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Species composition and population structure of phytopathogenic fungi in sugar beet agrocenoses of short-rotation crop rotations in the western forest-steppe of Ukraine

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Abstract. This study analyzed the species composition and population structure of phytopathogenic fungi in short-rotation sugar beet agrocenoses of the Western Forest-Steppe of Ukraine. Based on 150 samples (90 roots and 60 rhizosphere soil samples) collected from fields of PE “Zakhidnyi Buh”, a total of 240 fungal isolates were identified. The dominant taxa included *Fusarium oxysporum*, *F. solani*, *Phoma betae*, *Rhizoctonia solani*, and *Botrytis cinerea*, accounting for more than 90% of the rhizosphere mycobiota. The genus *Fusarium* was the most abundant (48 ± 3.5%), forming a stable infectious core of the agroecosystem. Short-rotation crop sequences (wheat-soybean-beet and maize-soybean-beet) were found to increase the isolation frequency of *F. oxysporum* by 25–30% and *Phoma betae* by 18–22% compared with other systems, while the share of *Rhizoctonia solani* in rotations with maize reached 16%. Soil type significantly influenced the species profile: *F. oxysporum* predominated in calcareous sandy soils (≈35%), whereas *F. solani* and *P. betae* were dominant in chernozems. Morphological variability of *Fusarium* isolates (pigmentation and sporulation level of 2.5×10^{5}–1.8×10^{6} spores mL^{-1}) indicated high adaptability and potential for the formation of virulent races. Ecological analysis revealed a low alpha-diversity level ($H' = 1.13$–1.32) and a high dominance index ($D = 0.42$–0.51), indicating structural simplification and increased pathogen specialization. Three functional fungal groups were distinguished – primary pathogens (*Fusarium* spp.), opportunists (*Phoma betae*), and necrotrophs (*Rhizoctonia*, *Botrytis*) – which form a hierarchical model of the parasitic complex. The results confirm the cumulative effect of short crop rotations and demonstrate the necessity of integrating biocontrol agents (*Trichoderma*, *Gliocladium*) and ecological soil sanitation measures to restore microbial balance and reduce infection pressure in short-rotation systems of the Western Forest-Steppe.

Key words: rhizosphere mycobiota, *Fusarium oxysporum*, *Phoma betae*, *Rhizoctonia solani*, population structure, alpha-diversity, phytopathogenic fungi, agroecosystem, ecological stability.

INTRODUCTION

Sugar beet (*Beta vulgaris* L.) is one of the most important industrial crops in temperate climates, and its stable production determines both food security and the development of the sugar industry in Europe. At the same time, modern beet cultivation is undergoing systemic transformation driven by shortened crop rotations, intensification of soil tillage, global climate change, and increasing phytosanitary pressure. The reduction in the share of cereals and legumes in crop sequences and the replanting of beets at intervals of only 3–4 years promote the formation of persistent populations of phytopathogenic fungi that affect the root system throughout the growing season. The accumulation of infectious potential in beet agrocenoses is not only an agronomic but also an ecological problem, as it alters the equilibrium of microbial communities in the rhizosphere, reduces the abundance of antagonistic microorganisms, and lowers the biological stability of the agroecosystem (Strausbaugh, 2019).

Phytopathogenic fungi play a central role in the degradation of beet agrophytocenoses, causing necroses, rots, and vascular wilt that reduce yield by 15–30% and deteriorate the technological quality of roots. The main soilborne pathogens belong to the genera *Fusarium*, *Rhizoctonia*, *Alternaria*, *Phoma*, *Cercospora*, and *Botrytis*, each forming a stable ecological niche under prolonged monocropping conditions. The evolutionary plasticity of these fungi provides a competitive advantage through rapid substrate colonization, adaptation to changes in humidity, pH, and temperature, as well as interactions with other microorganisms of the rhizosphere (Woeber et al., 2025).

