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A review of *Fusarium redolens* Wollenw. as an emerging plant pathogen in Iran

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Abstract: This study presents scientific research on *Fusarium redolens* Wollenw. A systematic search of the Scopus database from 1956 to 2023 yielded 201 indexed documents. *F. redolens* is an emerging pathogen with a significant impact on pulse crops. Population growth, especially in developing countries, creates a primary problem: food availability, especially protein sources. Chickpeas are an important crop in western Iran, especially in Kermanshah province. Until 2019, most studies attributed chickpea yellowing and root rot to *Fusarium oxysporum* and *Fusarium solani*, respectively. To manage this crop, previous recommendations included planting cereals such as barley and wheat due to the presence of *F. oxysporum* formae speciales in the soil. However, *F. redolens* has now been identified as the major cause of chickpea yellowing and root rot, especially in the western provinces. This Fusarium species have been isolated from 54 species of 50 genera and 29 plant families, with the highest frequency observed in Fabaceae, Poaceae and Asteraceae hosts. Given its pathogenicity to wheat and barley and the unknown presence of formae speciales, rotation with these cereals is no longer considered an appropriate management solution. Further research is needed to develop effective management strategies for the future.

Keywords: Forma specialis, Pathogenicity, Species-specific primer, VOSviewer, Wheat

INTRODUCTION

As a common pathogen, saprobe, and endophyte, Fusarium is one of the most ecologically important genera of soil-dwelling fungi (Summerell et al. 2011). The fungus has been isolated from a wide range of soil types throughout the world. This genus is a member of the class Sordariomycetes, order Hypocreales, division Ascomycota, subdivision Pezizomycotina, and family Nectriaceae (Kirk et al. 2008). Fusarium species exhibit niche differentiation within the complex microbial tapestry of the soil environment. In particular, some species are very efficient at breaking down organic matter in the soil. This decomposition process, known as mineralization, releases essential nutrients for plants and other soil organisms. This contributes significantly to the vital nutrient cycle within the soil ecosystem (Stoner 1981, Paul & Clark 1989, Ruiter et al. 1994). This is due to their capacity for saprobic digestion. Many Fusarium species are important plant pathogens that can cause a range of plant diseases, including foliar diseases, dieback, canker, vascular wilt, seed and fruit decay, onion rot, stem rot, and root rot (Dean et al. 2012, Chehri et al. 2017, Trabelsi et al. 2017, Sharma & Marques 2018). Several studies have demonstrated the endophytic colonization of the root cortex (endorhiza) by non-pathogenic species within the Fusarium genus (Dababat & Sikora 2007). The management of soil-borne plant diseases has proven to be a useful application of these non-pathogenic *Fusarium* (Steinberg et al. 2007, Zhang et al. 2015, Šišić et al. 2017, Shadmani et al. 2018).

Fusarium redolens Wollenw. has recently been reported as an emerging pathogen threatening chickpea production in Iran. Due to the economic importance of chickpea and its vast area of cultivation in Iran, especially in the western provinces, this crop has become the major host for *F. redolens* in the country. This fungus causes significant quantitative economic losses to chickpea production. The area under chickpea cultivation in Iran is about 439,872 hectares, 95% of which is rain-fed. Iran is the ninth largest producer of chickpeas in the world after India, Australia, Ethiopia, Turkey, Myanmar, the Russian Federation, Pakistan, and Mexico (FAOSTAT 2021). Iran produces about 168,000 tons of chickpeas per year, accounting for 2% of global production. More than 80% of chickpea production in Iran comes from the provinces of Kermanshah, Lorestan, Kurdistan, East Azerbaijan, and West Azerbaijan (Western Provinces). Worldwide, the average grain yield of chickpeas is 850 $kg \cdot ha^{-1}$, and in Asia, it is 919.7 $kg \cdot ha^{-1}$ (FAOSTAT 2021). Chickpea yield in Iran is

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much lower than the world average. The world average yield of chickpea is about 1800 kg·ha^{-1}. In Iran, however, the average yield is only 400 kg·ha^{-1}. Kermanshah province is the leading chickpea producer in Iran, accounting for nearly 28% of the total area (141,520 ha). The Bivanij cultivar dominates the region (except in cold and high-altitude areas) due to its faster maturity, higher biomass, and grain yield compared to other cultivars (Azad, Hashem, ILC482). However, pathogens and poor management practices significantly affect production. Studies show that *F. oxysporum* and related fungi (FOSC) are a major threat in western Iran, where rainfall exceeds 400 mm (Younesi et al., 2020). Therefore, accurate identification of Fusarium species is essential for the development of effective control measures.

Chickpea Fusarium disease history: World

Fusarium species are among the most devastating pathogens of chickpeas globally. The first documented instance of chickpea wilt occurred in India, reported by Butler in 1918. The disease was also reported in Myanmar in 1923, but the exact cause of the disease was unknown until Padwick's successful identification of the causative agent in 1940 (Erwin 1958). In a study conducted by Prasad and Padwick in 1939, a total of 300 Fusarium isolates were collected from chickpeas. These isolates were divided into three different groups. The first group included non-pathogenic isolates, while the second group was found to be responsible for wilt disease. The third group was found to cause seed rot. The Fusarium isolates in the second group were named *F. orthoceras* var. *ciceri*. Erwin isolated some strains of Fusarium from wilted chickpeas in California and named them *F. lateritium* (Erwin 1958). He divided them into two groups: *F. lateritium* f. sp. *crotalariae* (syn: *F. udum* var. *crotalariae*), which causes wilt of sunn hemp (*Crotalaria juncea*), and *F. lateritium* f. sp. *cajani* (syn: *F. udum* var. *cajani*), which causes wilt of lentil (*Cajanus cajan*).

