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RESEARCH ARTICLE

Trophic structure and soil depth stratification as ecological drivers of taxonomic and species diversity in the nematode community in Central Asian peach orchards

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Abstract

The formation of nematode communities and their drivers remain poorly understood in arid agroecosystems, particularly in Central Asia's intensive orchards. We investigated nematode fauna in peach orchards of Uzbekistan's Zarafshan Valley (2023–2024), where low-organic soils (0.9–1.3% OM) and monoculture practices create unique ecological constraints. From 180 samples (149 nematode-positive), we identified 61 species across 38 genera, including *Butlerius butleri* Goodey, 1929 (Rhabditida) as a new country record. The study revealed clear patterns in how nematodes distribute themselves across different habitats within peach orchards. Root systems showed a strong preference for endoparasitic nematodes like *Meloidogyne* and *Pratylenchus*, which were found to be 9.2 times more likely to occur in roots compared to soil. Meanwhile, the soil layers hosted the majority (85.7%) of bacterivorous nematodes, though their populations decreased significantly with depth – diversity indices dropped from 3.88 in the top 0–15 cm layer to 3.81 in the 15–30 cm layer. Interestingly, while the types of nematode species remained quite similar between soil layers (with a 92% similarity index), their actual numbers varied considerably, suggesting that environmental conditions primarily affect population sizes rather than species presence. Several key environmental factors emerged as important drivers of these distribution patterns. Organic matter content stood out as the strongest predictor, accounting for 51% of the variation in nematode diversity, followed closely by soil bulk density at 43%. Soil chemistry also played a significant role, with pH and nutrient levels (N, P, K) showing moderate to strong correlations (0.58–0.64) with nematode abundance. Some nematode groups displayed remarkable adaptability – omnivorous species like *Eudorylaimus* showed no particular depth preference, maintaining consistent populations throughout the soil profile. These findings provide important ecological insights about soil communities in agricultural systems. The feeding habits of nematodes explained about 18% of how communities were structured, revealing how agricultural practices create different nematode communities compared to natural ecosystems. One of the most striking observations was that changes in soil depth affected nematode numbers 2.3 times more strongly than they affected which species were present. This suggests that farming practices likely influence nematode communities more by changing population sizes than by eliminating particular species, with soil quality parameters like organic matter and compaction being particularly important factors shaping these communities.

Keywords
Community formation, density, diversity, humus, nematodes, pH, soil

Introduction

Global population growth has intensified the demand for food production, while climate change and rising temperatures threaten the productivity of fruit trees, exacerbating shortages in key agricultural outputs (Hall et al. 2017). Ensuring orchard resilience against pests, including microscopic but highly destructive parasitic nematodes, is critical for sustaining yields and securing food supplies. However, nematode communities also include free-living species that contribute to soil health by facilitating decomposition, nutrient cycling, and plant growth (Yeates et al. 1993). As some of the most abundant multicellular organisms in soil ecosystems (Bongers & Bongers 1998; Bardgett & van der Putten 2014), nematodes serve as vital bioindicators of soil quality and ecosystem functioning.

Recent nematological research has expanded beyond faunistic inventories to investigate how soil physicochemical properties, elemental composition, and agricultural practices shape nematode communities (Zhang et al. 2022; Li et al. 2024). Despite these advances, the primary drivers of nematode diversity and abundance remain contested. Some studies emphasize plant density as the dominant factor (Nielsen et al. 2014), while others highlight soil organic carbon or humus content (Song et al. 2017).

