



Investigation of Fungal Diseases of Potato (*Solanum tuberosum* L.) in Duhok Province/ Kurdistan Region/ Iraq

Goran R. Majid

Ministry of Agriculture and Water Resources/ Dohuk Agricultural General Directorate/ Bardarash
Agricultural Directorate

Ramadan Y. Mohamed

Department of Plant Protection/ College of Agricultural Engineering Sciences/
University of Salahaddin- Erbil/ Iraq

p-ISSN: 1608-9391

e-ISSN: 2664-2786

Article information

Received: 3/6/2025

Revised: 25/7/2025

Accepted: 6/ 8/ 2025

DOI:

10.33899/rsci.v35i3.65256

Corresponding Author:

Ramadan Y. Mohamed

ramadan.mohamed@su.edu.krd

ABSTRACT

This study identified prevalent fungal pathogens affecting potato crops in Duhok province, in three locations including: Bardarash, Rovia, and Shekhan, on three key cultivars (Arizona, Rashida, and Primabelle) during the 2024-2025 growing season. Field surveys recorded symptoms on leaves, stems, roots, and tubers. Symptomatic tissues were collected for pathogen isolation and identification via morphological characteristics and molecular analysis (ITS region sequencing). The confirmed fungi were registered in the NCBI GenBank.

Field assessments revealed stark differences among cultivars. Key pathogens identified included *Alternaria solani*, *A. alternata* (Early Blight), *Phytophthora infestans* (Late Blight), *Fusarium solani*, *F. oxysporum* (Dry rot/Wilt), and *Rhizoctonia solani* (Black Scurf/ Stem Canker). Other fungi (*Clonostachys solani*, *Allophoma labilis*, *Aspergillus flavus*, *Trichocladium acropullum*, *Penicillium puniceae*, *Fusarium concentricum*, *Phytophthora colocasiae*, and *Aspergillus oryzae*) were detected at lower frequencies.

This research marks the first combined field survey and molecular confirm the prevalence fungal pathogens affecting major potato varieties in Bardarash, Rovia, and Shekhan, Duhok province. Disease symptoms were identified and confirmed through visual inspection and genetic analysis. Results indicated that *Rhizoctonia* species were more prevalent in all three surveyed areas and across different parts of the potato crop.

This confirms the prevalence of pathogens such as *Alternaria* spp. and *P. infestans*. And highlights different levels of susceptibility among cultivars. In Bardarash and Rovia, Primabelle was identified as highly susceptible, while Rashida and Arizona appeared to be resistant in Bardarash, Rovia, and Shekhan under field conditions.

Keywords: Potato fungal diseases, *Alternaria*, *Phytophthora*, Molecular identification.

INTRODUCTION

Potato (*Solanum tuberosum* L.) holds substantial economic and nutritional importance across diverse agroecological regions, underpinning food security through its adaptive growth characteristics (Campos and Ortiz, 2020). However, potato yields are significantly limited by diseases, particularly those caused by fungi and fungi like organisms (Adolf *et al.*, 2020). Late blight *Phytophthora infestans* and early blight *Alternaria* spp. are major threats globally, causing substantial economic losses (Fry *et al.*, 2015). Other fungi like *Fusarium* spp. and *Rhizoctonia solani* also contribute to yield reduction. Effective management necessitates integrated strategies, including resistant cultivars, cultural practices, and targeted controls (Weng *et al.*, 2024).

In addition to its global economic relevance, the potato is a nutritionally rich crop, providing a significant source of carbohydrates, dietary fiber, essential amino acids, and vital micronutrients such as vitamin C, B-complex vitamins, potassium, and magnesium (Wubet *et al.*, 2022).

In Iraq, potatoes are increasingly viewed as a strategic horticultural crop, with the Kurdistan Region of Iraq (KRI) playing a dominant role in national production. While national figures report 229,069 tons of potato production in 2023 (FAO, 2023), regional data suggests that the KRI contributes between 45% and 50% of Iraq's total yield-estimated at 250,000 to 300,000 tons during the 2022–2023 seasons (Ministry of Agriculture and Water Resources – KRG, 2023). Within the KRI, Duhok Province has emerged as the leading production area, supported by favorable environmental conditions, including fertile alluvial soils, spring-fed irrigation, and a Mediterranean-type climate characterized by mild, wet winters and hot, dry summers (Waheed *et al.*, 2023).

