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Chapter

Current Status of *Fusarium* and Their Management Strategies

Amar Bahadur

Abstract

Fusarium spp. is one of the most economically important plant pathogens causing a wide range of plant diseases with significant crop losses globally. *Fusarium* wilt is a major problem all over the world. *Fusarium oxysporum*, *Fusarium solani*, *Fusarium fuji-kuroi* are economic importance species in worldwide. *Fusarium solani* causing disease in many agriculturally crops and favored by high temperatures and warm moist soils. The fungus produces three types of asexual spores; microconidia, macroconidia and chlamydospores serve as propagules in infecting host plants and found endophytes and saprophytes. The color of the colony, length and shape of the macroconidia, the number shape of microconidia and the presence or absence of chlamydospores are key features for the differentiation of *Fusarium* species. Pathogens, forms over 100 *formae speciales* cause disease in dicot and monocot plant species and infecting a variety of hosts. Vegetative compatibility Groups (VCG) is used to differentiate their races. Resistant cultivars and bio-control agents (*Trichoderma* spp., and *Psedomonas* spp.) have been used to manage the disease.

Keywords: Fusarium spp., formae speciales, symptoms, disease cycle, management

1. Introduction

Soil-borne pathogens caused infection in soil *via* the roots. *Fusarium* is a complex genus and worldwide distribution, causing diseases in plants, animals, and humans as well as the presence of non-pathogenic *Fusarium* in the natural ecosystem [1]. Fusarium wilt pathogen is one of the most destructive soil-borne pathogens around the world occurring in both saprophytic and pathogenic [2, 3]. Non-pathogenic and pathogenic *F. oxysporum* strains are in the soil, but the pathogenic strain causes severe vascular wilt disease in more than 150 agricultural crop species are banana, tomato, melon, watermelon, and cotton to be infected by vascular wilt [4]. Cereals and other food grains can be contaminated by Fusarium toxins and causes many diseases syndromes in mammals, moldy sweet potato toxicity, and poisoning in bean hulls [5]. *Fusarium* is one of the most important fungal genera that can produce mycotoxins. *Fusarium* mycotoxins are fumonisins, zearalenone, deoxynivalenol, and additional trichothecenes, cosmopolitan genus and numerous species are plant pathogens [6]. Cob rots in maize, caused mainly by F. graminearum and F. verticillioides, and both species produce mycotoxins which contaminate the grain and some strains of Fusarium solani cause collar rot of legume seedlings such as peas and bean. *Fusarium* species have their ability to grow on a wide range of substrates and their efficient mechanism for dispersal [7]. Many species are saprophytes which occur commonly in soil, colonize diseased roots, stems and grow quickly

on isolation media. It is important to test Fusarium isolates from diseased roots for pathogenicity to the plant. Diversity of host specificity within a single species into the 'forma specialis' each forma specialis exhibited a high level of virulence on a particular host species [8]. Fusarium oxysporum and their formae speciales that cause vascular wilt diseases, more than 100 Fusarium vascular wilt diseases worldwide and root rots cause with saprophytic strains as colonizing roots after the pathogen, forma specialis usually causes vascular wilt in only a single host specie. F. oxyspo*rum* mainly causes vascular wilt diseases, while *F. solani* mainly causes collar and root rots. Some strains of *F. oxysporum* can cause rots of melons and potato tubers. *Fusarium oxysporum* is an economically harmful species is a soil-borne phylogenetic diversified fungus with a wide host range including horticultural and grain crops that cause diseases such as wilt, rot, and damping-off [9, 10]. The pathogen has ranked fifth among the top 10 plant pathogenic fungi [11]. Fusarium wilt is one of the major diseases caused by *Fusarium oxysporum* strains and a major threat to agriculture [12]. Besides wilt disease, some strains can also cause foot- or root-rot resulting in serious yield losses in affected crops [13].

In the Cucurbitaceae family various *formae speciales* have been identified; among them, *F. oxysporum* f. sp. *cucumerium*, *F. oxysporum* f. sp. *niveum* and *F. oxysporum* f. sp. *niveum* is the most destructive pathogen of watermelon around the world [14]. Based on the host cultivar's resistance classified into four physiological races (0–3) [15]. The pathogen is responsible for yield losses of around 30–80% or even more [16, 17].

Fusarium is one of the most important groups of plant-pathogen causing diseases on crops. Plant-pathogenic fungi Fusarium graminearum, causes head blight of wheat and Fusarium oxysporum, which causes wilt and stem rot diseases [11]. Fusarium species produce a range of mycotoxins, most trichothecenes and fumonisins, which harm animal and human health [18]. Fusarium has a taxonomy with generic and species that diagnosing of diseases, identifying fungi, and developing management strategies. The generic concept of *Fusarium* was first diagnosed with the primary character of the banana-shaped conidia [19]. In *Die Fusarien*, which have a thousand species into 65 species, 55 varieties, and 22 forms in 16 sections and continued to use before 1960 [20]. In Russia, recognized and documented Fusarium [21, 22]. The Commonwealth Mycological Institute in the United Kingdom published The Genus Fusarium in understanding variability in Fusarium recognized 44 species and highlighted morphological characters, especially microconidia and the sexual reproductive structures, which used to differentiate species to identification [23]. A pictorial atlas to *Fusarium* that recognized more than 90 species [24]. A manual that recognized 41 species, and further 16 species were published [25]. Fusarium species use three predominant species concepts viz., morphological, biological, and phylogenetic to differentiate *Fusarium* species. Species concepts in *Fusarium* have been discussed [26]. Many "new" species of Fusarium discovered and described [27] and host species [28–30] are explored, grown in new areas [31–34]. Currently, there are more than 300 phylogenetically distinct species [35].

