Research Article

Diversity and Ecological Roles of Bacteriophagous and Omnivorous Nematodes in Potato Soils of Algeria (Ain Defla)

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Abstract | Nematodes play a crucial role in soil ecosystems, contributing to nutrient cycling and providing protection for plants. This study examined the diversity and potential biological roles of nematodes associated with potato (*Solanum tuberosum* L.) fields in Ain Defla, Algeria. A total of 30 samples of soil obtained from 150 sub-samples collected from potato plots between January and mid-April were collected from depths of 0–5, 5–10, 10–15, 15–20, 20–25, and 25–30 cm and analyzed for nematode diversity and their interactions with soil bacteria and fungi. Eight genera of nematodes were identified, predominantly bacterivorous and omnivorous, with no mycophagous nematodes. The study highlights the ecological importance of nematodes in sustainable agriculture and proposes potential strategies for integrating nematode ecology into biocontrol efforts.

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Keywords | Bacteriophagous, Biological control, Potato, *Pseudomonas fluorescens*, *Rhizoctonia*, Soil ecology

Introduction

The potato is the fourth most important food crop in the world, following rice, wheat, and maize (FAOSTAT, 2022). It is cultivated widely due to its high caloric value and short growth period cycle, making it a key crop in food security initiatives (Scott *et al.*, 2013). In Algeria, the National Agricultural Development Program (PNDA) has boosted potato productivity, particularly in the fertile lands of Aïn Defla province, where yields exceed 350 quintals per hectare (MADR, 2023). In 2024–2025, Aïn Defla produced over 2.1 million quintals on 6,500 ha with yields of 500 qx/ha, underscoring its critical economic role in Algeria's potato supply, seed sector, and food security (Renima, 2025).

Despite high levels of productivity, potato cultivation faces several challenges, including drought, extreme temperatures, pest outbreaks, and ineffective disease management (Jansky *et al.*, 2016; Haverkort *et al.*, 2013). Among these challenges, soil-dwelling

nematodes have become significant biological factors impacting both yield and tuber quality. These microscopic organisms are present in soils everywhere and occupy various ecological niches. They play important roles in organic matter decomposition, nutrient mineralization, and the suppression of plant pathogens (Neher, 2010; Yeates *et al*., 1993).

Soil nematodes occupy various ecological niches and are classified into trophic groups based on their feeding behavior (Yeates *et al*., 1993; Ferris *et al*., 2001). These groups include bacteriophagous nematodes (e.g., *Rhabditis, Cephalobus*), fungivorous nematodes (*Aphelenchus*), phytophagous nematodes (*Meloidogyne*), omnivorous nematodes (*Dorylaimus*), and predatory forms (Yeates *et al*., 1993). Each group performs distinct functions in the decomposition of organic matter, the mineralization of nutrients, and the suppression of pathogens (Neher, 2010). Intensive agricultural practices, such as the excessive use of pesticides and fertilizers, can diminish nematode diversity and their ecological functions (Bongers and Bongers, 1998).

Therefore, understanding nematode ecology and its interactions with soil microbes presents a promising avenue for sustainable agriculture and natural biocontrol strategies. Among soil microorganisms, certain bacterial and fungal taxa play crucial roles in shaping nematode communities. Beneficial bacteria such as *Pseudomonas fluorescens* are known for their biocontrol potential through the production of antimicrobial compounds, while pathogenic fungi like *Rhizoctonia solani* represent major threats to potato production. Understanding the interactions between these microorganisms and soil nematodes is essential for developing sustainable biocontrol strategies. This study aims to investigate the presence and diversity of nematodes in the potato-growing soils of Ain Defla and to assess their interactions with bacterial and fungal communities.

Materials and Methods

Study area and sampling

The study was conducted in El Amra, located in the Ain Defla province of Algeria (36°18′ 50″N, 2°09′ 50″E) (Figure 1). This region features a Mediterranean semi-arid climate, characterized by annual rainfall ranging from 500 to 600 mm. The landscape includes mountainous terrain and alluvial soils found in the Chellif Valley. Ain Defla is recognized for its high potato productivity, attributed to the favorable climate, effective irrigation, and the presence of diverse agricultural stakeholders.