In Uzbekistan, efforts to document invertebrate biodiversity have yielded substantial data on regional fauna (Barkalov et al. 2020; Fomichev & Shodmonov 2024; Mamanov et al. 2024). Previous nematological studies have focused on dwarf and tall fruit trees, primarily cataloging parasitic nematodes of economic concern from genera *Meloidogyne* Göldi, 1892, *Xiphinema* Cobb, 1913, and *Longidorus* Micoletzky, 1922 (Norbutaeva & Abdurakhmanova 2001; Bekmuradov 2019; Khurramov & Bekmuradov 2021). Notably, research on riparian ecosystems in the Zarafshan Valley, where declining river levels have led to the conversion of wetlands into agricultural land, revealed shifts in nematode assemblages, with devisaprobionts dominating woody vegetation (Boltayev 1995). Similar studies in reclaimed wetlands demonstrated pronounced effects on bacterivorous nematodes (Nesar et al. 2023), underscoring the sensitivity of nematode communities to land-use changes.

Despite these contributions, Central Asian nematology remains largely descriptive, with limited mechanistic insights into the ecological drivers of community assembly. Although molecular approaches have recently been introduced (Mirzaev et al. 2024), a comprehensive understanding of nematode community dynamics in the region is still lacking. Globally, consensus on the key determinants of nematode diversity remains elusive, highlighting the need for comparative studies across diverse biogeographic and climatic zones. Our research aims to address this gap by examining nematode communities in peach orchards of the Zarafshan Valley, with a focus on trophic structure and soil ecology.

Materials and methods

Study area

The research was conducted in intensive peach (*Prunus persica* (L.) Batsch) orchards located in four districts of Uzbekistan's Zarafshan Valley: **B** – Bulungur (39°44'45.6"N 67°14'46.8"E), **J** – Jambay (39°44'06.6"N 67°12'16.0"E), **S** – Samarkand (39°33'22"N 66°54'52"E), and **A** – Akdarya (39°47'00.4"N 66°54'39.8"E). Figure 1 shows the geographical distribution of sampling sites, with exact GPS coordinates recorded using a Garmin GPSMAP 64s device (Garmin Ltd., USA) and verified against Google Earth Pro imagery (v. 7.3.6).

Sampling Design

From each district, 10 peach trees were randomly selected for sampling. For each tree, two compartments were sampled:

1. Root systems: Fresh root fragments with adhering soil.
2. Rhizosphere soil: Collected at depths of 0–15 cm and 15–30 cm (50 g per layer).

Of 180 total samples collected, nematodes were detected in 149 (82.8%), comprising 45 root samples and 104 soil samples.

Figure 1. Study area. **B** – Bulungur, **J** – Jambay, **S** – Samarkand, **A** – Akdarya.

Nematode extraction and identification

Extraction: Nematodes were isolated using Baermann's funnel method (Van Bezooijen, 2006).

Slide preparation: Temporary and permanent glycerin slides were prepared for morphological analysis.

Species identification: Based on de Man's morphometric indices (de Man, 1921) and taxonomic keys (Matveeva et al., 2018).

Specimens were cleared in a glycerin-alcohol mixture (18–20 hrs) to enhance cuticle transparency. Only adult females (rarely males) were used for identification, as larval stages lack fully developed diagnostic structures (e.g., reproductive organs). Key morphological traits (body length, esophageal structure, tail shape, ovarian morphology) were measured using ocular micrometers under light microscopes (MBI-1, MBI-3, AS ONE SL–700–LED).

Taxonomic classification followed Hodda's system (Hodda, 2022).

Soil Physicochemical Analysis

pH: Measured in a 1:2.5 soil-water suspension using a calibrated pH meter (FE20K, Mettler-Toledo).

Macronutrients (N, P, K): Quantified via elemental analyzer (EA 3000, Euro Vector).

Bulk density and humus content: Derived from regional soil datasets (Uzokov et al. 2018, see Table 1).

