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ORIGINAL PAPER

Isolation and Characterization of Fungi Associated with Dry Rot of Potato Tubers in Minya Governorate

Mousa T.A.A.[1], Galal A.A.[1], Farag F.M.[2]. Armanious H.A.H[1], Abdel-latif M.R.[1*]

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ABSTRACT

Potato is one of the world's most significant food crops. During storage and transportation, potato tuber dry rots result in substantial losses that reduce quality and marketable production. Tuber losses from dry rots during storage range from 6.35 to 25 % annually. Dry rots of potato tubers, Cara cv., were surveyed in four counties: Minya, Samalut, Abu Qurqas and Matay, belonging to Minya governorate. The disease was detected in all potato storages in the three counties under investigation. Minya county had the highest disease incidence and severity followed by Matay, however Abu Qurqas county had the lowest disease incidence and severity. Nine isolates (presented 75%) of *Fusarium* sp., and three (25%) of *Alternaria* sp. were isolated from naturally rotted tubers of Cara cv. collected from different potato stores. PCR identification of the most virulent isolates, *Fusarium* isolate No.F4 and isolate No.A10 of *Alternaria* confirmed that *Fusarium* isolates were *Fusarium oxysporum* (accession No. PV400667) whereas *Alternaria* isolate was *Alternaria alternata* (accession No. PV390825). All genotypes of potato under study were susceptible to infection with all the five isolates evaluated, showing different degrees of DI% and DS%. Cara genotype was the highest susceptible one, while Lady Rosetta was more resistant. At the same time, isolate (F3) of *F. oxysporum* induced the maximum DI and DS, while A10 isolate of *A. alternata* showed the least DI and DS% on Cara, Sifra and Sponta genotypes, whereas F4 isolate of *F. oxysporum* induced the lowest disease severity and incidence on Pran, Metro and Lady Rosetta genotypes. The ability of different isolates to infect tomato, pepper, eggplant, cotton, hibiscus, and okra differed according to the host under study. Except hibiscus, isolate F4 of *F. oxysporum* was able to infect all tested plants. Whereas isolate F3 infected tomato, pepper, and eggplant. While isolates F1 and F2 infected tomato only. Isolate A10 of *A. alternate* infected tomato and eggplant. Hibiscus plants showed more resistance to any of the tested isolates.

Keywords: Potato, *Fusarium oxysporum*, *Alternaria alternata*, host range, potato genotypes

***Correspondence: Marzouk R. Abdel-latif**
E-mail: mrzukabdellatif@yahoo.com
Thanaa A.A. Mousa[1]
https://orcid.org/0009-0008-9648-5271
Anwar A. Galal[1]
Hanaa A.H. Armanious[1]
Marzouk R. Abdel-latif[1]
https://orcid.org/0000-0002-4289-9945
1- Plant Pathology Department, Fac. Agric., Minia Univ., Egypt.
Farag M. Farag [2]
https://orcid.org/0000-0003-0181-8296
2- Plant Pathology Research Institute, Agricultural Research Center (ARC), Giza, Egypt.

INTRODUCTION

Potatoes (*Solanum tuberosum* L.) rank as the fourth most important food crop globally, following rice (*Oryza sativa* L.), wheat (*Triticum aestivum* L.), and maize (*Zea mays* L.) (Saber et al., 2013 and FAOSTAT, 2023). A significant non cereal food crop is indispensable to the world's food supply. In addition to being a reliable source of macronutrients like carbohydrates and dietary fiber, potatoes are also a reliable source of micronutrients like vitamins and minerals. It is a significant source of antioxidants (Liu *et al.*, 2022). Li *et al.*, (2022) reported that 359 million tons of potatoes were produced worldwide in 2020. As a vegetable and industrial product, over 85% of potatoes must be stored for three to six months, and the disease-related losses during storage are significant (Xue *et al.*, 2013 and Xue *et al.*, 2023). Post-harvest diseases can be caused by certain bacteria, viruses, and fungi (Erper *et al.*, 2022). Among these, *Fusarium* sp. infection of potato tubers can induce severe dry rot during storage, which lowers the marketable yield in addition to causing quality degradation. Every year, dry rot during storage causes tuber losses ranging from

6.25% to 25%, and damage to potato tubers can result in losses of up to 60% (Saber *et al.*, 2013 and Fan *et al.*, 2021). Potato dry rot, caused by various *Fusarium* species, poses a significant threat to potato production worldwide. This soil- and seed-dwelling disease affects crop establishment by hindering sprout development and leads to severe rotting in seed tubers as well as potatoes intended for consumption and processing during cold storage (Wang et al., 2020). The present the aimed to isolate and characterize the fungi associated with dry rot of potato tubers.

MATERIALS AND METHODS

Survey of potato dry rot

Potato dry rots of cultivar Cara were assayed in January along two years, 2021 and 2022. One thousand eight hundred tubers of potato were randomly selected from potato stores, in 6 villages belonging to four counties, *i.e.* Al Birjayah, Tukh Al khayl and Bihdal **(** Minya county**)**, Soultan Hassan (Abu Qurqas county), Al Bayahu (Samalut county) and Kom El-Basal (Matay county), Minya Governorate. Samples from each village were put singly into sterile paper bags and brought to the laboratory of Pl. Pathol. Dept, Fac. Agric., Minia Univer. The diseased number of tubers and the disease severity of rotted tubers were assayed. Calculating disease incidence percentages (DI, %) was carried out according to the following formula:

DI (%) = (No. of rooted tubers/ The total no. of tubers) x 100.

Calculating of disease severity (DS, %) was carried out according a scale from 0 - 4 grades, which 0 = healthy tubers, 1 = 1-25% infection, 2 = more than 25-50% infection, 3 = more than 50-75% infection and 4 = more than 75-100 % infection, to assay the DS% according to the formula adopted by Hanounik (1986) as follows:

DS (%) = [Σ (NCC x CR)/ NTC x MSC] x100

Whereas: NCC= No. of potato tubers in each class rate , NTC= No. of total potato tubers, CR = Class rate and MSC= Maximum disease severity class rate.

Isolation of pathogen (s) associated with rotten potato tubers

Naturally infected potato tubers of the cultivar 'Cara' exhibit characteristic dry rot symptoms were washed under running tap water then air-dried, surface sterilized with 1% sodium hypochlorite ($NaOCl_3$) for 2 minutes, next washed 3 times in sterilized water, and dried with sterilized filter paper, then were cut into small segments (0.5-1.0 cm - size). Four sterilized segments of potato were placed in Petri plates holding PDA medium supplemented with Cefriaxone (100 mg\L, Sandoz, Egypt) as bactericide agent. Petri dishes were incubated at 25ºC for 7 days. For pure cultures, single spore method was applied to purify the obtained fungal colonies. The associated fungal colonies were transported into new PDA plates. Pure cultures were maintained on PDA slants at 4ºC for further analysis. The purified fungal isolates were identified microscopically based on their morphological characteristics as previously described by Ellis (1971), Nelson *et al.* (1983), Agarwal (1985), Booth (1985), Green *et al*., (2001), Leslie and Summerell (2006), Mangala *et al*., (2006) and Sharma and Ratnoo (2019)., then confirmed by Moubasher Mycological Center, Faculty of Science, Assiut University.

Frequency of fungal isolates associated with potato dry rot

The frequency of isolated fungi was calculated using the following formula: Frequency (%) = (Number of samples in which a particular fungus appears / Total number of samples) × 100.