2. Pathogens (*Fusarium* spp.)

Fusarium species are widely distributed in soil, aerial plant parts, plant debris, and other organic substrates. A genus *Fusarium* is a large group of hyaline filamentous fungi [19]. Fusaria are common soil saprophytes and are also known as phytopathogens [36]. The genus Fusarium currently contains over 20 species [37]. Some Fusarium species have a teleomorphic state [38]. The commonest species include *Fusarium solani*, *F. oxysporum*, *F. equisetti* and *F. chlamydosporum* [39]. Two

Fusarium species were recently included in the list of the top ten plant pathogenic fungi with both economic and scientific importance [11]. This genus interacst with plants as endophytic root colonizers [40]. they may be responsible for a wide range of human infections [41]. Fusarium genus has more than 1500 species and several strains occur on plants/animals producing mycotoxins. *Fusarium* belongs to Phylum—Ascomycota, Order—Hypocreales and Family—Nectriaceae. Fusarium species are complex includes plant pathogens, human pathogens, and non-pathogens. Pathogenic strains are morphologically indistinguishable from nonpathogenic strains. Fusarium pathogens are persisting in the soil as chlamydospores, cause infect through the feeder rootlets and then colonize the vascular system, leading to severe wilting and death of plants. Important species are Fusarium oxysporum, F. solani, F. fujikuroi and F. graminearum well known plant-pathogens. It's characterized by fast-growing colonies with floccose aerial mycelium, colony pigmentation from pale, rose, burgundy to bluish violet depending on species and growth conditions. Fusarium usually produces pale violet to the dark magenta pigment in agar media (some do not produce). Conidia are often produced in sporodochia which are slimy dots in the culture, macroconidia are fusiform, multi-celled by transverse septa and characteristic foot-shaped basal cell pointed apical cell. Some species also produce microconidia are mostly single-celled, in some cases three to five celled and vary from globose, oval and fusiform. A few species produce microconidia in chains and others in slimy. Fusarium characteristics by morphological conidia in size and shape of macroconidia, the presence or absence of microconidia and chlamydospores, colony color and conidiophore structure [42]. Macroscopic and microscopic features, such as the color of the colony, length and shape of the macroconidia, the number, shape and arrangement of microconidia, and presence or absence of chlamydospores are key features for the differentiation of Fusarium species [43]. The *Fusarium oxysporum* is a soil borne fungi found in cultivated and uncultivated soils worldwide [7]. *F. oxysporum* have high functional and genetic diversity [6]. F. oxysporum can affect perennial and annual plants, including aquatic plants (lotus), cause wilts and crown rot on field crops, garden, ornamental crops and weeds (broomrape and witchweed). Strains with the same host range are grouped into forma specialis. In some formae speciales are subdivided into races by cultivar specialization [44]. Based on size and shape of macroconidia, presence or absence of microconidia and chlamydospores, colony color, and conidiophore Fusaria classified [42]. Morphological pictures of plant pathogenic, saprophytic and bio-control strains of F. oxysporum are indistinguishable. Based on taxonomic fusaria recognizing more than 100 species [23–25]. Pathogenic strain is very host specific, attacking only one or a few species and certain cultivars and designated as formae speciales and race of the pathogen. Proposed a system of classification of *F. oxysporum* strains, on basis of vegetative compatibility group (VCG), but not a universal tool of identify formae speciales or non-pathogenic isolates [45]. Nitrate reductase and phosphate permease have been used successfully to distinguish *Fusarium* species [46]. The presence or absence of microconidia is a primary character in *Fusarium* taxonomy. Fusarium teleomorphs have been described, classified into several different genera (Gibberella, Nectria) (Figure 1) [47].

2.1 Identification

There are three basic concepts for identification of *Fusarium* sp., by morphology can differentiate species, biological as sexual viable and phylogenetic as the common origin of the same species. Colonies character on potato dextrose agar of *Fusarium* species. *F. oxysporum* and *F. solani* can establish in suppressiveness soil than other species. *Fusarium* microconidia are oval to kidney-shaped, generally

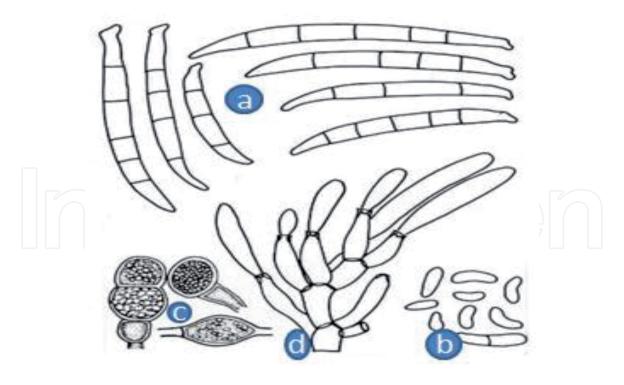


Figure 1. (*a*) macroconidia, (*b*) microconidia, (*c*) chlamydospores, (*d*) conidia and conidiophores of Fusarium spp.

one-celled produce on short conidiophores on aerial mycelia and enter into the sap stream transported upward, macroconidia are fusiform having three to five cells and produced large numbers on sporodochia and chlamydospores are usually two types one within the macroconidium and other within the mycelium, formed singly/in pairs or chains with thick-walled, survive in the soil for a long time. A system of classification of strains of *F. oxysporum*, based on their vegetative compatibility as a described method based on pairing nitrate non-utilizing mutants to determine the vegetative compatibility group (VCG) of each strain and use of various molecular tools that group together genetically similarity in strains [45]. VCG cannot be used as a universal tool to identify *formae speciales* or nonpathogenic isolates only molecular tools can provide information for a taxonomic framework for species identification to relationships among species. Sequences of the β -tubulin region have been useful to distinguish some Fusaria [48]. Use nuclear restriction fragnment length polymorphism (RFLP) and VCG to determine F. oxysporum f. sp. *radicis-lycopersici* [49]. Use random amplified fragment length polymorphisms (RAPD) to differentiate races of Fusarium oxysporum f. sp. vasinfectum on cotton [50]. DNA sequences of the ITS regions are very useful in distinguishing species in many eukaryotic organisms, but not is very informative for Fusarium [51]. Random amplified polymorphic DNA identify sequence-characterized amplified region (SCAR) markers. Many *formae speciales* are known to be polyphyletic, making it difficult to identify specific molecular markers [52, 53]. Molecular methods, such as 28S rRNA gene sequencing, may be used for rapid identification of Fusarium strains to species and subspecies levels [54]. Polymerase chain reaction (PCR) based rDNA detection method [55] and detection of protein banding patterns by SDS-PAGE and esterase isozyme electrophoresis [56]. Cultures of Fusarium species grown on Sabouraud Dextrose Agar at 25°C produce wooly, cottony, flat or spreading colonies [57]. F. oxysporum are responsible for severe damage on many economically important plant species and show a high level of host specificity, based on infection of the plant species and plant cultivars they are classified into more than 120 formae *speciales* and races [58]. Molecular tools are providing species identification as well as evolutionary relationships among species.