In an experiment, Fusarium strains isolated from chickpea in India were compared to those isolated from chickpea in California (Erwin 1958). Both strains were morphologically and pathogenically similar and were therefore introduced under the name *F. lateritium* f. sp. *ciceri*. Echandi (1970) separated Fusarium isolates from chickpea in Peru and reported them as *F. oxysporum*. It was shown that the isolated Fusarium strains causing wilt symptoms in chickpeas were all *F. oxysporum* and *F. lateritium* was not isolated (Echandi 1970). *F. oxysporum* f. sp. *ciceris* (Padwick) Matuo (Foc) and K. Sato, exhibits two main pathotypes: a yellowing type causing progressive leaf yellowing and vascular discoloration, and a wilting type inducing severe chlorosis, wilting, and vascular discoloration (Trapero-Casas & Jiménez-Díaz 1985). Additionally, eight pathogenic races (0, 1A, 1B/C, 2, 3, 4, 5, and 6) have been identified within this forma specialis (Haware & Nene 1982, del Mar Jiménez-Gasco et al. 2001). Within *F. oxysporum* f. sp. *ciceris*, races 0 and 1B/C are associated with a yellowing symptom, and the remaining races are associated with a wilting symptom (del Mar Jiménez-Gasco et al. 2001, 2003). Yield losses in chickpea due to the presence of this pathogen have been reported to be up to 15% and in some cases up to 70% (Halila & Strange 1996, Honnareddy & Dubey 2006).

At present, based on morphological characteristics, *F. oxysporum* f. sp. *ciceri* has been reported as the major causal agent of chickpea diseases in many parts of the world, including Australia, Canada, Egypt, Ethiopia, India, Pakistan, Peru, Turkey, Spain, Syria, Tunisia, the United States and other countries (Chattopadhyay & Sen Gupta 1967, Echandi 1970, Westerlund et al. 1974, Trapero-Casas & Jimnez-Diaz 1985, Bhatti & Kraft 1992, Haware et al. 1996, Nene et al. 1996, Demirei et al. 1998, Esmaeili Taheri et al. 2011). The morphological similarity between *Fusarium* spp., particularly *F. oxysporum* and *F. redolens*, can lead to misidentification based solely on these characteristics. This overlap raises the possibility that previous identifications of *F. oxysporum* may have included *F. redolens* (Jiménez-Fernández et al. 2011, Saeedi & Jamali 2021). An isolate of *F. redolens* previously thought to be *F. oxysporum* f. sp. *asparagi* was now shown to be *F. redolens* (Blok & Bollen 1997). Molecular techniques have revealed *F. redolens* as the causative agent of chickpea root rot in several countries, including Canada, Lebanon, Morocco, Pakistan, Spain, the Netherlands, and Tunisia (Baayen et al. 2000, Esmaeili Taheri et al. 2011, Leisso et al. 2011, Bouhadida et al. 2017, Rafique et al. 2020). A study by Jiménez-Fernández et al. (2011) showed that infection of chickpea with *F. redolens* induced a disease syndrome similar to that caused by the yellowing pathotype of *F. oxysporum* f. sp. *ciceris*. To date, at least nine Fusarium species have been reported to infect chickpeas around the world. These include *F. culmorum*, *F. equiseti*, *F. graminearum*, *F. hostae*, *F. oxysporum* f. sp. *ciceris*, *F. proliferatum*, *F. redolens*, *F. sporotrichioides* and *F. verticillioides* (Esmaeili Taheri et al. 2011, Jendoubi et al. 2017, Saeedi & Jamali 2021, Younesi et al. 2021, Geraminasab et al. 2023).

Chickpea Fusarium disease history: Iran

Fusarium wilt reduces both seed yield and seed weight in chickpea production in Iran. Chickpea yield losses of up to 15% annually and up to 70% in severe outbreak years have been reported. Chickpea wilting

and yellowing diseases were first reported in Iran by Manuchehri and Mesri from Khoy, Shapur, Ahar, Miandoab, Karaj, Gonbad, Shiraz, Isfahan, and Kashan (Manuchehri & Mesri 1966). At that time, the pathogen *F. lateritium* f. sp. *ciceris* was diagnosed by sending samples of the fungus isolated from infected chickpeas to California. *F. oxysporum* f. sp. *ciceri* was introduced by Banihashemi (1986) as the causal agent of chickpea wilt in Shiraz. In 1993, isolates obtained from the root and crown of wilted chickpea plants in rainfed fields in Lorestan province were identified as *F. oxysporum* (Nazari & Ershad 1993). In Fars province, the causal agent of chickpea root rot, *F. solani* f. sp. *pisi*, and the causal agent of chickpea yellowing and wilting, *F. oxysporum* f. sp. *ciceri*, were identified (Mohammadi & Banihashemi 2005). Graminasab et al. (2014) identified four species, including *F. oxysporum*, *F. solani* (Mart) sacc, *F. proliferatum* (Matsus) Nirenberg, and *F. equiseti* (corda) sacc, as the major causes of wilting and yellowing in chickpea. Since then, several reports have been published on the genetic variability of the pathogen. In Kermanshah province, Nourollahi et al. (2017) found nine fingerprint groups among 45 *F. oxysporum* f. sp. *ciceris* isolates from commercial chickpea fields using five microsatellite primers. Azimi et al. (2017) employed 12 inter simple sequence repeat (ISSR) primers to analyze the genetic diversity of *F. oxysporum* f. sp. *ciceris* isolates from chickpea in Ilam province, Iran. Their study identified 24 distinct fingerprint groups among 47 isolates. This contrasts with previous research in western Iran, which suggested only five pathogenic groups were present (Younessi 2004). Races 1, 2, and 4 were identified based on disease symptoms in chickpeas, as documented by Haware and Nene (1982). Earlier identifications relied primarily on morphological features of the pathogen. *Fusarium oxysporum* f. sp. *ciceris* is widely accepted as the main cause of Fusarium wilt in chickpeas. Until 2009, there were no reports on the pathogenicity of *F. redolens* on crops in Iran. Based on morphological and species-specific primers, Ghanbarzadeh et al. (2014) identified *F. redolens* as a pathogen of red onion, causing basal and bulb rot. Chehri (2016) showed that *F. redolens* is associated with tomatoes in Iran based on morphological and molecular phylogenetic analyses, and his research confirmed the prevalence of *F. redolens* in Iran. Chehri (2018) also showed that *F. redolens* is one of the most common fungi isolated from agricultural soils in Kermanshah province, Iran.

