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Identification of *Penicillium aeris* and *Penicillium egyptiacum* in saffron corms from Morocco: Implications for plant health and crop management

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ABSTRACT

In Morocco, saffron production plays a significant role in the local economies of certain regions and relies on high-quality planting material, strict adherence to good agricultural practices and effective post-harvest management. This study aimed to assess the quality of saffron corms used as propagation material and to identify the fungal agents associated with corm rot in the main saffron-growing areas of Taliouine and Taznakht, using an integrated approach combining morphological and molecular analysis. Surveys conducted in 2022 let to the isolation of a fungal complex from necrotic tissues of infected corms. Two species within this complex, *Penicillium aeris* and *P. egyptiacum*, were identified and confirmed as the causal agents of saffron corm rot marking their first report in Morocco. Pathogenicity tests demonstrated their ability to induce typical symptoms characterized by both superficial and internal rotting. These findings fill a major gap in the understanding of saffron diseases, provide new insights into the etiology of corms rot, and lay the foundation for developing targeted strategies to prevent and control this disease, ultimately contributing to the preservation of crop yield and commercial value.

Keywords: saffron, *Penicillium aeris*, *Penicillium egyptiacum*, Morocco, pathogenicity test, molecular analysis.

INTRODUCTION

Saffron is obtained from the dried stigmas of the plant *Crocus sativus* L. (*Iridaceae*), the world's most expensive spice (Plessner and Ziv, 1999; Ourras et al., 2022a). The main producing countries are Iran (90.1%), India (4.5%), Greece (2.8%) and Spain (0.5%) (Cardone et al., 2020; Kothari et al. 2021a, 2021b b; Ourras et al., 2022b, 2025a). with 6.8 tonnes produced over 1800 ha in 2018, Morocco stands as Africa's foremost saffron-producing country (Ourras et al. 2022), with an annual turnover of 50,000,000 MAD (Ben El Caid et al., 2018). Saffron is extensively grown in the mountainous zones of Taliouine (Taroudant province) and Taznakht (Ouarzazate province), where it represents an important source of income (El Aymani et al., 2023). Saffron cultivation in these regions plays a vital role in enhancing farmers' incomes, serving as a local product that greatly contributes to the livelihoods of the local populations (El Aymani et al., 2019a, b; Ourras et al., 2025a, 2025b).

Improving saffron production requires the use of high-quality plant material, strict control of crop management practices and post-harvest processes

(Devi et al., 2011). The use of plant growth-promoting rhizobacteria (PGPR) as biofertilizers in saffron production has gained considerable attention in recent studies. This approach can help reduce the negative environmental effects associated with the overapplication of synthetic fertilizers and pesticides use (Benjelloun et al., 2021; El Allaoui et al., 2023, 2024, 2025; Laanaya et al., 2025), providing a sustainable strategy for agriculture and environmental protection (Pérez-Montaño et al., 2014; Elbouazaoui et al., 2022a, 2022b).

The propagation of *Crocus sativus* occurs vegetatively through saffron corms or bulbs (Elouark et al., 2025b, 2025c). The cultivation and expansion of this species are influenced by three main limiting factors: 1) a low rate of bulb production, 2) a decline in the vigor and yield of propagated cultivars, and 3) the health status of the corms, particularly the presence of fungal pathogens that can cause diseases affecting saffron (Devi et al., 2011). In general, corms used by farmers for saffron plantations in Taliouine and Taznakht are not carefully selected, this lack of selection has significant implications for the quality and yield of saffron produced in these areas. Furthermore, the absence of a rigorous selection process could perpetuate the use of genetically inferior corms, which might be more susceptible to diseases and environmental stresses. Between 2019 and 2022, corm samples collected from farmers showed different types of symptoms, such as root rot and corm decay, ultimately impacting the saffron vigor (El Aymani et al., 2019b). These authors isolated a fungal complex from affected saffron corms composed of several pathogenic species such as *Fusarium* (*F. solani, F. oxysporum, F. culmorum, F. roseum*), *Aspergillus* (*A. fumigatus, A. niger), Trichoderma* sp., *Rhizopus oryzae,* and *Penicillium* sp.

Ourras et al. (2023) investigated the mycoflora of dormant safffron corms and found that the lesions contained both pathogenic and saprophytic fungi, including *Fusarium solani, F. roseum, F. oxysporum, F. culmorum, Aspergillus achraceus, A. fumigatus, A. niger*. The authors of this work have not yet reported the share of each species of the fungal complex affecting corms of saffron. In addition, a number of *Penicillium* species isolated from dormant corms, accounting for 10% to 14%, have not been identified.

In this study, we conducted an in-depth examination of two species from the genus *Penicillium*, specifically focusing on their impact on saffron corms. We aimed to assess the pathogenicity of these fungi, and understand their effects on saffron crops health and productivity. Initially, we identified the *Penicillium* species present in the saffron corms through morphological and molecular techniques. Following identification, we designed a series of experiments to test their pathogenic potential.

The results of our experiments will provide valuable insights into the role of these *Penicillium* species in saffron cultivation. By understanding their pathogenic characteristics, we can develop better management practices to mitigate their impact, ultimately contributing to the sustainability and productivity of saffron farming.

MATERIALS AND METHODS

Prospecting and sampling

Surveys were conducted in two regions in Morocco known for saffron cultivation: Taliouine and Taznaght, with the objective to identify pathogenic fungi associated with the deterioration of saffron corms destined for planting. Corms were gathered from farmers and were stored in sterile bags to avoid any possible contaminations. Subsequently, the corms were transported to the laboratory for in depth mycological analysis to detect any pathogenic fungi associated with corms deterioration.

Fungal isolation

Both healthy and symptomatic corms were placed in Petri dishes lined with sterile filter paper moistened with distilled water and incubated at 25 °C for 7 days, following the procedure outlined in previous studies (Benkirane et al., 1998, 1999a, 1999b; Ouazzani Touhami et al., 2000; Meddah et al., 2011) to isolate fungal species associated with these propagating organs. Subsequently, the developed mycelial growth were isolated and transferred onto PSA (Potato Sucrose Agar) or water agar media, following the procedure reported by Douira et al. (1989, 1993) and Qostal et al., (2025). Successive transplanting from the developed fungal colonies enabled the purification of isolates (Qostal et al., 2019, 2021). A macroscopic and microscopic description of these colonies was performed, and their pathogenic potential was evaluated.

Molecular analysis

DNA extraction

Genomic DNA was isolated using the OmniPrep fungi kit (G-Biosciences, St. Louis, MO; Cat. # 786-399) following the manufacturer's guidelines. DNA was quantified using the Implen N50 Nano spectrophotometer (Implen GmbH Schatzbogen, München Waltham, Germany).

