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Alternative cropping with *Ficus carica* reshapes rhizosphere fungal communities in kiwifruit decline-affected soils

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ABSTRACT

Kiwifruit Vine Decline Syndrome (KVDS) has caused severe yield losses in Italian kiwifruit orchards since 2012 and remains difficult to manage using conventional agronomic practices. Given the limitations of replanting kiwifruit in affected soils, the introduction of alternative tree species may represent a viable strategy to restore soil functionality. The present study evaluated the potential of *Ficus carica* to modulate rhizosphere fungal communities in soils affected by KVDS. Fig trees were established in a formerly diseased kiwifruit orchard in central Italy, and their rhizosphere fungal microbiomes were compared with those of KVDS-affected kiwifruit plants using high-throughput sequencing of the fungal ITS region. A significant variation in fungal community structure was identified between the two plant species, coupled with distinct patterns in alpha diversity. Specifically, fig rhizospheres demonstrated a higher relative abundance of saprotrophic and potentially beneficial fungal guilds, while kiwifruit rhizospheres exhibited a distinct functional composition. The findings suggest that fig not only exhibits tolerance to KVDS-affected soils but also actively contributes to the restructuring of the rhizosphere fungal community, thereby promoting a transition towards potentially beneficial functional assemblages. The plant-driven microbiome modulation suggests a role for alternative species in enhancing soil resilience and supports microbiome-based strategies for managing soils impacted by persistent soil-borne diseases.

1. Introduction

Kiwifruit Vine Decline Syndrome (KVDS) represents a major threat to the sustainability of kiwifruit production in Italy, where it has caused severe yield losses and orchard abandonment since its first report in 2012. Initially observed in the Veneto region, KVDS has rapidly expanded to all major Italian kiwifruit-growing areas, resulting in substantial economic damage and challenging the long-term viability of the crop (Sorrenti et al., 2019; Savian et al., 2020; Mian et al., 2023). Although primarily documented in Italy, KVDS-like syndromes have also been reported in other kiwifruit-producing countries, including Turkey and China, under comparable environmental conditions, suggesting a broader potential risk for global kiwifruit production (Kurbetli and Ozan, 2013; Wang et al., 2015). KVDS is a multifactorial syndrome characterised by progressive root system deterioration, leaf curling and twig wilting, ultimately leading to vine collapse (Donati et al., 2020). Its aetiology involves complex interactions between abiotic stressors—such as waterlogging, hypoxia, elevated soil temperatures and soil fatigue—and biotic components, including soil-borne oomycetes, fungi and bacteria. Although several microbial taxa have been consistently associated with affected plants, their presence alone does not fully explain disease onset or severity (Bardi, 2020; Spigaglia et al., 2020; Cardacino et al., 2025). Climate change further exacerbates these conditions by increasing the frequency of extreme precipitation events and altering soil moisture dynamics, thereby amplifying root stress and disease susceptibility (Manici et al., 2021, 2024).

In this context, increasing attention has been directed toward the role of the rhizosphere microbiome in mediating plant health and soil resilience. Root-associated microbial communities regulate nutrient cycling, suppress pathogens and modulate plant responses to environmental stress. Disruptions to these communities, often driven by intensive cultivation practices or adverse environmental conditions, can lead to microbial dysbiosis, favouring opportunistic pathogens and accelerating disease progression (Hinsinger et al., 2009; Babalola et al., 2020; Bergamaschi et al., 2024; Guaschino et al., 2024). Consequently, strategies that promote the reassembly of functionally balanced microbial communities are increasingly recognised as a sustainable approach for managing soil-borne diseases.

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One emerging strategy for KVDS-affected orchards is the replacement of kiwifruit with alternative, more resilient tree species capable of tolerating degraded soil conditions. Beyond their agronomic performance, such species may actively influence rhizosphere microbial assembly, potentially restoring soil functionality. *Ficus carica* is characterised by high ecological plasticity and tolerance to abiotic and biotic stressors, making it a promising candidate for orchard replacement in KVDS-affected areas (Rahmani and Aldebasi, 2017; Khadivi et al., 2018; Villard et al., 2019). However, whether replacement planting with fig can actively restructure rhizosphere fungal communities in diseased soils remains poorly understood.

In this study, we tested the hypothesis that *F. carica* modifies the structure and functional guild composition of rhizosphere fungal communities in KVDS-affected soils. We compared the fungal microbiomes associated with kiwifruit (*Actinidia chinensis* var. *deliciosa*) and fig (*F. carica*) grown in the same diseased orchard, sampling at two key phenological stages to capture temporal dynamics. By integrating community composition and guild-based analyses, we aimed to assess the capacity of fig to promote a rhizosphere fungal assemblage associated with soil resilience and to evaluate the potential of replacement planting as a sustainable management strategy for KVDS-impacted orchards.

2. Materials and methods

2.1. Site description

The experimental field was located in Cisterna di Latina (Lazio Region, central Italy; 41°32′13″ N, 12°46′09″ E; 41 m a.s.l.). According to the Köppen–Geiger climate classification (https://koppen.earth/), the study area is designated as part of the Mediterranean climate zone (Csa), distinguished by hot and dry summers and mild, wet winters. The field comprised two adjacent orchards: a kiwifruit plantation (10,791.83 m^2) established in 1998 (*Actinidia chinensis* var. *Deliciosa* cv. 'Hayward') and a fig plantation (7368.8 m^2) established in 2018 (*Ficus carica* cv. 'Paradiso'), the latter replacing a section of the former kiwifruit orchard following KVDS spread (Fig. S1). Kiwifruit Vine Decline Syndrome (KVDS) symptoms were first observed in the orchard in 2016, several years after the establishment of the kiwifruit plantation, indicating that disease onset occurred under long-term cultivation rather than immediately after transplantation. In 2018, *Ficus carica* trees were planted in the same affected area as an alternative crop species following the decline of kiwifruit plants. Fig trees have been regularly monitored and have not exhibited visible symptoms of decline or growth impairment, suggesting good adaptation to KVDS-affected soils.

