



***FUSARIUM CULMORUM* ASSOCIATED WITH ROOT ROT IN CHICKPEA (*CICER ARIETINUM* L.) IN UZBEKISTAN: MOLECULAR IDENTIFICATION AND PATHOGENICITY**

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SUMMARY

Root rot caused by *Fusarium* species is the major constraint in chickpea (*Cicer arietinum* L.) production under arid and semi-arid conditions of Central Asia. This study aimed to investigate the occurrence, pathogenicity, and molecular identity of *Fusarium culmorum* associated with chickpea root rot in Uzbekistan. During the growing season of 2025, collecting symptomatic chickpea plants transpired from fields in the Gallaarol District, Jizzakh Region, Uzbekistan, which yielded 10 *Fusarium* isolates. The selection of isolate GPEB-65 proceeded for detailed characterization. Morphological analysis revealed a rapid colony growth, reddish pigmentation, abundant chlamydospores, and the absence of microconidia, consistent with *F. culmorum*. The *TEF1-a* (translation elongation factor 1- α) gene sequencing confirmed species identity, with 99.8% similarity to reference strains. Phylogenetic analysis placed the isolate GPEB-65 within a strongly supported *Fusarium culmorum* clade, confirming its taxonomic identity. Two unique single-nucleotide polymorphisms (A7G and C205T) distinguished the Uzbekistani isolate from strains reported in Iraq and the United States. Pathogenicity assays demonstrated the highest virulence, with severe root necrosis and a disease severity index (79%), fulfilling Koch's postulates through re-isolation. The results confirmed the presence of a highly virulent and genetically distinct *F. culmorum* population affecting the chickpea crop in Uzbekistan and provided a robust foundation for improved molecular monitoring and resistance breeding strategies.

Keywords: Chickpea (*C. arietinum* L.), *Fusarium culmorum*, root rot, *TEF1-a* gene, molecular identification, phylogenetic analysis, single-nucleotide polymorphism (SNP)

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Key findings: This study confirmed *F. culmorum* as the causal agent of chickpea (*C. arietinum* L.) root rot in Uzbekistan. *TEF1-a* sequencing (99.8% similarity) and phylogenetic analysis placed the GPEB-65 strain within a considerably supported *F. culmorum* clade. Pathogenicity assays demonstrated the highest virulence, with a disease severity index at 79%, emphasizing the significant threat of this pathogen to regional chickpea production.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an important grain legume widely cultivated in semi-arid regions as a major source of plant protein. In Uzbekistan, the chickpea cultivated area has expanded steadily in previous years as part of national strategies aimed at diversifying crop production and strengthening food security. Likewise, these strategies seek to improve soil fertility through legume-based crop rotations and enhance the export potential of high-value pulse crops. However, despite this area expansion, the crop's yield potential remains constrained by several biotic stresses, particularly soil-borne fungal pathogens. Root and crown rot diseases are the most destructive constraints to chickpea production, especially under the arid and climatically diverse conditions of Central Asia, where drought stress predisposes plants to infection and further accelerates disease development (Suga *et al.*, 2014; Abduvaliev *et al.*, 2024; Sherimbetov *et al.*, 2024).

Among the fungal pathogens associated with root rot, *Fusarium culmorum* is recognizably highly prevalent and an economically considerable fungal species worldwide. This filamentous fungus infects a wide range of host plants and exhibits strong pathogenic potential. Its virulence largely refers to the secretion of cell wall-degrading enzymes and the production of toxic secondary metabolites, particularly trichothecenes, which facilitate host tissue colonization and suppress plant defense responses (Pasquali *et al.*, 2016; Munkvold, 2017; Akhmadaliev *et al.*, 2024). The ability of *F. culmorum* to survive in soil and crop residues further enhances its persistence and epidemiological importance in cereal- and legume-based cropping systems.

For effective phytosanitary monitoring and disease management, the accurate

identification of *Fusarium* species is crucial. Traditionally, species identification has relied on morphological and cultural characteristics, including colony pigmentation, growth rate, and microscopic features, such as macroconidia, microconidia, and chlamydospores (Leslie and Summerell, 2006). However, morphological traits often gain influences from environmental conditions and sometimes may overlap among the closely related taxa, resulting in misidentification and taxonomic ambiguity (O'Donnell *et al.*, 1998).