PCR amplification and sequencing

Amplification of the internal transcribed spacer (ITS) region of the rDNA was performed with a MultiGene OptiMax Thermal Cycler in a total reaction volume mixture of 20 µl containing 11 µl milli-Q water, 2 µl 10X PCR buffer, MgCl2, dNTPs, 0.2 µl x-VITA-Taq DNA polymerase, and specific primers (ITS1 and ITS4 described by White et al. (1990).), and 1µl of genomic DNA. The PCR program consisted of an initial denaturation at 95 °C for 3 min, followed by 35 amplification cycles comprising denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s), and extension at 72 °C for 1 min 25 swith a final elongation (7 min 25 s at 72 °C). PCR products were checked on a 1% agarose gel stained with innoQ DNA stain, and visualized under UV light. The products were then purified using the ExoSAP-IT kit, and ITS rDNA gene sequencing was conducted using an ABI PRISM BigDye Terminator kit and analyzed on an ABI PRISM 3130XL Genetic Analyzer.

DNA sequence alignment and phylogenetic construction

DNA sequence alignment and phylogenetic analysis were performed using the sequences generated in this study and other sequences retrieved from GenBank database. All sequences were aligned with MEGAX software (Kumar et al., 2018). The phylogenetic tree was inferred using the Neighbor-Joining (NJ) method (Saitou et al., 1987; El Alaoui et al., 2021) with 1000 bootstrap replicates to assess branch support.

Pathogenicity test

The pathogenicity test of the isolated species was conducted *in vitro* by inoculating saffron corms with mycelial explants (Msairi et al., 2025). Healthy saffron bulbs were selected, disinfected for three minutes with 5% NaClO (Sodium hypochlorite), rinsed several times with sterile distilled water and air-dried on sterile paper within a laminar flow hood. The surface-sterilized corms were slightly injured at two opposite points using a sterile needle and each wound was inoculated with a 4 mm mycelial plug taken from the actively growing margin of the two *Penicillium* isolates. The explants were placed on the corm wounds with the mycelium side down. Control corms received the same treatment but were inoculated only with an agar disc. All inoculated corms were incubated at 28 °C, and lesion development was periodically observed and recorded.

RESULTS

Morphological analysis

Incubation of symptomatic corms on moistened with sterile filter paper resulted in the appearance of bluish-green mycelial masses and conidia, identifying the isolates as belonging to the *Penicillium* genus (Figure 1).

Figure 1. The appearance of *Penicillium* sp. on saffron corms after 3 days of incubation using the blotter paper method under laboratory conditions

Observations of the colonies cultured on PSA medium provided both macroscopic and microscopic information for describing the two *Penicillium* isolates associated with saffron corms intended for planting.

On PSA medium (25 °C), the *Penicillium* sp.$_1$ colonies showed a slow growth, a diameter of 19 mm to 24 mm in 8 days (Figure 2 and 3). The colonies generally exhibit a central white cottony mycelium, while the reverse appears yellowish to pale. After 8 to 10 days of incubation, conidiogenesis remains scarcely visible, and the conidiophores show branching structures. The conidiophores exhibited branching structures that generated groups of monoverticulated, biverticulated or occasionally terverticillate metulae. These metulae measured about 9.50 × 2.4 µm and each supported 4 ampulliform phialides, approximately 6.1 × 2.2 µm in size. The conidia were smooth-walled, globose to subglobose, about 2.1 µm in diameter, and arranged in regular chains. Molecular analyses confirmed that this *Penicillium* isolate corresponded to *P. egyptiacum*. *Penicillium* sp.$_2$ colonies developped slowly on PSA medium at 25 °C (Figure 4 and 5). The surface coloration varied from greenish-white to yellowish-white, while the

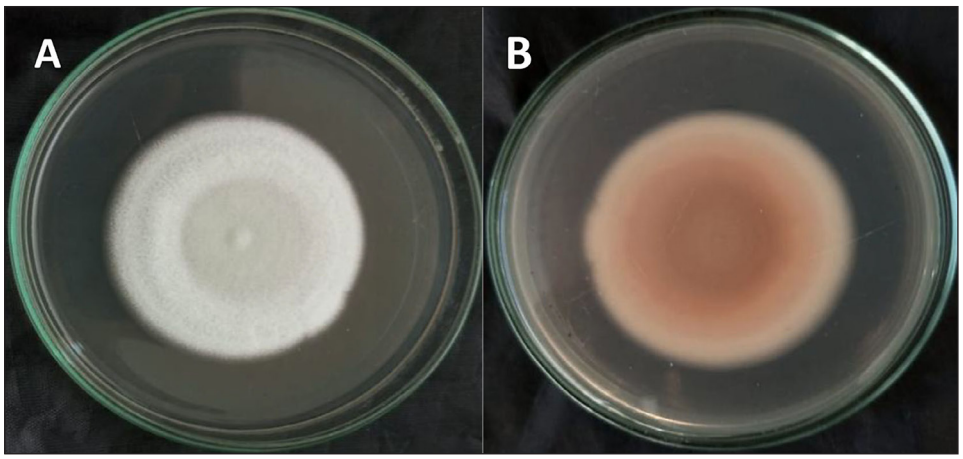

Figure 2. Macroscopic appearance of the colony of *Penicillium* sp.$_1$ (*Penicillium egyptiacum)* cultivated on PSA for 7 days (A) and (B) reverse side of the culture