Both orchards were irrigated via a micro-sprinkler system with an estimated seasonal volume of 10,000 m^3 ha^{-1}. Fertilization combined organic inputs (e.g., manure) with a fertigation program supplying nitrogen, phosphorus, potassium, and micronutrients. Plant protection was limited to tribasic copper sulphate applications to control *Pseudomonas viridiflava*. To mitigate waterlogging, raised beds were implemented in the kiwifruit root zone. The soil has a predominantly sandy texture (pH 6.8) and normal electrical conductivity (Table S1), with relatively high levels of nitrogen, phosphorus, calcium, and magnesium, and substantial organic matter (Table S2).

2.2. Sample collection

Plants were arranged in a randomized block design, with three blocks per species and four plants per block (24 plants in total). Sampling was carried out at two time points corresponding to kiwifruit flowering (May 2022) and fruit set (July 2022). Samples were collected on the same tagged plants at both time points. For each plant and time point, we obtained one rhizosphere soil sample and one root sample (two compartments), yielding a total of 96 composite samples (24 plants × 2 time points × 2 compartments). Leaf symptoms consistent with Kiwifruit Vine Decline Syndrome (KVDS) were used to select kiwifruit plants (Fig. 1); no disease symptoms were observed on fig plants.

2.3. Soil coring and root handling

For each plant, three soil cores (40–50 cm depth) were taken within a 50-cm radius using a handheld core drill and pooled to obtain one composite sample per plant × time point. Samples were transported in sterile bags at 4 °C. After soil coring, soil samples were air-dried at room temperature and subsequently sieved (2 and 4 mm mesh) to separate root fragments from the soil matrix. Root fragments were then manually collected and selected based on morphological characteristics, including color, texture, and diameter, to distinguish between kiwifruit and fig roots. Larger and well-developed root fragments were preferentially collected, as they could be more reliably attributed to the target plant species. Fine roots and fragments with uncertain origin were excluded to minimize the risk of contamination from non-target plant species. Kiwifruit roots were easily identified based on their characteristic morphological features and typical KVDS-associated symptoms, including reddish-brown discoloration, tissue decay, and a reduced presence of fine roots, as previously described (Savian et al., 2020; D'Ippolito et al., 2022; Malacrinò et al., 2026) and shown in Fig. 2. Adhering soil was detached from the root surface by ultrasonication at 20 °C and 40 kHz (60 s pulses with 15 s intervals). The resulting soil suspension was collected and defined as the rhizosphere soil fraction. Roots were subsequently washed with sterile phosphate-buffered saline (PBS, 1 × , pH 7.4) to remove residual particles. Prior to DNA extraction, root tissues were freeze-dried, finely ground using a sterile mortar and pestle, and stored at −80 °C.

2.4. DNA extraction and storage

Genomic DNA (gDNA) was extracted from both rhizosphere soil and root samples using the NucleoSpin® Soil Kit (Macherey-Nagel, Düren, Germany) following the manufacturer's instructions, using ~150 mg of soil and ~100 mg of root tissue per extraction. DNA was eluted in 50 µL TE buffer, quantified with the Qubit™ dsDNA BR Assay Kit (Thermo Fisher Scientific, MA, USA), and stored at −20 °C until downstream analyses.

2.5. ITS amplification and sequencing

DNA amplification, library preparation, and sequencing were carried out by Novogene GmbH (Munich, Germany). Each PCR reaction contained 15 µL Phusion® High-Fidelity PCR Master Mix (New England Biolabs, MA, USA), 0.2 µM of each primer, and 10 ng template DNA in a total volume of 30 µL. Cycling conditions were: 98 °C for 1 min; 30 cycles of 98 °C for 10 s, 50 °C for 30 s, and 72 °C for 30 s; final extension at 72 °C for 5 min. The fungal ITS2 region was amplified using primers ITS3 (5′-GCATCGATGAAGAACGCAGC-3′) and ITS4 (5′-TCCTCCGCTTATTGATATGC-3′). PCRs were run in triplicate per sample and pooled prior to cleanup. Libraries were prepared and indexed according to Novogene's amplicon workflow, quantified with Qubit™ and real-time qPCR, and size-profiled on an Agilent Bioanalyzer. Equimolar pooling was performed to achieve the target sequencing depth per sample. Pooled libraries were sequenced on an Illumina NovaSeq 6000.

2.6. Bioinformatic analysis

Microbiome characterization was performed using the QIIME2 pipeline (v.2023.2.0; Bolyen et al., 2019), following workflows adapted from Cardacino et al. (2025). Raw sequence reads were demultiplexed, chimera-filtered, and denoised using DADA2 algorithm to generate a feature table of Amplicon Sequence Variants (ASVs) and corresponding representative sequences in FASTA format. DADA2 processing was

Fig. 1. (A) Overview of the kiwifruit orchard in October 2022, at the end of the growing season. (B–E) Close-up views acquired in early July 2023 showing representative leaf symptoms, including lamina curling and desiccation.