Overcoming these hindrances has made molecular approaches become the standard for species delimitation within the genus *Fusarium*. Among various genetic markers, the translation elongation factor 1- α (*TEF1-a*), encoded by the *tef1* gene, has proven to be one of the most informative loci for phylogenetic inference and species identification (O'Donnell *et al.*, 1998). Compared with the internal transcribed spacer (ITS) region, which often lacks sufficient resolution within *Fusarium*, *TEF1-a* exhibited the higher interspecific variability and relatively low intraspecific divergence, enabling reliable differentiation among closely associated fungal species (Geiser *et al.*, 2004; O'Donnell *et al.*, 2015; Sherimbetov *et al.*, 2024).

Despite the global importance of *F. culmorum*, its genetic structure, evolutionary dynamics, and virulence variability in Central Asia, particularly in Uzbekistan, remain insufficiently characterized (Ma *et al.*, 2013). Therefore, a comprehensive understanding of the molecular identity and pathogenic diversity of the local *Fusarium* populations is essential for developing effective disease management strategies and resistant chickpea cultivars adapted to regional agroecological conditions. In light of the above discussion, the pertinent study aimed to identify *Fusarium culmorum* associated with chickpea root rot in Uzbekistan

using *TEF1-α* sequence analysis and evaluate its pathogenicity under controlled conditions. The results will contribute to improved phytosanitary monitoring and integrated disease management strategies for sustainable chickpea production in Uzbekistan.

MATERIALS AND METHODS

Sample collection and fungal isolation

During the growing season of 2025, chickpea plants with root rot symptoms (yellowing, wilting, stunting, and root necrosis) proceeded to collection from four fields in the Gallaarol District, Jizzakh Region, Uzbekistan. Twenty symptomatic plants entailed collection using a zigzag sampling pattern, with the samples transported to the laboratory at 4 °C–8 °C and processed within 24 h. Root segments sustained surface sterilization (1% NaOCl, 4 min), then rinsing with sterile distilled water, drying, and plating on the potato dextrose agar (PDA). Plates underwent incubation at 26 °C (16 h light) and 18 °C (8 h dark). Obtaining pure cultures continued with monohyphal isolation. Morphological identification took place on the PDA and potato sucrose agar based on standard taxonomic keys (Leslie and Summerell, 2006).

DNA extraction and molecular analysis

Genomic DNA extraction from 7-day-old mycelium used the Gene JET Genomic DNA Purification Kit (Thermo Scientific, USA). The DNA quality and concentration received assessment with a NanoDrop spectrophotometer. The translation elongation factor 1- α (*TEF1-α*) gene reached amplification using the primer pair EF1 (5'-ATGGGTAAGGA(A/G)GACAAGAC-3') and EF2 (5'-GGA(G/A)GTACCAGTSATCATGTT-3'), as described by O'Donnell *et al.* (1998). PCR amplification succeeded in 25 μ L reaction volumes with an initial denaturation at 95 °C for 3 min, followed by 35 cycles of 95 °C for 30 s, 55 °C for 30 s, and 72 °C for 1 min, with a final extension at 72 °C for 7 min. Amplicons

incurred visualization on 1.1% agarose gels, with purified products sequenced using the BigDye Terminator v3.1 kit (Applied Biosystems, USA). Sequence chromatograms underwent editing in BioEdit, alignment using the MUSCLE algorithm in MEGA12, and analysis for single nucleotide polymorphisms (SNPs). Phylogenetic trees' construction utilized the neighbor-joining method with 1000 bootstrap replicates.

Pathogenicity assay

Virulence evaluation employed a seed inoculation method following Koch's postulates. Surface-sterilized seeds of the chickpea cultivar Guliston bore immersion in a conidial suspension (1×10^6 conidia mL⁻¹) of the isolate GPEB-65. Both inoculated and control seeds acquired incubation at 25 °C $\pm$ 1 °C under a 12-h photoperiod. Disease symptoms entailed evaluation 7–10 days after inoculation using a 0–5 disease rating scale, with the disease severity index (DSI) calculated accordingly. Pathogenicity confirmation had the pathogen re-isolated from symptomatic seedlings and compared with the original isolate.

RESULTS

Fusarium isolates recovered from infected chickpea plant samples totaled 10 (Figure 1).