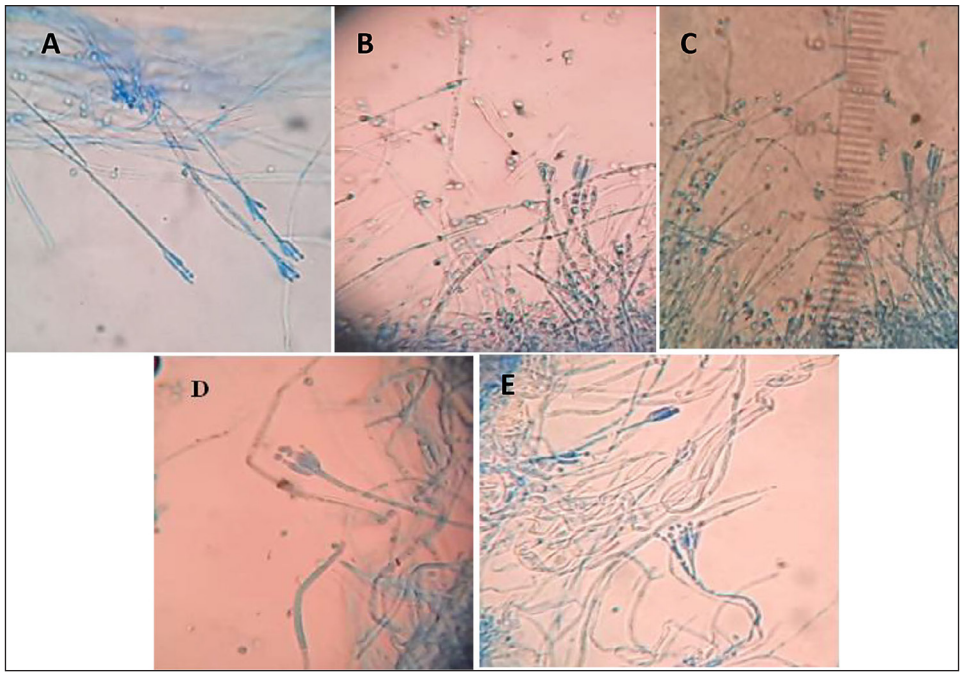

Figure 3. Microscopic observation of conidiophores, phialides and conidia of *P. egyptiacum* (x400)

reverse sides appeared greenish-orange to greyish-white. The conidiophores bear flask-shaped phialides whose dimensions range from 3.2–7.1 × 1.9–3.2 µm (average 4.8 ± 0.5 × 2.3 ± 0.2 µm, n = 50). Conidia were globose with rough to echinulate walls, ranging from 1.8–2.3 × 1.8–2.4 µm (mean = 1.9 ± 0.2 × 2.1 ± 0.23 µm, n = 50), with a width-to-length ratio close to 0.97. No sclerotia, Conservation organs, were detected. Molecular analyses confirmed the isolat as *Penicillium aeris*.

Molecular analysis

The rDNA ITS sequences from *Penicillium* isolates were deposited in GenBank under the accession numbers (GenBank: OP389143.1; OP389142.1; OP379573.1; OP389145.1; OP389144.1; OP389133.1) (Figure 6).

Pathogenicity test

Each of the fungal isolates was able to alter the inoculated corms on which light to dark brown lesions gradually developed, reaching an average diameter of 1.46 cm and 1.15 cm for *P. aeris* and *P. egyptiacum* respectively (Figure 7). No symptoms of disease were observed on the control. Corm rot, observed after 5 days of incubation, progressed significantly and the diameter of the lesions formed significantly enlarged transversely and longitudinally in the deep tissues of the corms, 15 days after inoculation. Over time, lesions expanded to cover about 30% to 80% of the corm surface, turning from brownish to bluish-grey as *P. aeris* and *P. egyptiacum* progressively colonized the tissues. The interior of the corms has also become necrotic (Figure 8). These

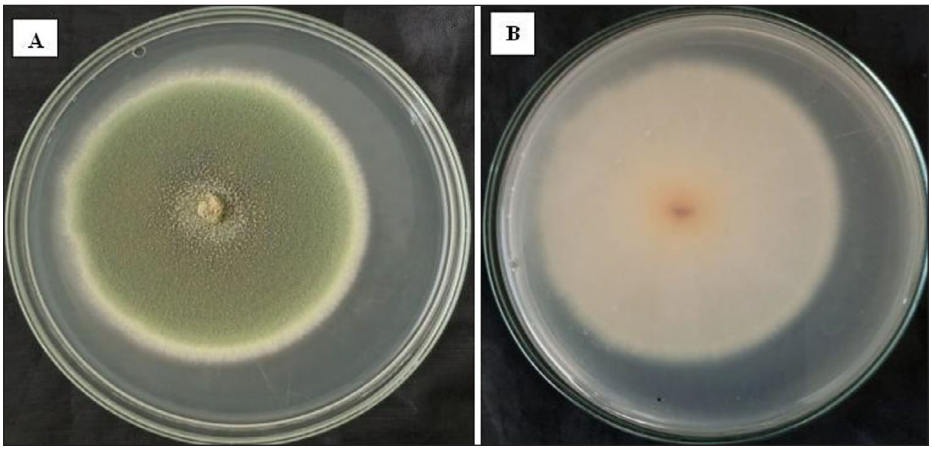

Figure 4. Macroscopic morphology of *Penicillium aeris* colony after 7 days of growth on PSA medium: (A) obverse and (B) reverse sides

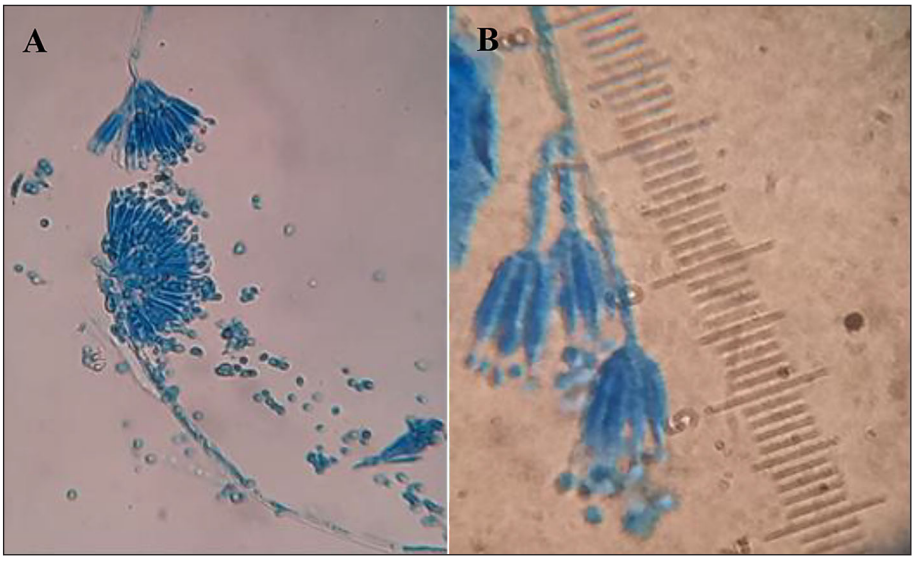

Figure 5. (A) and (B) Microscopic observation of conidiophores, phialides and conidia of P. aeris (×400)