The soil sampling protocol for nematode extraction was designed to capture variability across five plots. Within each plot, soil was sampled from six distinct depth layers (0–5, 5–10, 10–15, 15–20, 20–25, and 25–30 cm). For each depth, five individual soil cores (sub-samples of 200 g each) were collected randomly. To obtain a representative sample for extraction, the five sub-samples from the same depth and plot were thoroughly homogenized and mixed into a 1 kg composite sample. In total, 150 soil cores were collected, resulting in 30 composite samples (5 plots × 6 depths) prepared for nematological analysis.

The samples were placed in polyethylene bags and labeled with field coordinates and sampling cropping history. A composite sample was then prepared for each field.

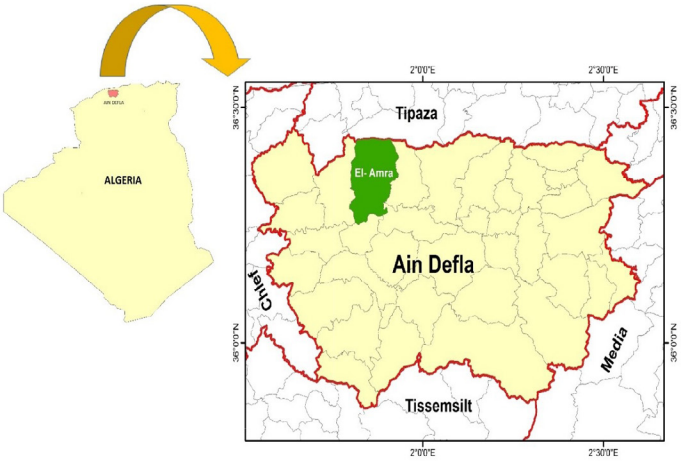

Figure 1: *The location sites of the samples in the representative case study.*

Nematode extraction and identification

The bucket method (Dalmasso, 1966) was employed for the extraction of nematodes. After sieving and decantation, the nematodes were recovered using a 40 µm mesh and collected in Petri dishes. Identification was carried out under a binocular microscope based on various morphological features, including body shape, esophageal structure, tail morphology, and the presence of stylets (Schmidt-Rhaesa, 2014).

Pathogen isolation (bacteria and fungi)

Bacteria were isolated from soil, roots, and tubers using King B medium and nutrient agar. Colonies

suspected to belong to the *Pseudomonas* species were identified based on fluorescence, catalase, oxidase, and hypersensitivity tests conducted on geranium leaves (Schaad *et al*., 2001). *Bacillus* species were isolated using a heat shock method and confirmed through spore staining and biochemical tests (Chilcott and Wigley, 1993).

Fungi were isolated from plant tissues after they were surface sterilized. The cultures were then incubated on Potato Dextrose Agar (PDA) at 25°C for 5–8 days. To identify *Rhizoctonia* species, we examined macroscopic and microscopic characteristics, including septation, hyphal structure, and conidia morphology (Botton *et al*., 1990; Chabasse *et al*., 2002).

Direct confrontation assay

Approximately 20–30 individual nematodes (mixed stages) were transferred to 5 cm Petri dishes containing either bacterial lawns (10^8 CFU/mL on nutrient agar) or fungal mycelia (7-day-old cultures on PDA). Nematode viability was assessed every 24h for 72h by observing movement under a stereomicroscope (40×). Mortality was expressed as a percentage of immobile individuals. Three independent replicates were conducted per treatment.

Two assays were conducted to study interactions between nematodes and isolated bacteria or fungi. Bacteriophagous nematodes were placed on bacterial lawns, and omnivorous nematodes were exposed to mycelial hyphae. Mortality was recorded over 72 hours and repeated three times.

Statistical analysis

The Principal Component Analysis (PCA) method reduces the dimensionality of a dataset by establishing correlations among variables. This reduction is achieved through the diagonalization of the correlation matrix, which generates a new orthogonal and uncorrelated dataset composed of principal components (PCs) ranked in decreasing order of importance (Singh *et al*., 2004; Helena *et al*., 2000). According to the Kaiser criterion (eigenvalue > 1) (Kaiser, 1960), the selected PCs facilitate the interpretation of underlying factors related to the variables. Factor loadings are commonly classified as follows: values greater than 0.75 are considered "strong," those between 0.50 and 0.75 are "moderate," and those ranging from 0.30 to 0.50 are "weak" (Liu *et al*., 2003). The analysis was performed using XLSTAT software (version 2016).

Results

Repartition of nematode population on different plots of land

Nematode distribution varied considerably across depths and plots (Figure 2). Surprisingly, the deepest layer sampled (25–30 cm) showed the highest densities in plots P1, P2, P4, and P5, with values approaching or reaching 100. Plot P3 was the exception, showing relatively balanced densities across all depths. The shallowest layer (5–10 cm) consistently had the lowest populations across all plots, suggesting less favorable conditions near the surface.