Morphological identification of *F. culmorum*

The fungal isolates obtained from symptomatic chickpea (*Cicer arietinum* L.) seedling roots gained initial identification based on their cultural and microscopic characteristics, following the standard diagnostic criteria described by Nelson *et al.* (1983). Colonies grown on the potato dextrose agar (PDA) showed rapid growth, reaching 70–85 mm in diameter after seven days of incubation at 25 °C $\pm$ 1 °C in darkness. The aerial mycelium was abundant, dense, and cottony, initially white to cream and gradually turning light pink



Figure 1. Chickpea plants exhibiting symptoms of root rot.

to reddish-brown with age. The reverse side of the colonies exhibited reddish-brown to pinkish-orange pigmentation (Figure 2).

On the carnation leaf agar (CLA), abundant sporulation was prominent. Macroconidia production surfaced in sporodochia, and these were typically thick-walled, moderately curved, and robust, with a blunt apical cell and a distinct foot-shaped basal cell. Most macroconidia were 3–5 septate and measured 25–45 μm $\times$ 4–6 μm . Microconidia were absent, which is a characteristic feature of *Fusarium culmorum*. Chlamydospores were abundant, formed singly, in pairs, or in short chains, both terminally and intercalary within the hyphae. They were globose to subglobose, thick-walled, and measured 7–12 μm in diameter.

The combination of rapid colony growth, reddish pigmentation, absence of microconidia, presence of thick-walled, 3–5 septate macroconidia with foot-shaped basal cells, and abundant chlamydospore formation corresponded well with the standard

morphological description of *Fusarium culmorum* (Figure 3) (Nelson *et al.*, 1983). One representative isolate, designated GPEB-65, reached selection for further pathogenicity testing and molecular characterization.

In vitro pathogenicity assessment

The pathogenicity assay clearly enunciated the aggressive nature of the *F. culmorum* isolate GPEB-65 toward chickpea (*C. arietinum* L.) under controlled laboratory conditions. The development of typical root rot symptoms occurred on inoculated seedlings within 5–7 days after inoculation and became severe by 10 days. In contrast, control seedlings treated with sterile distilled water remained healthy and exhibited normal germination, root elongation, and shoot growth and development. Inoculated chickpea seedlings showed pronounced disease symptoms, including extensive root browning, dark necrotic lesions along the primary root, cortical tissue disintegration, and marked suppression

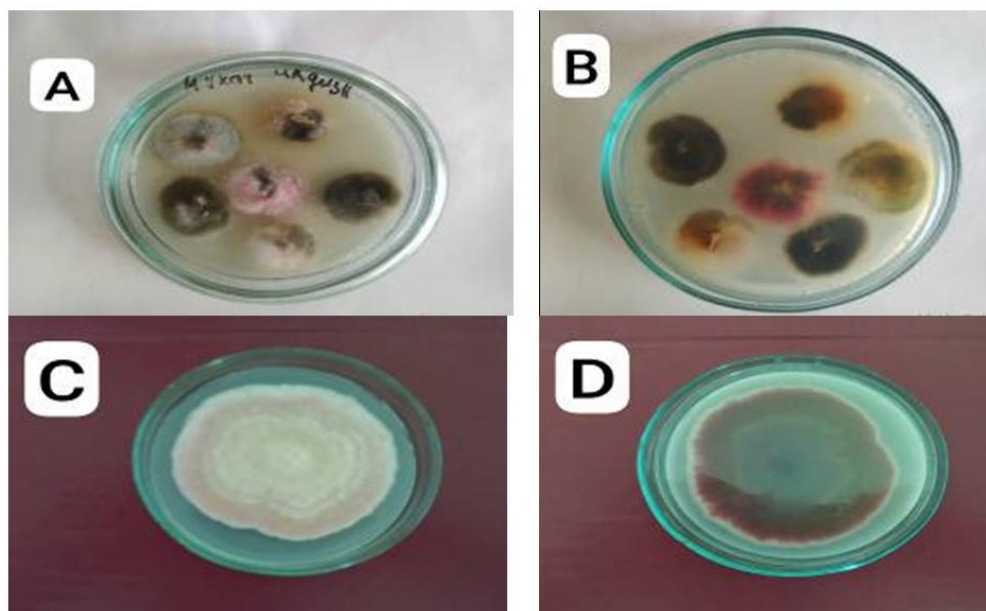


Figure 2. Macroscopic characteristics of colonies of some *F. culmorum* isolates: A) front side and B) back side; and GPEB-65 strain: C) front side and D) back side.