Fig. 2. Root segment from *Actinidia chinensis* collected from one of the observed plants, showing cortical browning and decay, thinning of lateral roots, and reduced fine root density.

conducted using a minimum overlap of 20 bp, with reads trimmed to a length of 240 bp. Fungal taxonomic classification was performed using the classify-consensus-blast algorithm against a custom reference database incorporating sequences from *Actinidia chinensis* (taxID 3625) and *Ficus carica* (taxID 3494), together with the NCBI Fungi RefSeq ITS database (PRJNA177353), in order to improve classification of plant-associated fungal taxa. ASVs assigned to host sequences, uncharacterized taxa, or low-frequency features (<10 reads across all samples; Bokulich et al., 2013) were removed prior to downstream analyses. The filtered feature table, taxonomy, and representative sequences were imported into RStudio (v.2024.09.0) and analyzed using the *phyloseq* package (v.1.50.0; McMurdie and Holmes, 2013). Rarefaction curves were generated using the *vegan* package (v.2.6.8; Dixon, 2003). Alpha diversity was estimated on rarefied ASV counts using Shannon, Simpson, Chao1, and ACE indices. Differences among experimental factors (host species, sampling time point, and sample type) were assessed using the Kruskal–Wallis test (two-sided, $\alpha = 0.05$). Beta diversity was evaluated using non-metric multidimensional scaling (NMDS) and principal coordinate analysis (PCoA) based on Bray–Curtis dissimilarities. Statistical significance of compositional differences was tested using permutational multivariate analysis of variance (PERMANOVA; 999 permutations). Relative abundances of the 30 most abundant fungal genera were visualized, with taxa contributing less than 1% grouped as "<1%". Set intersections were computed on the curated ASV table after filtering to remove host-related sequences, uncharacterized features, and low-frequency ASVs (<10 total reads across the dataset). Four sample groups were defined based on the host × compartment combination: *Actinidia chinensis* roots, *Actinidia chinensis* soil, *Ficus carica* roots, and *Ficus carica* soil. An ASV was considered present in each group if detected in at least one sample (pooled across the two sampling time points) with a post-filter count ≥1. Intersections among groups were visualized using an UpSet plot, which provides a scalable representation of shared and unique ASVs across multiple sets. Presence/absence analyses were conducted on non-rarefied data, as rarefaction does not influence binary occurrence-based comparisons. At least, functional guilds were assigned to fungal ASVs using the *fungaltraits* package (v.0.0.3), which integrates functional information from the FunGuild (Põlme et al., 2020) database.

3. Results

3.1. Plant host identity drives fungal community structure in KVDS-affected soils

Illumina sequencing generated a total of 4.8 million high-quality reads, with an average of approximately 600,000 reads per sample (Table S2). After quality filtering and removal of host-derived, unassigned and low-abundance features, the final dataset comprised 775 fungal taxa, which were used for downstream analyses.

Alpha-diversity analyses indicated comparable levels of fungal richness and evenness between the rhizospheres of *Actinidia chinensis* and *Ficus carica*. Neither richness estimators (Chao1, ACE) nor diversity indices (Shannon, Simpson) differed significantly between the two plant hosts (Fig. 3), suggesting that replacement planting did not alter overall fungal diversity. In contrast, sample compartment exerted a strong influence on alpha diversity, with rhizosphere soil consistently exhibiting higher richness than root-associated samples (Fig. S2). No significant temporal effect on alpha diversity was detected between sampling time points (Fig. S3). Together, these results indicate that differences between plant hosts are primarily reflected in community composition rather than diversity magnitude.