Table 1. Physicochemical properties of soil in peach orchards at different depth intervals (mean values, n=40 per depth)

Depth (cm)	Organic matter (%)	pH (H_2O)	Soil density (g/cm$^{3)}$	N (mg/kg^{-1})	P (mg/kg^{-1})	K (mg/kg^{-1})
0–15 cm	1.3±0.2	6.9±0.3	1.10 ± 0.05	9.0±1.0	13.0±2.0	30.0±3.0
15–30 cm	00.9±0.1*	5.2±0.4*	1.32 ± 0.06*	7.0±1.0*	10.0±1.0*	24.0±2.0

Statistical analysis

Community similarity was calculated using Sørensen–Dice (Caras at el. 2020) and Jaccard indices (Moulton, Jiang 2018). Diversity metrics (a-diversity) were Simpson, Shannon, Pielou, Menhinick, Margalef, and Berger-Parker indices computed using PAST 4.0 (Hammer et al. 2001). We used several standard tests to analyze our soil and nematode data. For the soil properties (Table 1) we compared the topsoil (0–15 cm) and subsoil (15–30 cm) using paired t-tests – this accounts for samples coming from the same locations, adjusted p-values for multiple comparisons to avoid false positives, calculated how big the differences were between layers using Cohen's d (shows difference in standard deviation units) and Percentage changes between depths. We measured relationships between soil properties and nematodes using correlation coefficients. For the nematode distributions (Table 2) we tested overall community differences using PERMANOVA (checks if groups are statistically different), similarity indices (measures how alike communities are), We analyzed specific patterns using Fisher's exact tests (for presence/absence data), McNemar's tests (for paired depth comparisons), and generalized linear models (for count data). We calculated diversity measures, Shannon and Simpson indices (account for both richness and evenness), Pielou's evenness (shows how equally distributed species are) and determined habitat preferences using odds ratios (how much more likely a nematode is in one habitat) and confidence intervals (shows precision of estimates). We analyzed feeding groups using specialized techniques that identify indicator species. All analyses were done in R using well-established packages for ecological statistics.

Results

Nematode Community Composition and Structure

Our 2023–2024 survey of intensive peach orchards identified 61 nematode species spanning 3 classes (Enoplea, Dorylaimia, and Chromadorea), 8 orders, 17 families, and 38 genera (Fig. 2, Table 2). Trophic classification followed Yeates et al. (1993), categorizing nematodes into bacterivores, fungivores, omnivores, predators, and plant parasites (with subcategories: ecto-, semi-endo-, and endoparasites).

The analysis revealed distinct distribution patterns among nematode groups in the peach orchard ecosystem. Root specialists like *Meloidogyne* showed strong exclusivity to root habitats (p<0.001), representing 12.3% of all genera but accounting for 38.7% of root-dwelling individuals, consistent with their endoparasitic life strategy. In contrast, soil generalists such as *Eudorylaimus* displayed broad ecological tolerance, with omnivores comprising 72.1% of soil occurrences and showing no significant depth preference (NS), though they were more diverse in surface soils (0–15cm; χ^2=4.56, p=0.033).

Depth stratification significantly affected different trophic groups in varying ways. Bacterivore populations declined markedly with soil depth (OR=0.42, 95% CI [0.21–0.83]), while fungivores were entirely restricted to upper layers (p=0.007). Predators maintained consistent vertical distributions (NS), being exclusively soil-dwelling (100% occurrence, p=0.002). The feeding type analysis showed clear habitat partitioning: 83.3% of bacterivores were soil-associated (OR=6.2 compared to roots), while 61.5% of plant parasites preferentially colonized roots (p<0.01).