Pathogenicity test

Pathogenicity tests of the isolated fungi were conducted in the Laboratory of Pl. Pathol. Dept., Faculty of Agriculture, Minia University in February 2021. Healthy potato tubers (cv. Cara) were tested in this study. Uniformed tubers (5-6 cm in diameter) and weight (85-100 grams) were washed by tap water to remove the attached soil, surface sterilized by $NaHCl_3$ (1%) for 2 minutes, rinsed three times by sterilized water (Lui and Kushalappa, 2002), then dried using sterilized filter papers. A sterile cork borer (5 mm in diameter and 1 cm in depth) was used to injure the tubers, and each one was aseptically infected in the holes using a disk

(5 mm in diameter) removed from the edge of the 7-day-old test tube. Sterile cork borer (5 mm in diameter and 1 cm in depth) was used to injure the tubers, and a disk (5 mm in diameter) removed from the edges of the 7-day-old of *Fusarium* sp. or *Alternaria* sp. cultures was used to individually inoculate each tuber in the prepared holes under aseptic conditions.. The check control was a set of tubers infected with PDA disks free of pathogens. For every fungal isolate that was tested, four tubers served as a replicate. Following Lui and Kushalappa's (2002) approach, the inoculated potato tubers were wrapped in paper bags and incubated for 10–14 days at 25 ± 1°C in the dark.

Disease assessment:

The tested potato tubers were sliced through the inoculation location at the conclusion of the incubation period, and DI% and DS% measurements were made of the breadth and depth of the rotten area as described before.

Molecular identification of potato dry rot pathogens

Among the twelve isolates, four of *Fusarium* sp. (F1 - F4) and one of *Alternaria* sp. (A10) were chosen on the basis of their pathogenic ability to represent the most aggressive isolate of each tested pathogen and used in further study. The most pathogenic fungal isolates F1, F2, F3, F4 and A10 were subjected for molecular identification. The fungal isolates were grown in sterile Petri plates containing autoclaved PDA medium and incubated for 7 days at 25±1°C. Cultures were sent to the Molecular Biology Research Unit, Cairo University, Egypt for DNA extraction using Patho-gene-spin DNA/RNA extraction kit provided by Intron Biotechnology Company, Korea. Fungal DNA samples were sent to SolGent Company, Daejeon, South Korea for polymerase chain reaction (PCR) and rRNA gene sequencing. PCR was performed using internal transcribed spacer (ITS1) (forward) and ITS4 (reverse) primers which were incorporated in the reaction mixture (Kim *et al*., 2024). Primers used have the following sequences: ITS1 (5- 'TCC GTA GGT GAA CCT GCG G - 3'), and ITS4 (5'- TCC TCC GCT TAT TGA TAT GC -3'). The purified PCR product (amplicons) was sequenced with the same primers with the incorporation of ddNTPs in the reaction mixture (White *et al*., 1990). The obtained sequences were analyzed using the Basic Local Alignment Search Tool (BLAST) from the National Center of Biotechnology Information (NCBI) website. Phylogenetic analysis of sequences was done with the help of MegAlign (DNA Star) software version 5.05 (Moghadam and Hosseinzadeh, 2013).

Response of different genotypes of potato to dry rot pathogens

This experiment was carried out to find out the most susceptible genotypes to the infection with the pathogen isolates obtained from rotted potato tubers under greenhouse conditions. Four pathogenic isolates of *Fusarium oxysporum* and an isolate of *Alternaria alternata* (designated as F1, F2, F3, F4 and A10, respectively) were tested. Pot experiment was carried out in the open experimental field of Plant Pathol. Dept., Fac. Agric., Minia University. In this study, surface sterilized apparently healthy potato tubers of Cara, Pran, Metro, Sifra, Spunta and Lady Rosetta genotypes were sown in previously dis-infected clay pots (30 cm in diameter), filled with disinfested Nile: sandy, 1:1V/V soil, previously individually inoculated with the different pathogens each alone during winter-spring seasons of 2022. Before planting, tested genotype tubers were surface sterilized by soaking them in a solution of sodium hypochlorite (2%) for two minutes. This eliminated the possibility of unintentional infection with saprophytic rotting bacteria or fungi. They were then repeatedly washed with sterile water.

Fungal inoculum. Preparation and soil infestation procedure:

Fungal isolates were cultured on potato dextrose agar (PDA) in 9 cm diameter Petri dishes and incubated in the dark at 25 ± 1 °C for 7 days. To prepare inocula, 150 g of autoclaved barley grains were mixed with 200 ml of water in 500 ml Erlenmeyer flasks. Each flask was inoculated with 5 mm discs

cut from the actively growing margins of 7-day-old PDA cultures. The inoculated flasks were incubated at 25 ± 1 °C for 15 days. After incubation, the inoculum was used to artificially infest soil. Soil infestation was carried out 7 days prior to planting by thoroughly mixing each fungal isolate into the soil at a concentration of 2% (w/w). The inoculum had been previously standardized to contain 4×10^5 conidia/ml. After infestation, the soil was irrigated daily until planting. For each treatment, five replicate pots were used, with one tuber planted per pot. Control pots received sterilized, un-inoculated barley grain medium only. All pots were irrigated as needed. Plants were regularly monitored for disease symptoms, with final observations recorded 90 days after planting. The harvested tubers of each genotype were collected, and fifteen uniformed tubers were randomly chosen and the percentage of infection and rot severity were calculated as mentioned before.

Host range of the potato dry rot pathogens

The pathogenic isolates of *Fusarium oxysporum* and *Alternaria alternata* were evaluated against six plant species, *e.g.*,Tomato (*Solanum lycopersicum*, cv. F1 023), Pepper (*Capsicum annuum*, cv. Balady), Eggplant (*Solanum melongena*, cv. Classic), Cotton (*Gossypium* sp., cv. Giza 95), Hibiscus (*Hibiscus sabdariffa*, cv. Balady), and Okra (*Abelmoschus esculentus*, cv. Balady). The tuber seeds of different hosts were surface sterilized using 2% NaHCl3 solution for 3 minutes, followed by three rinses with sterile distilled water to remove any residual disinfectant. Disinfected seeds were sown in sterilized Nile loamy soil previously infested individually with different pathogens. Inoculum preparation and soil infestation were carried out as described before in the experiment. Thirty days post-inoculation, wilt and root rot symptoms were carefully examined. The percentage of wilted plants and disease severity were calculated. A disease index was used to evaluate disease severity of wilt following to Jiménez-Fernández *et al.* (2013) with minor modification using a scale (0 to 4) based on root rot or leaf discoloration as follows: 0 = No symptoms (healthy), 1 = Yellowing on less than (25%) of the plants, 2= Yellowing on (25- 50%) of the plants, 3 = Yellowing on (75%) of the plants with root rot and 4 = Over 75 % of the plants with wilted and plant death. Disease severity (DS%) was calculated as mentioned before under pathogenicity tests using the following formula: Disease severity index (DSI) = (Σ d/ d max x N) x 100. where "d" = the disease rating possible, and "N" = the total number of plants.

Statistical analysis:

Least significant difference (LSD) values at $P< 0.05$ were determined to test the variants among treatments (Gomez and Gomez, 1984).

RESULTS

Survey of tuber dry rot of potato in Minya governorate:

A survey on dry rot disease was carried out in potato stores of 6 villages belonging to Abu-Qurqas, Minya, Samalut and Matay during 2021 and 2022. Table (1) shows that potato dry rot was found in all potato stores of all tested villages with different degrees. The highest DI% and DS% were recorded in Al Birjayah village (25 and 31.7% DI % and 16.9 and 21.2% DS% during 2020-2021), respectively. Followed by Kom El-Basal (18.3 and 21.9% DI% and 12.6 - 17.1% DS% at the first and the second seasons, respectively. The lowest disease incidences of 8.3 and 10.5% and severity (4.3-5.8%) were recorded in Soultan Hassan village.