In Duhok, systematic information on prevalent fungal pathogens and their impact on local cultivars, Arizona, Rashida, and Primabelle, are lacking. This study aimed to identify these pathogens through field surveys and laboratory analysis (morphological and molecular identification via ITS sequencing), focusing on target fungi, especially *Alternaria* spp. and *Phytophthora infestans*.

MATERIALS AND METHODES

Study area description

The study was conducted in Duhok province at three locations, including Bardarash (36.508874 N latitude, 43.588951 E longitude), which is the first representative district known for its potato cultivation and was selected as the site. Rovia (36.626174 N latitude, 43.701295 E longitude) and Shekhan (36.684083 N latitude, 43.349281 E longitude) are in the northern part of the Kurdistan Region of Iraq. Duhok province is characterized by a Mediterranean climate, featuring cold, rainy winters and hot, dry summers, with variations influenced by topography ranging from plains to mountainous areas. Agriculture, including potato cultivation, is a significant economic activity in the region (Hassan, 2023).

Field survey

Field surveys were conducted during the main potato growing season, typically from August 2024 and May 2025, coinciding with the period of maximum vegetative growth and potential disease development. A multi-stage sampling strategy was employed. Within each district, several commercial potato fields cultivating at least one of the target varieties (Arizona, Rashida, and Primabelle) were randomly chosen.

Within each selected field (typically 3–4 hectares), a systematic sampling pattern, such as an 'X' transect, was followed to ensure representative coverage (Zhang *et al.*, 2024). Along each transect, approximately 100 potato plants were randomly selected at regular intervals every 10–15 steps. For each selected plant, detailed visual inspections were performed on leaves, stems, roots, and tubers to record the presence and type of disease symptoms.

Isolation of fungal pathogens

The collected samples were brought to the Plant Protection Postgraduate Laboratory, College of Agricultural Engineering Sciences, Salahaddin University/Erbil-Iraq, where plant samples were processed immediately or stored at 4°C for a short period (max 24h). Isolation procedures were tailored based on the tissue type and suspected pathogen.

Tubers/ Roots/ Stems/ Leaf lesions

The advancing margins of the active areas had tiny tissue pieces cut off, measuring roughly 3-5 mm². The pieces were surface sterilized by sequential immersion in 70% ethanol for 30 to 60 seconds and 1 to 2% sodium hypochlorite (NaOCl) for 1 to 3 minutes, and then rinsed three times with sterile distilled water (SDW). Sterilized pieces were blotted dry on sterile filter paper (Bakir *et al.*, 2023; (Zhang *et al.*, 2024). A septic placement was done by transferring sterilized tissue pieces (4-5 pieces/plate) on the Potato Dextrose Agar (PDA) medium mixed with antibiotics, 100 mg/L streptomycin sulfate or chloramphenicol, to check for bacterial growth (Adolf *et al.*, 2020).

Morphological identification

Pure fungal isolates were initially identified based on their cultural and morphological characteristics. Cultural characteristics observed on PDA included colony color obverse and reverse, texture cottony, powdery, velvety, slimy, growth rate diameter after a specific incubation period of 7 days. Microscopic identification involved preparing slides from the pure cultures by single spore technic. Small portions of the fungal colony's mycelia and spores were mounted in a drop of lactophenol cotton blue stain or sterile water on a glass slide, covered with a coverslip, and examined under a compound light microscope at 4x, 10x, and 40x magnification. Key microscopic features recorded included: mycelial characteristics septation, branching pattern, diameter, color, conidiophore structure simple/complex, branched/unbranched, length, width, ornamentation, conidia/spore characteristics shape, size, color, septation, ornamentation, arrangement, chains, clusters, solitary, presence and morphology of specialized structures like sporangia for oomycetes like *Phytophthora*, chlamydospores, sclerotia size, shape, color for *Rhizoctonia*, and fruiting bodies pycnidia, perithecia if present. Identification to the genus level, and tentatively to the species level for distinct morphotypes, was performed by comparing observed characteristics with standard mycological keys, taxonomic descriptions, and monographs (Barnett and Hunter, 1998); (Leslie and Summerell, 2008, Woudenberg *et al.*, 2013).

Molecular identification

DNA extraction

According to molecular characterization of fungi: Methods and applications, various molecular techniques are discussed for characterizing fungi, including DNA extraction methods (Singh *et al.*, 2015).