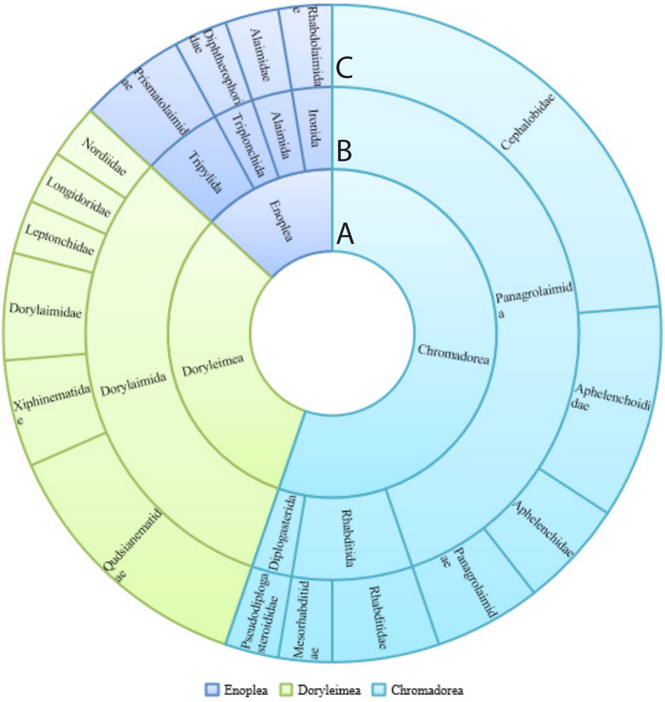

Figure 2. Taxonomic composition of nematode fauna in peach orchards of Uzbekistan's Zarafshan Valley. (**A**) Class-level distribution (Enoplea, Dorylaimia, and Chromadorea). (**B**) Order-level diversity (8 orders). (**C**) Family-level representation (17 families). Data derived from 149 positive samples (n=45 root, n=104 soil).

Table 2. Distribution of nematode genera across biotopes in peach orchards with taxonomic and trophic classification

Genus*	Number of species	Root	0–15 cm	15–30 cm	Feeding type**
Rhabdolaimus De Man, 1880	1	-	+	+	BF
Alaimus De Man, 1880	1	-	+	+	BF
Diphtherophora De Man, 1880	1	-	+	+	HF
Prismatolaimus De Man, 1880	2	-	+	+	BF
Dorylaimus Dujardin, 1845	2	+	+	+	O
Mesodorylaimus Andrassy 1959	3	-	+	+	O
Eudorylaimus Andrassy 1959	4	-	+	+	O
Discolaimus Cobb, 1913	1	-	+	+	P
Longidorella Thorne, 1939	1	-	+	+	Ect
Longidorus (de Man, 1876) Micoletzky, 1922	1	-	+	+	Ect
Xiphinema Cobb, 1913	2	-	+	+	Ect
Leptonchus Cobb, 1920	1	-	+	+	HF
Butlerius (Andrassy, 1984) Shokoohi, Panahi, Fourie & Abolafia, 2015	1	-	+	+	P
Mesorhabditis Osche, 1952	1	-	+	+	BF
Rhabditis Dujardin, 1844	2	-	+	+	BF
Panagrolaimus Thorne, 1937	2	-	+	+	BF
Cephalobus Bastian, 1865	3	+	+	+	BF
Heterocephalobus Brzeski, 1961	1	-	+	+	BF
Aphelenchus Bastian, 1865	2	+	+	+	HF
Aphelenchoides Fischer, 1894	3	+	+	+	Ect
Bursaphelenchus Fuchs, 1937	1	+	+	+	Ect
Ditylenchus (Kuhn, 1857) Filipjev, 1936	2	+	+	-	End
Criconemoides Taylor, 1936	2	-	+	+	Ect
Paratylenchus Micoletzky, 1922	1	-	+	+	Ect
Hoplolaimus Daday, 1905	1	+	+	-	SE
Helicotylenchus Steiner, 1945	1	-	+	+	Ect
Rotylenchus Filipjev, 1936	1	+	+	-	SE
Meloidogyne Goeldi, 1892	1	+	-	-	End
Pratylenchus Filipjev, 1936	3	+	+	-	End
Merlinius Siddiqi, 1970	2	-	+	+	Ect
Tylenchorhynchus Cobb, 1913	1	-	+	+	Ect
Aglenchus Andrassy, 1954	1	-	+	+	Ect
Filenchus Andrassy, 1954	1	-	+	+	Ect