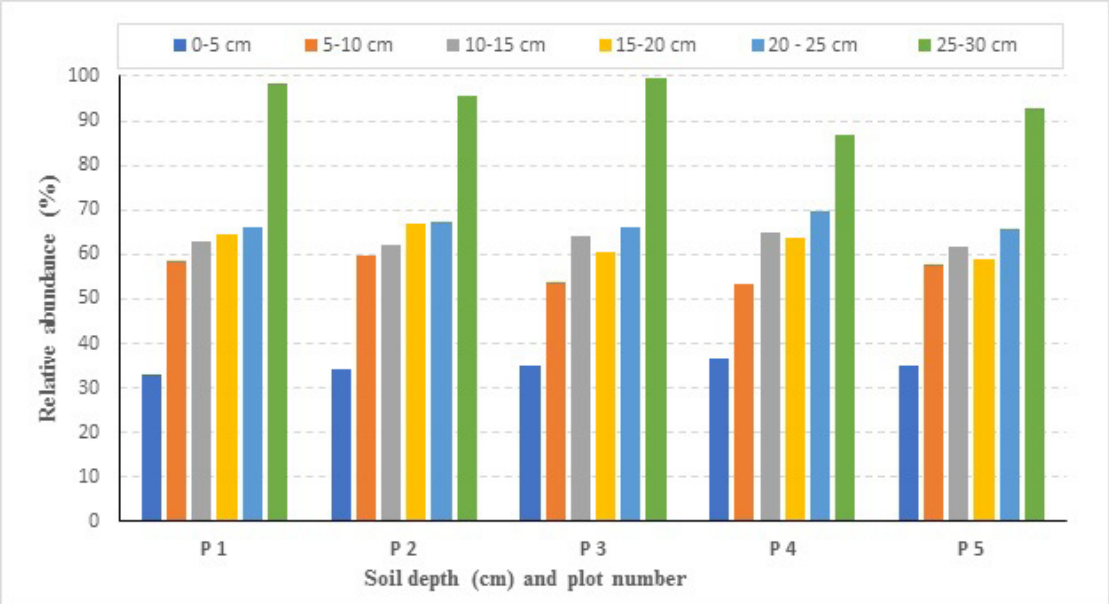

Figure 2: *Repartition of the nematode population across 5 plots of land, expressed as percentages, and at different depths (cm).*

Nematode diversity

Nematological analysis of the soil samples revealed the presence of a highly diverse nematode fauna comprising eight genera, distributed across four trophic groups (Table 1, Figure 3). This trophic diversity reflects both the availability of varied food resources and the state and functioning of the studied ecosystem.

Bacterial and fungal identification

The bacterium *Pseudomonas fluorescens* was identified through colony morphology, fluorescence, and metabolic profile analysis. *Rhizoctonia* was identified by the presence of septate hyphae, sclerotia production, and distinct branching patterns (Figure 4).

Nematode analysis at different elevations

The principal component analysis (PCA) reduced the dimensionality of the dataset to two main components, which together explained 84.18% of the total variance (59.65% for F1 and 24.53% for F2) (Table 2). The first axis (F1) opposes the variables "0–5," "10–15," and "20–25," which are strongly and positively correlated ($r > 0.83$), to the variables "5–10" and "25–30," which are negatively correlated ($r < -0.77$), thereby highlighting a clear structural contrast between two groups of variables. The second axis (F2) is primarily defined by the variable "15–20" ($r = 0.94$), capturing an independent source of variability (Figure 5a). At the observation level, P4 is strongly associated with the positive side of F1, while P1 and P2 are positioned on its negative side; P3 is characterized by a strong negative projection on F2, and P5 is located negatively on both axes.