Polymerase chain reaction (PCR) amplification large subunit 28s ribosomal RNA (rRNA)

PCR amplification for 28S rRNA partial gene was done in 50µl of reaction mixture containing; 25 µl of 2x Taq DNA Polymerase Master Mix (AMPLIQON A/S Stenhuggervej 22), 2µl of LSU forward primer (5'- ACCCGCTGAACCTAAGC-3'), 2µl LSU reverse primer (5'-CGCCAGTTCTGCTTACC -3'), 17µl DNase free water and 4µl DNA template by biosearch PTC-200 gradient thermocycler (Mohammad and Zrary, 2023).

The temperature profile consists of an initial denaturation step at 95°C for 5 minutes. This is followed by 35 cycles, which include denaturation at 95°C for 1 minute, primer annealing at 55°C for 60 seconds depend on the primer, and extension at 72°C for 1 minute. The final step involves an additional extension at 72°C for 5 minutes.

Sequencing of DNA

The fungi sample of the PCR product 28S rRNA partial gene was sequenced by ABI Prism Terminator Sequencing Kit (Applied Biosystem) at Macrogen Company of Korea. Chromatograms of 28S rRNA were edited and base calls checked using the Finch TV program software.

Sequence alignment and submission

The 28S rRNA gene sequences were submitted on Basic Local Alignment Search Tool (BLAST) is a search software that employs the technique of sequence alignment (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>), available at NCBI (National Center for Biotechnology Information) website to align and compare laboratory or query sequence with other biological sequence to identify more similarity with fungi species. A part of the 28S rRNA gene sequence of the samples was submitted to the National Center for Biotechnology Information (NCBI).

RESULTS AND DISCUSSION

Study area description

Field surveys were carried out across several key potato-growing districts within Duhok province, from three locations: Bardarash, Rovia and Shekhan, representing the diverse agro-ecological conditions where potato varieties Arizona, Rashida, and Primabelle are commonly cultivated. Selection criteria for fields included accessibility, farmer cooperation, and representation of typical cultivation practices in the area. Soil types in the surveyed areas generally range from clay loam to sandy loam, typical for the region.

Field survey results

Samples of symptomatic plant tissues were carefully collected from representative diseased plants in each field. Symptoms characteristic of major fungal and oomycete diseases noted, including leaf spots, concentric rings typical of early blight, water-soaked, rapidly expanding lesions typical of late blight, wilting, stem cankers, tuber rots, and sclerotia on potato species Fig. (1). Primabelle, Rashida, and Arizona. The most sensitive species is *Primabelle* by pathogenicity test.



Fig. 1: Fungal disease symptoms on potato (*Primabelle* cultivar) plant parts

Isolation of fungal pathogens

Fungal pathogens caused distinct symptoms across potato plant organs in cultivars Primabelle, Rashida, and Arizona. *Phytophthora infestans* (late blight) produced water-soaked leaf lesions progressing to necrosis, stem rot, and tuber sunken spots with internal decay. *Rhizoctonia solani* manifested as black sclerotia (black scurf) on tubers, stem cankers, and root rot. *Alternaria solani* (early blight) formed concentric ring-patterned leaf spots (bull's-eye lesions) and dry tuber rot. Primabelle showed high susceptibility to late/early blights; Rashida exhibited moderate *Rhizoctonia* resistance but brown rot vulnerability; Arizona demonstrated high yield potential yet late blight sensitivity in cool soils.

Morphological identification

Macroscopic pure fungal isolates were initially identified based on their cultural and morphological characteristics. Cultural characteristics observed on PDA included colony color, obverse and reverse, texture, growth rate, diameter, zonation patterns, and production of pigments (Table 1).

Table (1): Morphological Identification of isolated fungi from different parts of Potato cultivars