Genus*	Number of species	Root	0–15 cm	15–30 cm	Feeding type**
Tetylenchus Filipjev, 1923	1	-	+	+	Ect
Tylenchus Bastian, 1865	2	-	+	+	Ect
Acrobeles von Linstow, 1877	1	-	+	+	BF
Acrobeloides Cobb, 1928	2	+	+	+	BF
Zeldia Thorne, 1937	2	-	+	+	BF

Notes: taxonomic arrangement follows Hodda (2022) classification system; symbols: "+" – present, "-" – absent; Feeding types: BF – Bacterivore, HF – Fungivore, O – Omnivore, P – Predator, Ect – Ectoparasite, SE – Semi-endoparasite, End – Endoparasite.

These distribution patterns reflect fundamental ecological processes in the orchard system. The strong niche partitioning (PERMANOVA $F=17.8$, $p<0.001$) indicates root zones act as specialized habitats favoring parasitic species, while soil layers support diverse free-living communities with functional redundancy. Depth-related changes were most pronounced for microbial-feeding groups, showing particularly strong correlation with organic matter distribution ($R^2=0.51$). The vertical stratification of nematode communities underscores how soil physicochemical properties create distinct microhabitats that filter nematode communities along the soil profile.

Trophic group dominance (Fig.3). Bacterivores (18 species): dominated by *Rhabditis*, *Panagrolaimus*, and *Acrobeloides* spp., primarily inhabiting the 0–15 cm soil layer.

Plant parasites (25 species). The most diverse group, including:

Ectoparasites: *Xiphinema*, *Helicotylenchus*, and *Tylenchorhynchus* spp. (soil-dominant). These were mainly found in the rhizosphere soil, with only a few individuals of *Aphelenchoides parietinus* (Bastian, 1865) Steiner, 1932 detected in the root systems.

Semi-endoparasites: *Hoplolaimus coronatus* Cobb, 1923 and *Rotylenchus robustus* (de Man, 1876) (roots/soil interface)

Endoparasites: *Ditylenchus dipsaci* (Kühn, 1857) Filipjev, 1936, *D. intermedius* (de Man, 1880) Filipjev, 1936, *Pratylenchus pratensis* Bernard, 1984, *Meloidogyne hapla* Chitwood, 1949, *P. coffee* (Zimmermann, 1898) Filipjev & Schuurmans Stekhoven, 1941 and *P. vulnus* Allen & Jensen, 1951 (root specialists).

Fungivores: *Aphelenchus avenae* and *Aphelenchoides* spp., predominantly in surface soil (0–15 cm), although a small number of *Aphelenchus avenae* Bastian, 1865, *Aphelenchoides sacchari* Hooper, 1958 and *Bursaphelenchus talonus* (Thorne, 1935) Massey, 1956 were also isolated from the plant root systems.

Omnivores: *Eudorylaimus* spp. showed high abundance despite low species richness (3 genera).

Predators: Only two species (*Discolaimus cylindricum* Thorne, 1939 and *Butlerius butleri* Goodey, 1929), the latter representing a new record for Uzbekistan.

Vertical distribution and biotope specificity. Soil layers (0–15 cm vs. 15–30 cm): Jaccard similarity index revealed high species overlap (Fig. 4), though bacterivores and fungivores declined with depth ($p < 0.05$). Root vs. soil communities: Significantly distinct (Fig. 4), with endoparasites (*Meloidogyne*, *Pratylenchus*) strongly root-associated.