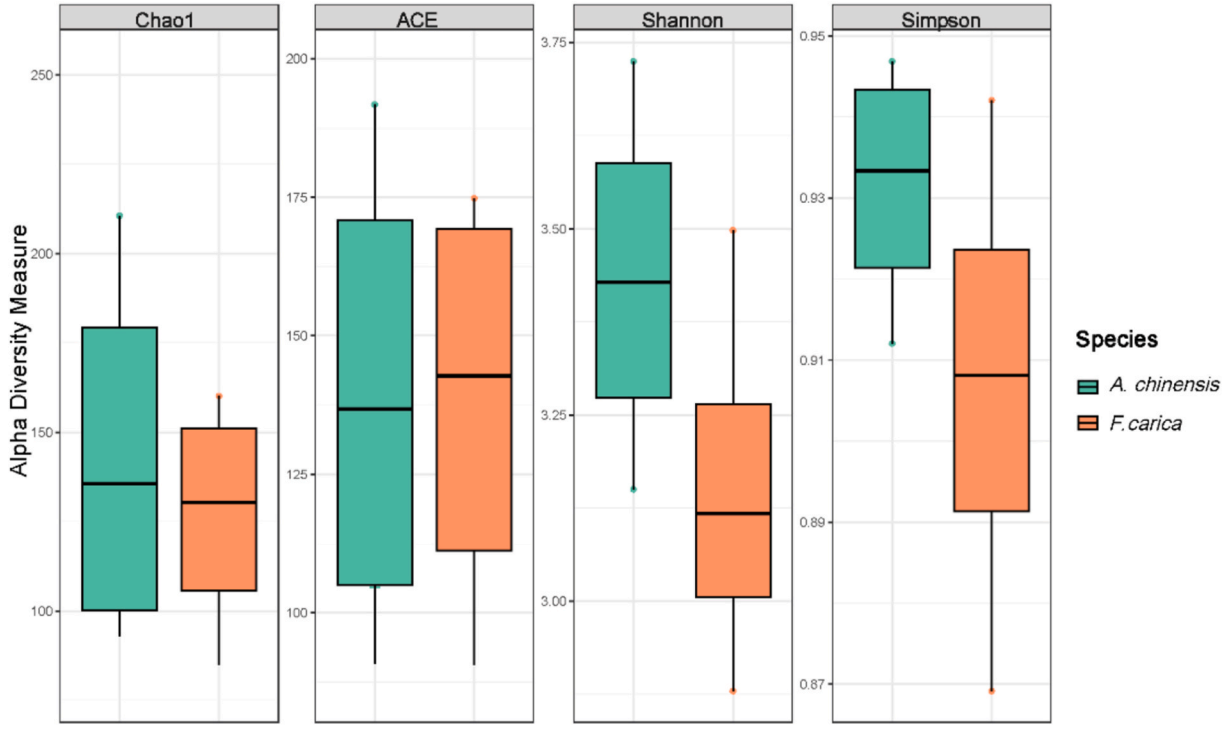

Fig. 3. Alpha-diversity of fungal communities associated with *Actinidia chinensis* and *Ficus carica* rhizospheres. Box plots show Chao1 and ACE richness estimators and Shannon and Simpson diversity indices. No significant differences were detected between plant hosts ($p > 0.05$), indicating comparable levels of fungal richness and evenness.

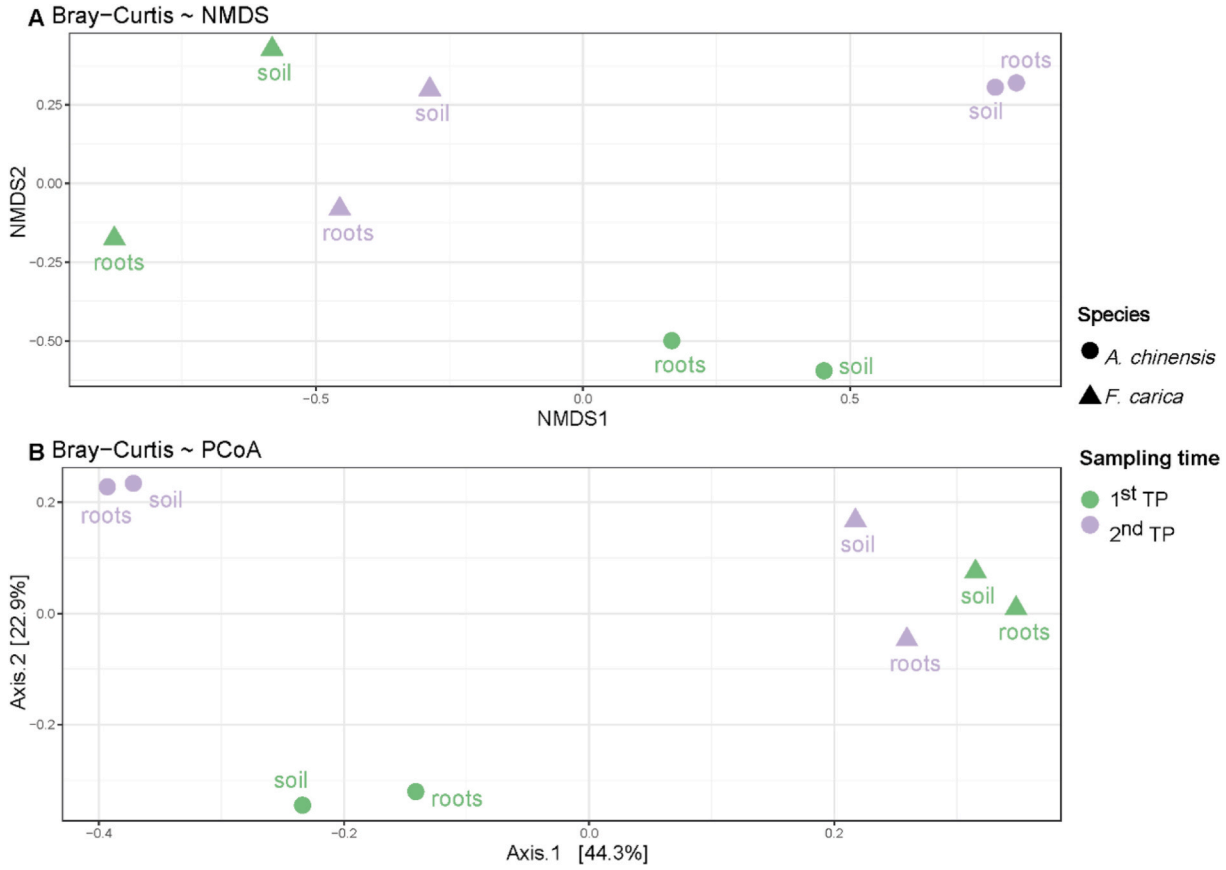

Fig. 4. (A) NMDS ordination and (B) PCoA based on Bray–Curtis dissimilarities. Shapes indicate plant host (*A. chinensis* circles; *F. carica* triangles), colours denote sampling time points, and labels indicate sample compartment (roots or rhizosphere soil). Ordinations reveal clear host-driven separation of fungal community composition.

3.2. Replacement planting rearranges fungal community composition

In contrast to alpha-diversity patterns, beta-diversity analyses revealed a pronounced separation of fungal communities according to plant host. Both NMDS (Fig. 4, panel A) and PCoA (Fig. 4, panel B) ordinations based on Bray–Curtis dissimilarities showed distinct and non-overlapping clustering of samples associated with *A. chinensis* and *F. carica*. This host-driven structuring was consistently observed across both roots and rhizosphere soil compartments.