Table (1): DI,% and DS,% of potato dry rot in El-Minya Governorate

Districts	*Villages	DI (%)		DS (%)	
		2021 season	2022 season	2021 season	2022 season
Abu Qurqas	S.H	8.3	10.5	4.3	5.8
EL-Minya	AL.Bi	25.0	31.7	16.9	21.2
	T.A	11.1	15.0	5.1	7.2
	B.	12.2	15.8	6.5	7.9
Samalut	AL.B	16.7	17.8	10.4	13.2
Matay	K.EL	18.3	21.9	12.6	17.1

*Villages;S.H=SoultanHassan,AL.Bi=Al Birjayah, T.A= Tukh Al khayl, B.= Bihdal, AL.B= Al Bayahu, and K.EL= Kom El-Basal

Frequency of fungi associated with potato dry rots:

Twelve fungal isolates were obtained from rotted tubers of potato. Fungi belonging to genera, *Fusarium* and *Alternaria* were isolated from potato dry rotted tubers (Table 2). The results indicated that *Fusarium* sp. was the dominant one, representing 75 % of the isolated fungi, whereas *Alternaria* sp. represented (25%) in this respect**.**

Table (2): Frequency of isolated fungi which associated with potato dry rot

Isolated fungi	No. of fungal isolates	Frequency (%)
***Fusariaum* sp.**	9	75
***Alternaria* sp.**	3	25
Total	12	100

Pathogenicity tests:

Data presented in Table (3) show that all the isolated isolates were able to infect potato tubers (Cara cv.) with different degrees of disease incidence and disease severity. The DI% and DS% ranged between 20 - 100 % and 10 - 65.0%, respectively, depending on the pathogen isolate. *Fusarium* sp. isolates were more aggressive than *Alternaria* sp. isolates, inducing 68.15 and 32.59% DI % and DS%, on the average respectively, while *Alternaria* isolates induced 57.78 and 27.22% DI% and DS%, respectively. Isolates F1, F2, F3 and F4. caused the highest disease incidence and severity (100 DI% and 40.00 – 63.33 DS%). Followed by isolate A10 of *Alternaria* sp., which caused 83.30 and 43.33% DI% and DS%, respectively.

Table (3): Pathogenicity test of Fungal isolates on potato tubers, Cara cv.

Fungi	Code of isolates	DI (%)	DS (%)
***Fusarium* sp.**	F1	100.00	40.00
***Fusarium* sp.**	F2	100.00	45.00
***Fusarium* sp.**	F3	100.00	65.00
***Fusarium* sp.**	F4	100.00	63.00
***Fusarium* sp.**	F5	40.00	14.17
***Fusarium* sp.**	F6	60.00	16.67
***Fusarium* sp.**	F7	20.00	10.00
***Fusarium* sp.**	F8	50.00	20,00
***Fusarium* sp.**	F9	43.00	19.17
Mean		68.00	32.59
***Alternaria* sp.**	A10	83.00	43.33
***Alternaria* sp.**	A11	30.00	15.00
***Alternaria* sp.**	A12	60.00	23.33
Mean		57.78	27.22
Control		00.00	00.00

Molecular identification of pathogenic isolates

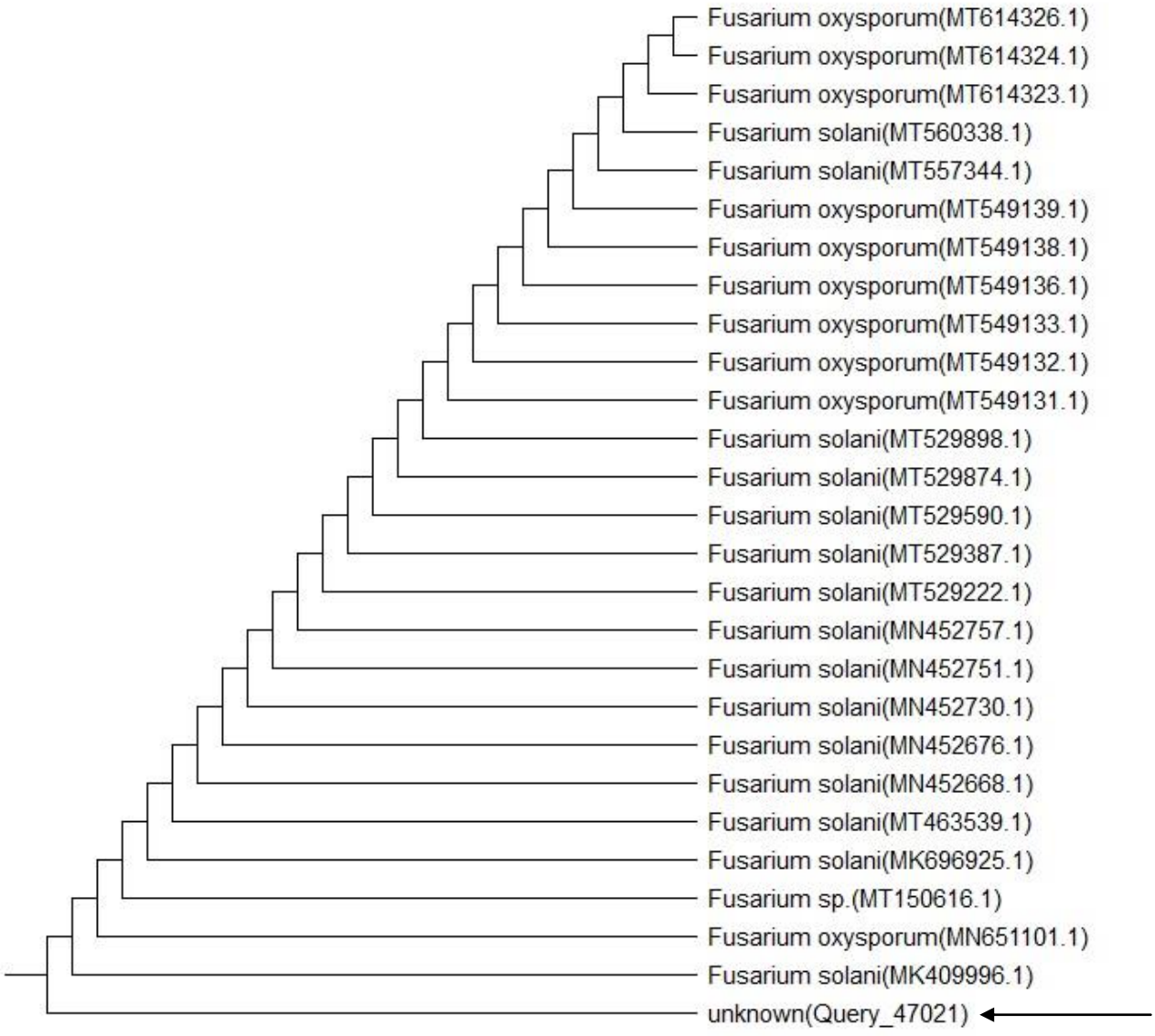
Isolates which previously were morphologically identified as *Fusarium* sp. (four isolates, 1- 4), and *Alternaria* sp. (one isolate), were further confirmed by molecular identification of the ITS region as *F. oxysporum* and *A. alternata* (Table 2). Four strains with 99% bootstrap support were found to be closely nested to *F. oxysporum* strains in the neighbor joining trees of the ITS region, and to strain of *A. alternate* with 100% bootstrap support (Fig. 1 and 2 respectively). The ITS sequence of F4 and A10 were deposited at the GenBank with the accession Nos. PV400667 and PV390825.