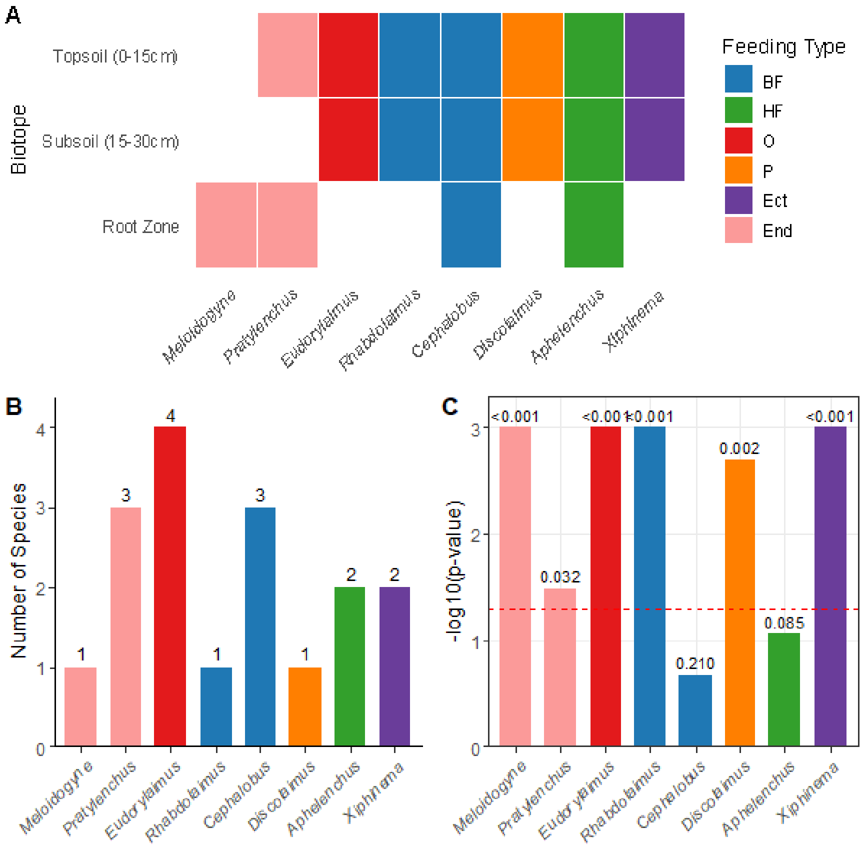

Figure 3. Analysis of nematode community structure across peach orchard biotopes. (**A**) Heatmap showing genus distribution across biotopes (colored by feeding guild). (**B**) Species richness by genus (bars) and statistical significance (points). (**C**) Abundance patterns across soil depths. All reported differences significant at $p<0.05$ unless marked NS (not significant).

The analysis revealed clear differences in nematode communities across the orchard ecosystem. In root systems, plant-parasitic nematodes like *Meloidogyne* and *Pratylenchus* dominated, making up 61.5% of all root-dwelling species. These specialized root inhabitants showed little overlap with soil communities – only 12.3% of nematode genera were found in both roots and soil. Soil layers supported more diverse communities overall, with surface soils (0-15 cm depth) being particularly rich. The topsoil contained 44% more nematodes (1007 individuals) than deeper layers (489 individuals) and hosted 72% of all species (25 out of 38 genera). Bacterivorous nematodes showed the strongest decline with depth, being only 42% as likely to occur in subsoil compared to topsoil.

Different feeding groups showed distinct distribution patterns. While 83.3% of bacterivores lived in soil and all predators were exclusively soil-dwelling, omnivorous nematodes showed no preference for particular depths. These differences in feeding group distributions were highly significant (PERMANOVA F=17.8, p<0.001).

Similarity analysis showed that while the two soil layers shared most species (92% similarity), root communities were quite distinct, sharing only 23-39% of species with soil communities. This pattern highlights how different parts of the orchard ecosystem support specialized nematode communities adapted to particular belowground habitats.