2.2 Fusarium oxysporum

F. oxysporum is soil-borne pathogen that survive in the soil for a long time in the form of chlamydospores, penetrates the roots and colonizes in xylem vessels, systemic appear as yellowing, wilting, and death in plants. *F. oxysporum* are saprophytic and able to grow and survive for long periods on organic matter in soil and in the rhizosphere of plant species [59]. Some strains of *F. oxysporum* are pathogenic on plant species causing wilt and responsible for severe damage on many economically important crops and show host specificity based on the plant species and plant cultivars. They are classified more than 120 *formae speciales* and races [58]. Some strains can penetrate roots, but do not invade the vascular system [60]. *F. oxysporum* strains are responsible for two types of symptoms, such as vascular wilting and rotting. Vascular wilt resulting in yellowing and wilting of the plant [61]. Rotting of root without reaching the vascular system is called basal rot, stem rot, crown, root rot and also affect storage organs such as bulbs, corms, tubers and rhizomes. The first rot reported on lupine was caused by *F. oxysporum*

Sl No.	Fusarium species	Host crops	
1	F. oxysporum	cereals, peas, beans, nuts, bananas, onions, potatoes, citrus fruits apples, spices	
2	F. solani	fruits and vegetables, spices	
3	F. avenaceum	cereals, peaches, apples, pears, potatoes, peanuts, peas, asparagu tomatoes in temperate climate	
4	F. cerealis	cereals, potatoes	
5	F. culmorum	Cereals, potatoes, apples, sugar beet in temperate climates	
6	F. equiseti	cereals and fruits contaminated with soil, vegetables, nuts, spices	
7	F. graminearum	Cereals and grasses in warmer to tropical regions	
8	F. poae	Cereals, soybeans, sugar cane, rice from the temperate region.	
9	F. proliferatum	Corn, rice, figs, fruits	
10	F. sambucinum	cereals, potatoes	
11	F. semitectum	nuts, bananas, citrus, potatoes, melons, tomatoes, spices	
12	F. sporotrichioides	cereals, pome fruits	
13	F. subglutinans	corn, pineapple, bananas, spices, sorghum	
14	F. tricinctum	cereals from temperate regions.	
15	F. venenatum	cereals, potatoes	
16	F. verticillioides	corn, rice, sugarcane, bananas, asparagus, spices, cheese, garlic from warm to tropical regions.	
17	Fusarium sacchari	sugarcane	
18	Fusarium moniliforme	sugarcane	
19	Fusarium fujikuroi	rice	
20	Fusarium mangniifera	mango	
22	F. verticillioides	maize	
23	F. pseudograminearum	wheat and barley	
24	Fustiaria circinatum	pinus	

Table 1.

Fusarium species and their host causing diseases.

Sl No.	'formae speciales' (f. sp.)	race	host plants
1	asparagi	—	asparagus
2	apii	1 to 4	celery
3	callistephi	1, 2, 3	African marigold
4	cubense	1, 2, subtropical race 4, tropical race 4	banana
5	cannabis	_	hemp
6	ciceris	0, 1A, 1B/C, 2 to 6	chikpea
7	cucumerinum	1 to 3	cucumber, muskmelon, watermelor
8	cepae		onion
9	conglutinans	1 to 5	cabbage, radish
10	carthami	1 to 4	safflower
11	chrysanthemi	3 races	chrysanthemum, gerbera, daisy
12	dianthi	1, 2, 4 to 11	carnations
13	elaeidis	_	Oil palm
14	fragariae	_	strawberry
15	gladioli	1 and 2	gladiolus
16	glycines	_	soybean
17	lactucae	1 to 4	lettuce
18	lagenariae	_	bottle gourd, winter squash
19	lupini	1 to 3	lupine
20	lentis	1 to 8	lentil
21	lycopersici	1, 2 and 3	tomato
22	melongena	_	egg plant
23	melonis	1 to7	muskmelon
24	niveum	0 to 3	watermelon, squash
25	pisi	1, 2, 5, 6	peas
26	phaseoli	1 to 7 and 27	common bean
27	radicis-cucumerinum	50	cucumber, muskmelon, sponge gourd, watermelon, squash
28	radicis-lycopersici		Tomato, eggplant, <i>Cucurbitaceae</i> sp
29	radicis-vanillae		vanilla
30	raphani	_	radish
31	rapae	_	Brassica rapa
32	saragae	_	witchweed
33	saffrani		saffron
34	spinaciae	1, 2	Spinach, beet
35	tracheiphilum	1 to 4	cowpea, soybean
-			
36	tulinae	_	tuline
36 37	tulipae vasinfectum	1, 2, 3, 4, 6, 8	tulipe cotton, okra alfalfa, soybean, tobacc

Table 2.Important 'formae speciales (f.sp.)' and race of Fusarium oxysporum.

f. sp. *radicis-lupini*. The term "*radicis*" can differentiate rot-producing strains from wilt-producing strains. The "*radicis*" name of the *forma specialis* to allow for identification of the type of symptoms. Some *formae speciales* such as *cepae*, *lilii*, and *opuntarium*, cause rotting but are not referred as *formae speciales* "*radicis*-host plant name. *F. oxysporum* causes disease on vanilla, described to as *forma specialis radicis-vanillae*. Two different *formae speciales* are causing two types of symptoms in tomato as the *forma specialis lycopersici* causing wilt and *radicis-lycopersici* causing rot, **Table 1** [62–66].

2.2.1 Fusarium oxysporum 'formae speciales (f.sp.)' and race

Host range of plant species are grouped into a *forma specialis* and subdivided into races by cultivar specialization [44]. More than 100 *formae speciales* of *F. oxysporum* causing diseases in different plant species. *Forma specialis* is determined by testing the fungus for pathogenicity on various plants species and race is determined by pathogenicity on cultivars of a single plant species. Molecular tools can identify pathogenic strains and in some cases races of the pathogen. A *forma specialis* of fusarium fungus normally affects only one primary host species, but colonize endophytically in the roots of secondary hosts. Many *formae speciales* were named according to the host plant either the genus name/species name. A reported 106 *formae speciales* and 58 additional host plants which have no *forma specialis* as characterized and races based on cultivar identified 25 of the 106 *formae speciales* (**Table 2**) [67].