Response of different potato genotypes to the tuber dry rot pathogens

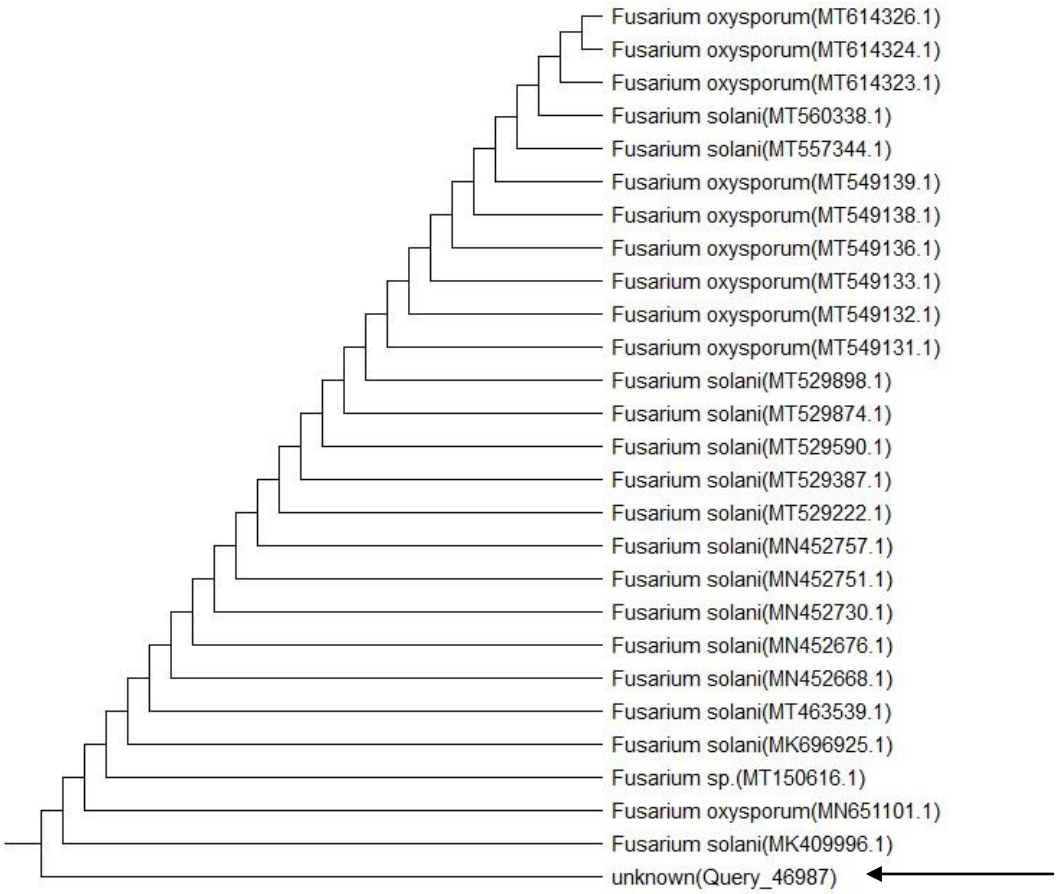
Pot experiment was conducted in 2022 to the response of 6 genotypes of potato to different isolates of *F. oxysporum* (F1, F2, F3 and F4) and A10 isolate of *A. alternate* which were the highest virulent isolates. Data in Figures (3-6) show that all genotypes under investigation were susceptible to all five isolates. Disease incidence ranged between 11.1 - 60%, and DS% was ranged between 6.1 - 36.1%. Cara genotype was the highest susceptible one, showing 51.56% DI and 25.66% DS, while Lady Rosetta was more resistant (19.12 and 8.98% DI and DS, respectively). Isolate F3 induced the maximum DI and DS (39.25 and 17.58%), respectively. While A10 isolate of *A. alternata* showed the least DI and DS%, (23.33 and 10.0) on Cara, Sifra and Sponta genotypes, while F4 of *F. oxysporum* caused the lowest disease severity and incidence on Pran, Metro and Lady Rosetta genotypes.

Response of some plants to infect pathogens which caused tuber dry rot of potato

Pot experiment was conducted to investigate response of tomato, pepper, eggplant, cotton, hibiscus, and okra to infection with *F. oxysporum* (isolates F1, F2, F3 and F4) and *A. alternata* (isolates A10). Data in Figures (7and 8) show that, except hibiscus, all tested plants were susceptible to infection by isolate F4, whereas isolate F3 infected tomato, pepper and eggplant. While mean isolates F1 and F2 infected tomato alone. Isolate A10 of *A. alternate* infected tomato and eggplant All tested isolates of *F. oxysporum* and *A. alternata* infected tomato plants causing DI% (13.3- 53.3%) and DS% (6.7-40%). Isolate F4 of *F. oxysporum* caused the highest DI and DS% on tomato plants (53.3 and 40%, respectively, while A10 of *A. alternata* induced the lowest DI and DS% (13.3 and 6.7%, respectively). Also, *F. oxysporum* isolate F3 was more aggressive on eggplant (causing 26.7% DI and 13.3% DS) than tomato (caused 20% and 10% DI and DS , respectively). Hibiscus plants were more resistance to any of the tested isolates.



