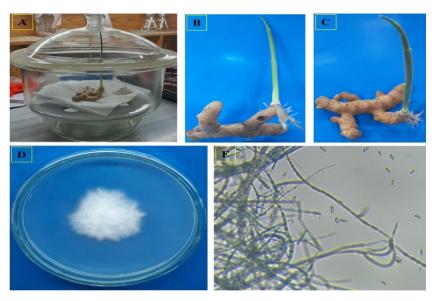
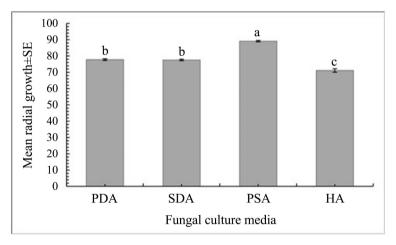
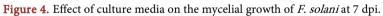
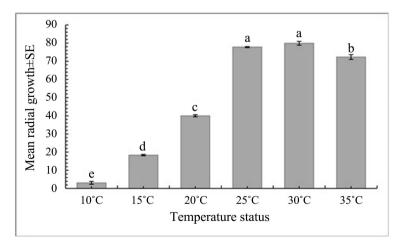
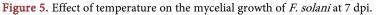


Figure 3. Pathogenicity test in *in vitro* condition (A—Experiment set up in desiccator; B—Reproduced rot symptom; C—Control; D—Re-isolated fungal pathogen on PDA medium; E—Microscopic view of *F. solani* (10X)).









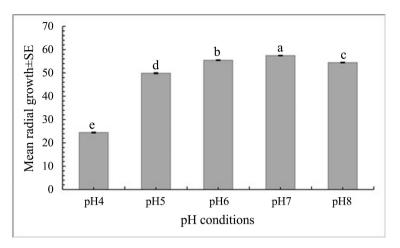


Figure 6. Effect of pH on the mycelial growth of *F. solani* at 7 dpi.

3.5. Growth Response of F. solani to pH

Five several pH levels of culture media *viz.*, 4.0, 5.0, 6.0, 7.0, and 8.0 were tested in the running investigation and the highest radial mycelial growth of *F. solani* was recorded at pH 7.0 and the lowest growth was recorded at pH 4.0 after 7 days of incubation (dpi) (**Figure 6**). Almost similar results were found at pH 6.0, 7.0 & 8.0, which indicate that *F. solani* favours a wide range of pH conditions. These findings are very comparable to antecedent works. The highest mycelial growth of *F. solani* occurred at pH 6.0, followed by pH 7.0, which is quite analogous to the current study [32]. The growth and bioactive metabolite production of *Fusarium solani* were optimized in India and pH 6.0 was noticed as the optimum condition for the proliferation of the fungus [35]. Optimum pH of 7.5 is favorable for the growth of all species of *Fusarium* [31].

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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