3. Diseases

The genus Fusarium species cause vascular wilts, root, stalk and cob rots, collar rot of seedlings, and rots of tubers, bulbs and corms, some species also produce mycotoxins in contaminating grain, diseases as ear and kernel rot of corn, scab of rice and wheat and stalk rot and grain mold infection of sorghum. Fusarium species are causing diseases such as crown rot, head blight and scab on cereal grains; vascular wilts on a wide range of horticultural crops; root rots; cankers; and other diseases such as pokkah-boeng on sugarcane and bakanae disease of rice. Wilts are important in many cultivated crops. Fusarium pathogens survive as chlamydospores in soil for long periods. Wilt pathogens colonize in the root cortex of some non-host plants. Chlamydospores form in the cortex when the plant dies. Fusarium produces harmful secondary metabolites known as mycotoxins [18]; toxicity to animals, humans, plant pathogens, and also in food and feeds [68]. Mycotoxins are secondary metabolites produced by *Fusarium* species and threat to animal and human health. Earlier infections during the harvesting some of them produce mycotoxins in agricultural products [69, 70]. Mycotoxins, are the trichothecenes, fumonisins, and zearalenone [71]. Vascular wilt fungus produces the characteristic xylem vessel clogging and wilting of plants. Colonization and clogging of vessels in addition to the secretion of several toxins by the fungus including fusaric acid, lycomarasmin, dehydrofusaric acid, play a major role in the development and progression of wilt symptoms [18]. First detected fusaric acid (in-vivo) in wilted cotton plants and suggested that responsible for the production of wilt symptoms [72]. Fusaric acid is a toxin in tomatoes and cotton [73]. Fusaric acid is well-known for its phytotoxicity and role in the pathogenesis of Fusarium wilts [74]. Fusarium species as plant pathogens, causing diseases such as crown rot, head blight, and scab on cereal grains; vascular wilts on a wide range of horticultural crops root rots; cankers; and other diseases such as pokkah-boeng on sugarcane and bakanae disease of rice [23].

4. Symptoms

The pathogen colonizes in the xylem, growing up the vascular system in the stem, disease development and symptom expression of host plants depend on the colonization of vessels by the pathogen [75]. Hyphae and chlamydospores of diseased plant debris in the soil infect young rootlets and enter the xylem vessels. Colonization in the plant causes a reaction, producing brown phenolic compounds and tyloses. Browning of vascular tissue is a key symptom of pathogens that cause vascular wilt disease. Blocking of the xylem decreases water movement, causing the infected plant to wilt and die. Yellowing, wilting and stunting are general symptoms of many diseases of the root and stems. Early symptoms appear as leaf yellowing, slight wilting during the day and stunting. Wilt starts vein clearing on the younger leaves and drooping of the older lower leaves, followed by stunting, yellowing of the lower leaves, defoliation, marginal necrosis and plant death. This seed and soilborne plant pathogen showing symptoms like chlorosis, necrosis, immature leaf fall, vascular system browning, and finally wilting. Fusarium vascular wilt diseases are more severe in warm, wet conditions. The *Fusarium* infects through wound sites as made by the nematode as associated with roots. Pathogenic strains of F. oxyspo*rum* are produce two types of symptoms, vascular wilting and rotting, penetrates the host roots and reach the xylem vessels, colonizes caused vascular wilt, and progressive yellowing and wilting [61].

4.1 Disease cycle

Fusarium is a monocyclic, soil-borne, diversified fungus including pathogenic and saprophytic [9, 10]. Dispersing by soil, plant debris, farm machinery [76] and seeds [77] and survive more than 15 years without host plants [78]. Pathogens spread through water and farm equipment over short distances but extensive areas through contaminated soil, seeds, or seedlings. A report indicated that spread by seeds [79]. Fusarium wilt does not spread from plant to plant within a season. The fungus infects the plants by germinating spores, growing through the wounds and openings near the root hair [80]. Fungal hyphae penetrate the vascular tissue produce microconidia [80]. Microconidia are released into the xylem, which travels upward though the water and colonizes the vascular tissue [81]. In stressful environmental fungi produce chlamydospores into the soil. *Fusarium* wilt accomplishes by spreading chlamydospores as the primary survival of the pathogen [15].

5. Management

Several *Bacillus* spp. strains suppressive effect against plant diseases caused by soil-borne diseases. *B. subtilis*, produce volatile compounds and activate plant defense mechanisms by triggering induced systemic resistance [82, 83]. Bacillusmediated plant growth promotion due to promote phytohormone, biosynthesis, thereby enhancing nutrient uptake ability in the host and stimulating plant defense responses against biotic and abiotic stresses [84, 85]. *Bacillus* species can produce lytic enzymes like chitinase and β -1,3-glucanase, involved in the degradation of the fungal cell wall [86]. *Trichoderma* spp. show a wide genetic diversity, and are producers of several extracellular proteins, enzymes. Arbuscular mycorrhizal fungi (AMF) protect plants against phytopathogens and abiotic stresses [87–89]. Chemicals can prevent infection, but do not cure a plant once infected and these compounds affect beneficial soil microbiota and accumulate in the food [90]. Resistant plant varieties carrying resistance genes is currently the most effective in terms of economy, ecology, and disease control. However, genetically encoded resistance is seldom durable and sooner or later new races emerge that overcome resistance [91, 92]. *Fusarium oxysporum* resistance genes are not available in the germplasm of all crops [93].