Fusarium redolens has been reported as pathogenic on a wide range of hosts in Iran, including *Cicer arietinum*, *Malus domestica*, *Mentha piperita, Salsola incanescens*, *Triticum aestivum* and *Zea mays* as pathogenic (Habibi et al. 2018, Jahedi et al. 2019, Fallahi et al. 2019, Razghandi et al. 2020, Younesi et al. 2021, Esmaili & Sharifnabi 2023). Interestingly, it has also been found as an endophyte in *Achillea millefolium*, *A. filipendulina* and *Hordeum vulgare* (Shadmani et al. 2021, Hatamzadeh et al. 2023). Studies suggest *F. redolens* may significantly contribute to chickpea black root rot in Iran. Younessi et al. (2021) found it caused high disease rates in certain chickpea varieties. Additionally, Saeedi and Jamali (2021) reported its frequent presence in uncultivated soil and its identification from symptomatic chickpea roots. Their findings warrant further investigation into F. redolens' role and biology in Iran's chickpea crops.

Fusarium redolens

History of research on *Fusarium redolens* between 1956 and 2024

In the period from 1956 to 2024, 201 and 99 published documents were identified fulfilling the search criteria in Scopus and Web of Science, respectively. Figure 1 shows the evolution of the number of publications per year. Between 1956 and 2010 (54 years), 65 documents were published and the number of publications per year was less than five. Most of these articles have been concerned with isolation and pathogenicity *F. redolens* on plants such as carnation (Gerlach & Pag 1961, Baayen et al. 1997), peas and beans (Hepple 1960, Clarkson 1978), asparagus (Gordon-Lennox & Gindrat 1987), oil palm (Ho et al. 1985), maize (O'Donnell et al. 1999), rose (Ypema et al. 1987) and white pine (Ocamb & Juzwik 1995). An increase in the number of publications was observed from 2010 onward (Figure 1), and a sharp rise in indexed documents was observed in 2021 (n=22). Fifty-six percent of the articles were published between 2016 and 2024. The first article titled "Pathogenicity of the fungus *Fusarium redolens* Wr.; clinico-experimental research" (Kozin 1956) was published in Vestnik venerologii i dermatologii Journal (30:28-31). The paper is written in Russian and focuses on the pathogenicity of the fungus *Fusarium redolens* Wr., through clinico-experimental research.

Figure 2 shows the areas of knowledge related to the studies of *F. redolens* published between 1956 and 2023. In this regard, (i) Agriculture and Biological Sciences (146 documents), (ii) Biochemistry, Genetics, and Molecular Biology (47 documents), and (iii) Immunology and Microbiology (29 documents), contributed with 47.7%, 15.5%, and 9.5% of the indexed documents, respectively. Agriculture and Biological Sciences was ranked first on this list because most of the publications consisted of the isolation, identification, and characterization of *F. redolens* populations associated with different plant species in various countries. The largest number of articles was published in Plant Disease (n=22), followed by Journal of Phytopathology (n=9). The

leading countries in studies related to *F. redolens* were China, the United States, the Netherlands, and Iran, which contributed 34, 25, 18, and 15 documents, respectively (Fig. 3).

Figures 4 and 5 show the research-topic map of *F. redolens* studies between 1956 and 2024. The network visualization contains 95 items grouped in four clusters (Fig. 4). In this regard, the biggest node, which corresponds to the keyword with the highest occurrences, was *F. redolens* (Fig. 4). Many isolates of this fungus from plants were initially misidentified as *F. oxysporum*. Both are within the same cluster (the red one) (Saeedi and Jamali 2021). Here, it is clear the special interest in the pathogenicity of *F. redolens* in plants. This species has been reported as a pathogenic agent in more than 50 host plants.

Figure 5 shows how the research topics moved from species specificity/asparagus/asparagus officinalis/biosynthesis/metabolism/beauvericin/*F. oxysporum* (2010 to 2012), passing by classification/biodiversity/microbiology/*F. edolens*/*F. hostae* (beginning of 2012), molecular analysis/ rDNA/ fungal DNA/ morphology/ phylogenetics /internal transcribed spacer/ morphology (beginning of 2012) to wheat/ controlled study/ root rot/pathogenicity/wilt/symptom/endophytes (end of 2018). Further studies should be focused on the effect of environmental parameters on the severity of *F. redolens* disease and control measures for future outbreaks of *F. redolens* (Saeedi and Jamali 2021).

Taxonomy of *Fusarium redolens*

The exact taxonomic placement of *F. redolens* is a subject of ongoing debate. Wollenweber (1913) first described *F. redolens* and maintained this nomenclature in subsequent publications (Wollenweber 1916-1935, 1931, Wollenweber & Reinking 1935). Traditionally, size differences in macroconidia were the primary way to distinguish *F. oxysporum* from *F. redolens* (Gordon, 1952). However, their similar morphology led to earlier classifications grouping them as the same species (Snyder & Hansen, 1940; Nelson et al., 1983), a variety of *F. oxysporum* (Gordon, 1952; Booth, 1975), or even *F. solani* (Bilaĭ, 1955). The use of molecular methods is necessary to correctly identify and separate *Fusarium* species. Almost all molecular studies for *Fusarium* identification have been based on comparison of rDNA internal transcribed spacers. Previous studies have shown that sequence data from the ITS rDNA region is not sufficient to distinguish the Fusarium taxa studied (Zhao et al. 2011, Raja et al. 2011, Šišić et al. 2018, Alhawatema et al. 2019). Baayen et al. (2000) have successfully used restriction fragment length polymorphism (RFLP) patterns of rRNA internal transcribed spacer (ITS) regions to diagnose *F. oxysporum* and *F. redolens*. *Fusarium oxysporum* is polymorphic for AluI and HinfI and has produced three RFLP fragments. *Fusarium redolens* cannot be distinguished from its close relative *F. hostae* by this technique (Baayen et al. 2001). Many researchers have reported that the *tef1-α* gene has a higher resolution than ITS and can provide a sufficient phylogenetic signal to distinguish between different Fusarium species. The transfer elongation factor gene contains both conserved and variable regions that allow inter- and intraspecific comparisons and is reliable for studying the phylogenetic relationships of *Fusarium* spp. (Kristensen et al. 2005). Modern DNA analysis reveals *F. redolens* as a separate species from *F. oxysporum* (O'Donnell et al., 1998; Baayen et al., 2000, 2001; Bogale et al., 2007). These studies even suggest they aren't closely related. Notably, Baayen et al. (2001) found the *F. nisikadoi-F. miscanthi* group to be closer to *F. oxysporum* than *F. redolens* and its relatives. Other research suggests *F. hostae* is closely related to *F. redolens*, with strong statistical support (Saeedi & Jamali 2021). Bogale et al. (2007) designed a specific primer set (Redolens-F: 5-ATC GAT TTTCCC TTC GAC TC-3; Redolens-R: 5-CAA TGA TGA TTGTGA TGA GAC-3) to identify *F. redolens* isolates. This method effectively differentiates *F. redolens* from other Fusarium species, enabling rapid and straightforward diagnosis. Compared to previous methods involving restriction fragment length polymorphism (RFLP) analysis, these primers allow a simpler distinction between *F. redolens* and *F. oxysporum*.

