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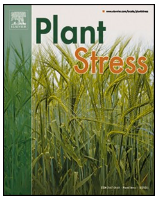

Review

Kiwifruit Vine Decline Syndrome: etiology, mechanisms, and management of a multifactorial disease

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ABSTRACT

The Kiwifruit Vine Decline Syndrome (KVDS) is becoming one of the most severe threats to kiwifruit cultivation in Italy, with potential to spread to other kiwifruit cultivation areas. KVDS is a complex, multifactorial disease induced by the combined action of abiotic stresses and biotic agents. Waterlogging, soil compaction, and high soil temperatures seem to be the main factors generating conditions that make roots highly vulnerable to colonization by soilborne pathogens, with *Phytopythium vexans* and other oomycetes playing a central role. Aboveground, impaired hydraulic function drives canopy collapse during periods of high evapotranspiration demand. Despite significant progress, major gaps remain in clarifying the precise etiology, identifying primary pathogens, and understanding the physiological mechanisms that lead to plant decline. This review is the first comprehensive report on the current understanding of KVDS, including the mechanisms behind its induction, and the first attempts to contrast its spread, discussing a path forward to identify strategies to safeguard kiwifruit production and manage other decline syndromes that may arise as consequence of global changes.

1. Introduction

The Kiwifruit Vine Decline Syndrome (KVDS) is an emerging disorder affecting kiwifruit vines (*Actinidia chinensis* Planch.), characterized by a progressive reduced plant vigor and canopy collapse as consequence of severe root system deterioration. In affected orchards, symptoms often manifest abruptly during periods of high evapotranspiration, ultimately leading to plant death (Fig. 1). Belowground, roots show marked necrosis, cortical degradation, and loss of fine roots critical for water and nutrient uptake. Increasing evidence indicates that KVDS results from complex interactions between abiotic stresses and biotic agents.

KVDS has been reported mainly in Italy, where it is known as *moria dell'actinidia* (pronounced as */moˈri.a delː aktiˈnidja/*) or *moria del kiwi* (pronounced as */moˈri.a del ˈkiː.wi/*). New outbreaks of KVDS are being officially reported in Türkiye (Polat *et al.* 2025) and France (Avignon *et al.* 2025). Previously, symptoms similar to KVDS have been reported in New Zealand (Smith *et al.* 1989), Türkiye (Polat *et al.* 2017; Türkkan *et al.* 2022), and Korea (Kim & Choi 2023). Earlier reports of kiwifruits root rots caused by *Phytopythium* spp. were made in China (Wang *et al.*

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2015) and Japan (Shimizu *et al.* 2005). Similarly, root rots caused by species of *Phytophthora*, were reported in France (Baudry *et al.* 1991) and Türkiye (Akilli *et al.* 2011; Kurbetli & Ozan 2013). In Italy, the syndrome affects both green- (var. *deliciosa*) and yellow-flesh (var. *chinensis*) genotypes, regardless of plant age (Spigaglia *et al.* 2020). The first documented cases of KVDS were reported in 2012 in Veneto (northeastern Italy) (Tacconi *et al.* 2019). Initially considered a localized anomaly, the disease spread rapidly across the country within a few years. Subsequent investigations revealed that similar symptoms had occurred sporadically in earlier years but had not been formally linked to a distinct syndrome. By 2015, new outbreaks were recorded in Piemonte (northwestern Italy) and, by 2017, KVDS was reported in Lazio (central Italy) and Calabria (southern Italy) (Savian *et al.* 2022). These outbreaks were often, but not always, observed in intensively managed orchards located in areas prone to periodic waterlogging.

KVDS initially affected about 10 % (around 2 900 hectares) of kiwifruit orchards across northern (Piemonte, Veneto, Friuli Venezia Giulia), central (Emilia Romagna, Lazio), and southern regions (Calabria) (Sorrenti *et al.* 2016). More recent estimates suggest that over 25 % of Italian kiwifruit orchards are currently affected by the syndrome (Savian *et al.* 2020). In heavily affected areas, annual yield can be reduced by 50 % or more, with some orchards becoming unproductive within a few years of planting. Although KVDS is currently almost exclusively confined to Italy, with very recent reports in France and Türkiye, the risk of spread to other Mediterranean regions is substantial.

While research on KVDS has progressed rapidly, driven by urgent demands from growers and industry stakeholders, findings remain fragmented across disciplines, making it challenging to synthesize a coherent picture of KVDS etiology and management. In addition, the accelerating pace of climate change is likely to heighten the abiotic stresses that make kiwifruit plants susceptible to KVDS, potentially triggering more frequent and severe outbreaks. In this context, a comprehensive review is needed to summarize the state of knowledge on KVDS and to frame it as a model for understanding and managing complex decline syndromes in perennial crops. Such synthesis is critical for guiding future research, informing extension efforts, and supporting the development of management strategies aimed at safeguarding kiwifruit production in Italy and beyond.