F. oxysporum are genetically varied in phytopathogens, saprophytes and bio-control agents. Management of Fusarium wilt use broad-spectrum chemical fumigates in the soil before planting that are environmentally unsafe and also living thinks, only cost-effective, environmentally safe method is resistant cultivars when these are available. Resistant crop varieties are available against some Fusarium wilt pathogens. However, resistant variety is not resistant to all races of the particular forma specialis. In case develop new races of the pathogen overcome host resistance. Managing Fusarium wilt is very difficult to manage because of chlamydospores persistent in nature for about 10 to 15 years and the development of new physiological races [15, 94]. Fusarium wilts diseases are difficult to control because the chlamydospores persist for a long time in soil. These fungi can survive infecting the root cortex of some symptomless, non-host crops. Only biocontrol agents are useful in the management of diseases. Non-pathogenic strains generally developed as bio-control agents and show several modes of action in their bio-control capacity, easy to massproduce and formulate. The use of nonpathogenic strains of F. oxysporum to control Fusarium wilt has been reported for many crops [94–104]. On the infection sites on the roots trigger plant defense reactions; plants protect themselves from microbes by activating defense reactions such as systemic acquired resistance. During growth, plants are continuously challenged by a wide spectrum of environmental stimuli, by abiotic and biotic. Plants usually protect themselves from microbes by activating defense reactions such as systemic acquired resistance (SAR) after recognizing microbial stimuli. When plants are exposed to abiotic stimuli, the plants can acquire an improved defense by chance. Chemical stimuli, such as probenazole (PBZ), acibenzolar-S-methyl (ASM), tiadinil (TDL), and isotianil, have been used as plant activators and can induce disease resistance in plants. Foliar spray with validamycin A effectively controls soil-borne *Fusarium* diseases tomato wilt, and banana panama disease by inducing SAR. Once soil-borne fusaria pathogens spread in the field, their removal is very difficult. Soil treatments often are less sufficient and need to reduce their usage because of adverse effects on the environment. Biological control and resistance cutovers are alternatives to control fusarium diseases. Trichoderma ligno*rum* was registered as a fungicide on the Agricultural Chemicals Regulation Law in Japan in 1954 to control *Rhizoctonia* disease in tobacco. This was the first registered bio-fungicide in the world. A non-pathogenic strain of F. oxysporum was registered in 2002 as a bio-fungicide to control soil-borne wilt of sweet potato plants caused by F. oxysporum f. sp. batatas. Trichoderma atroviride was registered as a bio-fungicide to control rice 'Bakanae' by seed or nursery-box treatment.

6. Conclusion

Fusarium is a large genus of imperfect fungi and numerous species are important plant pathogens. *Fusarium oxysporum* all strains are saprophytic, based on phenotypic and genetic characterize the strains and showed the diversity. Interactions between pathogenic and non-pathogenic strains result in the control of the disease. Complex fusarium species are the economic importance of their pathogenic/nonpathogenic activity. The development of molecular-based genomic tools to study in relation and its characterization. As 106 *formae speciales* have been clearly described within *F. oxysporum*. The pathogenic activity of *F. oxysporum* on plants of economic interest, many wild plants also infect by new *formae speciales*. Greater diversity in *F. oxysporum* and within *formae speciales* may be revealed over time by using new plant genotypes resulting from breeding. Fusarium species has a significant role in socio-economic and international trade for food security as ability to destroy crop yields and contaminate plant products. New populations of *Fusarium* pathogens will continue to emerge through micro-evolution and the invention of exotic pathogens. Need the research on the biology of the fungus to determine their role of non-host crops and length of survival of chlamydospores in soil.

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Author details

Amar Bahadur College of Agriculture, Tripura, Lembucherra, Agartala, India

*Address all correspondence to: amarpatel44@rediffmail.com; agcollege07@gmail.com

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References

[1] Gordon TR. *Fusarium oxysporum* and the Fusarium Wilt Syndrome. Annual Review of Phytopathology. 2017;55: 23-39

[2] Martyn RD. Fusarium Wilt of Watermelon: 120 Years of Research. In Horticultural Reviews: Volume 42; John Wiley & Sons, Inc.: Hoboken, NJ, USA, 2014; pp. 349-442.

[3] Zhou XG, Everts KL, Bruton BD. Race 3, a New and Highly Virulent Race of *Fusarium oxysporum* f. sp. *niveum* Causing *Fusarium* Wilt in Watermelon. Plant Disease. 2010;**94**:92-98

[4] Bertoldo C, Gilardi G, Spadaro D, Gullino ML, Garibaldi A. Genetic diversity and virulence of Italian strains of *Fusarium oxysporum* isolated from *Eustoma grandiflorum*. European Journal of Plant Pathology. 2015;**141**:83-97

[5] Kalagatur NK, Kamasani JR, Mudili V. Assessment of Detoxification Efficacy of Irradiation on Zearalenone Mycotoxin in Various Fruit Juices by Response Surface Methodology and Elucidation of Its in-vitro Toxicity. Frontiers in Microbiology. 2018;**9**

[6] Nelson PE, Toussoun TA. Cook RJ. Fusarium: Diseases, Biology and Taxonomy. Pennsylvania State University, University Park; 1981

[7] Burgess LW. General Ecology of the Fusaria. In: Nelson PE, Toussoun TA, Cook RJ, editors. Fusarium: diseases, biology and taxonomy. University Park, PA, USA: The Pennsylvania State University Press; 1981. pp. 225-235

[8] Snyder WC, Hansen HN. The species concept in *Fusarium*. American Journal of Botany. 1940;**27**:64-67

[9] Xiong W, Zhan A. Testing clustering strategies for metabarcoding-based investigation of communityenvironment interactions. Molecular Ecology Resources. 2018;**18**:1326-1338

[10] LeBlanc N, Essarioui A, Kinkel L,
Kistler HC. Phylogeny, Plant Species,
and Plant Diversity Influence Carbon
Use Phenotypes Among Fusarium
Populations in the Rhizosphere
Microbiome. Phytobiomes J. 2017;1:
150-157

[11] Dean R, van Kan JAL, Pretorius ZA, Hammond-Kosack KE, Di Pietro A, et al. The top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology. 2012;**13**:414-430

[12] Fisher MC, Henk DA, Briggs CJ, Brownstein JS, Madoff LC, McCraw SL, et al. Emerging fungal threats to animal, plant and ecosystem health. Nature. 2012;**484**(7393):186-194

[13] Michielse CB, Rep M. Pathogen profile update: *Fusarium oxysporum*.Molecular Plant Pathology. 2009;**10**(3): 311-324

[14] Keinath A.P, Hassell RL, Control of Fusarium Wilt of Watermelon by Grafting onto Bottlegourd or Interspecific Hybrid Squash Despite Colonization of Rootstocks by Fusarium. Plant Disease 2014;, 98: 255-266.