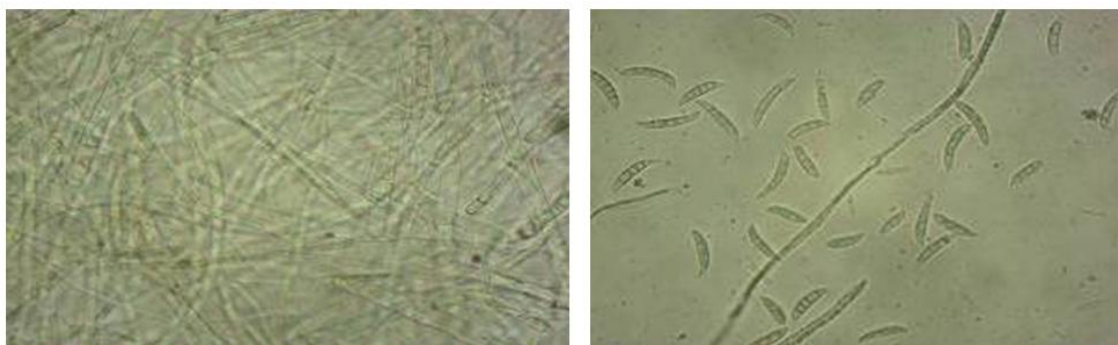


Figure 3. Microscopic characteristics of macroconidia and chlamydospores of *F. culmorum* GPEB-65 strain.

of the root and shoot growth and development. In several cases, advanced infection resulted in partial seedling collapse and severe decay of the root system. Germination percentage exhibited visible reduction in the inoculated treatments compared with the control, indicating the pathogen adversely affected the pre- and post-emergence stages.

Disease severity assessment using the 0–5 rating scale revealed an average severity score of four, corresponding to severe root necrosis and considerable growth inhibition.

The disease severity index (DSI) was 79%, indicating the highest level of virulence. This elevated DSI value quantitatively confirmed the robust pathogenic potential of the GPEB-65 strain and reflected extensive tissue colonization and damage under in vitro conditions. Infected chickpea seedlings displayed a substantial reduction in root and shoot length as compared with the control treatment, disclosing the detrimental impact of the infection on early seedling vigor.

Re-isolation of the pathogen from symptomatic tissues consistently yielded fungal colonies that were morphologically identical to the original isolate, confirming its identity and pathogenic role. However, no fungal growth was evident in the control seedlings. The successful re-isolation of the fungus that fulfills Koch's postulates provided definitive evidence that the *F. culmorum* isolate GPEB-65 was the causal agent of root rot symptoms observed in chickpea. Overall, the highest DSI value (79%) and severity rating underscore the considerable virulence of the tested isolate and highlight the potential threat posed by *F. culmorum* to chickpea production, particularly during early growth and developmental stages. The results emphasized the importance of accurate molecular identification and the development of integrated disease management strategies to mitigate yield losses in chickpea-growing regions of Uzbekistan.

Molecular identification and phylogenetic analysis

The identity of the strain GPEB-65 garnered an unequivocal confirmation by analyzing a 737 bp partial sequence of the translation elongation factor 1-alpha (*TEF1-α*) gene. BLASTn analysis against the NCBI nucleotide

database revealed 99.8% sequence identity with *F. culmorum* reference strains (Figure 4).

The phylogenetic tree enunciated that the *F. culmorum* strain GPEB-65 (PP003058; Uzbekistan) clusters robustly within the *F. culmorum* clade. The said clade includes multiple reference isolates from the USA (MW370273, MW370272, and MW370271; JF740860), Iraq (PV654536), and some other regions, revealing broad geographic representation. The *F. culmorum* clade achieved significant support with the highest bootstrap values ($\approx 99\%$ – 100%), confirming its monophyly. Within this clade, the strain GPEB-65 forms a closely related subgroup with the strain NRRL 52792 (USA) and the strain Karbala-1 (Iraq). The internal branching nodes showed the moderate bootstrap support ($\approx 58\%$ – 62%), suggesting some intraspecific genetic variation, but overall apparent genetic affinity. The short branch lengths among the *F. culmorum* isolates exhibited the limited genetic divergence within the species. The *F. culmorum* clade gave an obvious separation from other *Fusarium* species included in the said analysis. The species *F. graminearum* isolates created a distinct, well-supported clade (bootstrap $\approx 98\%$), while the species *F. equiseti* strains also clustered separately with robust support (bootstrap $\approx 100\%$).