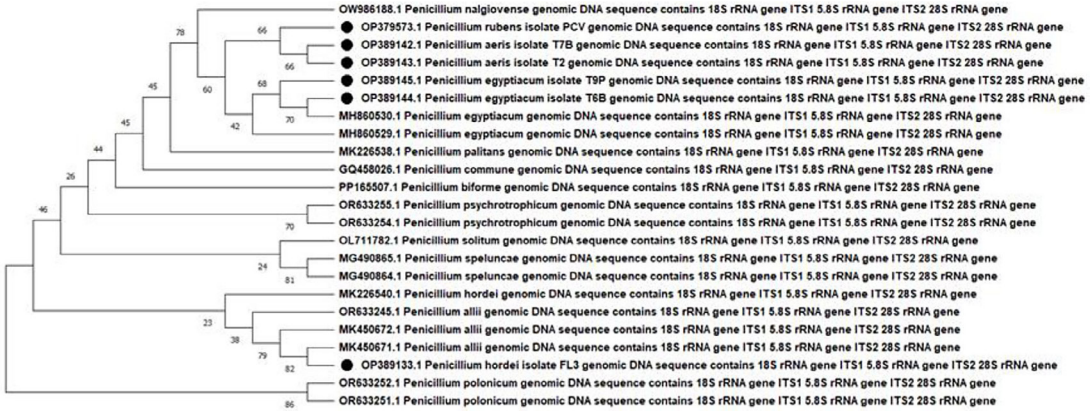

Figure 6. Neighbor-joining phylogenetic tree constructed from complete 18S SSU rDNA nucleotide sequences and other sequences retrived from GenBank. The black circle represents the isolates of the current study (GenBank: OP389143.1; OP389142.1; OP379573.1; OP389145.1; OP389144.1; OP389133.1)

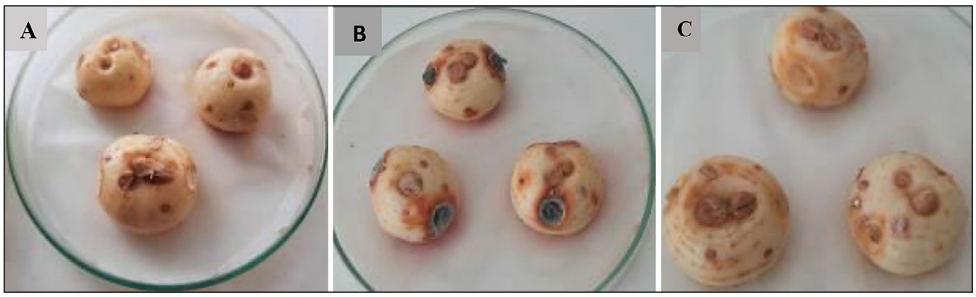

Figure 7. Appearance of necrotic lesions developed around bulb inoculation sites by *Penicillium* isolates tested after 7 days of incubation. Lesions on corms inoculated with saffron corms control (A), *Penicillium aeris* (B), and *P. egyptiacum* (C)

results show that *P. aeris and P. egyptiacum,* isolated from corms intended for planting saffron, are endowed with a significant pathogenic power on these seeds. Both species have been shown to induce necrotic lesions, rots, superficial and untenable, which develop, decolorize and deform, over time, the inoculated corms.

DISCUSSION

In their inventory of saffron-associated fungi, Mouden et al. (2024) reported 142 species belonging to three phyla: Ascomycota, Basidiomycota, Mucoromycota. Among these, 26 *Fusarium* species were identified, making this genus the most abundant, followed by *Aspergillus* with 15 species and *Penicillium* with 14. Almost all *Penicillium* species isolated from saffron corms are considered either true pathogens or facultative parasites of these propagation organs. Previous studies have reported several *Penicillium* species associated with saffron corms, including *P. crocicola* (Yamamoto et al., 1954), *P. corymbiferum* (Gupta et al., 2011), *P. canescens* (Taheri et al., 2021; Wani et al., 2016, 2017), *P. citrinum* (Belfiori et al., 2021; Tian et al., 2022), *P. citreosulfuratum* (Tian et al., 2022; Hu et al., 2022), *P. cyclopium* (Cappelli and Di Minco, 1999; Fiori, 2002), *P. chrysogenum* (Shuwen et al., 2019), *P. digitatum* (Saeedizadeh, 2014, 2016; Najjar et al., 2017; Zheng et al., 2012) and *P. pinophilum* (Wani et al., 2016, 2017). A number of these species have been reported to compromise postharvest quality, as well as the vitality, propagation and yield of saffron (Rubio-Moraga et al., 2013). worldwide saffron production has been negatively affected by come rot caused by pathogenic fungi, particularly species belonging to the genera *Fusarium, Rhizoctonia* and *Penicillium* (Belfiori et al., 2021; Mansotra et al., 2023). Other studies have also identified a broader range of fungi associated with corm decay, including *Macrophomina, Aspergillus, Sclerotium, Phoma, Stromatinia, Rhizoctonia, Rhizopus, Penicillium, Fusarium, Cochliobolus, Safostereum, Talaromyces*, as well

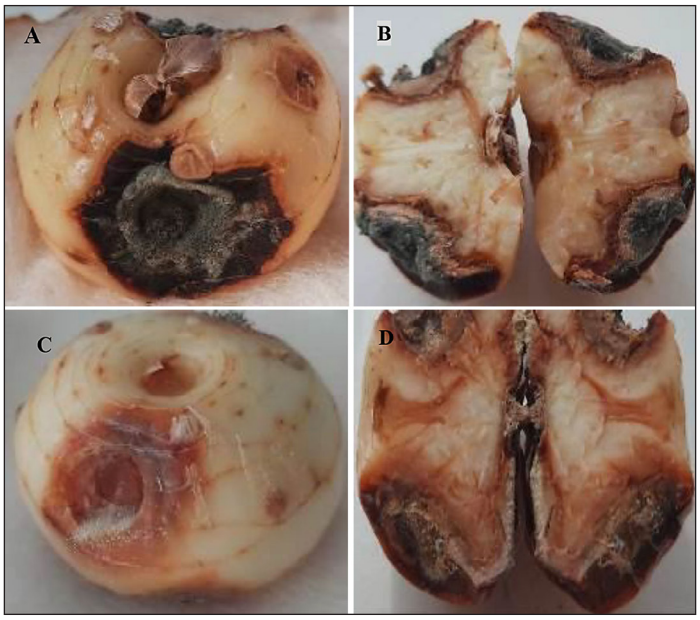

Figure 8. Rot developed after inoculation of corms by *Penicillium aeris* and *P. egyptiacum*: (A) superficial rot of corms, inoculated pat *P. aeris,* manifested by dark brown lesions, with development of a blue-greyish mycelial felting protecting from fructification; after 15 days of incubation; (B) rot spread to deep tissues, with an onset of atrophy of corm edges; (C) development of superficial dry rot, accompanied by discoloration of corms, reddish gray, and the onset of appearance of an airborne mycelial bearing fruit; (D) alteration of corms inoculated with *P. egyptiacum,* superficial and internal rot, with discoloration of corms, after 15 days of incubation

as *Penicillium aeris* and *P. egyptiacum.* These last two species, isolated from saffron corms cultivated in Morocco, have not previously been reported in the literature as saffron-related fungi (Wani et al., 2016, 2018; Ahrazem et al., 2010) and can be considered as two new species for saffron.