Table 1: *Taxonomic presentation of the identified nematodes.*

Order	Family	Genus	Species	Trophic group
Araeolaimida	*Plectidae*	*Plectus*	Plectussp.	Bacteriophagous
Rhabditida	*Cephalobidae*	*Cephalobus*	*Cephalobus* sp.	Bacteriophagous
	Rhabditidae	*Rhabditis*	*Rhabditis* sp.	Bacteriophagous
	Diplogasteridae	*Diplogaster*	*Diplogaster* sp.	Bacteriophagous
Dorylaimida	*Dorylaimidae*	*Dorylaimus*	*Dorylaimus* sp.	Omnivorous
	Qudsianematidae	*Discolaimus*	*Discolaimus* sp.	Omnivorous
Isolaimida	*Aulolaimidae*	*Aulolaimus*	*Aulolaimus* sp.	Undetermined
Tylenchida	*Hoplolaimidae*	*Helicotylenchus*	*Helicotylenchus* sp.	Phytophagous

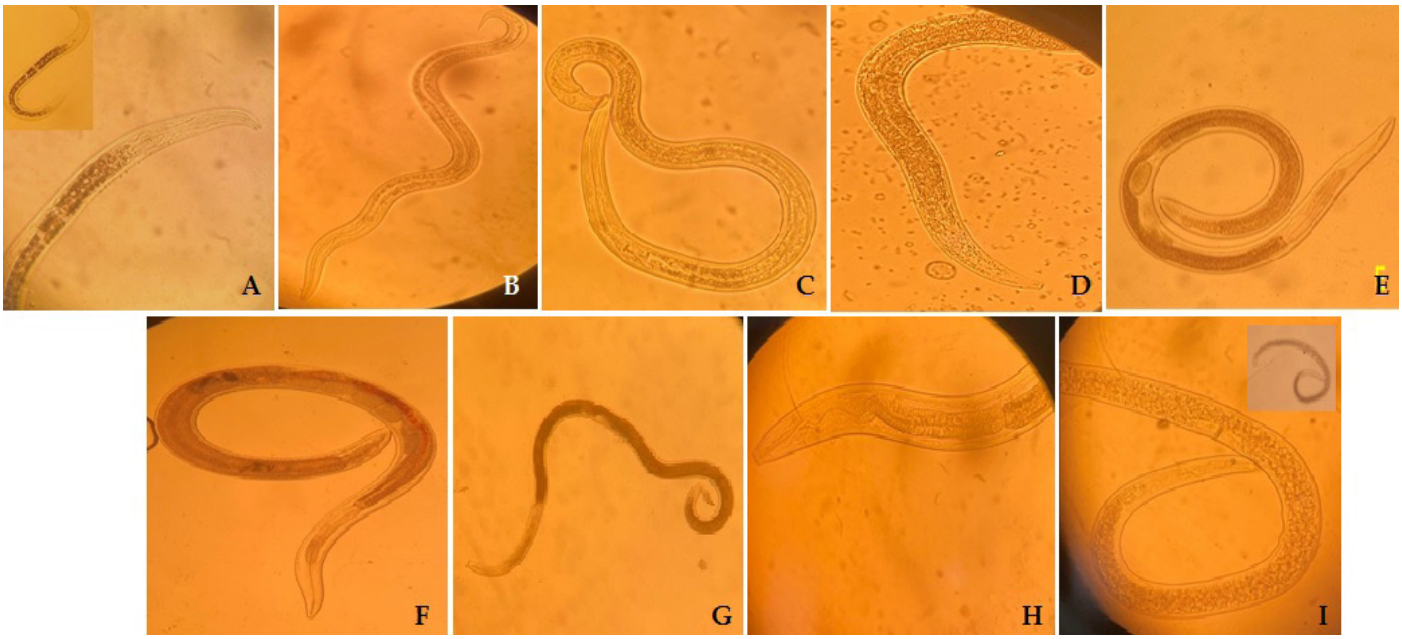

Figure 3: Nematodes identified in the study area (G:10×40). A) *Genus Diplogaster (Diplogasteridae); B) Genus Cephalobus (Cephalobidae); C) Genus Plectus (Plectidae); D) Genus Rhabditis (Rhabditidae); E–F) Genus Dorylaimus (Dorylaimidae); G) Genus Discolaimus (Qudsianematidae); H) Genus Aulolaimus (Aulolaimidae); I) Genus Helicotylenchus (Hoplolaimidae).*