No.	Location	Part of the plant	Cultivars	Identified Fungi	Season
1	Shekhan	Tuber	Arizona	<i>Fusarium solani</i>	2024
2	Shekhan	Tuber	Arizona	<i>Clonostachys solani</i>	2024
3	Shekhan	Tuber	Arizona	<i>Alternaria alternata</i>	2024
4	Shekhan	Tuber	Arizona	<i>Allophoma labilis</i>	2024
5	Shekhan	Stem	Arizona	<i>Aspergillus oryzae</i>	2024
6	Shekhan	Stem	Arizona	<i>Phytophthora colocasiae</i>	2024
7	Shekhan	Leaf	Arizona	<i>Phytophthora infestans</i>	2024
8	Shekhan	Root	Arizona	<i>Alternaria solani</i>	2024
9	Rovia	Tuber	Rashida	<i>Rhizoctonia solani</i>	2025
10	Rovia	Leaf	Primabelle	<i>Trichocladium acropullum</i>	2025
11	Rovia	Stem	Rashida	<i>Corynascus similis</i>	2025
12	Rovia	Root	Primabelle	<i>Phytophthora infestans</i>	2025
13	Rovia	Root	Primabelle	<i>Fusarium solani</i>	2025
14	Rovia	Root	Primabelle	<i>Aspergillus flavus</i>	2025
15	Bardarash	Tuber	Arizona	<i>Rhizoctonia solani</i>	2024
16	Bardarash	Root	Primabelle	<i>Fusarium oxysporum</i>	2025
17	Bardarash	Root	Primabelle	<i>Fusarium concentricum</i>	2025
18	Bardarash	Stem	Primabelle	<i>Penicillium punicae</i>	2025
19	Bardarash	Stem	Rashida	<i>Rhizoctonia solani</i>	2025
20	Bardarash	Leaf	Primabelle	<i>Rhizoctonia solani</i>	2025
21	Bardarash	Leaf	Rashida	<i>Fusarium oxysporum</i>	2025

Molecular Identification

DNA extraction:

Genomic DNA was extracted from twenty-one fungi isolates samples were extracted from Potato-infected leaves, stems, roots, and tubers by using FavorPrep™ Fungi Genomic DNA Extraction Mini Kit (FAVORGENT Biotech Corp-Taiwan). The DNA extract was loaded into a 1% agarose gel, and bands was viewed under UV transillumination.

PCR amplification of partial 28s rRNA gene

28S rRNA gene-specific primers were designed according to the sequences of the fungal ribosomal RNA made by Micro-gene Company (South Korea). The primers amplified a band with the expected size, 1200bp. The PCR product was electrophoresed and visualized by 1.5% agarose gel Fig. (2).

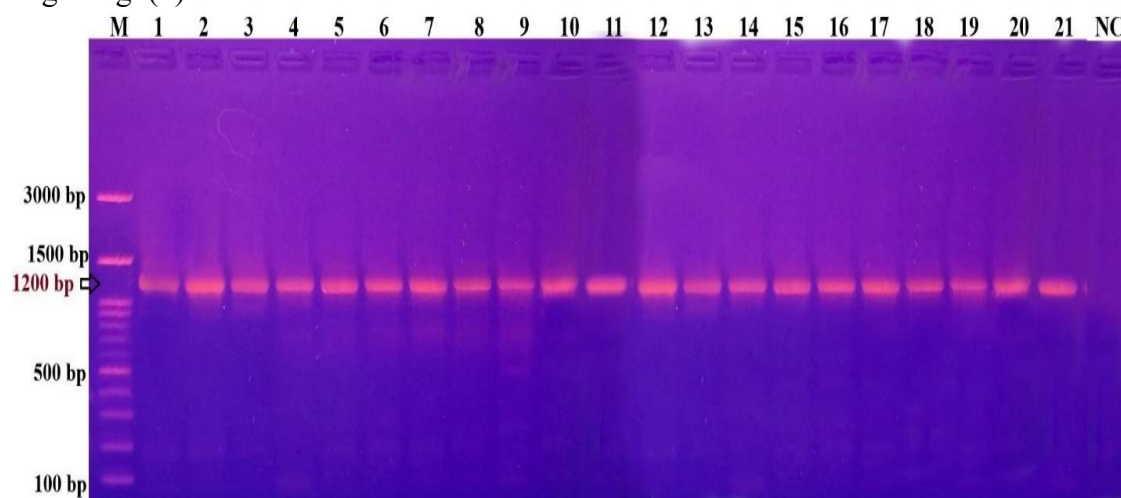


Fig. 2: PCR amplification of partial 28S rRNA, wells include M; Ladder (3000-100bp), lanes 1-21; gene bands with the size of 1200bp amplified, and NC indicates negative control without the band.

Molecular identification and submission of fungi species in GenBank

The BLAST program from GenBank (<http://blast.ncbi.nlm.nih.gov/>) was used to align a partial 28S rRNA sequence sample measuring 1200bp, allowing us to compare our amplified sequence with other fungal sequences stored in the database. The BLAST results showed that the top query sequence was a perfect 100% match with each fungus listed in (Table 2).