Permutational multivariate analysis of variance confirmed plant host

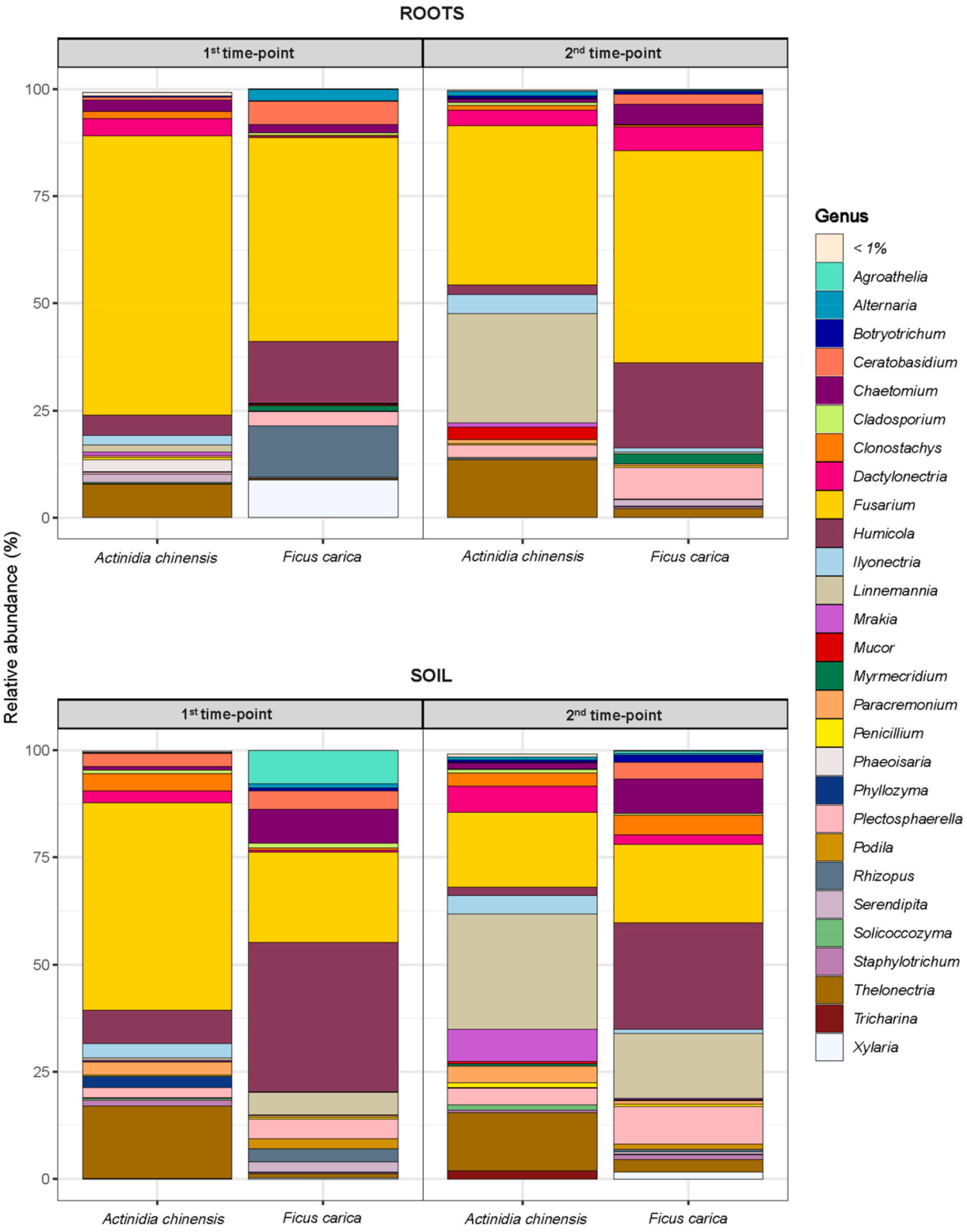

Fig. 5. Genus-level composition of fungal communities associated with *Actinidia chinensis* and *Ficus carica*. Relative abundances (%) of dominant fungal genera in root (top panel) and rhizosphere soil (bottom panel) samples are shown for each sampling time point. Taxa representing <1% of total relative abundance are grouped as "<1%".

identity as the main driver of fungal community composition ($R^2 = 0.423$, $P < 0.01$), exceeding the effect of sampling time ($R^2 = 0.164$, $P < 0.05$; Table S4). Temporal separation within each host species was evident, particularly in the PCoA ordination, but did not override host-associated differences. These results demonstrate that replacement planting with fig induces a substantial restructuring of fungal community composition in KVDS-affected soils.

3.3. Distinct taxonomic assemblages characterise Actinidia and Ficus rhizospheres

Taxonomic profiling at the phylum level revealed broadly similar distributions between hosts, with Ascomycota, Basidiomycota and Mucoromycota dominating both *Actinidia* and *Ficus* rhizospheres. However, marked differences emerged at finer taxonomic resolution.

Across sampling times, *Actinidia* rhizospheres were consistently dominated by *Fusarium* and closely related to other *Nectariaceae* genera, including *Thelonectria*, *Dactylonectria* and *Ilyonectria*. This dominance was observed in both root and soil compartments and persisted across phenological stages, indicating a stable host-associated fungal assemblage (Fig. 5). In contrast, *Ficus* rhizospheres exhibited a more heterogeneous taxonomic structure. Alongside *Fusarium*, fig-associated communities showed increased relative abundances of genera commonly associated with saprotrophic, wood-associated or multifunctional ecological roles, including *Humicola*, *Xylaria*, *Chaetomium*, *Agroathelia* and *Plectosphaerella* (Fig. 5). These taxa were particularly enriched in rhizosphere soil samples and displayed temporal variability, suggesting a more dynamic fungal assemblage under replacement planting.