(F1)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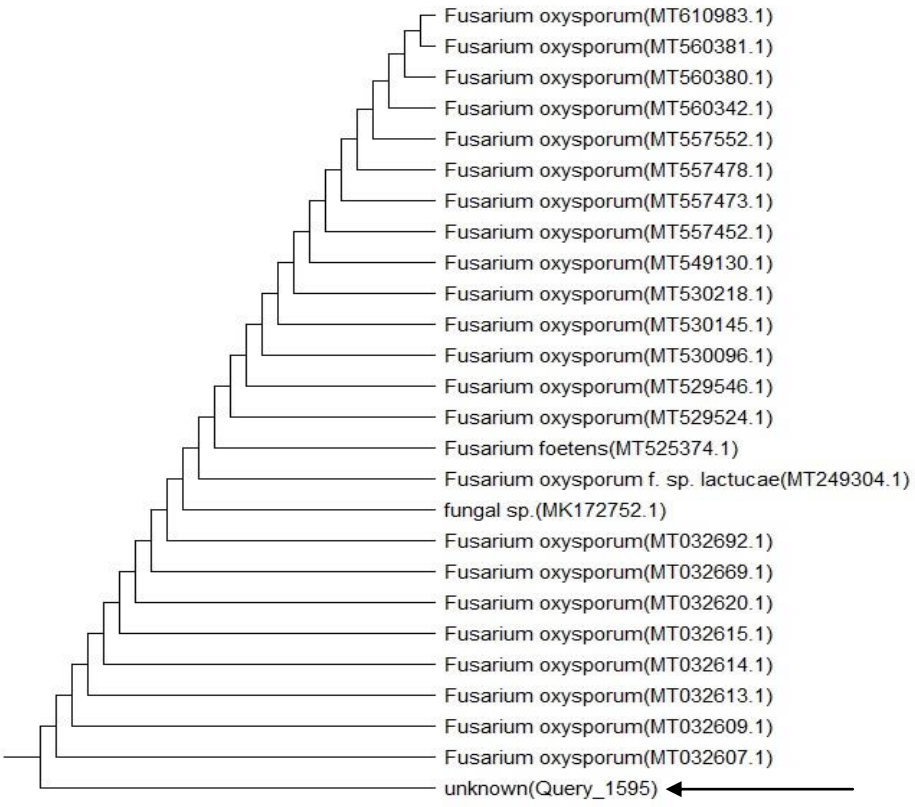
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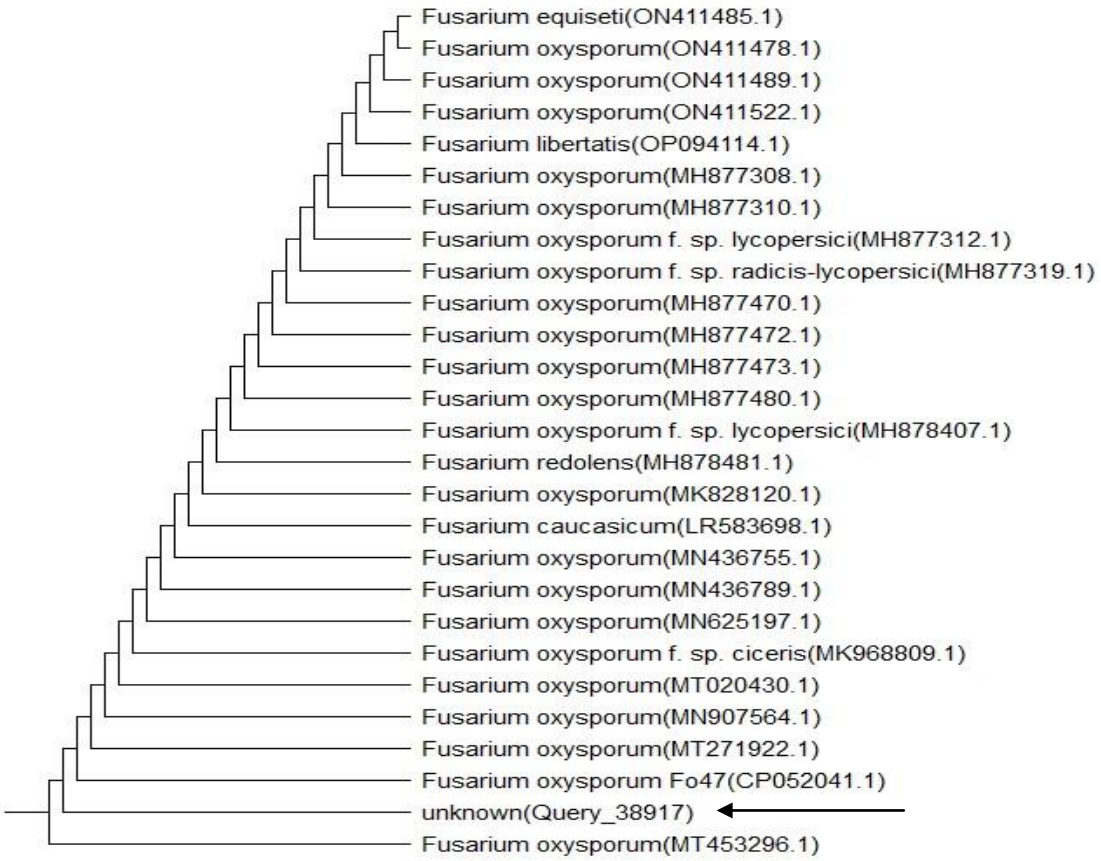
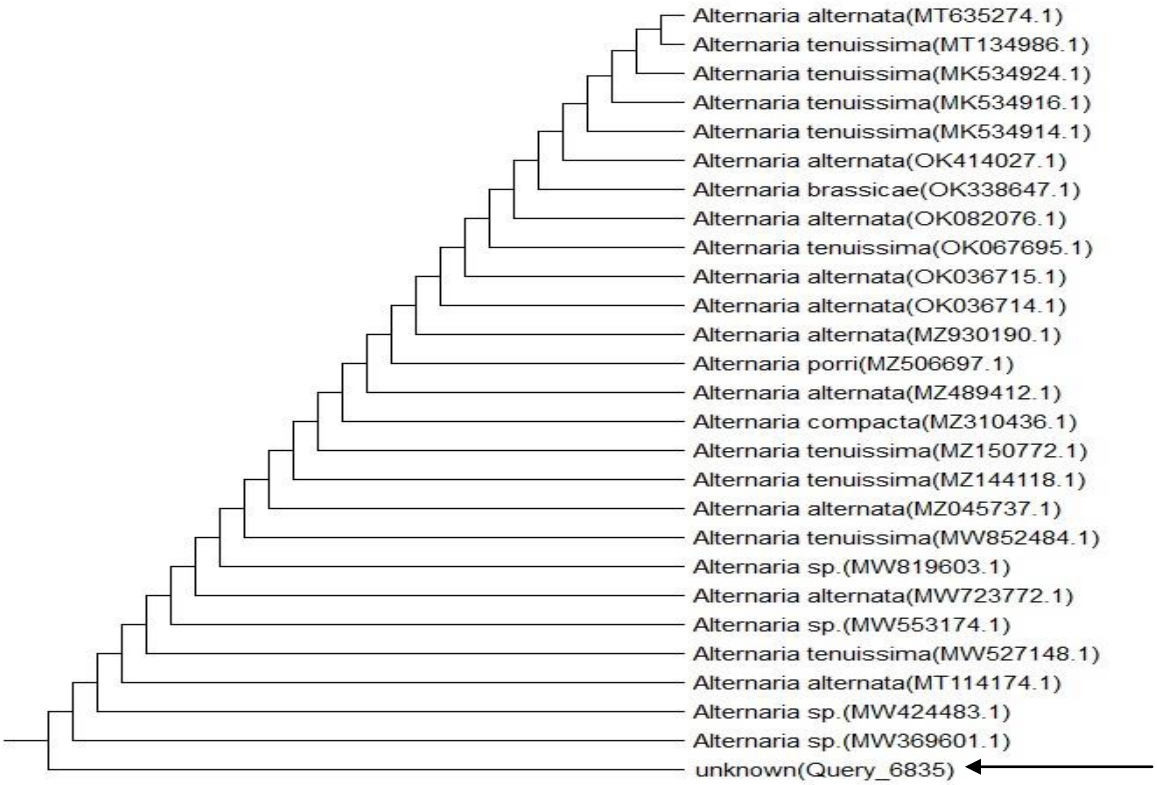
(F3)



(F4)

Fig. 1. ITS sequences are used to build the potato *Fusarium oxysporum* phylogenetic trees, (four isolates, F1- F4).



(A10)

Fig. 2. ITS sequences are used to build the potato *Alternaria alternata* phylogenetic tree.

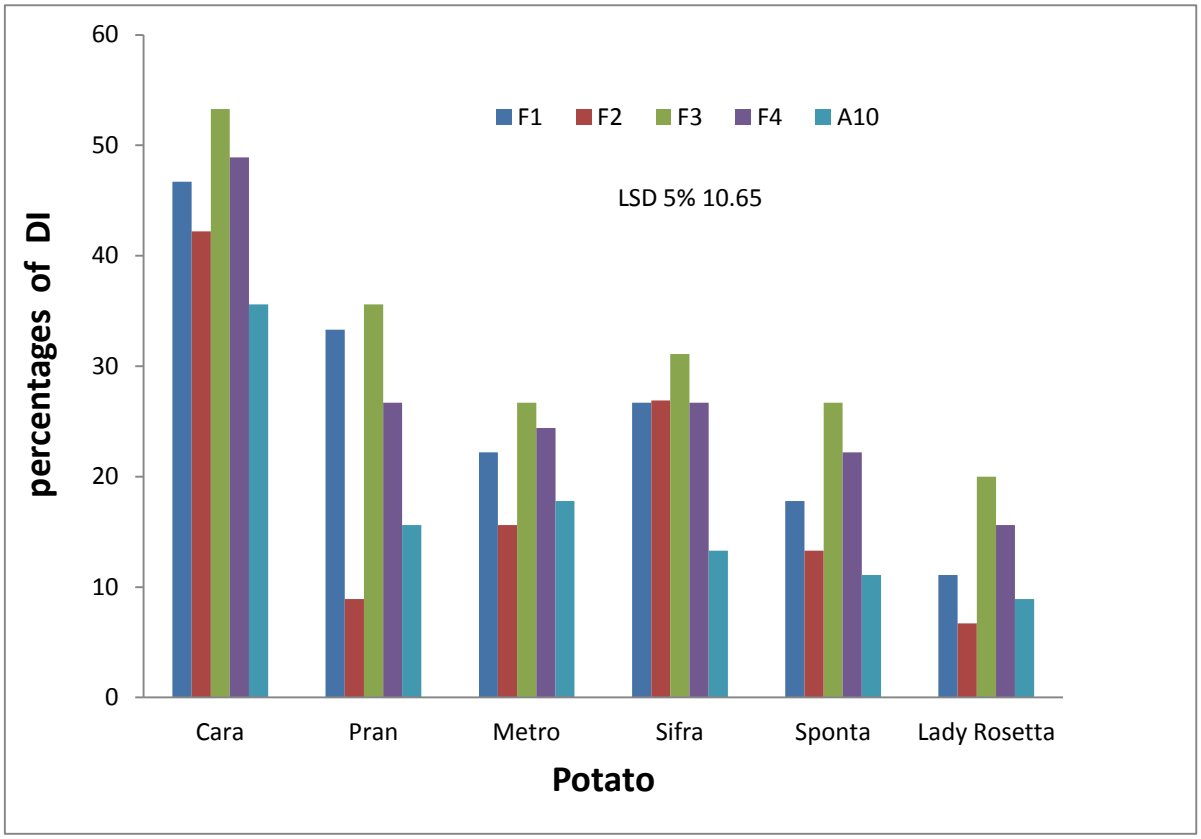


Fig. 3. Response of potato genotypes to infection (disease incidence %) with the tuber dry rot pathogens *F. oxysporum* (F1,F2,F3,F4) and *A. alternata* (A10) in 2022 season.