Inaccurate identification of Fusarium species has the potential to cause significant issues, including inappropriate management practices and the implementation of ineffective control strategies. Currently, the most reliable method for Fusarium identification is DNA sequencing. The gold standard for this involves targeting the translation elongation factor 1-alpha (TEF1) gene region. A publicly available database called FUSARIUM-ID exists for comparing TEF1 sequences against known Fusarium species (Geiser et al. 2004). In some cases, TEF1 alone might not be sufficient for differentiating closely related species. Multi-locus sequence typing (MLST) involves sequencing multiple gene regions, such as TEF1 and RNA polymerase II second largest subunit (rpb2) for a more robust identification.

Pathogenic *Fusarium redolens* isolates

Fusarium redolens has been reported as a pathogenic agent in more than 50 host plants including; soybean (*Glycine max*), Chinese skullcap (*Scutellaria baicalensis*), Tobacco (*Nicotiana tabacum*), alfalfa (*Medicago sativa*), asparagus (*Asparagus officinalis*), Rye (*Secale cereale*), wheat (*Triticum aestivum*), potato (*Solanum tuberosum*),

faba bean (*Vicia faba*), parsley (*Petroselinum crispum*), gastrodia (*Gastrodia elata*), lentil (*Lens culinaris*), American Ginseng (*Panax quinquefolius*), Duohua huangjing (*Polygonatum cyrtonema*), black cumin (*Nigella sativa*), Carnation (*Dianthus caryophyllus*), jojoba (*Simmondsia chinensis*), Barley (*Hordeum vulgare*), red clover (*Trifolium pratense*), cotton (*Gossypium hirsutum*), *Lilium candidum*, flax (*Linum usitatissimum*), lanzhou lily (*Lilium davidii* var. *unicolor*), Salsola (*Salsola* sp.), rice (*Oryza sativa*), spinach (*Spinacia oleracea*), onion (*Allium cepa*), rocket (*Diplotaxis tenuifolia*), maize (*Zea mays*), sugar beet (*Beta vulgaris*), white lupin (*Lupinus albus*), tomato (*Solanum lycopersicum*), sunflower (*Helianthus annuus*), roses (*Rosa* spp.), ragwort (*Jacobaea vulgaris*), pea (*Pisum sativum*), oat (*Avena sativa*), *Atractylodes chinensis* and date palm (*Phoenix dactylifera*) (Larsson & Olofsson 1994, Baayen et al. 2000, Riccioni et al. 2008, Jiménez-Fernández et al. 2011, Esmaeili Taheri et al. 2011, Al-Sadi et al. 2012, Shikur Gebremariam et al. 2015, Jing et al. 2016, Pearson et al. 2016, Bouhadida et al. 2017, Esmaeili Taheri et al. 2017, Chehri 2018, Taylor et al. 2019, Fallahi et al. 2019, Rafique et al. 2020, Le et al. 2020, Maymon et al. 2021, Qostal et al. 2021, Šišić et al. 2022, Abi Saad et al. 2022, Gibert et al. 2022, Li et al. 2022, Litovka et al. 2023, Olszak-Przybyś et al. 2023, Jiang et al. 2023, Armstrong-Cho et al. 2023, Gai et al. 2023, Wang et al. 2023, Jia et al. 2023, Xie et al. 2023). Several types of forest plants that have reportedly been attacked by *F. redolens* are Aleppo pine (*Pinus halepensis*), conifers (*Pinus*, *Cupressus*, *Picea*), and koa (*Acacia koa*) (Lazreg et al. 2014, Dobbs et al. 2023). Disease symptoms caused by *F. redolens* include root rot (Olszak-Przybyś et al. 2023, Armstrong-Cho et al. 2023), root and crown rot (Baayen et al. 2000), crown rot (Shikur Gebremariam et al. 2015), wilt (Jia et al. 2023), vascular wilt (Rafique et al. 2020), collar rot (Le et al. 2020), bulb rot (Cao et al. 2020), seedling blight (Wang et al. 2019), basal rot (Haapalainen et al. 2016), wilting and yellowing (Taylor et al. 2019), ear rot and kernel contamination (Fallahi et al. 2019), damping off (Lazreg et al. 2014), root, crown, and foot rot (Esmaeili Taheri et al. 2017), spear rot (Baayen et al. 2000), and black rot (Ypema et al. 1987).