Penicillium aeris and *Penicillium egyptiacum* have been shown to infect healthy, seemingly inoculated saffron corms. The necrotic lesions induced after inoculation developed both on the surface and within the corm tissues. Over time, these lesions caused bleaching and deformation of the corms, accompanied by the appearance of greenish mycelial felting and carriers of organs of asexual reproduction of *Penicillium.* Gupta and Vakhlu (2015) also isolated *Penicillium* sp. from infected corms with typical rot symptoms. Several *Penicillium* species have been identified as pathogens of saffron corms. For instance, *Penicillium citreosulfuratum* and *Penicillium citrinum* isolated within a fungal complex that also included *Fusarium solani, Stromatinia gladioli* and *Rhizopus oryzae,* have been reported to cause rot symptoms in saffron (Hu et al., 2021; Belfiori et al., 2021). Additionally, *P. digitatum* (Saeedizadeh, 2014, 2016), *P. pinophilum* (Wani et al., 2016, 2017) and *P. solitum* (Zhang et al., 2020) are known to contribute to corm rot. Studies by Wani et al. (2016, 2017) and Ahmad et al. (2022) noted that *P. pinophilum* can induce more severe rot in saffron corms. Moreover, *P. crocicola* and *P. chrysogenum* have been associated with seedling collapse, wilting of saffron shoots, and development of dark lesions beneath the plant sheaths (Ahrazem et al., 2010; Cappelli et al., 1991). In contrast, other species of the genus *Penicillium,* isolated from corms, are considered to be optional parasites, capable of inducing moderate corm rot, such as *Penicillium cyclopium* (Cappelli and Di Minco, 1999) and *Penicillium canescens* (Wani et al., 2016; 2017). Ambardar et al. (2016) noted that other *Penicillium* species are beneficial, acting as growth biostimulants and biological control agents (Hassine et al., 2022). some species, such as *P. rugulosum* and *P. bilaiae,* are also known to solubilize phosphate (Wakelin et al., 2004a,b; Fankem et al., 2014). Extending these findings, filamentous *Penicillium* species in general are recognized for colonizing the rhizosphere, where they interact beneficially with plant roots and contribute significantly to the phosphate cycle (Mehta et al., 2019). Recently, a strain of *P. guanacastense* was reported to solubilize aluminum phosphate, highlighting the continued discovery of functional traits in this genus that support plant nutrition (Qiao et al., 2020).

CONCLUSIONS

This study enriches current knowledge on saffron corm rot by identifying *Penicillium aeris* and *P. egyptiacum* as new pathogens and confirming their pathogenicity. The combined application of morphological and molecular tools proved effective for the accurate identification of the two fungal species. The results obtained provide a solid foundation for future epidemiological studies of saffron fungal pathogens and for understanding the role each pathogen plays in damaging the corms and consequently the plants that will grow from these corms. The presence of *Penicillium aeris* and *P. egyptiacum* on the corms suggests that serious economic losses are to be expected in the coming years. Therefore, it is important to consider these pathogens in future integrated pest management programs to reduce saffron yield losses in Morocco.

Acknowledgments

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REFERENCES

1. Ahmad T, Bashir A, Farooq S, Riyaz-Ul-Hassan S (2022) *Burkholderia gladioli* E39CS3, an endophyte of *Crocus sativus* Linn., induces host resistance against corm-rot caused by *Fusarium oxysporum*. *J. Appl. Microbiol. 132*, 495–508. https://doi.org/10.1111/jam.15190
2. Ahrazem O, Rubio-Moraga Á, Castillo-Lopez R, Trapero A, Gómez-Gómez L (2010) *Crocus sativus* pathogens and defense responses. Funct. Plant Sci. *Biotechnol. 4*(2), 81–90
3. Ambardar S, Singh H R, Gowda M, Vakhlu J (2016) Comparative metagenomics reveal phylum level temporal and spatial changes in mycobiome of belowground parts of *Crocus sativus*. *PloS One 11*, e0163300. https://doi.org/10.1371/ journal.pone.0163300
4. Belfiori B, Rubini A, Riccioni C (2021) Diversity of endophytic and pathogenic fungi of saffron (*Crocus sativus*) plants from cultivation sites in Italy. *Diversity. 13*, 535. https://doi.org/ 10.3390/d13110535
5. Ben El Caid M, Salaka L, Lachcheb M, Lagram K, Atyane L H, El Mousadik A, Serghini MA (2018) Provenance and site effects on progeny saffron corms *Crocus sativus* L.). *American Journal of Innovative Research and Applied Sciences 7*(4), 198–207.
6. Benjelloun I., Alami I.T., Khadir M.E., Douira A., Udupa S.M., (2021). Co-inoculation of mesorhizobium ciceri with either bacillus sp. or enterobacter aerogenes on chickpea improves growth and productivity in phosphate-deficient soils in dry areas of a mediterranean region. *Plants, 10*(3), 1–15, 571.
7. Benkirane R, Douira A, Selmaoui K, Lebbar S (1999a) Identification of pathotypes in moroccan population of the rice blast fungus (Magnoporthe grisea) originaire du riz et de Stenotaphrum secundatum. *Journal of phytopathology 148*: 95–99.
8. Benkirane R, Douira A, Selmaoui K, Lebbar S (1999b) Identification of pathotypes in a Moroccan population of the rice blast fungus Magnaporthe grisea. *Phytopathol. Mediterr 38*, 126–131.
9. Benkirane R, Tajani M, Selmaoui K, Lebbar S (1998) Maiting type of Magnaporthe grisea population in Morocco. *Phytopath. Medit 37*, 119–121.
10. Cappelli C, Buonaurio R, Polverari A (1991) Occurrence of *Penicillium corymbiferum* on saffron in Italy. *Plant Pathology 40*(1), 148–149.
11. Cappelli C, Di Minco G (1999) Three-years of trials on saffron diseases in Abruzzo (Central Italy) [*Crocus sativus* L.]. *Inf Fitopatologia 49*.
12. Cardone L, Castronuovo D, Perniola M, Cicco N, Candido V (2020) Saffron (*Crocus sativus* L.), the king of spices: an overview. *Sci Hortic 272*, 109560
13. Devi K, Sharma M, Singh M, Singh Ahuja P (2011) In vitro cormlet production and growth evaluation under greenhouse conditions in saffron (*Crocus sativus* L.)–a commercially important crop. *Eng Life Sci 11*, 189– 194.
14. Douira A, Benkirane R, Touhami A, Ouazzani T, Okeke B, Lahlou H (1993) Verticillium Wilt of Pepper (*Capsicum annuum*) in Morocco. *Journal of Phytophathology 143*, 467–470.
15. Douira A, Lahlou H (1989) Variabilité de la spécificité parasitaire chez Verticillium albo-atrum Reinke et Berthold, forme à microsclérotes. Cryptogamie Mycologie 10:19–32
16. El Alaoui, M. A., Msairi, S., Kaissoumi, H. E., Chliyeh, M., Selmaoui, K., Benkirane, R., Ouazzani Touhami, A., Douira, A. (2021). Phylogenetic diversity of a natural population of Colletotrichum spp. isolated from different substrates in Morocco. *Plant Cell Biotechnology and Molecular Biology 22*(1–2), 84–94.
17. El Allaoui N., Douira A., Benbouazza A., Ferrahi M., Achbani E/L, Habbadi K., (2024). Effect of plant