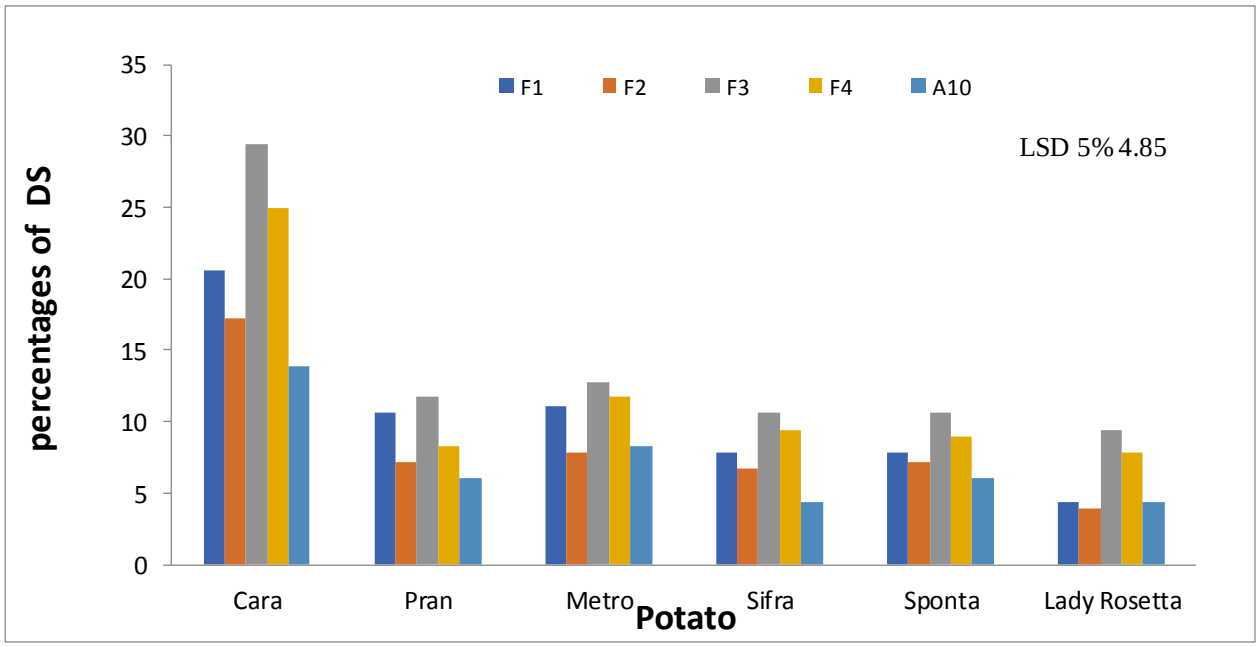


Fig. 4. Response of potato genotypes to infection (disease severity %) with the tuber dry rot pathogens *F. oxysporum* (F1,F2,F3,F4) and *A. alternata* (A10) infection at 2022season.

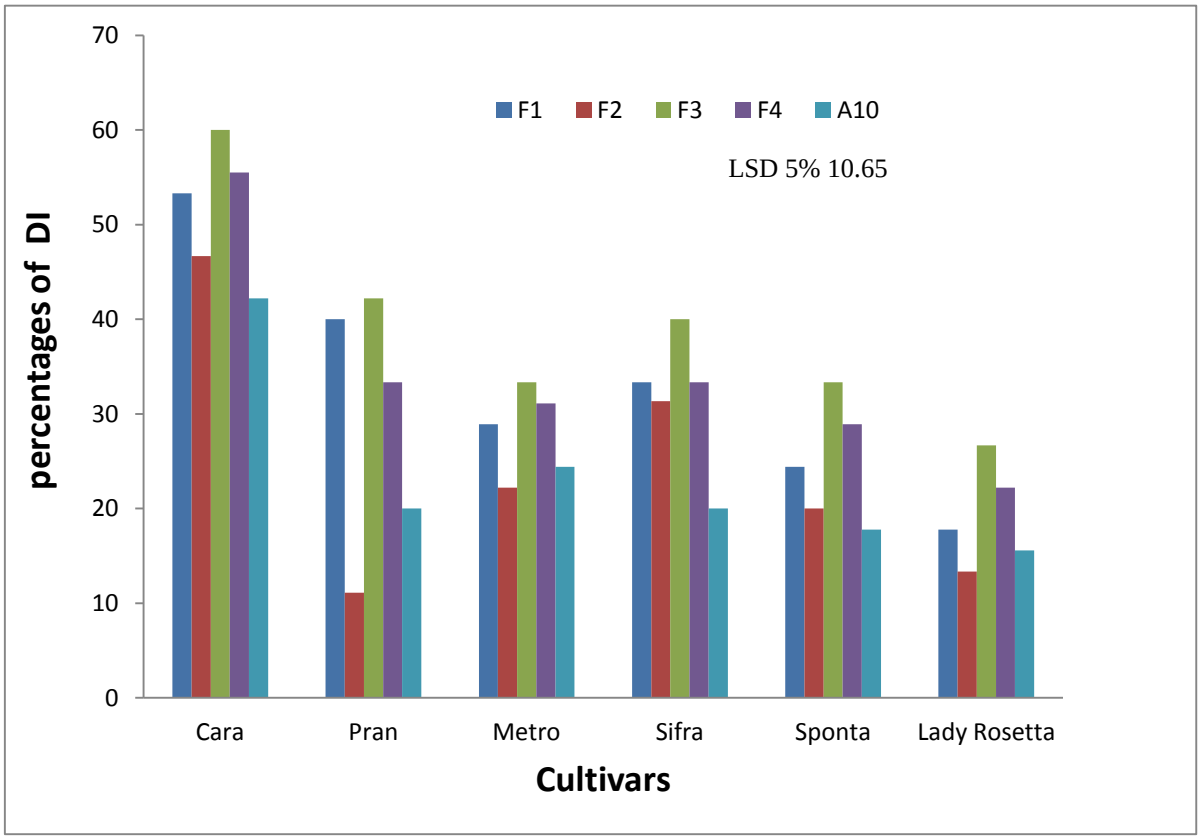


Fig. 5. Response of potato genotypes to infection (disease incidence %) with the tuber dry rot pathogens *F. oxysporum* (F1,F2,F3,F4) and *A. alternata* (A10) in 2023 season