Non-pathogenic *Fusarium redolens* isolates

Non-pathogenic *F. redolens* isolates have been shown to grow endophytically in the endorhiza of many plants including; rice (*Oryza sativa*), olive (*Olea europaea*), Russian wormwood (*Artemisia Sacrorum*), Salsola (*Salsola* sp.), maigoya (*Coleus forskohlii*), barley (*Hordeum vulgare* L.), oriental paperbush (*Edgeworthia chrysantha*), lemon bergamot (*Monarda citriodora*), Himalayan yew (*Taxus wallichiana*), esparto or needle grass (*Macrochloa tenacissima*), cocoa (*Theobroma cacao*), Chinese foxglove (*Rehmannia glutinosa*), *Stipa grandis*, *Fritillaria unibracteata* var. *wabuensis*, and *Dioscorea zingiberensis* (Su et al. 2010, Xu et al. 2010, Garyali et al. 2013, Pan et al. 2015, Katoch & Pull 2017, Shadmani et al. 2018, Mastan et al. 2019, Razghandi et al. 2020, Gargouri et al. 2020, Ambele et al. 2020, Hong-juan et al. 2021, Nazir et al. 2022, Roy et al. 2023).

Extracted beauvericin from non-pathogenic *F. redolens* isolates of *Dioscorea zingiberensis* has been used effectively as an antibacterial against several bacteria. These include *Agrobacterium tumefaciens*, *Bacillus subtilis*, *Escherichia coli*, *Pseudomonas lachrymans*, *Staphylococcus haemolyticus* and *Xanthomonas vesicatoria* (Xu et al. 2010). Recently, ethyl acetate was isolated from *F. redolens*, increasing the interest in strains of this species, since ethyl acetate showed significant cytotoxic potential against HepG2 cells (Nazir et al. 2022). Metabolites such as 3,4-dihydrocoumarin, 5'-deoxyribonucleoside, harmala alkaloid, benzofuran, and benzothiazole have also been obtained from *F. redolens*, which have inhibitory effects on wheat scab (*Fusarium graminearum*) (Hong-Juan et al. 2021). Mastan et al. (2021) used a consortium of *Trichoderma viride* and *F. redolens* and observed significant enhancement in plant growth, root biomass, and forskolin content of the medicinal plant *Coleus forskohlii*. The peimisine produced by *F. redolens* relieves sputum and cough, has anti-tumour activity and is a potent inhibitor of the angiotensin-converting enzyme (Feng et al. 2015). Taxol is a diterpenoid derived from *F. redolens* with an anti-tumor activity that inhibits microtubulin depolymerization, thereby affecting spindle formation and preventing the mitosis of tumor cells (Garyali et al. 2014). In the study by Roy et al. (2023), the antagonistic activity of *F. redolens* against the rice pathogen *Magnaporthe grisea* was observed. Inoculation of rice plants with *F. redolens* also increased the production of enzymes such as peroxidase, polyphenol oxidase, chitinase, and superoxide dismutase. Katoch and Pull (2017) have shown the antagonistic activity of *F. redolens* against *Sclerotinia* sp. and *Colletotrichum capsici*. They mentioned that the endophyte *F. redolens* could be used effectively to control a wide range of phytopathogens.

Management and formae speciales

To control this disease, various crop management techniques have been suggested, such as crop rotation, sanitation, the use of bacterial or fungal antagonists, and the use of resistant chickpea cultivars. One of the primary methods used in Iran to

control *Fusarium* in chickpeas is the rotational planting of wheat and barley. To reduce the Fusarium inoculum in the soil, this is advised. The majority of research in Iran is based on morphological characteristics, and in the majority of the country, *F. oxysporum* has been identified as the most pathogenic agent of chickpeas, causing yellowing and black root rot symptoms (Afshari-Azad 1998, Mohammadi & Banihashemi 2005, 2006, Zamani et al. 2001, 2004, Hasanzade et al. 2008, Haji-Allahverdipoor et al. 2011, Zokaee et al. 2012, Nourollahi et al. 2017). This could be the reason this species hasn't been identified as one of the fungi associated with root disease in Iranian cereal and chickpeas crops in the past. The increase in chickpea cultivation within wheat rotations might be linked to a higher prevalence of *F. redolens* in these fields. Notably, three formae speciales of *F. redolens* have been formally described: *F. redolens* Wollenw. f. sp. *asparagi* Baayen, *F. redolens* f. sp. *spinaciae* (Sherb.) Subramanian, and *F. redolens* f. sp. *dianthi* (Gerlach & Pag 1961, Baayen et al. 1997, 1999)**.**

The concept of forma specialis may limit our understanding of *F. redolens* isolates. Researchers need to consider both aggressiveness and host range variation among individual isolates. A study by Esmaeili Taheri et al. (2011) found *F. redolens* strains isolated from durum wheat caused severe disease in peas, indicating a broader host range for this fungus. Chittem et al. (2015) showed that cereal Fusarium pathogens, including *F. culmorum*, *F. graminearum*, and *F. avenaceum*, are capable of causing disease on pulse crops and dry peas. Moparthi et al. (2021) showed that *F. redolens* from dry pea, chickpea, and pea seeds were aggressive on pulses, wheat, and barley. Kraft and Pfleger (2001) identified F. solani f. sp. pisi as the main cause of pea root rot in Washington fields. This fungus exhibits a broad host range, infecting not only chickpeas but also other non-legumes such as ginseng and mulberry. One isolate of *F. redolens*, previously believed to be part of *F. oxysporum* f. sp. *asparagi*, has been reclassified as *F. redolens* (Blok & Bollen 1997). This isolate was found to be pathogenic on pea and lupin, indicating that it is not host-specific. Borrell et al. (2016) showed that *F. redolens* poses a risk to wheat production, which is greater when rotated with pulse crops. In Iran, particularly in the western provinces, millions of hectares of rain-fed chickpeas are grown each year in rotation with rain-fed wheat. The emergence of *F. redolens* as a pathogen on Iranian crops highlights the need for a deeper understanding of its biology and ecological role. This knowledge is crucial to assess its economic impact and develop effective control strategies, particularly if resistant cultivars prove to be the most viable option. Building on the points above and considering the evidence of cross-pathogenicity, the current forma specialis definition may need revision.