growth-promoting rhizobacteria (PGPRs) on tuber storage of two potato varieties. *Arab Society for Plant Protection, 42*(2). https://doi.org/10.22268/AJPP-001242

18. El Allaoui N., Yahyaoui H., Douira A., Benbouazza A., Achban, E. H., Habbadi K., (2025). Mitigating the effects of climate conditions on potato cultivation: exploring hydroabsorbents and pgprs as sustainable alternatives. *Journal of Microbiology, Biotechnology and Food Sciences, 14*(5), e10926. https://doi.org/10.55251/jmbfs.10926
19. El Allaoui, N., Yahyaoui, H., Douira, A., Benbouazza, A., Ferrahi, M., Achbani, E.H., Habbadi, K., (2023). Assessment of the impacts of plant growth-promoting micro-organisms on potato farming in different climatic conditions in Morocco. *Microbiol. Res. 14*, 2090–2104. https://doi.org/10.3390/microbiolres14040141
20. El Aymani I, Chliyeh M, Selmaoui K, Mouden M, El Gabardi S, Ouazzani Touhami A, Benkirane R, Douira A (2019a) Effect of a composite endomycorrhizal inoculum on the growth of saffron plants (*Crocus sativus* L.) and the multiplication of corms. *Plant Cell Biotechnology and Molecular Biology. 20*(23&24), 1122–1136.
21. El Aymani I, El Gabardi S, Artib M, Chliyeh M, Selmaoui K, Ouazzani Touhami A, Benkirane R, Douira A (2019b) Effect of the number of years of soil exploitation by Saffron cultivation in Morocco on the diversity of endomycorrhizal Fungi. *Acta Phytopathologica et Entomologica Hungarica, 54*(1), 71–86.
22. El Aymani I, Ourras S, Mouden N, Chliyeh M, Selmaoui K, Msairi S, Benkirane R, El Modafar C, Ouazzani Touhami A, Douira A (2023) Effect of endomycorrhizal fungi inoculum on agro morphological behavior and productivity of saffron (*Crocus sativus* L.) under water and salinity stress. *Acta Universitatis Agriculturae et Silviculturae Mendelianae Brunensis, 71*(4), 183–192. https://doi.org/10.11118/actaun.2023.013
23. Elbouazaoui A, Sijilmassi B, Maafa I, Douira A, Kemal SA, (2022a). Biocontrol activity of Bacillus, Paenibacillus and Pseudomonas against Fusarium wilt of chickpea in Morocco. *Acta Agriculturae Scandinavica, Section B-Soil & Plant science, 72*(1), 847–859. https://doi.org/10.1080/09064710.2022.2100819
24. Elbouazaoui A, Douira A, Ilyass Maafa I, Kemal SA, (2022b). Integrating sowing date with chickpea genotypes in managing fusarium wilt in Morocco. *Agriculture (Switzerland), 12*(6), 773.
25. Elouark M, El Aymani I, Ourras S, Mouden N, Chliyeh M, Karima Selmaoui S, Msairi M, Benkirane R, El Alaoui MA, Ouazzani Touhami A, Douira A, (2025b). *Safran (Crocus sativus L.): A Bibliographic Review*. Book chapter in Technical Innovation and Modeling in the Biological Sciences, ed. Jamal Mabrouki, 433–490. IG-Global. https://www.igi-global.com/chapter/safran-crocus-sativus-l/378418
26. Elouark M, Ourras S, Selmaoui K, El Alaoui MA, Ouazzani Touhami A, Douira A, (2025a). Moroccan Trichoderma species: a distinctive source of volatile organic compounds. *Egyptian Journal of Botany, 65*(2), 89–108.
27. Fankem H, Ngo Nkot L, Nguesseu Njanjouo G, Tchuisseu Tchakounte Gylaine V, Tchiazé Ifoué AV, Nwaga D, (2014) Rock phosphate solubilisation by strains of *Penicillium* Spp. Isolated from Farm and Forest Soils of three Agro Ecological Zones of Cameroon. *American Journal of Agriculture and Forestry, 2*(2), 25–32. https://doi.org/10.11648/j.ajaf.20140202.12
28. Fiori M, (2002) *Avversità*. In: Zafferano. Storia, Cultura, Coltivazione e Impiego a San Gavino Monreale e in Sardegna. (F. Sanna, ed.) E.R.S.A.T. Centro Zonale di Guspini. Medio Campidano, Sardinia, Italy, 68–73.
29. Gupta R, Vakhlu J, (2015) Native *Bacillus amyloliquefaciens* W2 as a potential biocontrol for *Fusarium oxysporum* R1 causing corm rot of *Crocus sativus*. *Eur. J. Plant Pathol. 143*, 123–131. https://doi.org/10.1007/s10658-015-0670-3
30. Gupta V, Kalha CS, Razdan VK, Dolly, (2011) Etiology and management of corm rot of saffron in Kishtwar District of Jammu and Kashmir, India. *J Mycol Plant Pathol 41*(3), 361–366.
31. Hassine M, Aydi BAR, Jabnoun KH, Daami RM, (2022) Soil-borne and compost-borne *Penicillium* sp. and *Gliocladium* spp. as potential microbial biocontrol agents for the suppression of anthracnose-induced decay on tomato fruits. *Egypt J Biol Pest Co. 32*, 1–12. https://doi.org/10.1186/S41938-022-00519-5
32. Hu S, Sun W, Wang X, Wang L, Li W, (2021) First report of black spot caused by *Penicillium citreosulfuratum* on saffron in Chongming Island, China. *Plant Dis 106*(2), 346–776. https://doi.org/10.1094/PDIS-05-21-1038-PDN
33. Hu S, Sun W, Wang X, Wang L, Li W, (2022) First report of black spot caused by *Penicillium citreosulfuratum* on saffron in Chongming Island, China. *Plant Disease, 106*(2), 760.
34. Kothari D, Thakur M, Joshi R, Kumar A, Kumar R, (2021a) Agro-climatic suitability evaluation for saf fron production in areas of Western Himalaya. *Front Plant Sci 12*, 408.
35. Kothari D, Thakur R, Kumar R, (2021b) Saffron (*Crocus sativus* L.): gold of the spices—a comprehensive review. Hortic Environ Biotechnol 1–17.
36. Kumar S, Stecher G, Li M, Knyaz C, Tamura K (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular*