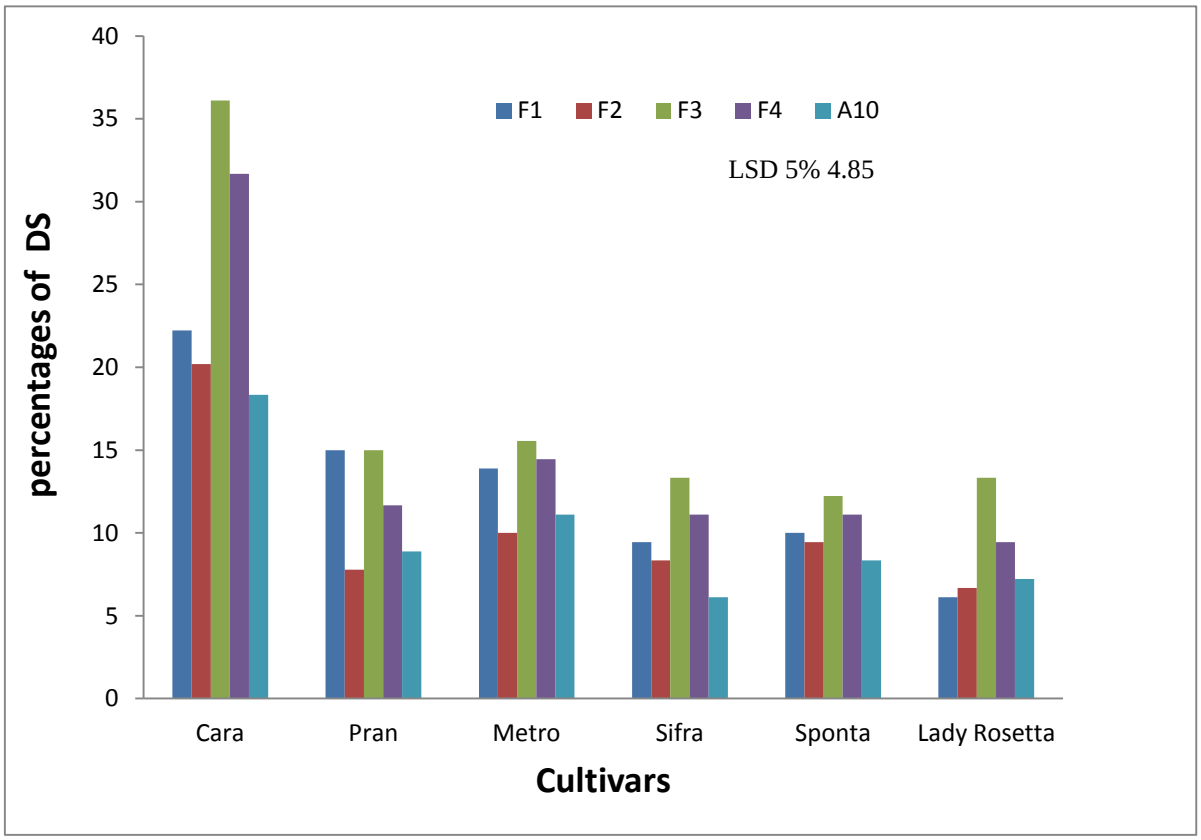


Fig. 6. Response of potato genotypes to infection (disease severity %) with the tuber dry rot pathogens *F. oxysporum*(F1,F2,F3,F4) and *A. alternata*(A10) infection at 2023 season.

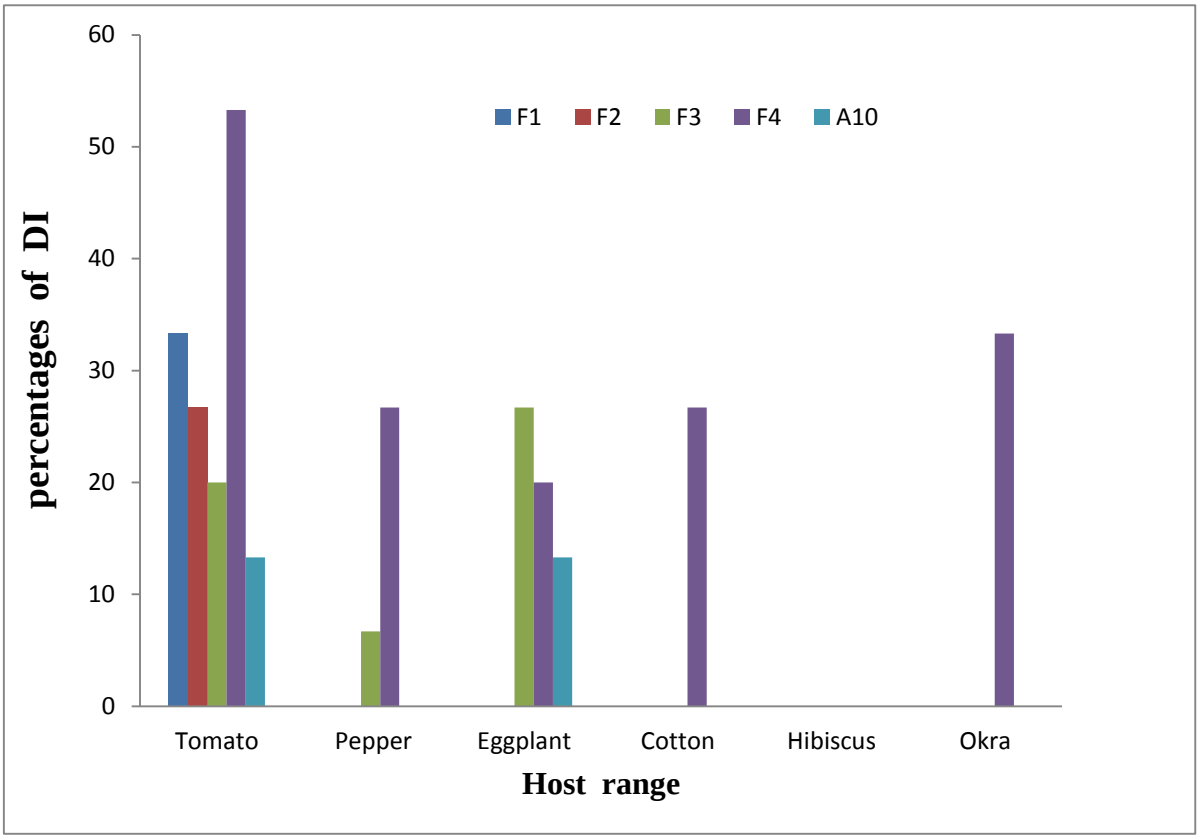


Fig. 7. Host range of various plant species to infection (disease incidence %) by dry rot of potato tubers isolates F1, F2, F3, F4 and A10.

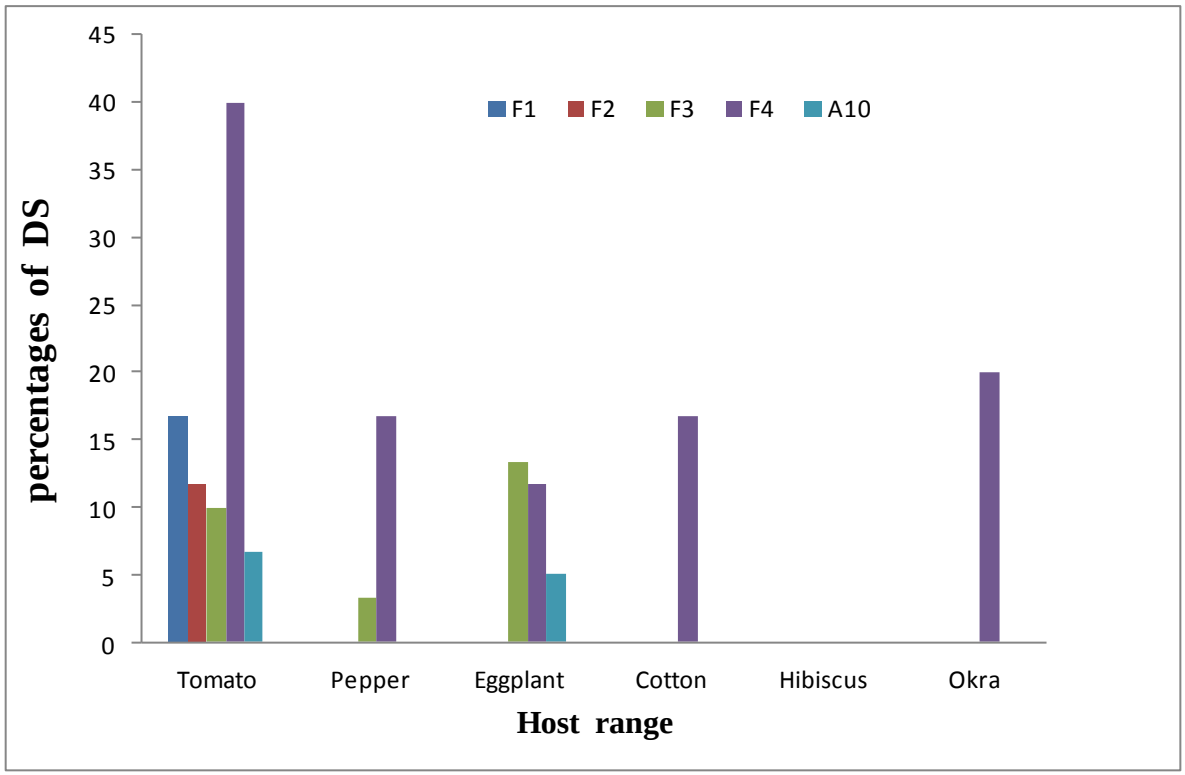


Fig. 8. Host range of various plant species to infection (disease severity %) by dry rot of potato tuber isolates F1, F2, F3, F4 and A10.