3.4. Replacement planting alters fungal core membership and host-specific ASV patterns

To resolve shared and host-specific fungal assemblages, ASV distribution patterns were analyzed using an UpSet plot (Fig. 6). A limited core microbiome of 70 ASVs (9% of the total dataset) was shared across all sample groups, indicating a small set of ubiquitous fungi in KVDS-affected soils.

Host-specific patterns revealed clear differences between plant species. *Actinidia* samples harboured a larger host-associated core dominated by taxa commonly linked to plant pathogenic or root-associated lifestyles, including *Fusarium*, *Thelonectria* and *Dactylonectria*. In contrast, *Ficus* rhizospheres were characterised by a smaller but taxonomically distinct core, enriched in genera such as *Xylaria*, *Chaetomium*, *Ceratobasidium*, *Agroathelia* and *Serendipita*. Rhizosphere soil samples from both hosts exhibited a high number of unique ASVs, reflecting strong environmental filtering at the soil–root interface. These patterns suggest that fig selectively recruits a distinct subset of fungal taxa when established in KVDS-affected soils, consistent with host-driven restructuring of the rhizosphere microbiome.

3.5. Functional guild composition differs between plant hosts

Functional annotation of fungal taxa revealed pronounced differences in guild structure between *Actinidia* and *Ficus* rhizospheres (Fig. 7). Communities associated with *Actinidia* were dominated by plant-associated guilds, particularly plant pathogens and endophytes, largely represented by *Fusarium*, *Alternaria*, *Cladosporium* and *Penicillium*.

In contrast, *Ficus* rhizospheres exhibited an increased representation of saprotrophic and multifunctional guilds, including wood saprotrophs

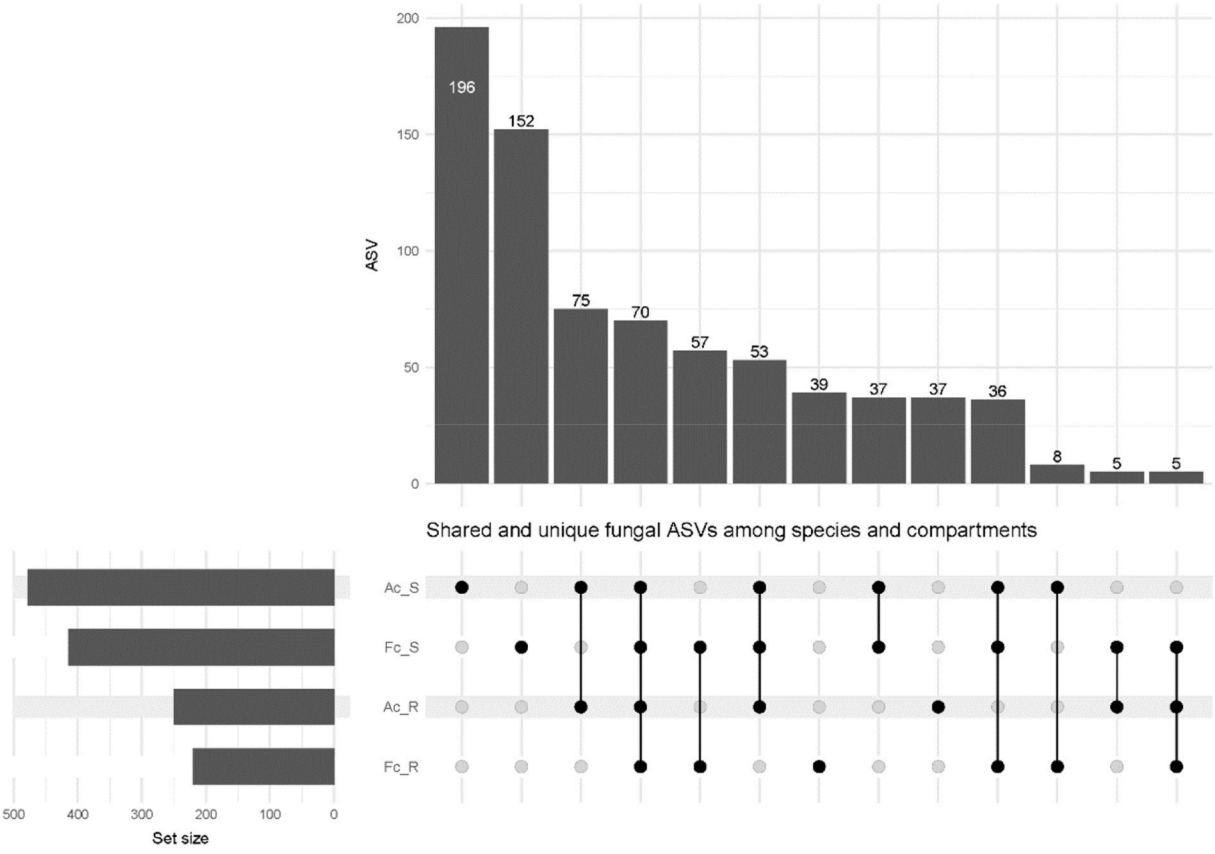

Fig. 6. UpSet plot showing the intersections of amplicon sequence variants (ASVs) across host × compartment groups. Sets correspond to *Actinidia chinensis* roots (Ac_R), *Actinidia chinensis* soil (Ac_S), *Ficus carica* roots (Fc_R), and *Ficus carica* soil (Fc_S). Bars indicate the number of shared and unique ASVs among groups.