Table (2): Molecular identification and partial 28S rRNA gene sequences submitted for 21 query isolates in NCBI GenBank

Samples	Accession Numbers	Fungous Identified
1	PV739830	<i>Fusarium solani</i>
2	PV739831	<i>Clonostachys solani</i>
3	PV739832	<i>Alternaria alternate</i>
4	PV739833	<i>Alophoma labilis</i>
5	PV739834	<i>Aspergillus oryzae</i>
6	PV739835	<i>Phytophthora colocasiae</i>
7	PV744056	<i>Phytophthora infestans</i>
8	PV744057	<i>Alternaria solani</i>
9	PV744058	<i>Rhizoctonia solani</i>
10	PV744059	<i>Trichocladium acropullum</i>
11	PV749117	<i>Phytophthora colocasiae</i>
12	PV744060	<i>Phytophthora infestans</i>
13	PV744061	<i>Fusarium solani</i>
14	PV744062	<i>Aspergillus flavus</i>
15	PV744063	<i>Rhizoctonia solani</i>
16	PV744064	<i>Fusarium oxysporum</i>
17	PV744065	<i>Fusarium concentricum</i>
18	PV744066	<i>Penicillium punicae</i>
19	PV744067	<i>Rhizoctonia solani</i>
20	PV744068	<i>Rhizoctonia solani</i>
21	PV744069	<i>Fusarium oxysporum</i>

Phylogenetic inferences

Phylogenetic analysis utilizing the 28S rRNA nucleotide sequence demonstrated that the examined fungal species grouped as anticipated. The sequence divergence similarity data and the resulting phylogenetic tree indicated that species within the same genus were closely related. Each sampled species formed distinct clusters within its species group. Additionally, the relatedness of the fungal samples to other species in GenBank was determined using the Mega BLAST program from NCBI, as shown in (Table 3) and Fig (4).

Table (3): Percentage distribution of fungal species based on partial 28S rRNA sequences according to BLASTn analysis in NCBI GenBank

Accession Numbers	Fungi	Query Cover %	Identical Number %	Genbank Accession Number
PV739830 PV744061	<i>Fusarium solani</i>	100	100	MH866510
		100	100	MT533279
		100	100	MZ399199
PV744064 PV744069	<i>Fusarium oxysporum</i>	100	100	MK981956
		100	100	MH869602
		100	100	KT207705
PV744065	<i>Fusarium concentricum</i>	100	100	PP425403
		100	100	PQ304466
		100	100	NG_069847
PV739831	<i>Clonostachys solani</i>	100	100	MW19906
		100	100	PQ385862
		100	100	MW291605
PV739832	<i>Alternaria alternata</i>	100	100	PQ449778
		100	100	OM337556
		100	100	ON088979
PV744057	<i>Alternaria solani</i>	100	100	KM233368
		100	99.76	OK036418
		100	99.76	PP831848
PV739833	<i>Alophoma labilis</i>	100	100	GU238091
		100	100	MH257424
		99	100	MN973062
PV739834	<i>Aspergillus oryzae</i>	100	100	PQ424717
		100	100	MH094244
		100	100	MK204934
PV744062	<i>Aspergillus flavus</i>	100	98.85	PQ571952
		100	98.85	MF590165
		100	98.85	KX765883
PV739835 PV749117	<i>Phytophthora colocasiae</i>	100	100	KX250570
		100	100	KX250563
		100	99.88	OR519212
PV744056 PV744060	<i>Phytophthora infestans</i>	100	100	XR_009934489
		100	99.88	FJ869957
		100	99.88	XR_009934745
PV744058 PV744063 PV744067 PV744068	<i>Rhizoctonia solani</i>	100	100	MN970164
		100	100	MH867320
		100	100	MH873230
PV744059	<i>Trichocladium acropullum</i>	100	100	MH875680
		100	100	JX280662
PV744066	<i>Penicillium puniceae</i>	100	100	MH875529