Fusarium redolens: Ecology and Environment

The composition of soil fungal communities, including Fusarium species, is shaped by climate. Different Fusarium species adapt to specific climatic and environmental conditions, leading to variations in their distribution across regions (Saremi & Burgess 2000). Despite existing knowledge on the impact of environmental factors on Fusarium distribution, the specific factors influencing the distribution of *F. redolens* in both agricultural and natural soils remain poorly understood. Elucidating the environmental and climatic determinants of Fusarium distribution would enable predictive modeling of species presence across diverse locations. While prior research has established strong correlations between Fusarium distribution and climatic factors, the broader field of modeling Fusarium species distribution using advanced software tools remains understudied, despite its potential utility. Studies have consistently shown that climatic factors play a significant role in shaping the distribution patterns of Fusarium species (Burgess et al. 1993, Saremi et al. 1997).

Several Fusarium species exhibit distinct geographic distributions. Non-pathogenic species like *F. oxysporum*, *F. solani*, and *F. equiseti* appear widespread (cosmopolitan), while *F. acuminatum* and *F. sambucinum* seem restricted to cooler temperate regions (Abbas et al. 1987, Backhous & Burgess 1995, Burgess et al. 1988, Backhous et al. 2001). This variation likely reflects the influence of environmental factors like temperature, soil properties (texture and organic matter), rainfall patterns, and local vegetation, as previously documented (Summerell et al. 2010).

Saeedi and Jamali (2021) demonstrated a highly significant correlation between species and environmental parameters. In their study, all sampled soils were predominantly alkaline, with pH levels ranging from 7.2 to 9. Jones and Woltz (1981) found that soils with a pH value greater than 7 were the most suppressive for Fusarium wilt (*F. oxysporum*). Several studies have shown that soil pH can influence Fusarium species and disease development. Alkaline soils (higher pH) tend to suppress *F. oxysporum*, a fungal pathogen causing wilt (Borrero et al., 2004; Fang et al., 2012; Deltour et al., 2017). In contrast, *F. redolens* appears to thrive in soils with neutral to slightly alkaline pH, while *F. oxysporum* and *F. solani* prefer more acidic environments. Saeedi and Jamali (2021) demonstrated that *F. redolens* thrives in alkaline conditions. Mycelial growth was highest at a pH of 9.72, while significantly lower at pH 5.8. This aligns with the naturally alkaline soil found in most parts of Iran, including Kermanshah province, where

soil pH typically ranges from 7.4 to 8.2 (Qadir et al., 2008; Heidari et al., 2008). These findings suggest that F. redolens may be a significant contributor to chickpea root rot in this region. It's important to note that soil pH also impacts the availability of various nutrients crucial for plant health, including copper, iron, manganese and zinc (Collins & Buol, 1970). Micronutrient acquisition by many organisms relies on siderophores, but their effectiveness is heavily influenced by environmental pH. This is because pH affects both the solubility of metals and the stability of the metal-siderophore complexes (chelation). Consequently, different species have varying abilities to compete for these essential micronutrients depending on the surrounding pH (Boukhalfa & Crumbliss, 2002; Dhungana & Crumbliss, 2005).

A recent study identified several key environmental factors influencing the distribution of Fusarium species in soil (Saeedi and Jamali, 2021). These factors, listed in order of decreasing importance, included soil texture (specifically the ratio of sand, silt, and clay), altitude, calcium carbonate content ($CaCO_3$), electrical conductivity (EC), organic matter content, and lastly, soil pH. Interestingly, the study found that *F. redolens* thrived in soils with a higher clay content compared to *F. oxysporum* and *F. solani*, which preferred soils with very low clay content. Studies have shown that higher clay content in soil can be associated with a decrease in Fusarium wilt severity (Deltour et al., 2017). Clay can affect pH buffering, nutrient availability, and oxygen diffusion, which may contribute to suppression (Lavie & Stotzky 1986, Dominguez et al. 2001). Saeedi and Jamali (2021) revealed that *F. redolens* was most abundant in soils with low levels of carbon and organic matter. This aligns with observations that loam and sandy loam soils, which typically have low clay content, also tend to have lower organic matter content (Vujanovic et al., 2006). Previous studies have shown a positive link between organic matter content in soil and reduced Fusarium disease in chrysanthemum, flax, and melon (van Rijn et al. 2007, Saadi et al. 2010).

Soil organic matter plays a crucial role in soil health, impacting not only its structure but also factors like pH, buffering capacity, and nutrient availability (Brady & Weil, 2000; Baum et al., 2015). However, the influence of organic matter on Fusarium disease can be complex. While Gehlker and Scholl (1974) found low pH, high organic matter, and clay content to favor the disease in asparagus, Saeedi and Jamali (2021) observed the highest abundance of Fusarium redolens in uncultivated soils with specific electrical conductivity (EC) and calcium carbonate (CaCO3) levels. Interestingly, Nam et al. (2018) reported no significant effect of increasing EC in hydroponic nutrient solutions on lettuce Fusarium wilt. Research on the impact of CaCO3 on Fusarium survival remains limited. Although CaCO3 is used to adjust soil pH and increase calcium (Ca2+) content (He et al., 2014), Benson et al. (2009) suggest Ca2+ might influence various soil-borne diseases, warranting further exploration in the context of Fusarium.

Summary and prospects

While the recent identification of *Fusarium redolens* as a chickpea pathogen in Iran represents a significant advancement, substantial knowledge gaps remain regarding its impact and management. Current research highlights its presence; however, a more comprehensive understanding of *F. redolens* and its interaction with environmental factors is critical for developing effective control strategies.

In-depth investigations are needed to determine how soil properties (texture, pH, electrical conductivity (EC), calcium carbonate (CaCO3) content), temperature, nutrient availability, and organic matter levels influence *F. redolens* disease severity. This knowledge will enable the development of region-specific management practices that consider prevailing soil conditions.

Phylogenetic studies suggest *F. redolens* might be responsible for chickpea black root rot in other Iranian regions. Further research is necessary to confirm this hypothesis. Comparative pathogenicity studies with *F. oxysporum* isolates previously identified from these regions should be conducted. Additionally, morphological identification methods should be complemented with molecular techniques for more precise diagnosis.

A nationwide survey is crucial to map the geographical distribution and prevalence of *F. redolens* affecting chickpeas. Furthermore, the characterization of *F. redolens* isolates from different regions will provide insights into potential strain diversity and virulence variations. This information is essential for developing broadly effective management strategies.