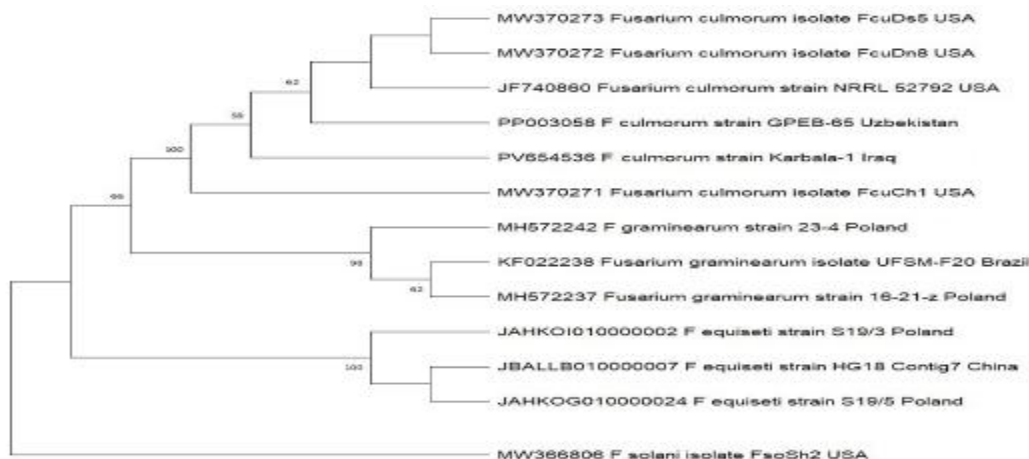


Figure 4. Phylogenetic analysis of *Fusarium culmorum* strain GPEB-65 (PP003058; Uzbekistan) and related species performed using the Neighbor-Joining method with the Tamura-Nei model. Bootstrap values > 50% (1000 replicates) are shown at branch nodes, with *Fusarium solani* (MW366806; USA) as the outgroup.

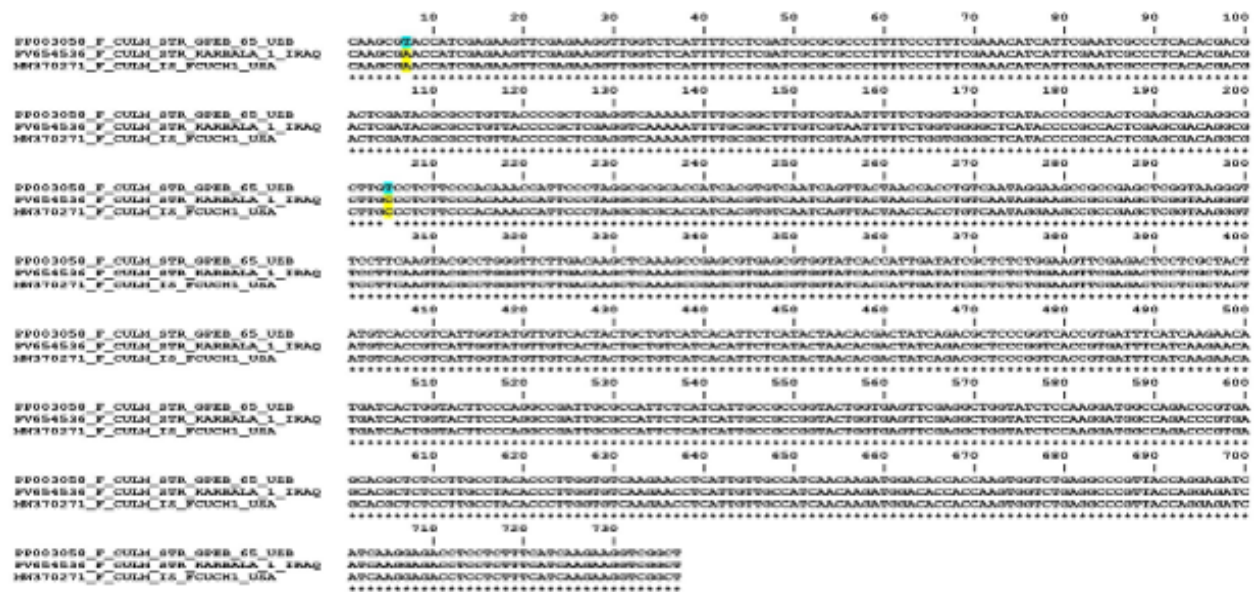


Figure 5. Multiple sequence alignment of the *Fusarium culmorum* *TEF1-a* gene from three strains: Uzbekistan GPEB-65, Iraq Karbala 1, and USA FCUCH1. Asterisks (*) indicate conserved sites; colored bases highlight SNPs among the strains. Position numbers refer to the Uzbekistan GPEB-65 sequence.

