

A study on root and stalk rot disease of broad bean caused by *Rhizoctonia Solani* (Kuhn) in Babylon and its biological control

Najat Hameed Jasim¹, Sarah Raheem Hamza²

¹ Department of Intelligent Medical System, Collage of Sciences, Al-Mustaqbal University, Babylon, Iraq

² Department of Medical Biotechnology, Collage of Sciences, Al-Mustaqbal University, Babylon, Iraq

DOI: <https://doi.org/10.66856/ijar.2026.2.2.2100>

Abstract

Broad beans (*Vicia fabae*) belong to the legume family, *Fabaceae*, which is second in importance only to the grass family (Poaceae). The area cultivated with broad beans worldwide is approximately 180 million hectares, or 12-15% of the Earth's arable land. Global production accounts for about 27% of the world's cereal production, and the beans contain 33% protein (Vance *et al.*, 2000; Graham and Vance, 2003) [11, 16]. Broad beans rank third in importance after beans vulgaris (Graham and Vance, 2003). Broad bean cultivation is widespread, particularly in the Near East, North Africa, some Asian countries, America, and Europe. It is also an important food source for some populations (Graham and Vance, 2003) [11]. The pea species is **Phaseolus sativum** (Pisum). Activate Windows se here to search Its importance lies in its nutritional value, as its seeds contain a high percentage of protein, which plays an important role in compensating for the deficiency in animal protein, especially in poor countries suffering from food crises. Its seeds also contain a considerable percentage of sugars, starches, and some vitamins such as B and A (Al-Khashan and Abdel-Bari, 1985) [1]. In addition, crop residues or seeds are used as animal feed (Al-Khashan and Abdel-Bari, 1985) [1]. Leguminous crops, including broad beans, play a role in improving soil properties by fixing atmospheric nitrogen through the symbiotic relationship between the roots of these plants and rhizobia bacteria.

Keywords: Broad bean (*Vicia fabae*), *Fabaceae*, legume crops, protein content, nutritional value

Introduction

This gives them importance in crop rotations for field crops. The amount of atmospheric nitrogen fixed by leguminous plants is estimated at 40-60 million metric tons annually (Mil 1999). The cultivated area for broad beans in Iraq exceeds 100,000 dunams, with an average yield of 1355 kg per dunam and a total production exceeding 120,000 tons. This crop is susceptible to numerous agricultural pests, including insect infestations, fungal and viral diseases, nematodes, and parasitic flowering plants. Among the most significant fungal diseases affecting this crop are Ascochyta blight, broad bean rust, and root and stem base rot. The latter is considered the most critical in impacting the crop in many parts of the world (Matloub & Mohammed, 2015) [4]. Given the increasing severity of this disease, this study aimed to evaluate the effectiveness of the fungus *Penicillium* and the bacterium *Pseudomonas fluorescens*, which are widely used microorganisms in controlling root and stem rot diseases (Khaleel *et al.*, 2019; Alwan, 2018) [6, 17], according to the following axes:

1. Isolation and diagnosis of the causes of seedling death and root rot in broad beans.
2. Testing the effectiveness of some biological agents in controlling the pathogen.

Literature Review

Diagnostic Characteristics of the Fungus *Rhizoctonia Solani* and its Economic Importance

After the fungus *Rhizoctonia solani*, one of the most widespread species of the genus *Rhizoctonia*, it was first recorded as a genus in 1815 by Decandall. The species was recorded by Kuhn in 1855 on a potato crop. The fungus *R. solani* reproduces asexually in nature and lives in the form

of a vegetative mycelium or as sclerotia. However, sometimes, under certain conditions, the fungus forms sexual spores of the basidiomycete type, which were first observed by Prillieux and Delacroix in 1891, based on which the fungus was considered a member of the Basidiomycetes. The sexual stage of the fungus *R. solani* has been subject to several names since 1891 and is now known as *Thanatephorus cucumeris*, which develops in high humidity and appears as a thin, downy growth on soil, leaves, and infected stems. It was first recorded on cotton plants (1969) and others the fungus *R. solani* attacks underground plant parts such as seeds, seedlings, and roots. It can also infect above-ground plant parts such as buds, fruits, leaves, and stems. The most common disease symptoms of fungal infection include the failure of some infected seeds to germinate. Seedlings are infected before or after emergence above the soil surface. Infected but not dead seedlings develop lesions, either on the roots or the stem area near the soil surface, where they appear as sunken, reddish-brown lesions (Ogoshi, 1987, and in Figure 3) [12].