One of the most pressing problems of modern beet cultivation is the reduction in the number of crops in rotation, which leads to a shift in the population balance among saprotrophic, antagonistic, and pathogenic microorganisms. Continuous beet cultivation or its reintroduction to the same field after only 3–4 years contributes to the accumulation of fungal infection structures – particularly chlamydospores and sclerotia – that can remain viable for more than ten years. As demonstrated by Cui et al. (2022), repeated sugar beet cropping alters the structure of the rhizosphere microbiota, reducing the share of beneficial bacteria (*Bacillus*, *Pseudomonas*) and fungi (*Trichoderma*) with antagonistic functions, while stimulating the development of *Fusarium oxysporum* and *Rhizoctonia solani*. The authors note that microbial disequilibrium is the key prerequisite for the emergence of soil infections and the replanting syndrome.

Long-term experiments on beet fields in Europe have shown that shortening rotations leads to yield decline and an increased risk of root diseases (Brauer-Siebrecht et al., 2018). At the same time, excessive intensification of chemical crop protection aimed at compensating for these effects increases selective pressure on soil mycobiota, resulting in the emergence of resistant pathogen races. Consequently, a new structure of the fungal complex develops in agrocenoses, dominated by species with a high capacity to produce toxins, secondary metabolites, and biofilms.

According to Koch et al. (2022), nitrogen dynamics in short-rotation systems directly influence the composition of the microbial community, including its fungal component. The biomass of cover crops determines the intensity of nitrogen release and, correspondingly, the degree of activation of phytopathogenic fungi. Excessive nitrogen promotes the growth of necrotrophic fungi, whereas nitrogen deficiency suppresses symbiotic interactions and disrupts natural mechanisms of microbial balance control.

Thus, changes in the agro-technological environment create conditions for transformation of the population structure of mycobiota and for a shift in dominance toward pathogenic forms.

The use of metagenomic techniques in recent years has refined our understanding of the composition and functional role of microbial communities in beet agrocenoses. Lin et al. (2023) demonstrated that beet hybrids resistant to root rots are dominated by bacteria of the genera *Paenibacillus* and *Burkholderia*, as well as fungi of the genera *Mortierella* and *Trichoderma*, which play a crucial role in suppressing *Rhizoctonia solani* and *Fusarium culmorum*. In contrast, rot-susceptible variants are dominated by *Alternaria* and *Aspergillus*, which produce phytotoxic secondary metabolites. This supports the hypothesis that the stability of microbial interactions in the rhizosphere is a decisive factor determining beet resistance to soilborne diseases.

The problem of phytopathogenic fungi extends beyond the field phase. A substantial portion of yield loss occurs during storage, when fungal infections continue to develop within root tissues. Strausbaugh (2018) showed that during long-term beet storage under high humidity, fungi such as *Fusarium*, *Botrytis*, *Penicillium*, and *Mucor* become active, causing secondary rots. Subsequent research confirmed that, during storage, not only do diseases progress, but the population composition of pathogens also shifts toward more aggressive strains (Kandel et al., 2024). As roots age, the expression of genes responsible for phytoncide synthesis and oxidative stress enzymes decreases, making tissues more susceptible to fungal penetration.

Understanding the ecological regularities governing fungal population formation in the beet rhizosphere requires an integrated approach combining microbiological, molecular, and ecological analyses. Wolfgang et al. (2023), in their 'sugar beet holobiont' concept, consider the plant as an integrated ecosystem in which roots, symbiotic bacteria, mycorrhizal fungi, and pathogens interact. The balance of these interactions determines long-term crop stability. Disturbance of this balance due to anthropogenic pressure or repeated cropping leads to pathogen dominance and degradation of microbial diversity.

Climate change also influences the structure of fungal communities. Keller et al. (2021) showed that autumn cooling activates reactive oxygen species metabolism in beet tissues and alters carbohydrate metabolism, changing plant susceptibility to low-temperature fungi such as *Botrytis* and *Fusarium tricinctum*. This mechanism determines not only seasonal disease dynamics but also the potential impact of future climate change on phytopathogenic situations.