Importantly, the species *F. solani* (MW366806; USA), signifying the position as an outgroup, appeared distinctly and separated from the group taxa. Its long branch length relative to the other species revealed the greater genetic divergence, supporting its vital role in rooting the tree and confirming the evolutionary separation between *F. solani* and the *F. culmorum*–*F. graminearum*–*F. equiseti* complex. Overall, the inclusion of the species *F. solani* as an outgroup further strengthens the phylogenetic interpretation by clearly rooting the tree and confirming that the strain GPEB-65 belongs unambiguously to the *F. culmorum* lineage. The analysis further detailed that the strain GPEB-65 shared a close evolutionary relationship with the globally distributed *F. culmorum* isolates while remaining genetically distinct from other species of *Fusarium*.

Performing multiple sequence alignment of the *F. culmorum* *TEF1-a* gene from three geographically distinct strains, viz., Uzbekistan GPEB-65 (PP003058), Iraq Karbala-1 (PV654536), and USA FCUCH1 (MW370271), used the MUSCLE (Multiple Sequence Comparison by Log-Expectation) algorithm.

The alignment revealed the highest sequence conservation across all the *Fusarium* strains, with several single-nucleotide polymorphisms (SNPs) considerably distinguishing the Uzbekistani isolate from the others (Figure 5). Two unique SNPs entailed identification within the Uzbekistani GPEB-65 strain: an A to G transition at position 7 (A7G) and a C to T transition at position 205 (C205T). However, these nucleotide substitutions were not evident in the strains Iraq Karbala-1 and the USA FcuCh1, authenticating distinct genetic signatures within the Uzbekistan population. The identified SNPs could serve as molecular markers for strain differentiation and population genetic studies of the species *F. culmorum*.

DISCUSSION

The potential study provided the first comprehensive characterization of the species *F. culmorum* associated with chickpea (*C. arietinum* L.) root rot in Uzbekistan and positioned the local populations within a broader global framework. By integrating

pathogenicity assays, morphological analysis, and *TEF1-α*-based phylogenetics, the results revealed Uzbekistani isolates were highly virulent and genetically aligned with globally distributed lineages, while also exhibiting signs of regional differentiation (Backhouse *et al.*, 2003; Sherimbetov *et al.*, 2024).

Among the 10 recovered isolates, the strain GPEB-65 exhibited the highest aggressiveness, inducing severe root necrosis within 5–7 days and showing a disease severity index (DSI) of 79%. This value falls within the upper range reported for chickpeas in other regions, including Iraq and Europe (Chatterton *et al.*, 2015), and is comparable with results reported from Australia and the United States for cereals and legumes (Alderman *et al.*, 1989). Such high virulence observed across different regions highlights the ecological adaptability and pathogenic potential of *Fusarium culmorum*. In this presented study, the relatively high DSI value may reflect the pathogen's adaptation to local chickpea germplasm and the semi-arid climatic conditions of Uzbekistan, where temperature fluctuations, irrigation practices, and crop rotation systems can influence pathogen aggressiveness (Backhouse *et al.*, 2003; Khan *et al.*, 2010; Makhmudov *et al.*, 2026).

The rapid onset of symptoms confirmed the pathogen's capacity to impair the chickpea seedling establishment at both pre- and post-emergence stages. Reports of similar infection dynamics have emerged in wheat crown rot, where early root colonization leads to significant yield losses (Smiley *et al.*, 2005). In chickpeas, early root damage restricts nutrient uptake and predisposes plants to additional abiotic stress conditions, reinforcing the pathogen's primary role in the disease development.

Molecular analysis based on *TEF1-α* sequencing confirmed 99.8% similarity with reference strains and placed GPEB-65 within a considerably supported *F. culmorum* clade, suggesting affiliation with a globally conserved lineage. Nevertheless, two unique SNPs (A7G and C205T) revealed the intraspecific genetic variability and could serve as useful markers for epidemiological surveillance. Although minor nucleotide substitutions in housekeeping

genes require further validation, and such variation may correlate with the adaptive traits and toxin production (Suga *et al.*, 2014).