Generally, basidiospores do not represent the primary inoculum of infection, as most diseases caused by the fungus *Rhizocinia* are produced by fungal mycelium or sclerotia found on the debris of infected plants, which can survive for several years in the soil. Basidiospores are believed to have no significant effect on the epidemiology of most root rot and damping-off diseases caused by the fungus *Rhizoctonia* during the growing season (Ogoshi, 1987; Cubeta & Vilgal, 1997) [9, 12]. The fungus *R. solani* attacks more than 188 plant species belonging to 32 species. Root rot diseases are among the most important diseases affecting broad beans and other legume crops (Saxena,

2002)^[14]. The fungus *R. solani* is a major causative agent of root rot, and other pathogens of equal importance include *Fusarium solani* and *Pythium ultimum*. These fungi are found in the soil and can attack the seeds, seedlings, and roots of legume crops, causing rot and significant crop losses (Gabr, 2001; El-Mosallomy *et al.*, 1990). Losses resulting from root rot caused by *R. solani* on legume plants in Minnesota were estimated at \$4 million annually (Graham and Vance, 2003)^[11]. A study by Hussein (2011)^[5] demonstrated the impact of the pathogenic fungus *R. solani*, showing a 40% germination rate, which causes root and stem base rot in broad beans.

Use of *Pseudomonas fluorescens* Bacteria in Biological Control

There is a group of bacteria found in the root zone, including *P. fluorescens*, commonly known as plant growth-promoting rhizobacteria (seeder bacteria).

Or abbreviated as PGPR, and it is clear from the name that it stimulates plant growth as a result of nitrogen fixation and increased availability of essential elements in the soil solution, affecting root growth and shape, the ability to build or change the concentration of growth regulators, and the ability to antagonize or reduce the effect of pathogens by forming free compounds (iron) and some enzymes such as chitinase and other compounds such as cyanide and antibiotics. The bacteria can build the enzyme ACC deaminase, which reduces the concentration of ethylene and thus stimulates growth. The bacteria also improve nutrient absorption, accelerate the onset of stress resistance, contribute to the solubility of inorganic phosphates (chelating siderophores) of iron (Al-) B-1,3-glucanase, convert organic phosphates, and build the enzyme Solubilization (*in vitro*, 2006). *P. fluorescens* is a Gram-negative, obligate aerobic rod-shaped bacterium that is flagellated and heterotrophic. It produces a small green fluorescent pigment when grown on iron-free media, hence the name *fluorescens*. It grows in a wide temperature range of 4-41°C. (Holt, Krieg, 1974; Gibbons and Buchanan, 1984)^[19] Bautista *et al.* (2007)^[20] demonstrated the high ability of *P. fluorescens* to inhibit the growth of the fungus *R. solani* on potato plants. Ten strains of *P. fluorescens* isolated from the root zone of rice crops exhibit strong inhibitory action against the pathogenic fungus *R. solani*, which causes root rot. The bacteria reduced the growth of the pathogenic fungus on the PDA culture medium. (Reddy and Battu, 2009) 3 of 58 Ali *et al.* (2001)^[21] achieved good results in inhibiting root pathogenic fungi such as *R. solani* when using the bacteria by seed loading or by adding them directly to the soil. Karim (2012)^[3] also reported the ability of the bacteria to inhibit the growth of pathogenic fungi *F. solani*, *R. solani*, and *M. phaseolina* by PDA on the culture medium: 71.00% and 78.25%, respectively

The bacterium *P. fuchuescens* showed an inhibitory effect on the fungi *F. solani* and *R. solani*, which cause the death of zucchini plants, with inhibition rates of 79.66% and 77.44%, respectively (Al-Hijazi, 2010)^[7]. Alwan *et al.* (2015) demonstrated the ability of the bacterium to inhibit the growth of the pathogenic fungus *R. solani*, the causative agent of root and stem base rot in cucumbers, with an inhibition rate of 100%.