At the same time, the role of biocontrol in beet protection systems is growing. Antagonistic fungi such as *Trichoderma harzianum* and *T. viride* exhibit strong inhibitory effects against *Fusarium* and *Rhizoctonia* pathogens (Yassin et al., 2021), and they also enhance enzyme activities responsible for phytohormone and antioxidant synthesis (Harman et al., 2021). The use of such bioagents is environmentally safe and promotes the gradual restoration of natural soil biodiversity. Farhaoui et al. (2023) emphasize that microbial antagonists are key elements of biotic control, acting not only through direct antagonism but also through systemic plant resistance.

In studying the population structure of phytopathogens, the use of quantitative diversity assessment methods is of particular importance. The Shannon-Weaver, Simpson (1949), and Magurran (2003) indices, along with the approaches described by

Krebs (1999), allow evaluation of dominance, evenness, and stability of fungal populations. These methods enable temporal comparison of pathogenic assemblages, identification of structural trends, and assessment of anthropogenic impacts. Increases in dominance indices under shortened rotations indicate simplification of fungal community structure and reduced ecological stability of agrocenoses.

Based on the analysis of these trends, it can be concluded that the species composition of phytopathogenic fungi in beet agrocenoses is gradually shifting-from dominance of single local species to the formation of multi-component pathogenic complexes that interact synergistically. This conclusion is supported by studies by Woeber et al. (2025) and Wolfgang et al. (2023), which demonstrated that modern agroecosystem pathogenesis results not from the activity of a single species but from cooperative interactions among multiple groups of fungi and bacteria.

Thus, the current phytopathological situation in sugar beet agrocenoses is determined not only by the species composition of pathogens but also by the balance of the entire microbial system. In short-rotation crop systems, the disruption of this balance becomes the main factor of phytosanitary destabilization, manifested in decreased biodiversity and increased pathogen specialization.

The aim of this study was to identify and quantitatively assess the fungal species associated with sugar beet roots and rhizosphere soil in short-rotation agroecosystems of the Western Forest-Steppe of Ukraine, and to analyze their population structure in terms of frequency, relative abundance, and morphological variability across different soil types and crop rotation schemes.

MATERIALS AND METHODS

The study was conducted in 2024 on production fields of Private Enterprise "Zakhidnyi Buh" (25.02447586727863°, N 50.1143476192611°; E 25.39262543909438°, N 50.10784363281620°; E 25.38856869450137°, N 49.85219098052827°; and E 25.02549005342688°, N 49.85872962175164°). The first and second sites are characterized by chernozem soils, whereas the third and fourth sites are located on sandy soils. The soil was characterized by a humus content of 3.2–3.5%, hydrolyzable nitrogen 10–12 mg per 100 g soil, available phosphorus (Chirikov method) 12–15 mg per 100 g soil, and exchangeable potassium 18–20 mg per 100 g soil. The soil reaction was slightly acidic (pH 6.2–6.4). Within the crop rotations, soils differed in moisture capacity and compensatory potential–ranging from high-productivity chernozems to calcareous sandy soils. The climate of the study area is moderately continental and, according to the Köppen-Geiger climate classification, corresponds to the Dfb type (humid continental climate with warm summers and no dry season).

A total of 150 samples were collected–90 root samples and 60 rhizosphere soil samples – from three crop rotation systems (wheat-soybean-sugar beet, soybean-wheat-sugar beet, and maize-soybean-sugar), with 50 samples per rotation system, including 30 root samples and 20 rhizosphere soil samples from each system.

Isolation of fungal pathogens

Isolation procedures followed standard mycological protocols recommended in international practice (Leslie & Summerell, 2006; Misra et al., 2023). Diseased sugar beet roots were carefully cleaned from soil and surface-sterilized in 1% sodium hypochlorite solution for 1–2 min, followed by three rinses in sterile distilled water. Sterilized fragments (3–5 mm) were aseptically transferred to potato glucose agar (PGA), a medium widely used for cultivation of phytopathogenic fungi (Booth, 1971). Plates were incubated at 25–27 °C in darkness for 5–7 days.

For soil samples, the dilution plate method was used to determine species composition and relative abundance of micromycetes in the rhizosphere. Serial dilutions of soil suspension were plated on PGA supplemented with streptomycin (50 mg L^{-1}) to suppress bacterial growth.