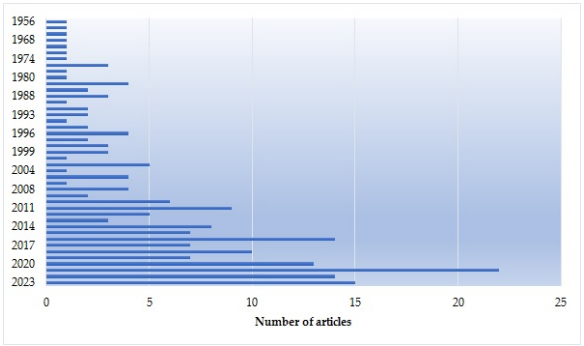

Fig. 1. Annual growth of publications in focus area of *Fusarium redolens* (1956-2023).

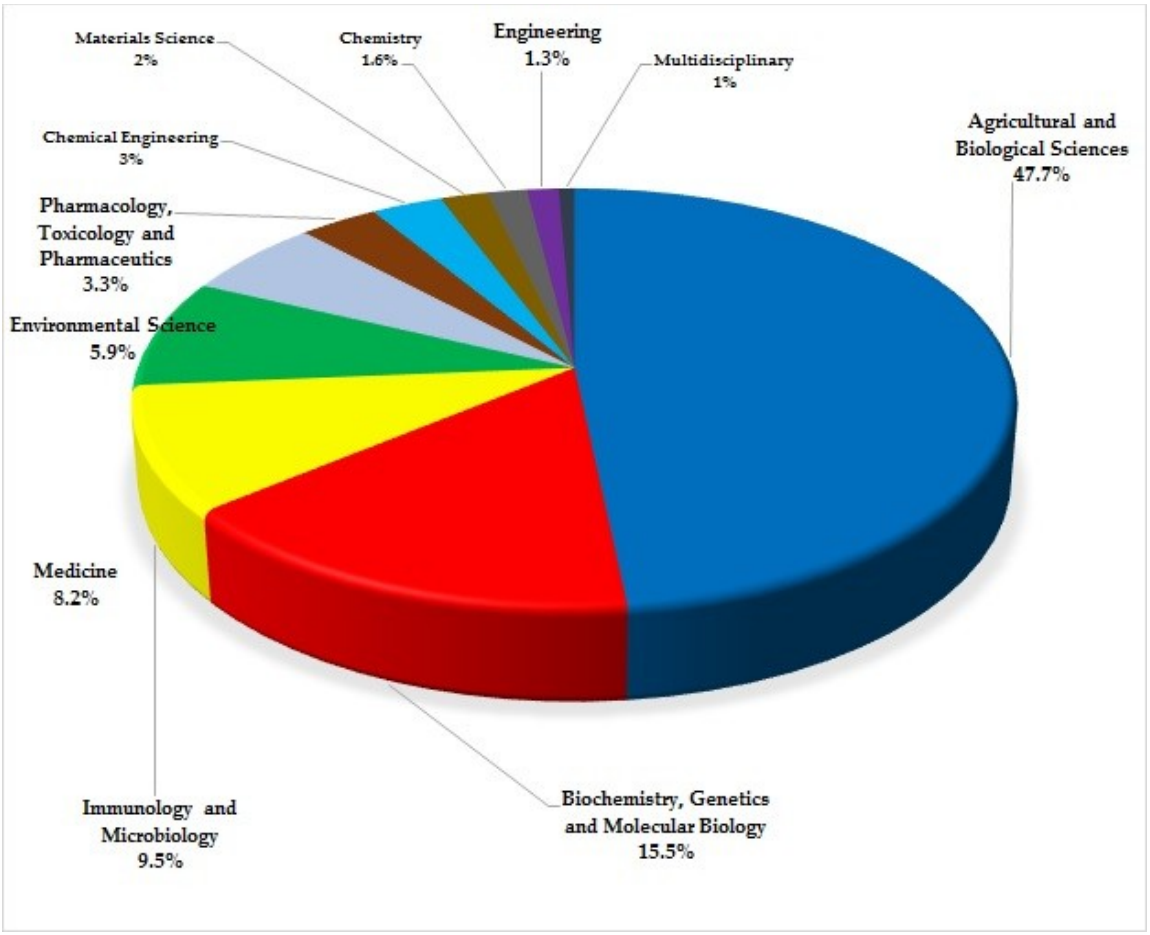

Fig. 2. Evolution of the number of publications related to *Fusarium redolens* between 1956 and 2023.

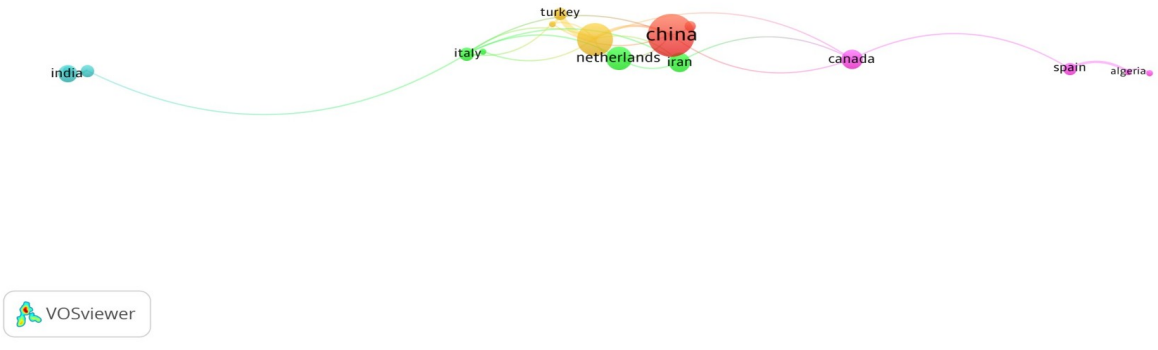

Fig. 3: The network map of co-authorship based on affiliation of authors belonging to different countries.