3-2- The Fungus **penicillium** and its Role in Biological Control

The fungus *Penicillium*, in its asexual stage, belongs to the division Eumycota Moniliales and the order Hyphomycetes,

specifically the Deuteromycotina subfamily Moniliaceae. Its sexual stage and classification are similar to that of *Aspergillus*, where the sexual stage is called Talaromyces. The number of known species in the genus *Penicillium* is estimated at approximately 300, with new species being added periodically.

These fungi are recorded in various regions of the world (2004). *Penicillium* spp. is a widespread fungus, found wherever decaying matter is present. Its spores are ubiquitous, and species of this fungus are abundant in soil, air, and food (Webster and Weber, 2007)^[23]. It is a widespread saprophytic fungus, and one of its most distinctive characteristics is the formation of conidia with characteristic dimensions. This is a diagnostic feature for differentiating between fungal species, as are the culture characteristics

Colony colors are secondary characteristics for distinguishing between fungal species, in addition to the secretion of pigments that appear behind the colony (Petit *et al.*, 2009)^[24].

Penicillium fungi are characterized by possessing several mechanisms by which they inhibit the growth and pathogenicity of pathogens or promote plant growth. The fungus *P. corylophilum* has the ability to produce a range of secondary compounds, the most important of which are antibiotics and antimicrobials. Some of these contribute to promoting plant growth and resistance to pathogens. A group of compounds produced by *P. corylophilum* has been identified, including alkaloids, alkanes, fatty acids, and essential oils such as methylenecyclohexane, 2-1,3,8- and -P-mentatriene, among them oxalic acid and anthracene, as well as several other compounds such as acid alkane hydrocarbons, hexadecanoic acid, dibenzothiophene acid, and neoisolongifolene, which were identified in the fungus's culture media (Yin 2014 *et al.*, Tajick 2011, Keller and Refai *et al.* 2015)^[25, 27] showed that the fungus *Corylophilum* secretes substances that promote plant growth, including the compound Gliotoxin. Al-Jubouri (2017)^[8] also demonstrated in her study that the fungus *P. Corylophilum* has a high antagonistic ability against pathogenic fungi such as *R. solani*, *F. solani*, and *M. phaseolina*. She showed that treating the soil with the fungus *P. Corylophilum* was the most efficient in reducing the severity of infection with the aforementioned pathogenic fungi, as it led to the absence of infection compared to treatments with the pathogenic fungi alone, in which the percentage of infection severity reached 83%, 80%, and 72% respectively under wooden shade conditions. The mentioned fungus also promoted plant growth in a study conducted by Al-Bahadli (2009), it was found that the bio-resistance fungus *Penicillium* reduced the effect of the pathogenic fungus *R. solani* and increased the germination rate. The *R. solani* treatment recorded a germination rate of 35.3%, while the *Penicillium* treatment, in the presence of the pathogenic *R. solani*, recorded a germination rate of 73.3%.

References

1. Al-Khashan, Ali, Abdul-Bari Ahmed Anwar. Crop Production. Part Two: Transactions. Dar Al-Matbouat Al-Jadeeda. Egypt, 1985.
2. Jabr Kamel Salman. A Survey of Broad Bean Root, Base, and Stem Rot Disease, Identification of the Causative Fungi, and Biological Control. Journal of Agricultural Sciences, 2001:32(2):127-132, Iraqi.