Primary pathogen colonies were subcultured using the hyphal-tip or single-spore isolation technique to prevent species mixing (Leslie & Summerell, 2006). This approach is standard for *Fusarium* and other fungi prone to mixed colony formation.

Identification of isolates

Identification was based on morphological and agronomic characteristics according to modern atlases and taxonomic keys (Booth, 1971; Williamson et al., 2007; Aveskamp et al., 2008; Summerell et al., 2010; Jash & Sarkar, 2025). The main diagnostic criteria were as follows: for *Fusarium* spp. – shape and size of macro- and microconidia, presence of chlamydospores, colony pigmentation; for *Phoma betae* – dark concentric necrotic spots, slow sporulation, formation of pycnidia with unicellular conidia; for *Rhizoctonia solani* – morphology of sclerotia, absence of sporulation, right-angle branching of hyphae with constrictions at septa; for *Botrytis cinerea* – gray conidial coating, multicellular oval conidia, rapid colony growth.

Microscopic examinations were performed using a light microscope at magnifications of ×400–1,000.

Data analysis

Quantitative analysis of phytopathogenic fungal communities was performed based on culture-based isolation data. Species richness, relative abundance, and alpha-diversity indices were calculated for each crop rotation system and soil type. Alpha-diversity was assessed using the Shannon diversity index (H′), while relative abundance was expressed as the proportion of isolates of each taxon relative to the total number of isolates per sampling unit.

Statistical analyses were conducted using Microsoft Excel and R software (version 4.3.1; R Core Team, Vienna, Austria). Differences in fungal abundance and diversity indices among crop rotation systems and soil types were evaluated using analysis of variance (ANOVA). When significant effects were detected, mean comparisons were performed using post hoc tests at a significance level of $p < 0.05$.

RESULTS AND DISCUSSION

Species composition of phytopathogenic fungi

During the mycological analysis of 90 root samples and 60 rhizosphere soil samples collected in 2023 from production fields of PE "Zakhidnyi Buh" (Lviv and Chernivtsi regions, Ukraine), a total of 240 fungal isolates were obtained. Five dominant species of phytopathogenic fungi were identified: *Fusarium oxysporum*, *F. solani*, *Phoma betae*, *Rhizoctonia solani*, and *Botrytis cinerea* (Fig. 1 (a and b). These taxa accounted for over 90% of all isolates, forming a stable core of the complex of soilborne and postharvest pathogens affecting sugar beet.

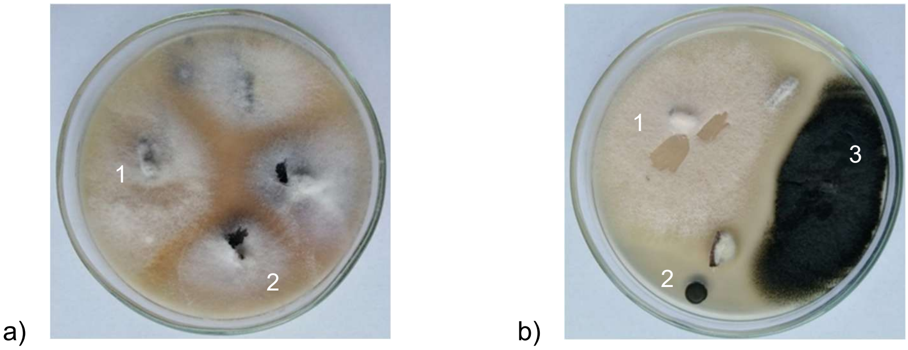

Figure 1. Example of isolated mycobiota from sugar beet samples a) 1 – *Fusarium oxysporum,* 2 – *Fusarium solani*; b) 1 – *Fusarium oxysporum,* 2 – *Gliocladium roseum,* 3 – *Phoma betae.*

On average, the genus *Fusarium* dominated the populations, representing 48 ± 3.5% of all isolates, of which *F. oxysporum* accounted for 30 ± 2.8% and *F. solani* for 18 ± 1.9%. *Phoma betae* was detected in 19 ± 2.1%, *Rhizoctonia solani* in 13 ± 1.7%, and *Botrytis cinerea* in 10 ± 1.5% of samples (Fig. 2). This species spectrum closely corresponds to results reported for European sugar beet agroecosystems (Lin et al., 2023; Misra et al., 2023; Cui et al., 2022; Kandel et al., 2024).