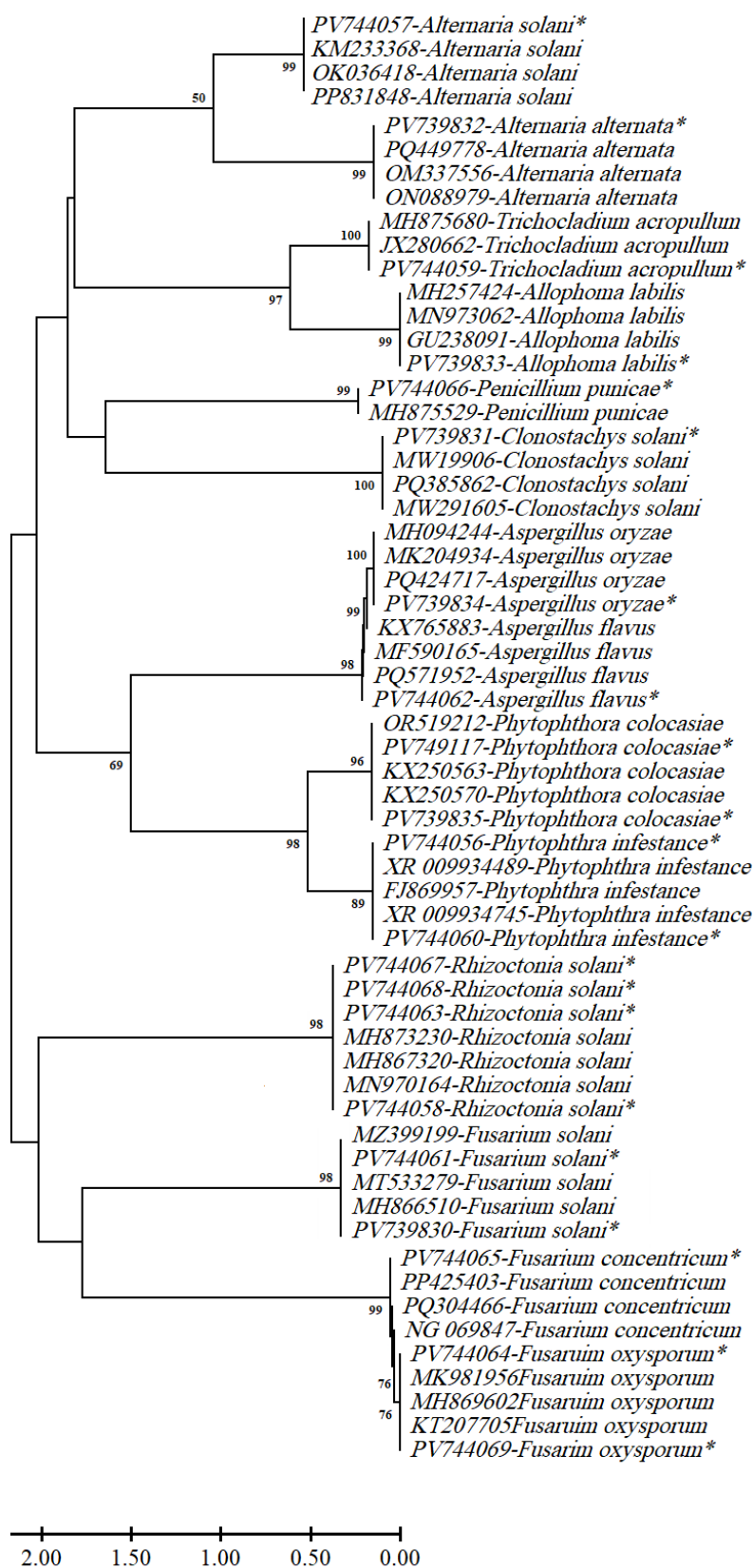


Fig. (4): Evolutionary analyses were conducted in MEGA 12, blastn shows phylogenetic positioning of twenty-one isolated fungal samples according to sequences of 28S rRNA employing maximum likelihood available in GenBank sequences.

The present investigation offers substantive, empirical insights into the fungal pathogen complex affecting potato cultivation across Duhok province, specifically in Bardarash, Rovia, and Shekhan districts, in the Kurdistan Region of Iraq. Field survey data revealed pronounced differential susceptibility patterns among the evaluated potato cultivars Arizona, Rashida, and Primabelle.

Comprehensive morphological and molecular characterization confirmed the presence of economically significant fungal pathogens, including *Alternaria solani*, *A. alternata*, *Phytophthora infestans*, *Fusarium solani*, *F. oxysporum*, and *Rhizoctonia solani*, establishing their association with observed disease symptoms in the surveyed regions. The predominance of *Alternaria spp* and *P. infestans*, particularly on the susceptible Primabelle cultivar, emphasizes the critical importance of implementing effective management strategies against early and late blight diseases, which constitute major constraints to global potato production systems (Adolf *et al.*, 2020; Fry *et al.*, 2015).