[15] Egel DS. Martyn RD. Plant Health Instr: Fusarium wilt of watermelon and other cucurbits; 2013

[16] Lü G, Guo S, Zhang H, Geng L, Song F, Fei Z, et al. Transcriptional profiling of watermelon during its incompatible interaction with *Fusarium oxysporum* f. sp. *niveum*. European Journal of Plant Pathology. 2011;**131**: 585-601

[17] Martyn RD, Netzer D. Resistance to Races 0, 1, and 2 of Fusarium Wilt of Watermelon in Citrullus sp. PI-296341-FR. HortScience. 1991;**26**:429-432

[18] Desjardins AE. *Fusarium Mycotoxins: Chemistry*, *Genetics and Biology*. Am. Phytopathol. Society: St. Paul, MN; 2006

[19] Link HF. Observationes in ordines plantarum naturals. Dissetatio I. *Magazin Ges.* Nat. Freunde Berlin.1809;**3**:3-42

[20] Wollenweber HW, Reinking OA. Die Fusarien, ihre Beschreibung, Schadwirkung, und Bekämpfung. Berlin: Paul Parey; 1935

[21] Raillo A. *Fungi of the Genus* Fusarium. Moscow, USSR: Publ. State Agric. Lit; 1950

[22] Bilai VI. *The Fusaria* (*Biology and Systematics*). Acad. Sci. Ukr. SSR: Kiev, USSR; 1955

[23] Booth C. *The Genus* Fusarium. Commonw. Mycol. Inst: Kew, UK; 1971

[24] Gerlach W, Nirenberg H. *The Genus* Fusarium: *A Pictorial Atlas*. Berlin: Biol. Bundesanst. Land Forstwirtsch; 1982

[25] Nelson PE, Toussoun TA, Marasas WFO. *Fusarium Species: An Illustrated Manual for Identification*. Pa. State Univ. Press: University Park, PA; 1983

[26] Leslie JF, Zeller KA, Summerell BA. Icebergs and species in populations of *Fusarium*. Physiological and Molecular Plant Pathology. 2001;**59**:107-117

[27] Laurence MH, Walsh JL,
Shuttleworth LA, Robinson DM,
Johansen RM, et al. Six novel species of *Fusarium* from natural ecosystems in
Australia. Fungal Diversity. 2015;77:
349-366

[28] Aoki T, Smith JA, Mount LL, Geiser DM, O'Donnell K. *Fusarium* *torreyae* sp. nov, a pathogen causing canker disease of Florida torreya (*Torreya taxifolia*), a critically endangered conifer restricted to northern Florida and southwestern Georgia. Mycologia. 2013; 105: 312-319.

[29] Elmer WH, Marra RE. New species of *Fusarium* associated with dieback of *Spartina alterniflora* in Atlantic salt marshes. Mycologia. 2011;**103**:806-819

[30] Skovgaard KL, Rosendahl S, O'Donnell K, Nirenberg HI. *Fusarium commune* is a new species identified by morphological and molecular phylogenetic data. Mycologia. 2003;**95**: 630-636

[31] Aoki T, Vaughan MM,

McCormick SP, Busman M, Ward TJ, et al. *Fusarium dactylidis* sp. nov., a novel nivalenol toxin-producing species sister to *F. pseudograminearum* isolated from orchard grass (*Dactylis glomerata*) in Oregon and New Zealand. Mycologia. 2015; 107: 409-18.

[32] Edwards J, Auer D, de Alwis SK, Summerell BA, Aoki T, et al. *Fusarium agapanthi* sp. nov, a novel bikaverin and fusarubin-producing leaf and stem spot pathogen of *Agapanthus praecox* (African lily) from Australia and Italy. Mycologia. 2016;**108**:981-992

[33] Herron DA, Wingfield MJ, Wingfield BD, Rodas CA, Marincowitz S, Steenkamp ET. Novel taxa in the *Fusarium fujikuroi* species complex from *Pinus* spp. Studies in Mycology. 2015;**80**:131-150

[34] Lima CS, Pfenning LH, Costa SS, Abreu LM, Leslie JF. *Fusarium tupiense* sp. nov., a member of the *Gibberella fujikuroi* complex that causes mango malformation in Brazil. Mycologia. 2012;**104**:1408-1419

[35] O'Donnell K, McCormick SP, Busman M, Proctor RH, Ward TJ, et al. Marasas et al. 1984 "Toxigenic *Fusarium*

Species: Identity and Mycotoxicology" revisited. Mycologia. 2018;**27**:1058-1080

[36] Coleman JJ. The *Fusarium solani* species complex: ubiquitous pathogens of agricultural importance. Molecular Plant Pathology. 2016;**17**:146-158

[37] Wang H, Xiao M, Kong F, Chen S, Dou H, Sorrell T, et al. Accurate and Practical Identification of 20 Fusarium Species by Seven-Locus Sequence Analysis and Reverse Line Blot Hybridization, and an In Vitro Antifungal Susceptibility Study. Journal of Clinical Microbiology. 2011;**49**(5): 1890-1898

[38] Booth C. Perfect states (teleomorphs) of Fusanium species. In: Nelson PE, Toussoun TA, Cook RJ, editors. Fusarium: diseases, biology, and taxonomy. University Park: Pennsylvania State University Press; 1981. pp. 446-452

[39] Chimbekujwo IB. Frequency and pathogenicity of Fusarium wilts (*Fusarium solani* and *Fusarium equiseti*) of cotton (*Gossypium hirsutum*) in Adamawa. Nigeria. Revista de Biología Tropical. 2000;**48**(1):1-5

[40] Bacon CW, Yates IE. "Endophytic root colonization by *Fusarium* species: histology, plant interactions, and toxicity," in *Microbial Root Endophytes*, eds B. J. E. Schulz, C. J. C. Boyle, and T. N. Sieber (Heidelberg: Springer), 2006; 133-152.

[41] Garnica M, Nucci M. Epidemiology of fusariosis. *Curr.* Fungal Infect. Rep. 2013;. 7: 301-305.

[42] Windels CE. Fusarium. In: Singleton LL, Mihail JD, Rush CM, editors. Methods for research on soilborne phytopathogenic fungi. St Paul, MN, USA: American Phytopathological Society; 1992. pp. 15-128 [43] De Hoog GS, Guarro J, Gene J,Figueras MJ. Atlas of Clinical Fungi.2nd ed. Vol. 1. Utrecht, TheNetherland: Centraalbureau voorSchimmelcultures; 2000

[44] Gordon TR, Martyn RD. The evolutionary biology of *Fusarium oxysporum*. Annual Review of Phytopathology. 1997;**35**:111-128

[45] Puhalla JE. Classification of strains of *Fusarium oxysporum* on the basis of vegetative compatibility. Canadian Journal of Botany. 1985;**63**:179-183

[46] Skovgaard K, Nirenberg HI, O'Donnell K. Rosendahl S. Evolution of *Fusarium oxysporum* f. sp. *vasinfectum* races inferred from multigene genealogies. Phytopathology. 2001;**91**: 1231-1237

[47] Burgess LW, Knight TE, Tesoriero L, Phan HT. Diagnostic manual for plant diseases in Vietnam. ACIAR Monograph No. 129, ACIAR: Canberra 2008; 210 pp.