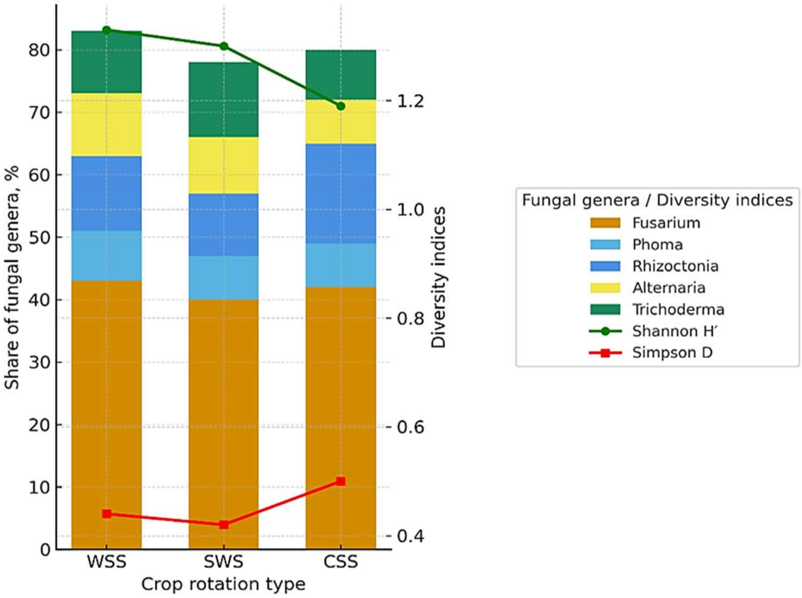

Figure 2. Species composition of phytopathogenic fungi and ecological diversity indices (Shannon H′ and Simpson D) in the rhizosphere of sugar beet under different short-rotation systems: wheat-soybean-sugar beet (WSS), soybean-wheat-sugar beet (SWS), and maize-soybean-sugar beet (CSS).

Effect of crop rotation systems on pathogen abundance and diversity

All investigated systems-wheat-soybean-sugar beet, soybean-wheat-sugar beet, and maize-soybean-sugar beet-were classified as short-rotation crop systems (3-year cycles). Compared with the soybean–wheat–sugar beet system, rotations including maize (maize-soybean-sugar beet) exhibited significantly higher soil infection pressure.

In particular, the frequency of *F. oxysporum* isolation increased by 25–30%, while *Phoma betae* increased by 18–22%. The maize–soybean–sugar beet system showed the highest incidence of *Rhizoctonia solani*, reaching up to 16% of isolates (Fig. 2), consistent with findings that maize acts as a favorable pre-crop for *R. solani* development (Koch et al., 2022; Misra et al., 2023). These results demonstrate the cumulative effect of short rotations, expressed not only as increased pathogen abundance but also as shifts in dominance structure.

Influence of soil type on population structure

Analysis of pathogen populations by soil type revealed statistically significant differences between chernozems and calcareous sandy soils (ANOVA, $p < 0.05$). These results are summarized in Table 1.

In calcareous sandy soils, *F. oxysporum* reached 35% of isolates, whereas in chernozems its share remained near 25%. Conversely, *F. solani* and *Phoma betae* were more abundant in chernozems, likely due to higher organic matter content and improved moisture conditions that favor saprotrophic – parasitic fungi.