Furthermore, the concurrent identification of *Fusarium* species and *R. solani* indicates the complexity of the pathosystem, characterized by the simultaneous presence of both foliar and soilborne pathogens, thereby necessitating comprehensive disease management approaches (Weng *et al.*, 2024). The findings presented herein, while consistent with established phytopathological principles, contribute region-specific epidemiological data for the Duhok potato production sector.

The observed differential cultivar responses provide valuable information for agricultural extension services and local producers regarding the strategic importance of cultivar selection as a fundamental disease management component. Implementation of integrated disease management protocols, potentially incorporating prophylactic fungicide applications guided by disease forecasting models in conjunction with appropriate cultural practices, would be particularly beneficial for susceptible cultivars.

CONCLUSION

This research establishes a foundational baseline for subsequent investigations into fungal diseases affecting potato production in the Duhok region. Future research directions could encompass longitudinal surveys to elucidate temporal dynamics in pathogen populations, controlled pathogenicity assays to quantify virulence characteristics, fungicide sensitivity profiling of predominant pathogens such as *P. infestans* and *Alternaria spp*, and exploration of biological control agents with antagonistic potential. The molecular characterization of pathogen isolates conducted in this study provides a robust platform for these subsequent investigations, ultimately contributing to enhanced sustainability and productivity of potato cultivation systems in the Kurdistan Region of Iraq.

REFERENCES

- Adolf, B.; Andrade-Piedra, J.; Bittara Molina, F.; Przetakiewicz, J.; Hausladen, H.; Kromann, P.; Lees, A.; Lindqvist-Kreuze, H.; Perez, W.; Secor, G.A. (2020). Fungal, oomycete, and plasmodiophorid diseases of potato. In: "The Potato Crop: Its Agricultural, Nutritional and Social Contribution to Humankind". Cham: Springer International Publishing, pp. 307-350. DOI: 10.1007/978-3-030-28683-5_9
- Bakir, M.Z.; Ahmed, K.M.; Mohamed, R.Y. (2023). Isolation and identification of *Xylella fastidiosa* that causes oleander leaf scorch. *Raf. J. Sci.*, **32**(1), 102–109. DOI: 10.33899/rjs.2023.177292
- Barnett, H.L.; Hunter, B.B. (1998). "Illustrated Genera of Imperfect Fungi". 4th ed. Minneapolis: Burgess Publishing.
- Campos, H.; Ortiz, O. (eds.) (2020). "The Potato Crop: Its Agricultural, Nutritional and Social Contribution to Humankind". Cham: Springer Nature. DOI: 10.1007/978-3-030-28683-5
- FAO (2023). Food and Agriculture Organization of the United Nations. Crops – Potatoes (Production quantity, Area harvested, Yield), Rome. <https://www.fao.org/faostat/en/#data/QC>. (Accessed: 10 June 2024).
- Fry, W.; Birch, P.; Judelson, H.; Grünwald, N.; Danies, G.; Everts, K.; Gevens, A.; Gugino, B.;

- Johnson, D.; Johnson, S. (2015). Five reasons to consider *Phytophthora infestans* a reemerging pathogen. *Phytop.*, **105**(8), 966–981. DOI: 10.1094/PHYTO-01-15-0005-FI
- Hassan, N. E. (2023). Statistical analysis of rainfall variations in Duhok City and Semel District, Kurdistan Region of Iraq. *Intern. J. Rese. Envir. Sci.*, **9**(1), 31–38. DOI: 10.20431/2454-9444.0903004
- Leslie, J.F.; Summerell, B.A. (2008). "The Fusarium Laboratory Manual". Hoboken: Wiley-Blackwell.
- MOHAMMAD, A.O.; ZRARY, T.J. (2023). Detection of seed-borne pathogens in wheat (*Triticum durum*). *Journal of Survey in Fisheries Sciences*, **10**(3S), 5151-5163. DOI: 10.17762/sfs.v10i3S.1759
- Singh, R.P.; Kumari, P.; Reddy, C.R.K. (2015). Antimicrobial compounds from seaweeds-associated bacteria and fungi. *Appl. Microb. Biotechn.*, **99**(4), 1571–1586. DOI: 10.1007/s00253-014-6334-y
- Waheed, A.; Li, C.; Muhammad, M.; Ahmad, M.; Khan, K.A.; Ghramh, H.A.; Wang, Z.; Zhang, D. (2023). Sustainable potato growth under straw mulching practices, Sustainability, **15**(13), 1-26. DOI: 10.3390/su151310442
- Weng, L.; Tang, Z.; Sardar, M. F.; Yu, Y.; Ai, K.; Liang, S.; Alkahtani, J.; Lyv, D. (2024). Unveiling the frontiers of potato disease research through bibliometric analysis. *Front. Microb.*, **15**, 1430066. DOI: 10.3389/fmicb.2024.1430066
- Woudenberg, J.; Groenewald, J.; Binder, M.; Crous, P. (2013). *Alternaria* redefined. *Stud. Mycol.*, **75**, 171–212. DOI: 10.3114/sim0015
- Wubet, G.K.; Zemedu, L.; Tegegne, B. (2022). Value chain analysis of potato in Farta District of South Gondar Zone, Amhara National Regional State of Ethiopia, *Heliyon*, **8**(3), e09142. DOI: 10.1016/j.heliyon.2022.e09142
- Zhang, X.; Chen, H.; Wu, J.; Wang, X.; Wang, S.; Chen, J.; Yu, Q.; Zhang, Z.; Zheng, X.; Zeng, J. 2024. A field survey of eight common potato pathogens in China based on integrated-loop-mediated isothermal amplification assays. *Phytopath. Rese.*, **6**(1), 1-14. DOI: 10.1186/s42483-024-00284-3
-