biology and evolution 35(6), 1547–1549. https://doi.org/10.1093/molbev/msy096

37. Laanaya J Soukaina Msairi S Ouazzani Touhami A Douira A, (2025). Unlocking the potential of Cannabis sativa L. – interactions with microorganisms for growth, protection and cannabinoid production: A review. *Ecological Engineering & Environmental Technology, 26*(9), 364–375.
38. Li Y, Guo Q, Wei X, Xue Q, Lai H (2019) Biocontrol effects of *Penicillium griseofulvum* against monkshood (*Aconitum carmichaelii* Debx.) root diseases caused by *Sclerotium rolfsi* and *Fusarium* spp. *J. Appl. Microbiol. 127*, 1532–1545. https://doi.org/10.1111/jam.14382
39. Mansotra R, Ali T, Bhagat N, Vakhlu J (2023) Injury and not the pathogen is the primary cause of corm rot in *Crocus sativus* (saffron). *Front. Plant Sci. 14*, 1074185. https://doi.org/10.3389/fpls.2023.1074185
40. Meddah N, Ouazzani Touhami A, Benkirane R, Douira A, (2011). Etude du pouvoir pathogène de quelques espèces de Fusarium sur le bananier sous serre au Maroc, *Bulletin de La Société Royale Des Sciences de Liège, 80*, 939–952.
41. Mehta P, Sharma R, Putatunda C, Walia A, (2019) *Endophytic fungi: role in phosphate solubilization.* In Advances in Endophytic Fungal Research. Fungal Biology (ed. Singh B.), 183–209.
42. Mouden N, Ourras S, Elouark M, El Aymani I, El Alaoui MA, Ouazzani Touhami A, Douira A (2024) Checklist of fungal species associated with saffron plants (*Crocus sativus* L.). *Community Practitioner. 21*(7), 2279–2310.
43. Najjar S, Mohammadi A, Asgari B, Mohammadi AH, (2017) Aflatoxin-producing *Aspergillus* species from saffron field soils in the South Khorasan province of Iran. *Archives of Phytopathology and Plant Protection. 50*(7–8), 349–360. https://doi.org/10.1080/03235408.2017.1316040
44. ORMVAO, (2019) Office régional de mise en valeur agricole d'Ouarzazate. 2019. *Les registres de la production et des prix de vente du Safran.* Ministre Marocain de l'Agriculture et de la Pêche Maritime, Ouarzazate, Morocco.
45. Ouazzani Touhami A, Ennafah B, El Yachioui M, Douira A, (2000) Pathogénie comparée de 4 espèces *d'Helminthosporium* obtenues à partir des plantes malades de riz au Maroc. *Journal of Phytopathology. 148*, 221–226.
46. Ourras S, El Aymani I, Mouden N, El Gabardi S, Adnani M, Selmaoui K, Artib M, Benkirane R, El Modafar C, Ouazzani Touhami A, Douira A, (2022) *Saffron endomycorrhizae: diversity and effect on plant growth and corm formation.* Book Chapter in Arbuscular Mycorrhizal Fungi in Agriculture - New Insights, Edited by Rodrigo Nogueira de Sousa, 13–14.
47. Ourras S, El Aymani I, Mouden N, Selmaoui K, Msairi S, Elouark M, Benkirane R, El Modafar C, Ouazzani Touhami A, Douira A, (2023) Mycoflora of Dormant Crocus Sativus Corms in Morocco. In: Kacprzyk, J., Ezziyyani, M., Balas, V.E. (eds) *International Conference on Advanced Intelligent Systems for Sustainable Development*. AI2SD 2022. Lecture Notes in Networks and Systems, vol 713. Springer, Cham. https://doi.org/10.1007/978-3-031-35248-5_43.
48. Ourras S, EL Gabardi S, El Aymani I, Mouden N, Chliyeh M, Selmaoui K, Msairi S, Benkirane R, El Modafar C, Ouazzani Touhami A, Douira A, (2022) Diversity of arbuscular mycorrhizal fungi in the rhizosphere of saffron (*Crocus sativus*) plants along with age of plantation in Taliouine region in Morocco. *Acta Biologica Szegediensis 65*(2), 199–209. https://doi.org/10.14232/abs.2021.2.199-209
49. Ourras S, El Ouark M, El Aymani I, Msairi S, Selmaoui K, El Alaoui MA, Mouden N, Ouazzani Touhami A, Douira A, (2025). *Antifungal potential of Trichoderma sp. against three species of fusarium genus: responsible for the root rot of the saffron corms (Crocus sativus L.).* Book chapter in Obstacles Facing Hydrogen Green Systems and Green Energy, ed. Jamal Mabrouki, 33–50. IGI GLOBAL, https://www.igi-global.com/chapter/antifungal-potential-of-trichoderma-sp-against-three-species-of-fusarium-genus/379734
50. Ourras S, El Ouark M, El Aymani S, Msairi S, Selmaoui S, El Alaoui ME, Mouden N, Ouazzani Touhami A, Douira A, (2025) *Quantitative Estimation of Phosphate-Solubilizing Capacity in Fungal Endophytes of Saffron Corms.* Book chapter in Technical Innovation and Modeling in the Biological Sciences, ed. Jamal Mabrouki, 407–432. IGGlobal. ttps://www.igiglobal.com/chapter/quantitative-estimation-of-phosphate-solubilizing-capacity-in-fungal-endophytes-of-saffron- corms/378417
51. Ourras S, El Ouark M, Msairi M, El Aymani I, Mouden M, Selmaoui K, Mouria A, Benkirane R, Ouazzani Touhami A, Douira A, (2025) *Fungal Species Carried by Corms Intended for Saffron Cultivation in Morocco*. Book chapter in Technical Innovation and Modeling in the Biological Sciences, ed. Jamal Mabrouki, 181–216. IGGlobal. https://www.igi-global.com/chapter/fungal-species-carried-by-corms-intended-for-saffron-cultivation-in-morocco/378406
52. Ourras S, Elouark M, El Aymani I, Msairi S, Chliyeh M. Selmaoui K, El Alaoui MA, Mouden N, Ouazzani Touhami A, Douira A, (2025) *First Report of Botrytis Cinerea on Saffron Corms in Morocco.* Book chapter in Technical Innovation and Modeling in the Biological Sciences, ed. Jamal Mabrouki, pp: 165-180.. IGGlobal. https://www.igi-global.com/chapter/first-report-of-botrytis-cinerea-on-saffron-