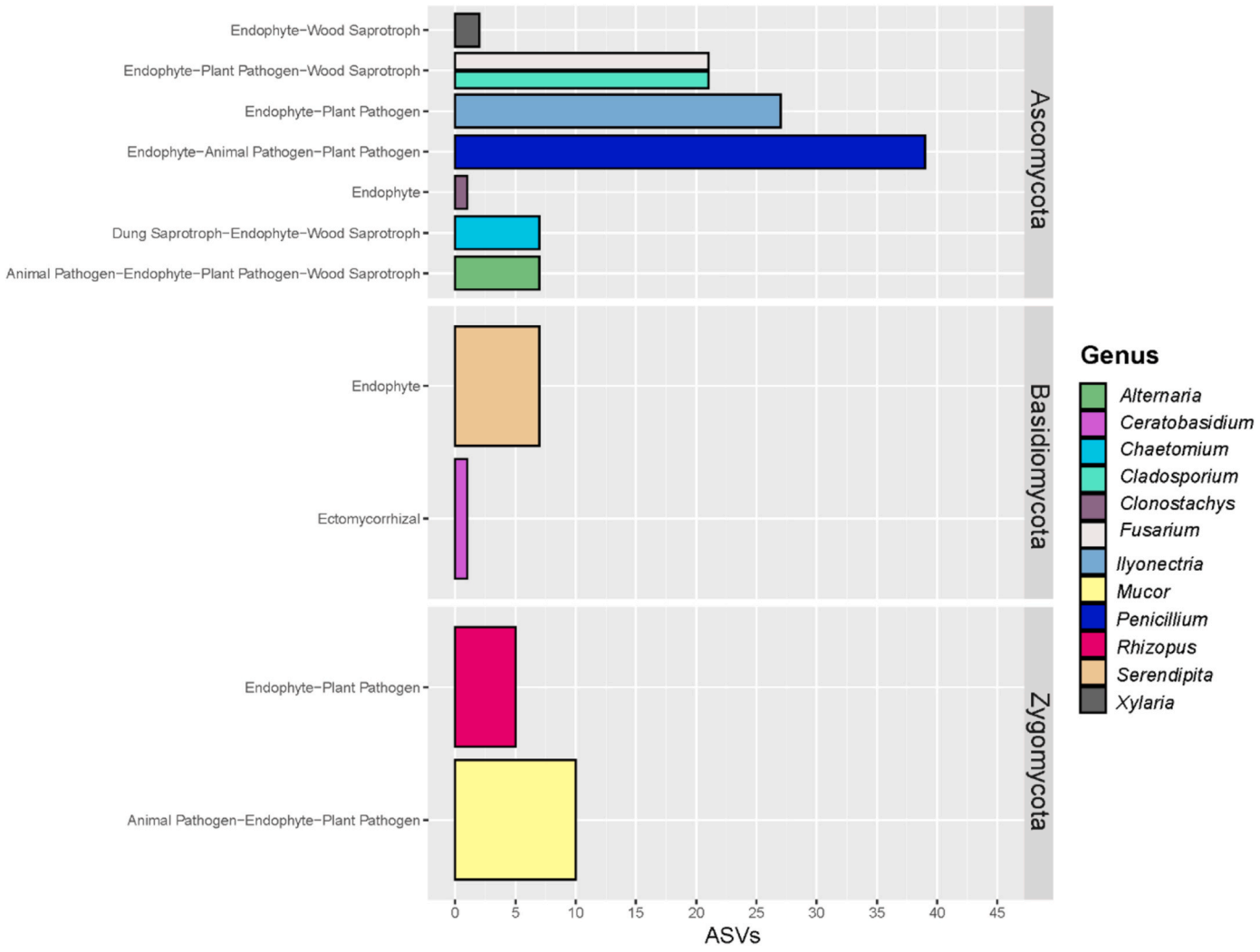

Fig. 7. Functional guild composition of fungal communities associated with *Actinidia chinensis* and *Ficus carica* rhizospheres. Bars represent the number of ASVs assigned to each ecological guild using the FungalTraits framework, grouped by fungal phylum. Multi-guild assignments reflect consolidated ecological roles reported for each taxon.

and taxa with combined endophytic and saprotrophic lifestyles, such as *Xylaria*, *Chaetomium* and *Humicola*. Basidiomycetous taxa with putative mutualistic or endophytic roles, including *Serendipita* and *Ceratobasidium*, were also more prominent in fig-associated samples.

Although multi-guild annotations were common due to genus-level taxonomic resolution, the overall shift in functional guild composition indicates that replacement planting with fig promotes a rhizosphere fungal assemblage less dominated by strictly pathogenic guilds and potentially more supportive of soil resilience.

4. Discussion

The present study demonstrates that replacement planting with *Ficus carica* in soils affected by kiwifruit decline leads to a marked restructuring of the rhizosphere fungal community, despite comparable levels of overall fungal diversity between fig and kiwifruit. By disentangling diversity, composition, and functional guild structure, the results highlight plant host identity as a key driver of fungal community assembly in degraded orchard soils, emphasizing the active role of alternative crops in shaping rhizosphere microbiomes.

Soil type and management history are widely recognised as dominant factors shaping rhizosphere microbiomes, often exerting stronger effects than plant species. In long-term monocultures and intensively managed systems, soil legacy effects can constrain microbial community assembly, limiting the influence of newly established plants. In the present study, both *Actinidia chinensis* and *Ficus carica* were grown in the same KVDS-affected orchard, sharing identical soil properties and environmental conditions. Nevertheless, fungal community composition differed strongly between plant hosts, with plant species explaining a substantial proportion of variance in beta-diversity analyses. These findings suggest that, even in soils severely impacted by disease and environmental stress, the identity of the plant host can take precedence over the effects of the soil's history, thereby influencing the composition of rhizosphere fungal communities. This supports the concept of plants as active ecological filters, capable of selectively recruiting microbial taxa through root exudation patterns, root architecture and rhizosphere physicochemical modification (Canarini et al., 2019; Seitz et al., 2022).