From phytopathological perspectives, the identification of a highly aggressive and genetically distinct *F. culmorum* population in Uzbekistan underscores the need for integrated management strategies. Integration of resistant cultivars, crop rotation, seed treatment, and molecular monitoring will be essential to mitigate the disease pressure and ensure sustainable chickpea production under regional agroecological conditions.

CONCLUSIONS

The promising study confirmed *Fusarium culmorum* as the causal agent of chickpea (*Cicer arietinum* L.) root rot in Uzbekistan through integrated morphological, pathogenicity, and molecular analyses. The isolate GPEB-65 showed high virulence, with a disease severity index of 79%, indicating its significant pathogenic potential toward chickpea seedlings. Molecular identification based on *TEF1-α* gene sequencing revealed 99.8% similarity with reference *F. culmorum* strains, and phylogenetic analysis confirmed its placement within the *F. culmorum* clade. The detection of two unique single-nucleotide polymorphisms (A7G and C205T) suggests the presence of genetic variation within local populations of *F. culmorum*. These findings provide the first molecular evidence of a genetically distinct and highly virulent *F. culmorum* population associated with chickpea root rot in Uzbekistan. The results highlight the importance of continuous phytosanitary monitoring and incorporation of pathogen diversity into chickpea breeding programs aimed at improving disease resistance and sustainable crop production.