[48] O'Donnell K, Kistler HC, Tacke BK, Casper HH. Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of *Fusarium graminearum*, the fungus causing wheat scab. Proceedings of the National Academy of Sciences, USA. 2000;**97**:7905-7910

[49] Rosewich UL, Pettway RE, Katan T, Kistler HC. Population genetic analysis corroborates dispersal of Fusarium oxysporum f. sp. radicis lycopersici from Florida to Europe. Phytopathology. 1999;**89**:623-630

[50] Assigbetse KB, Fernandez D, Dubois MP, Geiger JP. Differentiation of *Fusarium oxysporum* f. sp. *vasinfectum* races on cotton by random amplified polymorphic DNA (RAPD) analysis. Phytopathology 1994; 84: 622-626

[51] O'Donnell K, Cigelnik E. Two divergent intragenomic rDNA ITS2 types within a monnophyletic lineage of the fungus Fusarium are non orthologous. Molecular Phylogenetics and Evolution. 1997;7:103-116

[52] Baayen RPO, Donnell K, Bonants PJM, Cigelnik E, Kroon LPNM, Roebroeck EJA, et al. Gene genealogies and AFLP analyses in the *Fusarium oxysporum* complex identify monophyletic and nonmonophyletic *formae speciales* causing wilt and rot disease. Phytopathology. 2000;**90**: 891-900

[53] O'Donnell K, Kistler HC, Cigelnik E, Ploetz RC. Multiple evolutionary origins of the fungus causing panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. Proceedings of the National Academy of Sciences, USA. 1998;**95**:2044-2049

[54] Hennequin C, Abachin E, Symoens F, Lavarde V, Reboux C, Nolard N, Berche P. Identification of Fusarium species involved in human infections by 28S rRNA gene sequencing. Journal of Clinical Microbiology. 1999;. 37: 3586-3589

[55] Lacmanova I, Pazlarova J, Kostelanska M, Hajslova J. PCR-based identification of toxigenic Fusarium species. Czech Journal of Food Science. 2009;**27**(2):90-94

[56] El-Kazzaz MK, El-Fadly GB, Hassan MAA, El-Kot GAN. Identification of some Fusarium spp. using molecular biology techniques. Egyptian Journal of Phytopathology. 2008;**36**(1-2):57-69

[57] Mui-Yun W. *Fusarium oxysporum* f. sp. *lycopersici* (Sacc.): PP728 Soil-borne Plant Pathogen Class Project. North Carolina State University. 2003.

[58] Armstrong GM, Armstrong JK. *Formae speciales* and races of *Fusarium oxysporum* causing wilt diseases. In: Nelson PE, Toussoun TA, Cook RJ, editors. Fusarium: disease, biology, and taxonomy. University Park, PA, USA: State University Press; 1981. pp. 391-399

[59] Garrett SD. Pathogenic rootinfection fungi. London, UK: Cambridge University Press; 1970

[60] Olivain C, Alabouvette C.
Colonization of tomato root by a nonpathogenic strain of *Fusarium oxysporum*. New Phytologist. 1997;137: 481-494

[61] Olivain C, Alabouvette C. Process of tomato root colonization by a pathogenic strain of *Fusarium oxysporum* f.sp. *lycopersici* discussed in comparaison to a non-pathogenic strain. New Phytologist. 1999;**141**:497-510

[62] Burgess LW, Summerell BA, Bullock S, Gott KP, Backhouse LW. Laboratory Manual for Fusarium Research. 3rd ed. Sydney, Australia: University of Sydney/Royal Botanic Gardens; 1994

[63] Summerell B, Salleh B, Leslie JF. A utilitarian Approach to Fusarium Identification. Plant Disease.2003;87(2):117-128

[64] Geiser DM et al. A DNA sequence database for identifying Fusarium.European Journal of Plant Pathology.2006;**110**:473-479

[65] Burgess LW, Bryden WL. Fusarium: a ubiquitous fungus of global significance. Microbiology Australia.2012:22-25

[66] Thrane U. FUSARIUM. Encyclopedia of Food Microbiology. 1999:901-906

[67] Edel-Hermann V, Lecomte C. Current status of *Fusarium oxysporum Formae Speciales* and races. Phytopathology. 2019;**109**:512-530

[68] Ramana MV, Nayaka SC, Balakrishna K, Murali HS, Batra HV. A novel PCR–DNA probe for the detection of fumonis in producing Fusarium species from major food crops grown in southern India. Mycology. 2012;**3**: 167-174

[69] Mudili V, Siddaih CN, Nagesh M, Garapati P, Naveen KK, Murali HS, et al. Mould incidence and mycotoxin contamination in freshly harvested maize kernels originated from India. Journal of the Science of Food and Agriculture. 2014;**94**:2674-2683

[70] Chandra NS, Udaya SAC, Reddy M.S, Niranjana SR, Prakash HS, Shetty HS, Mortensen CN. Control of *Fusarium verticillioides*, cause of ear rot of maize, by Pseudomonas fluorescens. Pest Management Science 2009; 65: 769-775.

[71] Bakker M.G, Brown DW, Kelly AC, Kim HS, Kurtzman CP, Mccormick SP, O'Donnell KL, Proctor RH, Vaughan MM, Ward TJ. *Fusarium mycotoxins*: A trans-disciplinary overview. Canadian Journal of Plant Pathology 2018; 40: 161-171.

[72] Lakshminarayanan K, Subramanian D. Is fusaric acid a vivotoxin? Nature. 1955;**176**:697-698

[73] Gaumann E. Fusaric acid as a wilt toxin. Phytopathology. 1957;**47**:342-357

[74] Pegg, G. Biochemistry and physiology of pathogenesis. In Fungal Wilt Diseases of Plants; Academic Press, Inc.: New York, NY, USA, 1981; 7: pp.
193-253, ISBN 0124644503

[75] Di X, Takken FLW, Tintor N. How Phytohormones Shape Interactions between Plants and the Soil-Borne Fungus *Fusarium oxysporum*. Frontiers in Plant Science. 2016;7

[76] Bruton BD, Fish WW, Zhou XG, Everts KLRP. Fusarium wilt in seedless watermelons. In Proceedings of the 2007 Southeast Regional Vegetable Conference, Savannah, GA, USA, 5-7 January 2007; pp. 93-98.