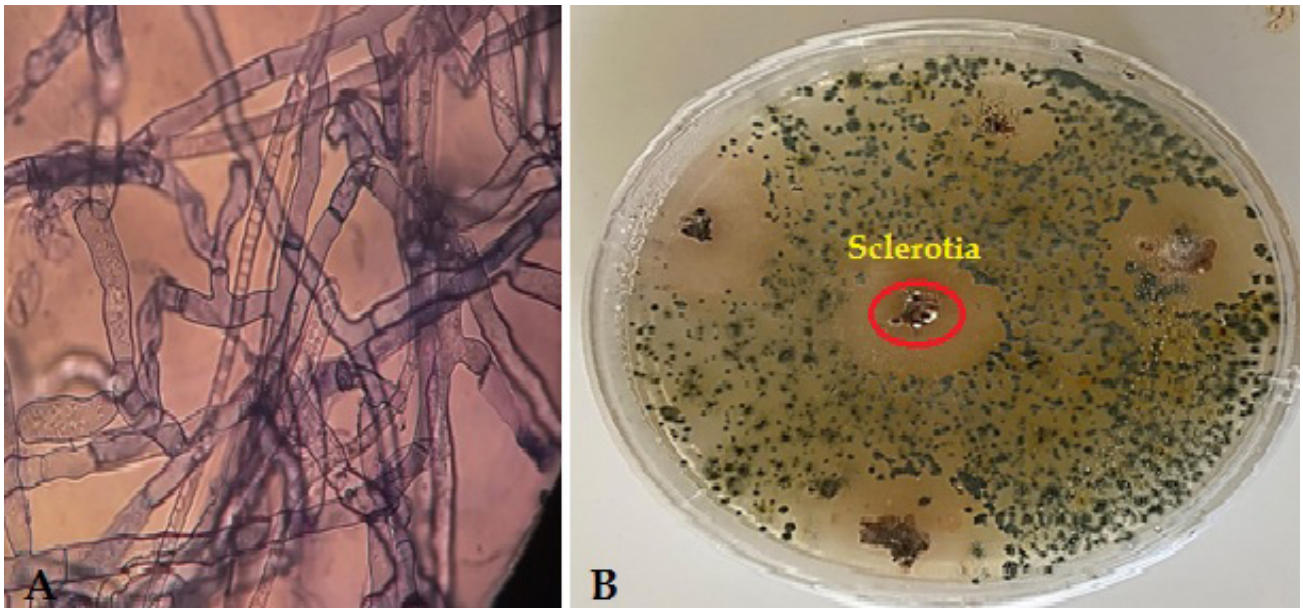

Figure 4: *Macroscopic and microscopic observations of fungi: Rhizoctonia A) Mycelium Cells; B) Sclerotia.*

Table 2: *The score of PCA according to nematode distribution.*

	F1	F2	F3	F4
0–5	0.919	-0.152	-0.292	0.218
5–10	-0.841	0.420	-0.337	-0.053
10–15	0.845	-0.067	0.514	-0.130
15–20	-0.140	0.940	0.296	0.098
20–25	0.834	0.551	0.016	-0.003
25–30	-0.773	-0.286	0.545	0.153
Eigen values	3.579	1.472	0.849	0.101
Variance (%)	59.652	24.529	14.142	1.677
Cumulative variance (%)	59.652	84.181	98.323	100.000

Overall, the PCA results reveal a well-structured separation of variables into two opposing sets on F1, complemented by a distinct factor carried by the "15–20" interval on F2, thus providing a robust basis for distinguishing the studied populations (Figure 5b). Finally, the populations can be classified into three distinct groups: P1 and P2 form the first group (Group 1); P5 and P3 constitute the second group (Group 2); and P4 characterizes the third group (Group 3).

The PCA highlighted, across the five studied plots, a significant and non-linear distribution of nematodes according to soil depth. The first axis (F1), accounting for 59.65% of the variance, opposes one group of depths (0–5 cm, 10–15 cm, and 20–25 cm) to another (5–10 cm and 25–30 cm), confirming that nematode abundance varies contrastingly with depth. The second axis (F2, 24.53% of the variance) is primarily defined by the 15–20 cm layer, whose unique character likely reflects specific ecological conditions at this depth, such as humidity, nutrient availability, or soil structure.

This structuring allowed us to distinguish three groups of plots: Group 1 (P1, P2), characterized by abundance at deeper layers; Group 2 (P3, P5), marked by a low nematode presence, particularly in the lower horizons; and Group 3 (P4), distinctly associated with superficial and intermediate layers. This differentiation strongly suggests that distinct farming practices applied to each plot directly influence the vertical distribution of nematode communities.

Nematode/pathogen interaction

Interactions between nematodes and pathogens

Exposure of nematodes to bacterial or fungal isolates resulted in notable mortality. The dry environment and lack of organic debris affected nematode survival, consistent with Wallace (1963).