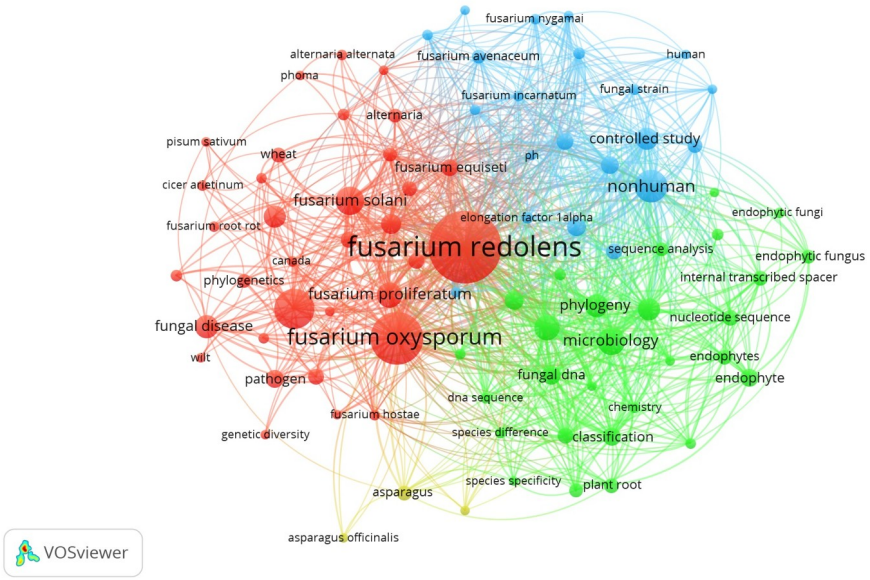

Fig. 4. Network visualization of the research-topic map of studies related to *Fusarium redolens* between 1956 and 2023. The minimum number of occurrences of a keyword is 5.

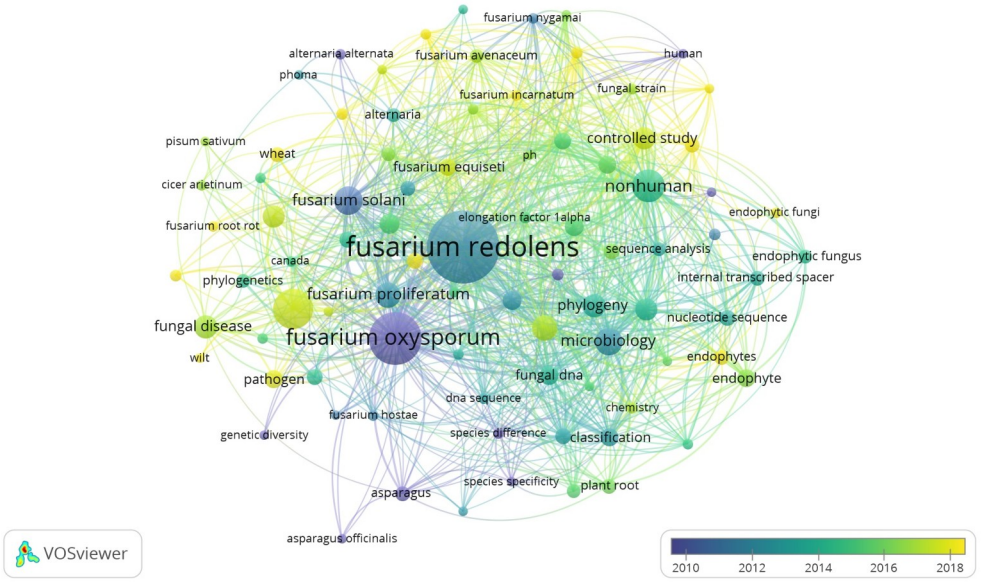

Fig. 5. Overlay visualization of the research-topic map of studies related to *Fusarium redolens* between 1956 and 2023. The minimum number of occurrences of a keyword is 5.

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مروری بر قارچ *Fusarium redolens* Wollenw. به عنوان یک عامل بیماری‌زای گیاهی نوظهور در ایران

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چکیده: مطالعه حاضر مروری بر تحقیقات انجام شده در مورد قارچ *Fusarium redolens* ارائه می‌دهد. جستجوی سیستماتیک در پایگاه داده اسکوپوس از سال ۱۹۵۶ تا ۲۰۲۳، ۲۰۱ سند مرتبط با این قارچ را شناسایی کرد. این قارچ به عنوان یک عامل بیماری‌زای نوظهور، تأثیر قابل توجهی بر حبوبات به ویژه نخود دارد. رشد جمعیت، به ویژه در کشورهای در حال توسعه، یک مشکل اصلی ایجاد می کند که آن دسترسی به غذا، به ویژه منابع پروتئین می‌باشد. نخود یکی از محصولات مهم کشاورزی در غرب ایران محسوب می‌شود و تا پیش از سال ۲۰۱۹، زرد شدن و پوسیدگی ریشه آن عمدتاً به گونه‌های *F. oxysporum* و *F. solani* نسبت داده می‌شد. توصیه های قبلی برای مدیریت این محصول، کشت غلات مانند جو و گندم به دلیل وجود فرم های ویژه *F. oxysporum* در خاک بود. با این حال، مطالعات اخیر نشان می‌دهند که *F. redolens* عامل اصلی این بیماری، به ویژه در استان‌های غربی کشور است. این گونه از طیف وسیعی از گیاهان شامل ۵۴ گونه متعلق به ۵۰ جنس و ۲۹ خانواده گیاهی جداسازی و گزارش شده است که بیشترین فراوانی آن در خانواده‌های نخود، گندمیان و آفتابگردان مشاهده شده است. با توجه به بیماری‌زایی این قارچ برای گندم و جو، تناوب کشت با این غلات دیگر به عنوان یک راهکار مناسب برای مدیریت بیماری در نظر گرفته نمی‌شود و تحقیقات بیشتری برای توسعه استراتژی‌های موثر مدیریت مورد نیاز است.

کلمات کلیدی: فرم‌های تخصصی، بیماریزایی، آغازگرهای اختصاصی گونه، نرم‌افزار VOSviewer، گندم

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