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DISCUSSION

Potato (*Solanum tuberosum*), a member of the family *Solanaceae*, is ranked as the world's fourth most important food crop after rice, wheat, and maize. However, soil-borne diseases such as dry rot, root rot, blackleg, and black scurf pose serious threats to potato production. These diseases are particularly severe in areas where potatoes are continuously cultivated, creating a bottleneck that limits crop productivity and sustainability. Potato is able to attack with several soil borne pathogens such as *F. oxysporum*, *F. oxysporum* f.sp. *tuberosi*, *F. solani* and *F. sambucinum*, *F. moniliforme*, *F. avenaceum*, *F. tricinctum*, *Verticillium nonalfalfae*, *V. albo-atrum*, *Vdahliae.*,*V. nubilum*, *V. nigrescens* and *Vtricorpus.* (Wang *et al*., 2014-a and b and Azil *et al*., 2021,) which reduce both the yield and tuber quality of potatoes. Our investigation showed that the disease was found in all locations and potato stores under investigation in Minya Governorate with different degrees of DI,% and DS, %. The highest DI% and DS% were recorded in Al Birjayah village which belonging to Minya county, followed by Kom El-Basal (Matay county), while the lowest disease occurred was in Soultan Hassan (Abu Qurqas county). Both *Fusarium oxysporum* and *Alternaria alternata* are soil-borne fungi (Gilman, 1957) known to cause symptoms such as wilting, rot, and yellowing in plants. To date, there have been no documented cases of co-infection by *Fusarium* spp. and *Alternaria* spp. in a single potato tuber. However, co-infection involving *F. oxysporum* and *Alternaria tenuis* has been reported as the primary cause of stem blight in sweet potato (Qian et al., 2017). In cotton, co-infection by *Fusarium* spp. and *A. alternata* has also been observed. Specifically, *F. oxysporum* f. sp. *vasinfectum* is known to cause Fusarium wilt in cotton, while *Verticillium dahliae* remains the only species currently reported to cause Verticillium wilt in this crop (Wagner et al., 2020 and Zhang et al., 2020). In this investigation, *Fusarium* sp. and *Alternaria* sp. co-existed in the diseased tubers, Nine isolates of *Fusarium* sp. and three isolates of *Alternaria* sp. were isolated using collected samples obtained from different regions under study. Pathogenicity test revealed that these isolates were differed in their ability on inducing rot in potato tubers. ITS1 and ITS4 gene primers were used in DNA sequencing by PCR amplification to confirm the fungal identity. By comparing fungal DNA sequences to the information in NCBI/GenBank, the nBLAST algorithm was able to identify the fungal species. The fungal species that were isolated were determined to be *Alternaria alternata* (isolates A10) and *Fusarium oxysporum* (isolates F1–F4). This is in agree with Trabelsi *et al*., (2016) who reported that *Fusarium sambucinum* and *F. solani* were the major agents inducing dry rot disease of potato in Tunisia. While 76 isolates of fungi, including *Fusarium oxysporum, F. foetens, F. boothii, F. circinatum, F. citricola , F. iranicum, F. longifundum, F. pseudoanthophilum, F. solani, Botryotinia ranunculi, Clonostachysrosea,* and *Humicolanigrescens* were obtained from potato rotted tubers (Kim *et al*., 2024). Also, they reported that *F. oxysporum* and *F. solani* were the dominant species involved in domestic potato dry rot disease. *Alternaria tenuissima* was reported by Liu *et al* (2019) as the pathogen of rotted potato tubers, causing significant losses in crop throughout storage period. *Alternaria* species, such as *Alternaria alternata* and *Alternaria solani*, were reported as the major fungal pathogens of potatoes. These species cause significant amounts of tuber rot during postharvest storage (Platt, 1994 and Iftikhar, 2017), in addition to infecting potato plants (Weber and Jansky, 2012, Gu *et al*., 2017 and, Meng *et al*., 2018). All local genotypes evaluated under investigation were susceptible to all the five isolates of fungi, showing different degrees with significant differences in disease incidence and severity. Cara genotype showed the highest susceptibility to both *Fusarium oxysporum* and

Alternaria alternata, whereas Lady Rosetta genotype was the most resistant one. Isolates F4 and A10 induced the lowest incidence and severity of infection of the different genotypes. These results are in agreement with that obtained by Park *et al.*, 2024, who found that among seven genotypes of potatoes tested, the genotypes Golden Ball, Arirang-2ho, and Arirang-1ho were resistant to the pathogen: *A. alternata*. They suggested that this result indicates that these genetic distinctions might not be significant. Both plant pathogenic and nonpathogenic strains of the *Fusarium oxysporum* species complex is frequently detected in soils. For over a century, plant pathologists have paid close attention to *F. oxysporum* because of its wide host range and the financial losses it causes. The idea of formae speciales (f. sp.), which group strains with the same host range, was inspired by the limited host specificity of pathogenic strains. This host range, which was initially limited to a single plant species, was later discovered to be wider for numerous forma speciales (f. sp.). Furthermore, races were found in certain f.sp., usually exhibiting specialization at the cultivar level. Its remarkable plant host range, which includes both dicots (like beans, carnations, and tomatoes) and monocots (like bananas, orchids, and palms), is proof of its variety.Both annual and perennial plants, mostly terrestrial ones, as well as aquatic ones (like lotuses), can be afflicted by pathogenic *F. oxysporum* strains. Practically, pathogenic strains of *F. oxysporum* damage economically significant field crops (*i.e.*, banana, cotton, soybean), a variety of market garden crops (i.e., potato, tomato, onion and melon), ornamental crops (gerbera, cyclamen and orchids), and even weeds or parasitic plants (witchweed and broomrape) by causing wilts or root and crown rots. Individual strains, however, are selectively harmful to a few host plants. Our study revealed that isolate F4 of *Fusarium oxysporum* is able to infect tomato, pepper, eggplant, cotton, and okra, while isolating F3 infected tomato, pepper and eggplant and isolates F1 and F2 infected only tomatoes plants. The isolate A10 of *Alternaria alternate* infected both tomatoes and eggplant. Hibiscus was resistant to infection with any of these isolates.

CONCLUSION

Dry rot causes tubers lose approximately 6.35 to 25% annually. Minya county had the highest DI and DS followed by Matay, and Abu Qurqas county. Identification of isolates were *F. oxysporum* (accession No. PV400667) and *A. alternata* (accession No. PV390825). All genotypes of potato under study were susceptible to infection. Cara genotype was the highest susceptible and isolate (F3) of *F. oxysporum* induced the highest DI and DS, on Cara, Sifra and Sponta genotypes.

AUTHOR CONTRIBUTIONS

Majority contribution for the whole article belongs to the author(s). The authors read and approved the final manuscript.

COMPETING INTERESTS

The authors declare that they have no competing interests. The contents of the manuscript have neither been published nor under consideration for publication elsewhere.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

The author (s) hereby declare that NO generative AI technologies such as Large Language Models (Chat GPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

STATEMENT AND ETHICS DECLARATIONS

The authors declare that they have no known competing financial interests or personal relationships that could have influenced the work reported in this article. Ethical approval was not required for this study, as it involved only plant and microbial samples, which are exempt from

human or animal ethical review regulations.

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