Confrontation tests revealed rapid and marked mortality in both groups of nematodes when exposed to their respective pathogens (Figure 6). Bacteriophagous nematodes (*Rhabditis, Cephalobus, Diplogaster, Plectus*) exhibited substantial mortality upon contact with *P. fluorescens* bacterial lawns within 24–72 hours, whereas control nematodes maintained on sterile agar showed minimal mortality. Omnivorous nematodes (*Dorylaimus, Discolaimus*) experienced marked mortality when confronted with *R. solani* mycelial hyphae, contrasting sharply with the low mortality observed in control treatments.

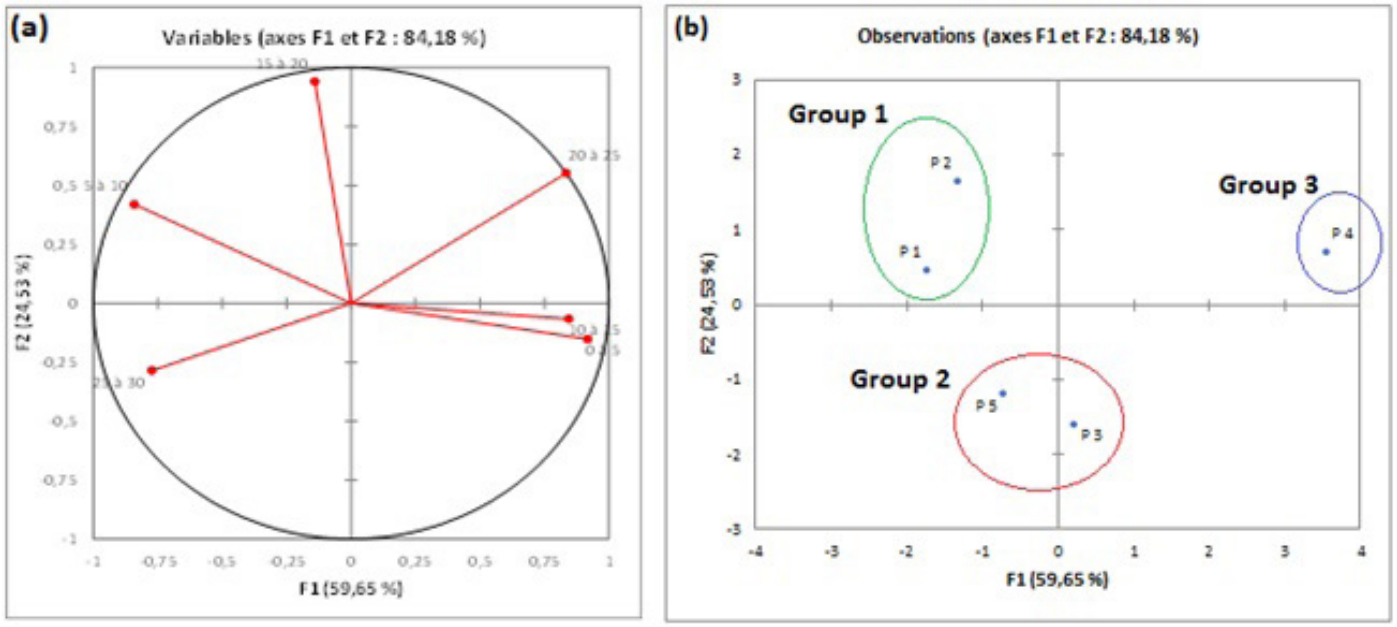

Figure 5: *(a) 2D Variables' projection on the factors plan (F1 × F2); (b) Samples projection plot on F1 and F2.*