[77] Boughalleb N, Mahjoub M. El Frequency of *Fusarium oxysporum* f. sp. *niveum* and *F. solani* f. sp. *Cucurbitae* from Watermelon Seeds and Their Effect on Disease Incidence. Res. J. Parasitology. 2007;**2**:32-38

[78] Zhang M, Xu JH, Liu G, Yao XF, Li PF, Yang XP. Characterization of the watermelon seedling infection process by *Fusarium oxysporum* f. sp. *niveum*. Plant Pathol. 2015; 64: 1076-1084.

[79] Martyn RD, Vakalounakis DJ.
Fusarium Wilts of Greenhouse
Cucurbits: Melon, Watermelon, and
Cucumber. In Fusarium Wilts of
Greenhouse Vegetable and Ornamental
Crops; The American Phytopathological
Society: St. Paul, MN, USA, 2017; pp.
159-174, ISBN 978-0-89054-482-2.

[80] Agrios G. Plant Pathology. 5th ed. Cambridge, MA, USA: Academic Press; 2005

[81] Di Pietro A, Madrid MP, Caracuel Z, Delgado-Jarana J, Roncero MIG. *Fusarium oxysporum:* Exploring the molecular arsenal of a vascular wilt fungus. Molecular Plant Pathology. 2003;**4**:315-325

[82] Raaijmakers JM, De Bruijn I, Nybroe O, Ongena M. Natural functions of lipopeptides from Bacillus and Pseudomonas: more than surfactants and antibiotics. FEMS Microbiology Reviews. 2010;**34**:1037-1062

[83] Cawoy H, Mariutto M, Henry G, Fisher C, Vasilyeva N, Thonart P, et al. Plant defense stimulation by natural isolates of bacillus depends on efficient surfactin production. Molecular Plant-Microbe Interactions. 2014;**27**:87-100

[84] Chen XH, Koumoutsi A, Scholz R, Eisenreich A, Schneider K,

Heinemeyer I, et al. Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium Bacillus amyloliquefaciens FZB42. Nat.Biotechnol. 2007;**25**: 1007-1014

[85] Harman GE. Multifunctional fungal plant symbionts: new tools to enhance plant growth and productivity. The New Phytologist. 2011;**189**:647-649

[86] Kumar DP, D, A.P., Singh, R. K., Thenmozhi, R., Nagasathya, A., Thajuddin, N., et al. Evaluation of extracellular lytic enzymes from indigenous Bacillus isolates. J. Microbiol. Biotechnol. Res. 2012;**2**:129-137

[87] Parniske M. Arbuscular mycorrhiza: the mother of plant root endosymbioses. Nature Reviews. Microbiology. 2008; **6**:763

[88] Bonfante P, Genre A. Mechanisms underlying beneficial plantfungus interactions in mycorrhizal symbiosis. Nature Communications. 2010;**1**:48

[89] Lenoir I, Fontaine J, Lounès-Hadj Sahraoui A. Arbuscular mycorrhizal fungal responses to abiotic stresses: a review. Phytochemistry. 2016;**123**: 4-15

[90] Lopez-Aranda JM, Dominguez P, Miranda L, de los Santos, B., Talavera, M., Daugovish, O., et al. Fumigant use forsStrawberry production in Europe: the current landscape and solutions. Int. J. Fruit Sci. 2016;**16**:1-15

[91] Takken FLW, Rep M. The arms race between tomato and *Fusarium oxysporum*. Molecular Plant Pathology. 2010;**11**(2):309-314

[92] de Sain M, Rep M. The role of pathogen-secreted proteins in fungal vascular wilt diseases. International Journal of Molecular Sciences. 2015;**16**(10):23970-23993 [93] Ploetz RC. Fusarium Wilt of Banana. Phytopathology. 2015;**105**(12): 1512-1521

[94] Lin YH, Chen KS, Liou TD, Huang JW, Chang PFL. Development of a molecular method for rapid differentiation of watermelon lines resistant to *Fusarium oxysporum* f. sp. *niveum.* Bot. Studia. 2009;**50**:273-280

[95] Gerlach KS, Bentley S, Moore NY, Aitken EAB, Pegg KG. Investigation of Non Pathogenic Strains of *Fusarium oxysporum* for Suppression of Fusarium Wilt of Banana in Australia, 28. In: Alabouvette C, ed. Second International Fusarium Workshop. Dijon, France: INRA-CMSE, 1999; p 54.

[96] Fravel DR, Larkin RP. Reduction of Fusarium wilt of hydroponically-grow basil by *Fusarium oxysporum* strain CS-20. Crop Protection. 2002;**21**: 539-543

[97] Garibaldi A, Brunatti F, Gullino ML. Suppression of Fusarium wilt of carnation by competitive non pathogenic strains of Fusaria. Medical Fac Landbouww Rijksuniv Gent. 1986;**51**:633-638

[98] Mandeel Q, Baker R. Mechanisms involved in biological control of Fusarium wilt of cucumber with strains of nonpathogenic *Fusarium oxysporum*. Phytopathology. 1991;81:462-469

[99] Minuto A, Migheli Q, Garibaldi A. Evaluation of antagonistic strains of *Fusarium* spp. in the biological and integrated control of Fusarium wilt of cyclamen. Crop Protection. 1995;**14**: 221-226

[100] Magie RO. Fusarium disease of gladioli controlled by inoculation of corms with non-pathogenic Fusaria. Proceedings of the Florida State Horticultural Society. 1980;**93**:172-175

[101] Rouxel F, Alabouvette C, Louvet J. Recherches sur la résistance des sols aux

maladies. IV – Mise en évidence du rôle des Fusarium autochtones dans la résistance d'un sol à la *Fusariose vasculaire* du Melon. Annales de Phytopathologie. 1979;**11**:199-207

[102] Lemanceau P, Alabouvette C. Biological control of fusarium diseases by fluorescent Pseudomonas and non-pathogenic Fusarium. Crop Protection. 1991;**10**:279-286

[103] Tezuka N, Makino T. Biological control of Fusarium wilt of strawberry by nonpathogenic *Fusarium oxysporum* isolated from strawberry. Annals of Phytopathology Society of Japan. 1991;**57**:506-511

[104] Larkin RP, Hopkins DL,
Martin FN. Suppression of fusarium wilt of watermelon by nonpathogenic Fusarium oxysporum and other microorganisms recovered from a disease suppressive soil.
Phytopathology. 1996;86:812-819