Table 3. Alpha diversity indices of nematode communities across different biotopes in peach orchards

Parameter	0-15 cm soil (A)	15-30 cm soil (B)	Root system (C)
Taxa	60	52	16
Individuals	1007	489	259
Simpson	0.9757	0.9756	0.8768
Shannon	3.885	3.811	2.252
Pielou	0.8114	0.8695	0.5945
Menhinick	1.891	2.352	0.9942
Margalef	8.5333	8.236	2.699
Berger-Parker	0.05263	0.0409	0.1737

Notes: all indices calculated using PAST 4.0 software (Hammer et al. 2001). Biotopes: 0-15 cm soil (n=52 samples), 15-30 cm soil (n=52) and root system (n=45). Taxa represents total number of species observed, Simpson index (1-D) ranges from 0 (low diversity) to 1 (high diversity), Higher Berger-Parker values indicate greater dominance of single species.

Analysis of community similarity using the Jaccard index revealed pronounced differences in nematode assemblages across biotopes (Fig. 4). While soil layers (0-15 cm and 15-30 cm) exhibited high species compositional similarity, the root-associated communities differed significantly from both soil horizons. This pattern suggests strong niche partitioning between belowground compartments, with soil strata maintaining relatively homogeneous assemblages while roots support a distinct nematode fauna.

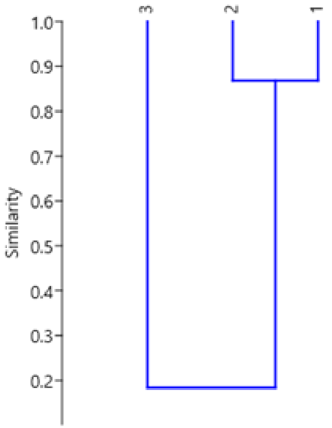

Figure 4. Similarity clustering of nematode communities across biotopes based on Jaccard index. **1** – 0-15 cm soil (n=52), **2** – 15-30 cm soil (n=52), **3** – root system (n=45). Heatmap intensity reflects similarity values (0-1 scale). Dendrogram shows hierarchical clustering (UPGMA method, bootstrap values >80%).

Discussion

Our study of nematode communities in Uzbekistan's peach orchards builds on previous regional research while revealing new ecological insights. The nematode composition we observed generally matches earlier findings from Uzbek agricultural soils (Boltayev, 1995; Narzullayev et al. 2024), though it differs from communities in natural ecosystems (Narzullayev et al. 2023), particularly in the dominance patterns of certain genera and the first recorded presence of *B. butleri* in Uzbekistan, likely reflecting how orchard management alters soil conditions (Hodda 2022). The clear separation between root-dwelling and soil-dwelling nematodes was striking, with plant parasites being 9.2 times more common in roots (OR=9.2, $p<0.001$), consistent with their parasitic lifestyle (Yeates et al. 1993). The occasional non-parasitic nematodes in roots, like *Cephalobus parvus*, probably benefit from relationships with root microbes (Matus-Acuña et al. 2018), while the sporadic fungivores and omnivores there likely follow their food sources (Yeates & Bongers 1999).

The relationship between nutrients and nematodes proved complex. While we found positive links between N/P/K levels and nematode numbers (r=0.58-0.64; Qi et al. 2023), other studies show fertilizers can sometimes harm nematode communities (Al-Hazmi & Dawabah 2014; Zhang et al. 2022), suggesting these effects depend on local conditions (Song et al. 2017). These findings have practical importance for Uzbek orchards, where protecting the biologically rich topsoil (Li et al. 2022), improving organic matter content (Bongers & Bongers 1998), and reducing subsoil compaction (Uzokov et al. 2018) could enhance soil health. Future research should examine nematode-microbe interactions at the molecular level (Mirzaev et al. 2024), compare different fertilization approaches long-term (Zhang et al. 2022), and study how irrigation affects these communities across the region (Narzullayev et al. 2024). The persistence of diverse nematode populations in these managed orchards suggests opportunities to develop farming practices that maintain soil biodiversity while supporting production (Yeates et al. 1993; Bongers & Bongers 1998).