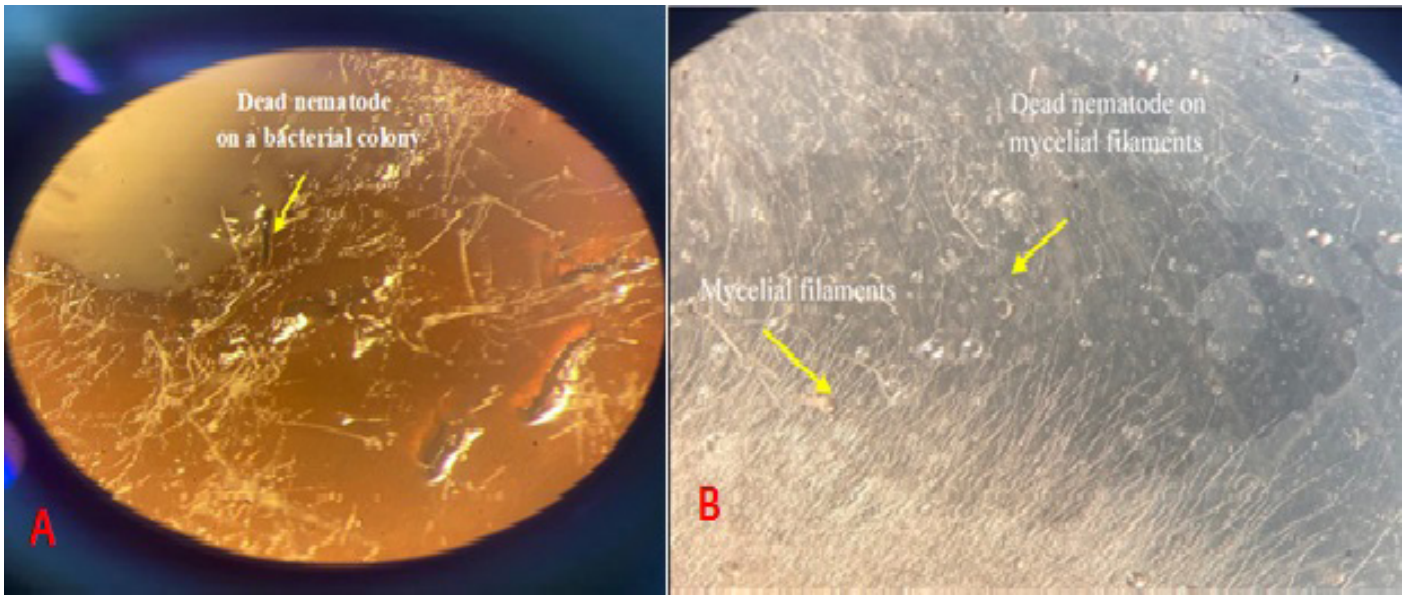

Figure 6: *Lethal interactions of nematodes with microbial pathogens (mortality observed 24–72 h post-exposure). (A) Nematode-fungal hypha encounter; (B) Nematode near bacterial cluster.*
Note: Data were obtained from three independent replicate assays, each involving 20–30 mixed-stage nematodes per treatment, with controls maintained on sterile agar. Detailed quantitative mortality data and time-course analyses are available upon request.

The antagonistic activity of *P. fluorescens* against nematodes has been well documented and involves multiple mechanisms. These include the production of secondary metabolites such as hydrogen cyanide (HCN) (Siddiqui *et al.*, 2006), extracellular proteases (AprA) (Siddiqui *et al.*, 2005), and 2,4-diacetylphloroglucinol (DAPG) (Siddiqui and Shaukat, 2003). These compounds can degrade nematode cuticles and interfere with their physiological processes. Similarly, *R. solani* is known to produce toxic metabolites as a defense mechanism against competing microorganisms (Kerry, 2000). However, whether these compounds directly caused nematode mortality in our assays remains to be determined through biochemical characterization of fungal exudates.

The rapid mortality observed in both trophic groups suggests active pathogenic mechanisms operating at the nematode-pathogen interface. However, the precise cause of mortality, whether through direct toxin secretion, enzymatic degradation of protective

structures, or modification of micro-environmental conditions, requires further investigation. Quantitative assessment of mortality rates and identification of specific bioactive compounds are currently underway and will be reported in future studies.

Discussion

The nematode community of Ain Defla soils is composed predominantly of bacteriophagous and omnivorous types, supporting soil nutrient cycling (Yeates, 1999; Neher, 2010). The dominance of *Rhabditis* and *Cephalobus* suggests the presence of active bacterial decomposition zones. Omnivorous nematodes, such as *Dorylaimus* and *Discolaimus*, contribute to the regulation of both bacteria and fungi. The unique presence of *Aulolaimus* warrants further ecological study. *Helicotylenchus*, although present in low numbers, indicates the potential for plant parasitism under favorable conditions (Yeates *et al*., 1993).

Environmental parameters, especially humidity, critically influence nematode survival and activity (Nouh, 2022; Guan *et al*., 2023; Matuska-Łyżwa*et al*., 2024). The use of *E. coli* OP50 and liquid media has shown promise in culturing bacteriophagous nematodes, such as *Caenorhabditis elegans* (Stiernagle, 2006).