Table 1. Relative abundance (%) of dominant phytopathogenic fungi by soil type

Species	Chernozems, %	Calcareous sandy soils, %
Fusarium oxysporum	25	35
Fusarium solani	27	15
Phoma betae	16	10
Rhizoctonia solani	12	14
Botrytis cinerea	10	11

Morphological diversity and adaptive traits of dominant taxa

A higher prevalence of *F. oxysporum* in sandy soils aligns with international observations: this species efficiently colonizes substrates with low buffering capacity and nitrogen deficiency, gaining a competitive advantage through chlamydospore formation and rapid root penetration (Bhuiyan, 2022). Conversely, *Phoma betae* predominated in more fertile soils with higher organic content, consistent with the findings of Farhaoui et al. (2023), who reported its activation in humid chernozems.

Microscopic observations combined with culture-based observations revealed high morphological diversity among *Fusarium* isolates. Colony pigmentation ranged from white-pink to orange-violet, and sporulation intensity varied from 2.5×10^5 to 1.8×10^6 spores·mL^{-1}, corresponding to international isolates (Cui et al., 2022) and indicating high adaptability of the pathogen.

Typical diagnostic features of *F. oxysporum* included sickle-shaped macroconidia with 3–5 septa and light violet pigmentation of the medium. *F. solani* produced shorter microconidia and had a denser mycelial structure, enhancing its survival in soil. *Phoma betae* formed small dark-brown pycnidia (100–150 µm) with hyaline unicellular conidia (4–6×2 µm). Sporulation in culture was slow, reaching its peak on the 12th–15th day of incubation. *Rhizoctonia solani* formed dark-brown sclerotia (150–200 µm) and did not produce spores; its hyphae exhibited characteristic right-angle branching with constrictions at septa. *Botrytis cinerea* demonstrated rapid colony growth and abundant sporulation at 25 °C under high humidity.

Comparison of *Fusarium* morphotypes showed that isolates with orange-green pigmentation and high conidial productivity exhibited the most vigorous growth, potentially correlating with increased virulence, as reported by Farhaoui et al. (2023) and Summerell et al. (2010). Combined analysis revealed that rotations involving maize ('maize-soybean-beet') showed the highest *R. solani* infection rates (up to 16%), while the frequency of isolation from wheat-preceded fields decreased to 10%. This relationship is explained by the presence of common hosts for *Rhizoctonia* among maize and beet crops, as noted by Koch et al. (2022) and Misra et al. (2023).

In contrast, rotations involving legumes (soybean–beet) exhibited an almost twofold reduction in *F. solani* incidence, likely due to nitrogen fixation and competition from symbiotic microbiota. This observation agrees with trends reported by Li et al. (2025) and Harman et al. (2021), where bioinoculation improved the balance between pathogens and antagonists.

Thus, short-rotation systems demonstrated an elevated level of pathogenic load, with soil type and preceding crop determining not only overall isolate density but also species dominance. The high proportion of *Fusarium* in short rotations indicates the formation of a stable infectious background that persists even with one-year breaks between crops. This persistence results from chlamydospore formation and the ability of the fungi to survive saprotrophically in crop residues. *Phoma betae* can persist on plant residues for more than two years, while *R. solani* can survive up to four years in the form of sclerotia (Misra et al., 2023).

Although the field frequency of *B. cinerea* did not exceed 10%, its epidemic potential during storage is considerably higher. According to Kandel et al. (2024), this species can actively develop even at low temperatures (2–4 °C), causing >15% mass losses and reducing sugar content by 2–3%. Hence, even a small field infection acts as a critical factor for postharvest losses.

Ecological dominance and population configuration of phytopathogenic fungi

The species composition of pathogenic fungi detected in short-rotation sugar beet agro-ecosystems of the Western Forest-Steppe of Ukraine reveals a stable, multi-species consortium with pronounced dominance of the genus *Fusarium*. In terms of ecological dominance (Magurran, 2004), this configuration corresponds to a monocentric population system in which a single genus (*Fusarium*) contributes >45% of total abundance. Such a pattern is typical for agroecosystems under sustained anthropogenic pressure, where repeated cropping creates selective conditions favoring specialized saprotroph-parasite complexes (Cui et al., 2022; Lin et al., 2023).