Although alpha-diversity metrics did not differ significantly between fig and kiwifruit rhizospheres, marked differences emerged at the compositional and functional levels. This decoupling between diversity and community structure indicates that microbial diversity alone is a poor predictor of soil health and disease suppressiveness.Instead, the identity and functional roles of dominant taxa appear to be more relevant indicators of ecosystem functioning in KVDS-affected soils. Kiwifruit rhizospheres were consistently dominated by *Fusarium* and related *Nectriaceae* genera, taxa commonly associated with root diseases and

decline syndromes in perennial crops (Bustamante et al., 2024; De Benedetti et al., 2025; López-Moral et al., 2024). The persistence of these taxa across sampling times suggests a stable, pathogen-enriched community potentially reinforced by plant stress and unfavourable soil conditions, such as periodic waterlogging and hypoxia. In contrast, fig rhizospheres exhibited a more heterogeneous fungal assemblage, characterised by increased representation of saprotrophic and multifunctional taxa, including *Humicola*, *Xylaria* and *Chaetomium*. These genera are frequently linked to organic matter turnover, microbial antagonism and indirect disease suppression, suggesting a functional redirection of the fungal community under replacement planting (Elias et al., 2018; Lavanya et al., 2025; Sharma et al., 2025).Functional guild analysis further supported the host-driven restructuring of the rhizosphere microbiome. Communities associated with kiwifruit were dominated by plant-associated pathogenic and endophytic guilds, whereas fig rhizospheres showed a relative enrichment of saprotrophic, wood-associated and multifunctional guilds. Although genus-level annotations inevitably result in multi-guild assignments, the overall shift in guild composition points toward a fungal community less centred on strictly pathogenic lifestyles in fig-associated soils. These patterns are consistent with well-established dynamics in agroecosystems, where the continuous monoculture of crops often promotes the accumulation of soil-borne pathogens and reduces microbial functional diversity (McDonald and Stukenbrock, 2016; H. Wu et al., 2022). Conversely, crop rotation and diversification strategies have been adopted extensively to disrupt the life cycles of pathogens and enhance beneficial microbial communities (Li et al., 2025; Wang and Sugiyama, 2024). In this context, the introduction of alternative plant species, such as *Ficus carica*, may represent a form of biological soil management capable of redirecting rhizosphere microbial assembly. It has been reported that analogous shifts in microbial community composition have been observed in systems where the suppression of disease is achieved through the application of microbial inoculants or the adoption of rotation schemes that favour antagonistic or competitive microorganisms (Aravindharajan et al., 2024; Xiao et al., 2025; Zhou et al., 2023). Furthermore, plant-driven mechanisms such as root exudation and potential allelopathic interactions may further contribute to shaping microbial assemblages and limiting pathogen dominance (Seitz et al., 2022; Steinauer et al., 2023; D. Wu et al., 2024). The increased presence of taxa such as *Humicola* and *Chaetomium*, which have been reported to exhibit antagonistic activity against soil-borne pathogens, may contribute to the establishment of a more balanced and resilient rhizosphere. Similarly, the detection of basidiomycetous taxa such as *Serendipita* and *Ceratobasidium* in fig rhizospheres suggests the potential involvement of mutualistic or stress-mitigating interactions (Mahdi et al., 2022; Rawat et al., 2025), although their functional roles in this system warrant further investigation.

Notably, fig trees established in KVDS-affected soils did not exhibit decline symptoms, despite growing near diseased kiwifruit plants. This resilience likely reflects a combination of physiological tolerance to abiotic stress and the ability to establish distinct rhizosphere microbial assemblages. Fig trees are well adapted to Mediterranean environments and have lower water requirements than kiwifruit (Ammar et al., 2022; Elmeknassia et al., 2025), reducing the risk of prolonged soil saturation, a key factor favouring pathogen proliferation. From an ecological perspective, replacement planting with fig should therefore be viewed not merely as a crop substitution strategy, but as an active intervention capable of redirecting rhizosphere microbial assembly. By promoting fungal communities with potentially beneficial or multifunctional roles, fig cultivation may contribute to the gradual restoration of soil functionality in KVDS-affected orchards.

5. Conclusions

This study provides a robust comparative assessment of rhizosphere fungal communities associated with different plant species growing under the same soil and environmental conditions. This approach is intended to minimize confounding factors and highlight the role of plant identity in shaping microbial assemblages. However, it should be noted that the findings are based on a single sampling campaign, and further multi-year studies are required to evaluate the temporal stability of these patterns. Furthermore, subsequent research should integrate functional predictions with targeted isolation, transcriptomic analyses, or functional assays in order to validate the ecological roles of key taxa. The extension of this approach to other resilient tree species has the potential to provide further support for sustainable strategies for managing soil-borne decline syndromes in perennial cropping systems.

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CRediT authorship contribution statement

Antonella Cardacino: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Validation, Visualization, Writing – original draft, Writing – review & editing. **Silvia Turco:** Data curation, Formal analysis, Software, Supervision, Visualization, Writing – review & editing. **Mattia Animobono:** Conceptualization, Investigation, Methodology, Writing – original draft, Writing – review & editing. **Giorgio Mariano Balestra:** Funding acquisition, Resources, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.rhisph.2026.101336.

Data availability

The link is shared on manuscript file

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