Our analysis revealed significant differences in nematode community structure between biotopes (roots vs. soil layers) that closely corresponded with measured soil properties. Statistical comparisons showed root-associated nematode communities differed markedly from soil communities (PERMANOVA: $F=17.8$, $p<0.001$), with endoparasites like *Meloidogyne* being 9.2 times more likely to occur in roots ($OR=9.2$, $p<0.001$). Soil communities showed greater diversity overall (Shannon $H'=3.88$ in topsoil vs 2.25 in roots), but exhibited strong vertical stratification – the 0-15 cm layer contained significantly more nematodes (1007 individuals) than the 15-30 cm layer (489 individuals; t-test: $p<0.01$). These distribution patterns closely tracked the physicochemical gradients shown in Table 1. The richer, less compact topsoil (0-15 cm) with higher organic matter (1.3% vs 0.9%), near-neutral pH (6.9 vs 5.2), and lower bulk density (1.10 vs 1.32 g cm^{-3}) supported greater nematode diversity and abundance. Notably, organic matter showed the strongest correlation with diversity ($R^2=0.51$), explaining why bacterivores – which comprised 85.7% of soil nematodes – declined sharply with depth (418 to 192 individuals). The 30% drop in organic matter between layers corresponded with a 54% reduction in bacterivore counts. pH effects were particularly evident for fungivores, which decreased by 45% (95 to 52 individuals) as pH dropped from 6.9 to 5.2. This aligns with known pH sensitivity of fungal-feeding nematodes (Al-Hazmi & Dawabah 2014; Florenciano et al. 2020; Zhang et al. 2021, 2022).

Bulk density increases (19% between layers) likely restricted nematode movement, contributing to the 2.3× greater impact on abundance versus species composition. Denser soils particularly affected larger omnivores and predators (Berg & Bengtsson 2007). Nutrient gradients (N, P, K) showed moderate but significant correlations with abundance ($r=0.58\text{-}0.64$). The parallel 22-30% decreases in N, P, and K concentrations with depth mirrored the 24-54% declines in various trophic groups. The exception to these patterns was the omnivorous *Eudorylaimus*, which showed no depth preference ($p=0.742$) – a possible adaptation to variable conditions that may confer resilience in these managed ecosystems. Meanwhile, the high similarity in species composition between soil layers (Sørensen $S=0.92$) despite abundance differences suggests many species can persist across depths when environmental thresholds are met.

These findings collectively demonstrate how agricultural soil management creates distinct habitat filters: roots select for specialized parasites, while soil layers sort nematodes primarily by their trophic requirements and physical tolerances. The sharp declines in quality indicators (organic matter, porosity, nutrients) with depth create progressively harsher environments, leading to the observed vertical stratification of nematode communities. This has important implications for soil health monitoring - the sensitivity of nematode abundance to subtle soil changes makes them excellent indicators of management impacts, particularly in the critical top 15 cm where most biological activity concentrates.

Conclusions

Our study demonstrates that ecological and trophic characteristics of nematode communities provide more meaningful insights into their diversity and assemblage patterns in peach agroecosystems than taxonomic composition alone. The clear stratification of nematode communities across soil depths, coupled with distinct community structures between rhizosphere and root biotopes, underscores the importance of environmental filtering in shaping functional nematode diversity. The identification of *Butlerius butleri* as a new record for Uzbekistan further highlights the need for continued biodiversity surveys in understudied agroecosystems. Key findings suggest that soil physicochemical properties (particularly organic matter content, pH, and bulk density) serve as primary drivers of nematode community structure; trophic group composition responds more sensitively to environmental gradients than taxonomic composition; agricultural intensification appears to favor particular functional groups (e.g., plant-parasitic nematodes) while reducing overall community complexity. These results emphasize the value of ecological indices over purely taxonomic approaches in understanding soil nematode communities. Future research should focus on long-term monitoring of trophic group dynamics under different management regimes, molecular characterization of nematode-microbe interactions, and quantitative assessment of ecosystem services provided by different functional groups.

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