Successional stabilization and diversity compression under short rotations

Ecologically, this dominance indicates a transition of the pathogen community from a sub-climax to a climax-like stabilization stage characterized by minimal external dependence and high internal renewal of inoculum. This is supported by the presence of long-lived survival structures – *Fusarium* chlamydospores, *Rhizoctonia solani* sclerotia, and *Phoma betae* pycnidia – capable of persisting in soil for years (Misra et al., 2023; Kandel et al., 2024). Consistent with population-ecology principles, the community exhibits low alpha diversity (H′ = 1.13–1.32) and high Simpson dominance (D = 0.42–0.51), reflecting a simplified species structure and increasing ecological specialization. Relative to long rotations (H′ ≈ 1.9), short rotations narrow rhizosphere mycobiome niches and compress functional redundancy (Fig. 2.).

Functional stratification of the pathogen complex

Within the detected complex, three functional groups dominated. Primary pathogens (*Fusarium oxysporum*, *F. solani*) operate as obligatory or near-obligate parasites with broad host ranges and a high capacity for latent persistence within beet tissues (Farhaoui et al., 2023). Opportunists (*Phoma betae*) readily shift from saprotrophy to parasitism under stress, especially excess moisture (Woeber et al., 2025). Secondary necrotrophs (*Botrytis cinerea*, *Rhizoctonia solani*) preferentially exploit weakened plants or mechanical injuries, yet they are key agents of postharvest losses (Strausbaugh, 2018; Kandel et al., 2024). Functionally, the structure conforms to an adaptive stratification paradigm across the soil-root-clamp continuum: *Fusarium* maintains the baseline infectious pressure, whereas *Phoma betae* and *R. solani* intensify after homeostatic disruption in the agroecosystem. This succession model agrees with field-crop pathogen ecology reported elsewhere (Strausbaugh, 2018; Woeber et al., 2025).

Morphological plasticity and within-genus diversity of Fusarium

Marked morphological variation within *Fusarium* (colony pigmentation, growth rate, sporulation intensity) demonstrates high geno-ecological plasticity that supports survival across diverse edaphic regimes. The observed distribution of morphotypes–42% white-pink (low sporulation), 28% orange green (intermediate), and 30% violet (high sporulation; putatively greater aggressiveness)–parallels international observations linking intense pigmentation/rapid growth to higher virulence and reduced fungicide sensitivity (Leslie & Summerell, 2006; Cui et al., 2022; Farhaoui et al., 2023).

The within-genus Shannon diversity index (H′ = 0.85) indicates a quasi-stable configuration dominated by *F. oxysporum* with *F. solani* as a co-dominant species. This balance appears to be maintained by spatial segregation, with *F. oxysporum* preferentially associated with calcareous-sandy soils and *F. solani* with chernozems.

Spatial heterogeneity and indicator taxa in the rhizosphere

The rhizosphere mycobiome thus emerges as a mosaic system shaped by soil – climate factors and agronomic parameters. Spatial segregation manifested as a higher frequency of *F. oxysporum* on calcareous-sandy sites and of *Phoma betae* on chernozems, reflecting ecological complementarity of niches. Short rotations further promoted a regional cohort of indicator taxa – *F. oxysporum*, *P. betae*, *R. solani* – with high constancy (C = 70–85%), providing robust markers of phytosanitary status in Western Forest-Steppe beet fields. Comparable spatial heterogeneity has been documented at continental scale, where *Fusarium* and *Phoma* anchor axes of ecological differentiation along moisture gradients (Wolfgang et al., 2023).

Implications for agroecosystem stability and management

From an ecosystem-stability perspective, short rotations create a low-entropy environment in which simplified species structure diminishes resistance to biotic stress. The elevated share of *Fusarium* increases the parasite-pressure index (≈ 0.48–0.52), shifting homeostasis toward a pathogen-dominated model (Magurran, 2004). Strategically, *F. oxysporum* displays r-traits (high reproductive rate, rapid colonization), whereas *P. betae* and *R. solani* tend toward K-traits (slower development, long-term survival). This r/K complementarity stabilizes the pathogenic complex across seasonal and management fluctuations (Magurran, 2004; Misra et al., 2023).