3. Karim Fatima Hadi. Isolation and Identification of Fungal Causes of Okra Root Rot and Integration of Control in Babylon Governorate. Master's Thesis, Technical College/Al-Musayyib, 2012.
4. Matloub Ahed, Abdul-Ali Hadi, Muhammad Ahmed, Imran Kaif Al-Kaif. Isolation and Identification of Some Fungi Causing Broad Bean Root and Stem Base Rot Disease and Controlling Them with Some Plant Extracts and the Biological Fungus *Trichoderma viride*. Karbala Journal of Agricultural Sciences, 2015, 2(4).
5. Hussein Iman Radhi Testing the efficiency of the fungi *Aspergillus niger* and *Penicillium oxalicum* in controlling root and stem base rot disease in broad beans caused by the fungus *Rhizoctonia solani* (Kuhn). Technical Institute / Najaf, 2011.
6. Alwan Kawthar Fadhil Using some isolates of the fungi *Aspergillus*, *Penicillium chrysogenum*, and *Niger* as biofertilizers in wheat crops. PhD dissertation. College of Agriculture / University of Kufa, 2018.
7. Al-Hijazi Ali, Fahim Muhammad. Studying the effect of some biotic factors on fungi isolated from zucchini roots *in vitro* and on improving crop growth and production and protecting fruits from infection by the fungus *Rhizopus stolonifer*. Master's thesis. College of Agriculture. University of Basra, 2010.
8. Al-Jubouri Nadia Muhammad Mujawed. Evaluating the efficiency of some biotic control agents in controlling the pathogens of pepper root rot disease. Master's thesis, College of Agriculture Technology – Musayyib, 2017.
9. Cubeta MA, Vilgalys R. Population Biology of the *Rhizoctonia solani* complex. *Phytopathology*, 1997;87:480-484.
10. El-Mosallamy HM, Elain ML, Yonis S, Shalaby MS. Histopathological studies on root rot of broad bean plant induced by *Rhizoctonia solani* Kuhn, *Fusarium oxysporium* Shlech and *Macrophomina phaseolaina* Taub, 1990.
11. Graham PH, Vance CP. Legumes: Importance Zagazig Journal of Agriculture research, 2003;13(2):437-449. and constraints to greater use. *Plant physiology* 131:872-
12. Ogoshi A. Ecology and Pathogenicity of Anastomosis 877. and intraspecific group of *Rhizoctonia solani* Kühn. *Anna. Rev. phytopathol*, 1987;25:125-143.
13. Parmeter JR, Sherwood J, Platt WdA. Anastomosis grouping among isolate of *Thanatephorus cucumeris*. *Phytopathology*, 1969;59:1270-1278.
14. Saxena SC. Bio-Intensive integrated disease management of banded leaf and sheath blight of maize. Proceeding of the 8th Asian regional maize workshop, 2002.
15. Bangkok, Thailand: August 5-8.2002. Smil, V. Nitrogen in crop production. *Global Biogeochem. Cycles*, 1999;13:647–662.
16. Vance CP, Graham PH, Allen DL. Biological nitrogen fixation Phosphorus: a critical future need. In Fo Pedrosa M, Hungria MG, Yates WE, Newton eds, *Nitrogen fixation: from molecules to crop productivity*, Kluwer Acadmic publishers, dordercht, The Netherlands, 2000, 506-514.
17. Khaleel AI, Fatima HK, Kawther FA. The Efficiency of Plant Extracts and Biological Control Agents on Some Pathogens Causing Damping-off and Root Rot Disease of Cucumber. *Biopesticides International*, 2019.
18. AL-Waibi MH. Role of diazotrophic bacteria in some non-leguminous plant. *J. saudi soc. For Agreic. Scis*, 2006, 2.
19. krieg N, JG. Holt. Bergys manul of systematic Bacteriology.vol. I. williams and wlikius. London, 1984.
20. Bautista Gb, H. Mendoza, D. Vride. biocontol of *Rhizoctonia solani* in native potato (*solanum phueja*) plants using native *pseudomonas fluorescens*. *actabiol. Colomb*, 2007;12(1):32-19.
21. Ali NI, IA Siddiqui, M J-Zaki. varations between strains of *pseudomonas bacterium* I. effects on rootinfecting. *funqi, pak.J. Biol.Sci*, 2001;4:17-19.
22. Asan A. *Aspergillus*, *Penicillium* and related species reported from Tarkey; *Mycotaxon*, 2004;89(1):155-157.
23. Webster J, Weber RWS. Introduction to Fungi. Thirded. Combridge University Press. New York, 2007, 696.
24. Petit P, Lucas EMF, Abreu LMP, fenning LH, Takahashi JA. Novel antimicrobial secondary metabolites from a *Penicillium* sp. Isolated from Brazilian cerrado soil. *Electron.J. Biotechnol*, 2009;12:8-9.
25. Yin W, Keller NP. Transcriptional regulatory elements in fungal secondary metabolism *J. Microbiol*, 2011;49:329-339.
26. Tajick MA, Mohammad Khani HS, Babaeizad V. Identification of biological secondary metabolites in three *Penicillium* species, *P. goditanum*, *P. moldavicum*, and *P. corylophilum*, 2014;4(1):53-61.
27. Refai M. Abo El-azid H, Tawakkol W. Monograph on the genus *Penicillium*. Research in cairo University. Egypt, 2015, 157.