corms-in-morocco/378405

53. Pérez-Montaño F, Alías-Villegas C, Bellogín RA, Del Cerro P, Espuny M R, Jiménez-Guerrero I,… Cubo T, (2014) Plant growth promotion in cereal and leguminous agricultural important plants: from microorganism capacities to crop production. *Microbiological research*, *169*(5–6), 325–336.
54. Plessner O, Ziv M, (1999) *In vitro propagation and secondary metabolite production in Crocus sativus L.* In: Negbi M (ed) Saffron: Crocus sativus L. Harwood Academic Publishers, Amsterdam, pp 137–148.
55. Qiao H, Zhang SH, Dong Y, Yang Y, Xu R, Chen B, … Li CW, (2020) Chrysomutanin and related meroterpenoids from a DES mutant of the marine-derived fungus *Penicillium chrysogenum* S-3-25. *Natural Product Research. 36*(7), 1834–1841. https://doi.org/10.1080/14786419.2020.1819271
56. Qostal S., Kribel S., Chliyeh M., Mouden N., Selmaoui K., Ouazzani Touhami A., Serghat S., Benkirane R., Douira A., (2021). First report of Fusarium redolens causing root rot disease of wheat and barley in Morocco. *Current Research in Environmental & Applied Mycology (Journal of Fungal Biology), 11*(1), 263–273.
57. Qostal S, Kribel S, Chliyeh M, Selmaoui K, Ouazzani Touhami A, Serghat S, Benkirane R, Douira A, (2019) *Curvularia spicifera*, a parasite of the fungal complex of root rot of wheat and barley in Morocco. *Plant Cell Biotechnology and Molecular Biology 20*(9&10), 354–365.
58. Qostal S, Kribel S, Mouden N, El Alaoui MA, Selmaoui K, Benkirane R, Ouazzani Touhami A, Douira A, (2025). *Fusarium falciforme*, another causal agent of root rot of wheat and barley varieties in Morocco. *3 Biotech 15*, 165. https://doi.org/10.1007/s13205-025-04333-2
59. Rubio-Moraga Á, Gómez-Gómez L, Trapero A, Castro-Díaz N, Ahrazem O, (2013) Saffron corm as a natural source of fungicides: the role of saponins in the underground, *Ind. Crops Prod. 49*, 915–921, https://doi.org/10.1016/j.indcrop.2013.06.029
60. Saeedizadeh A, (2014) Identification of some saffron corm rot fungi and their control. *Saffron Agronomy & Technology. 2*(3), 213–205.
61. Saeedizadeh A, (2016) Identification of some Saffron corm rot fungi and their control. *Saffron Agronomy & Technology 4*, 37–37.
62. Saitou N, Masatoshi N, (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular biology and evolution 4*(4), 406–25. https://doi.org/10.1093/oxfordjournals.molbev.a040454
63. Shuwen H, Xi Y, Liqin L, Yumei Y, Guifen Z, Chong Y, Yan D, Xiaodong Q, (2019) Limiting factors of saffron corm production from the perspective of microorganisms. Sci. Hortic 247, 165–174.
64. Taheri F, Habibipoor R, Rajabi M (2021) Isolation and molecular identification of endophytic fungi in Saffron (*Crocus sativus* L.). *12th National and 4th International Biotechnology Congress of the Islamic Republic of Iran*, Auhust 22–24, Iran.
65. Tian L, Hu S, Wang X, Guo Y, Huang L, Wang L, Li W, (2022) Antagonism of rhizosphere *Streptomyces yangpuensis* CM253 against the pathogenic fungi causing Corm Rot in Saffron (*Crocus sativus* L.). Pathogens. 11, 1195. https://doi.org/10.3390/pathogens11101195.
66. Wakelin SA, Warren RA, Harvey PR, Ryder MH (2004b) Phosphate solubilization by *Penicillium* spp. closely associatedwith wheat roots. Biol. Fertil Soils. 40: 36–43
67. Wakelin SA, Warren RA, Ryder MH (2004a) Effect ofsoil properties on growth promotion of wheat by *Penicillium radicum*. *Aust. J. Soil Res. 42*, 897–904.
68. Wani ZA, Ahmad T, Nalli Y, (2018) *Porostereum* sp., associated with saffron (*Crocus sativus* L.), is a latent pathogen capable of producing phytotoxic chlorinated aromatic compounds. *Curr. Microbiol. 75*, 880–887.
69. Wani ZA, Kumar A, Sultan P, Bindu K, Riyaz-Ul Hassan S, Ashraf N, (2017) Mortierella alpina CS10E4, an oleaginous fungal endophyte of Crocus sativus L. enhances apocarotenoid biosynthesis and stress tolerance in the host plant. *Sci. Rep. 7*, 8598.
70. Wani ZA, Mirza DN, Arora P, Riyaz-ul-Hassan S, (2016) Molecular phylogeny, diversity, community structure, and plant growth promoting properties of fungal endophytes associated with corms of saffron plant: An insight into the microbiome of *Crocus sativus* Linn. *Fungal Biol. 120*, 1509–1524.
71. White TJ, (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In *PCR protocols a guide to methods and applications*, 315–322.
72. Yamamoto W, Omatsu T, Takami K, (1954) Studies on the corm rots of *Crocus sativus* L. on saprophytic propagation of *Sclerotinia gladioli* and *Fusarium oxysporum* f. sp. *gladioli* on various plants and soils. *Sci. Rep. Hyogo Univ. Agric. 1*: 64–70.
73. Zhang T, Huang C, Deng C, Zhang Y, Feng Y, Hu, Wang R, Zhao L, Wang Y, Kai G, (2020) First report of corm rot on saffron caused by *Penicillium solitum* in China. *Plant Disease 104*(2), 579–579.
74. Zheng CJ, Li L, Zou J Ping, Han T, Qin LP, (2012) Identification of a quinazoline alkaloid produced by *Penicillium vinaceum*, an endophytic fungus from *Crocus sativus*. *Pharmaceutical Biology. 50*(2), 129–133. https://doi.org/10.3109/13880209.2011.569726