For agronomic practice, these data imply that conventional rotational intervals of 2–3 years no longer guarantee a reduction in infectious background. Effective stabilization requires integrating biological regulation (antagonists *Trichoderma* spp., *Gliocladium* spp.), ecological soil sanitation (organomineral amendments, cover crops), and molecular population monitoring (qPCR-based diagnostics). Evidence suggests such measures can reduce pathogen dominance indices by 20–30% within two seasons (Yassin et al., 2021). Overall, the population structure is monocentric with *Fusarium* dominance and low diversity; *Fusarium* plasticity confers a competitive advantage and a persistent infectious substrate; spatial heterogeneity follows soil-type complementarity; functional stratification aligns with a hierarchical parasite-complex model (primary pathogens → opportunists → necrotrophs). Agronomic stability, therefore, depends on transitioning from a rotation-only paradigm to an integrated model combining longer rotations, residue management, cover crops, risk-triggered fungicide interventions, and deployment of biocontrol antagonists under molecular surveillance of inoculum dynamics. Given the sensitivity of community structure to both predecessor crop and soil context, differentiated rotational scenarios for sandy versus chernozem fields, prioritization of legumes as sanitary phases, and hybrid stratification by *Fusarium/Phoma* tolerance are recommended. Study limitations (single season, regional sampling) motivate multi-year monitoring that couples metabarcoding and microbiome profiling with quantified storage losses to model epidemic thresholds in short-rotation systems of the Western Forest-Steppe.

CONCLUSIONS

Based on mycological analysis of 150 samples (90 roots, 60 soils) collected in 2024 from PE “Zakhidnyi Buh” fields (Lviv and Chernivtsi regions), the sugar beet phytopathogen complex is a stable multi-species consortium with clear genus-level dominance by *Fusarium*–48 ± 3.5% of 240 isolates (*F. oxysporum* 30 ± 2.8%, *F. solani* 18 ± 1.9%). A secondary block–*Phoma betae* (19 ± 2.1%), *Rhizoctonia solani* (13 ± 1.7%), *Botrytis cinerea* (10 ± 1.5%)–collectively exceeds 90% of all cultures, defining a monocentric dominance type with low alpha diversity. Rotational comparison confirmed a cumulative short-rotation effect: in wheat-soybean-beet and maize-soybean-beet links, *F. oxysporum* isolation frequency rose by 25–30% and *P. betae* by 18–22%, while *R. solani* peaked (up to 16%) specifically after maize. Conversely, legume-based links displayed an almost twofold reduction in *F. solani*, highlighting the regulatory potential of N-fixing/symbiotic microbiota. Soil type was decisive (ANOVA, $p < 0.05$): calcareous-sandy soils favored ecologically plastic *F. oxysporum* (≈ 35%), whereas chernozems supported higher shares of *F. solani* (≈ 27%) and *P. betae* (≈ 16%), consistent with greater water-holding capacity and organic matter. The morpho-cultural variability of *Fusarium* (pigmentation gradient; sporulation 2.5×10^5–1.8×10^6 spores mL^{-1}) reflects strong adaptive potential and explains the persistence of infectious pressure under short rotations (via chlamydospores and saprotrophic survival on residues). Although field frequency of *B. cinerea* did not exceed 10%, its postharvest risk in clamps is substantial, necessitating targeted preventive measures during storage. Collectively, the results show that short-rotation schemes involving maize and soybean intensify pathogenic pressure and reshape dominance profiles; soil type determines spatial segregation of key taxa; sustaining agroecosystem resilience requires an integrated control model-longer rotations, residue/cover-crop management, risk-based fungicide use, and biocontrol (*Trichoderma/Gliocladium*) under qPCR monitoring. Given the observed sensitivity to predecessor and soil environment, practical recommendations should include differentiated rotation blueprints for sandy versus chernozem fields, prioritization of legumes as sanitary phases, and hybrid stratification by tolerance to *Fusarium/Phoma*. Multi-year, region-wide surveillance combining high-resolution microbiome tools with quantitative loss assessments is warranted to parameterize robust epidemic thresholds for short-rotation sugar beet systems.

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