دراسة الأمراض الفطرية على البطاطا *Solanum tuberosum* في محافظة دهوك/ إقليم كردستان/ العراق

كوران رشيد مجيد

وزارة الزراعة والموارد المائية/ المديرية العامة للزراعة في دهوك/ مديرية زراعة بردرش

رمضان يوسف محمد

قسم وقاية النبات/ كلية علوم الهندسة الزراعية/ جامعة صلاح الدين - اربيل/ العراق

الملخص

كشفت هذه الدراسة عن مسببات الأمراض الفطرية السائدة في محصول البطاطا بمحافظة دهوك، في ثلاثة مواقع شملت بردرش وروفا وشيخان، وذلك على ثلاثة أصناف رئيسية (أريزونا، رشيدة، بريمايل) خلال موسم الزراعة 2024-2025. سُجّلت المسوحات الحقلية الأعراض على الأوراق والسيقان والجذور والدرنات، حيث جُمعت الأنسجة المصابة لعزل وتحديد الممرضات باستخدام الخصائص المورفولوجية والتحليل الجزيئي وسُجّلت الفطريات المؤكدة في بنك الجينات العالمي (NCBI GenBank). أظهرت التقييمات الميدانية تبايناً واضحاً بين الأصناف وشملت الفطريات الرئيسية: *Alternaria solani* و *alternata* *A.* المسبب للفحة المبكرة *Phytophthora infestans* المسبب للفحة المتأخرة *Fusarium solani*، *F. oxysporum* المسبب للعفن الجاف/ الذبول *Rhizoctonia solani* المسبب للجرب الأسود/ تفرح الساق. كما اكتُشفت فطريات أخرى: (*Clonostachys* *Penicillium*، *Trichocladium* *acropullum*، *Aspergillus* *flavus*، *Allophoma* *labilis*، *solani* *punicae*، *Fusarium concentricum*، *Phytophthora colocasiae*، *Aspergillus oryzae*) بترددات أقل. يمثل هذا البحث أول دراسة ميدانية وجزيئية متكاملة للممرضات الفطرية التي تصيب أصناف البطاطا الرئيسية في بردرش وروفا وشيخان بمحافظة دهوك. تم تشخيص أعراض الأمراض وتأكيدها عبر الفحص البصري والتحليل الجيني. أظهرت النتائج أن الجنس *Rhizoctonia* كان الأكثر انتشاراً في المواقع الثلاثة وبين مختلف أجزاء المحصول، مما يؤكد هيمنة الفطريات مثل *Alternaria spp.* و *P. infestans*، ويبرز مستويات مختلفة من الحساسية بين الأصناف. ففي بردرش وروفا، سجّل صنف بريمايل أعلى حساسية، بينما أظهر صنفا رشيدة وأريزونا مقاومة في بردرش وروفا وشيخان تحت الظروف الحقلية تُعد هذه النتائج حاسمةً لوضع إستراتيجيات متكاملة مستهدفة لإدارة الأمراض، بما في ذلك اختيار الأصناف المقاومة، لدعم زراعة البطاطا المستدامة.

الكلمات الدالة: أمراض البطاطا الفطرية، *Alternaria*، *Phytophthora*، التشخيص الجزيئي.