In confrontation assays, isolates of *Pseudomonas fluorescens* and *Rhizoctonia solani* exhibited a rapid lethal effect on bacterivorous and omnivorous nematodes, respectively. This potent antagonism indicates that these pathogens deploy active defense strategies, likely through toxin production or other secondary metabolites, to suppress saprophagous nematodes, which are crucial actors in soil health.

While our study provides a foundational description, its scope has inherent limitations. The snapshot nature of our sampling and the complexity of multipartite interactions in the soil necessitate deeper investigation. A critical unanswered question is the precise biochemical mechanism of nematode mortality, including the identity of the involved toxins or virulence genes.

Future work will focus on characterizing the antifungal and nematicidal compounds produced by these pathogens. We also propose evaluating how alternative farming practices could restore the nematofauna, specifically mycophagous groups. Furthermore, harnessing the antagonistic potential of local, non-pathogenic *P. fluorescens* strains presents a promising biocontrol strategy against pests like *Helicotylenchus*.

The absence of fungivorous nematodes such as *Aphelenchus* or *Aphelenchoides* in our samples represents a notable finding, particularly when compared to their presence in organic potato systems reported by Ferris *et al*. (2001). Several factors may explain this absence. Fungicide applications likely reduce fungal populations that serve as food sources for these nematodes. Additionally, intensive soil management practices, including repeated mechanical tillage, can disrupt mycelial networks and compact soil structure, creating unfavorable conditions for fungivorous nematodes. Short crop rotation cycles may also limit the establishment of these slow-colonizing organisms.

The ecological implications of this absence are significant. Fungivorous nematodes play an important role in regulating soil-borne pathogens, including *R. solani*, through their predation on fungal hyphae (Kerry, 2000; Kerry and Bourne, 2002). Their absence may reduce natural biocontrol capacity within the system. Future research should investigate whether modified agricultural practices, such as reduced tillage or organic amendments, could facilitate the re-establishment of this functional group.

Conclusion

Our investigation into the nematode community across potato fields in El-Amra (Aïn Defla, Algeria) yielded insights into its composition and interactions with bacterial and fungal pathogens. We observed a moderate diversity of nematodes under stereomicroscopy, identifying eight genera spanning four trophic groups: bacterivores (e.g., *Rhabditis*, *Cephalobus*), omnivores (e.g., *Dorylaimus*), phytoparasites (*Helicotylenchus*), and one undetermined genus (*Aulolaimus*).

The Principal Component Analysis (PCA) revealed a significant and non-linear vertical distribution of nematodes across the studied plots. The first axis (F1), explaining 59.65% of the variance, contrasted depth clusters (0–5, 10–15, and 20–25 cm) with the remaining layers, while the second axis (F2) isolated

the 15–20 cm interval as ecologically unique. This spatial structuring segregated the populations into three distinct groups (Group 1: P1–P2; Group 2: P3–P5; Group 3: P4), strongly suggesting that plot-specific farming practices are the primary drivers of community architecture.

The complete absence of mycophagous nematodes indicates that intensive agricultural management may have depleted native fungal host populations, potentially disrupting natural regulatory pathways for soilborne pathogens such as *Rhizoctonia solani*.

In summary, our findings advocate for the intentional integration of nematode ecology into agricultural management. Fostering nematode diversity emerges as a viable strategy for enhancing soil ecosystem services, boosting potato yields, and reducing reliance on pesticides in Algeria.

Acknowledgement

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Novelty Statement

This study provides the first simultaneous characterization of nematode trophic diversity in Algerian potato-growing soils, revealing a complete absence of mycophagous nematodes under intensive agriculture and demonstrating antagonistic nematode–pathogen interactions, thereby offering new insights for ecologically based biocontrol strategies.

Author's Contribution

Meziane Boukhatem Malika: Conceived and supervised the study, guided data interpretation, and contributed to manuscript drafting
Ali-Arous Samir: Collected samples, conducted experiments and analyses, and supported manuscript preparation.
Bradai Abdelhamid: Provided support for methodology, statistical analysis, and critical revision.
Madani Nacira: Contributed to nematode extraction, quantification, and data processing.
Medjahed Khaldia: Provided technical and field assistance.
Lankri Elhassen: Contributed to sampling strategy, data curation, and assisted in data interpretation and validation.
Rouam Djawad: Translated content, contributed to editing, and refined the final revision of the manuscript.
Meziane Ahmed Malika: Reviewed the manuscript, contributed to final editing, and approved the version for submission

Generative AI and AI assisted technology statement
The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interest
The authors have declared no conflict of interest.

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