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REFERENCES

- Abduvaliev B, Akhmadaliev B, Adilov B, Sherimbetov A, Ruzmetov DR, Abdikarimov B (2024). First report of soybean mosaic virus on soybean (*Glycine max* L.) in Uzbekistan. *J Plant Pathol.* <https://doi.org/10.1007/s42161-024-01783-0>
- Akhmadaliev B, Abduvaliev B, Adilov B, Aripova SH, Kadirova Z, Abdikarimov B, Makhmudov T, Sherimbetov A, Ruzmetov DR, Eshchanov B (2024). Preparation of polyclonal antiserum to Tomato mosaic virus and its application as a viral diagnostic test. *J Plant Biotechnol.* 51: 265–272. <https://doi.org/10.5010/JPB.2024.51.025.265>
- Alderman SC, Ocamb CM, Mellbye ME (1989). Occurrence and pathogenicity of *Fusarium culmorum* on wheat in the Pacific Northwest. *Plant Dis.* 73(4): 331–334. <https://doi.org/10.1094/PD-73-0331>
- Backhouse D, Abubakar AA, Burgess LW, Dennis JI, Hollaway GJ, Wildermuth GB, Wallwork H, Henry FJ (2003). Survey of *Fusarium* species associated with crown rot of wheat and barley in eastern Australia. *Australas. Plant Pathol.* 32(2): 255–261. <https://doi.org/10.1071/AP03014>
- Chatterton S, Harding MW, Gossen BD (2015). Pathogenicity and aggressiveness of *Fusarium* spp. causing root rot on pulse crops. *Can. J. Plant Pathol.* 37(3): 343–354. <https://doi.org/10.1080/07060661.2015.1071550>
- Geiser DM, Jiménez-Gasco MM, Kang S, Makalowska I, Veeraraghavan N, Ward TJ, Zhang N, Kuldau GA, O'Donnell K (2004). FUSARIUM-ID v.1.0: A DNA sequence database for identifying *Fusarium*. *Eur. J. Plant Pathol.* 110(5–6): 473–479. <https://doi.org/10.1023/B:EJPP.0000032386.75915.a0>
- Khan MR, Fischer S, Egan D (2010). Effect of soil moisture and temperature on crown rot development caused by *Fusarium culmorum*. *Plant Pathol.* 59(6): 1031–1038. <https://doi.org/10.1111/j.1365-3059.2010.02339.x>
- Leslie JF, Summerell BA (2006). The *Fusarium* Laboratory Manual. Blackwell Publishing, Ames, IA, USA. <https://doi.org/10.1002/9780470278376>
- Ma LJ, van der Does HC, Borkovich KA, Coleman JJ, Daboussi MJ, Di-Pietro A, Dufresne M, Freitag M, Grabherr M, Henrissat B, Houterman PM, Kang S, Shim WB, Woloshuk C, Xie X, Xu JR, Antoniw J, Baker SE, Bluhm BH, Breakspear A, Brown DW, Butchko RAE, Chapman S, Coulson R, Coutinho PM, Danchin EGJ, Diener A, Gale LR, Gardiner DM, Goff S, Hammond-Kosack KE, Hilburn K, Hua-Van A, Jonkers W, Kazan K, Kodira CD, Koehrsen M, Kumar L, Lee YH, Li L, Manners JM, Miranda-Saavedra D, Mukherjee M, Park G, Park J, Park SY, Proctor RH, Regev A, Ruiz-Roldán MC, Sain D, Sakthikumar S, Sykes S, Schwartz DC, Turgeon BG, Wapinski I, Yoder O, Young S, Zeng Q, Zhou S, Galagan J, Cuomo CA, Kistler HC, Rep M (2010). Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature* 464(7287): 367–373. <https://doi.org/10.1038/nature08850>
- Makhmudov TK, Adilov BS, Kadirova ZN, Ziyaev ZM, Sherimbetov AG, Ruzmetov DR, Abdikarimov BQ, Chorshanbiev NE, Adegbola RO, Brown JK (2026). First report of Beet western yellows virus infecting wheat in Uzbekistan. *Plant Disease* 110 (1): 253.
- Munkvold GP (2017). *Fusarium* species and their associated mycotoxins. *Plant Health Prog.* 18(3): 173–175. <https://doi.org/10.1094/PHP-03-17-0012-RV>
- Nelson PE, Toussoun TA, Marasas WFO (1983). *Fusarium* species: An Illustrated Manual for Identification. Pennsylvania State University Press, University Park, PA, USA.
- O'Donnell K, Cigelnik E, Nirenberg HI (1998). Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. *Mycologia* 90(3): 465–493. <https://doi.org/10.1080/00275514.1998.12026933>
- O'Donnell K, Rooney AP, Proctor RH, Brown DW, McCormick SP, Ward TJ, Frandsen RJN, Lysøe E, Rehner SA, Aoki T, Robert VARG, Crous PW, Groenewald JZ, Kang S, Geiser DM. (2015). Phylogenetic analyses of *Fusarium* and related taxa. *J. Clin. Microbiol.* 53(6): 1949–1960. <https://doi.org/10.1128/JCM.00062-15>
- Pasquali M, Beyer M, Logrieco A, Audenaert K (2016). Comparative genomics of *Fusarium* species producing trichothecenes. *Int. J. Food Microbiol.* 234: 21–30. <https://doi.org/10.1016/j.ijfoodmicro.2016.06.009>
- Ruzmetov DR, Sherimbetov AG, Adilov BSh (2024). First report of *Macrophomina phaseolina* causing charcoal rot in soybean (*Glycine max*) plants in Uzbekistan. *Plant Dis.* 108(7): 1958. <https://doi.org/10.1094/PDIS-12-23-2798-PDN>

- Sherimbetov AG, Adilov BSh, Ruzmetov DR (2025). First report of *Exserohilum pedicellatum* causing root rot of wheat (*Triticum aestivum*) in Uzbekistan. *Plant Dis.* 109(2): 420. <https://doi.org/10.1094/PDIS-08-24-1788-PDN>
- Sherimbetov SG, Sherimbetov AG, Adilov BSh, Ruzmetov DR, Shavkiev J (2024). Rapid detection of *Alternaria* spp. by PCR in the newly created forest plantations on the drained bottom of the Aral Sea. *Regul. Mech. Biosyst.* 15(2): 361–366. <https://doi.org/10.15421/022451>
- Smiley RW, Gourlie JA, Easley SA, Patterson LM (2005). Pathogenicity of *Fusarium* spp. associated with crown rot of wheat in the Pacific Northwest. *Plant Dis.* 89(9): 949–957. <https://doi.org/10.1094/PD-89-0949>
- Suga H, Kitajima M, Nagumo R, Tsukiboshi T, Uegaki R, Nakajima T, Kushiro M, Nakagawa H, Shimizu M, Kageyama K (2014). A single nucleotide polymorphism in the translation elongation factor 1 α gene correlates with the ability to produce fumonisin in Japanese *Fusarium fujikuroi*. *Fungal Biol.* 118(4): 402–412. <https://doi.org/10.1016/j.funbio.2014.02.005>