2. Symptoms

KVDS is characterized by a progressive decline in plant vigor, typically observed over one or more growing seasons. The first signs often become evident in late spring to early summer, when affected plants display reduced shoot growth and a general loss of canopy density compared to healthy plants. This is the result of severe root damage (Fig. 2 B-F), which leads to a marked reduction in the ability of the plant to adsorb water and nutrients, leading to wilting during periods of high evapotranspiration.

In plants affected by KVDS, the root system shows clear morphological and anatomical abnormalities, with cortical decay and brown discoloration of the stele. The cortical tissue loses its rigidity and detaches from the central stele due to the dissolution of an entire layer of cortical cells surrounding the endodermis causing the peculiar symptom known as “rat tail” (Fig. 2 C) (Bardi 2020). The fine roots, which are crucial for water and nutrient uptake, undergo almost complete decay and, when present, are typically confined to the top 5–10 cm of soil (Fig. 2 B) (Tacconi *et al.* 2015).

Symptoms aboveground typically appear only after significant root damage has occurred, making early diagnosis challenging. Kiwifruit vines have large xylem vessels that enable rapid water uptake and transport, allowing them to tolerate reductions in root system size (Dichio *et al.* 2013). However, this efficient water absorption can mask underlying root deterioration. As a result, plants may develop a vigorous canopy in spring, then suddenly wilt during heat waves when high transpiration rates exceed the ability of the compromised root to supply water (Black *et al.* 2011). This generally occurs in mid to late summer, when high temperatures increase transpiration rates, leading to leaf epinasty, chlorosis, marginal deformation, progressive desiccation from the leaf edges inward, and twig desiccation, particularly in 1- to 2-year-old plants (Donati *et al.* 2020). Eventually, widespread leaf margin desiccation and extensive premature defoliation lead to canopy collapse (Fig. 1 A and C), severely affecting plant growth, and fruit production and quality (Bardi 2020; Bardi *et al.* 2020; Donati *et al.* 2020; Spigaglia *et al.* 2020). Symptomatic plants might prematurely drop most of their fruits, and remaining berries are impaired in their development, showing a stunted growth often associated to skin wrinkling at harvest (Donati *et al.* 2020).

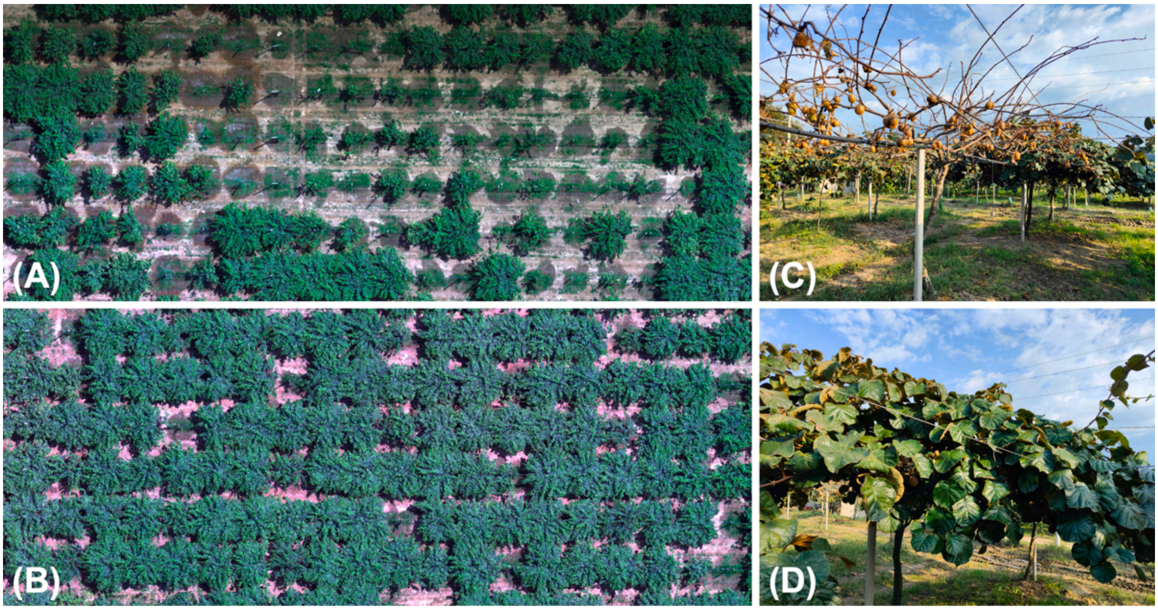

Fig. 1. Example of the impact of the Kiwifruit Vine Decline Syndrome (KVDS) (top, A, C) compared to sites where KVDS is not present (bottom, B, D). Drone pictures showing a significant impact of KVDS on a kiwifruit orchard (A) compared to another field where KVDS is currently absent (B). On the right side, we have an example of a kiwifruit plant collapsed as a consequence of KVDS (C), compared with an asymptomatic plant (D).

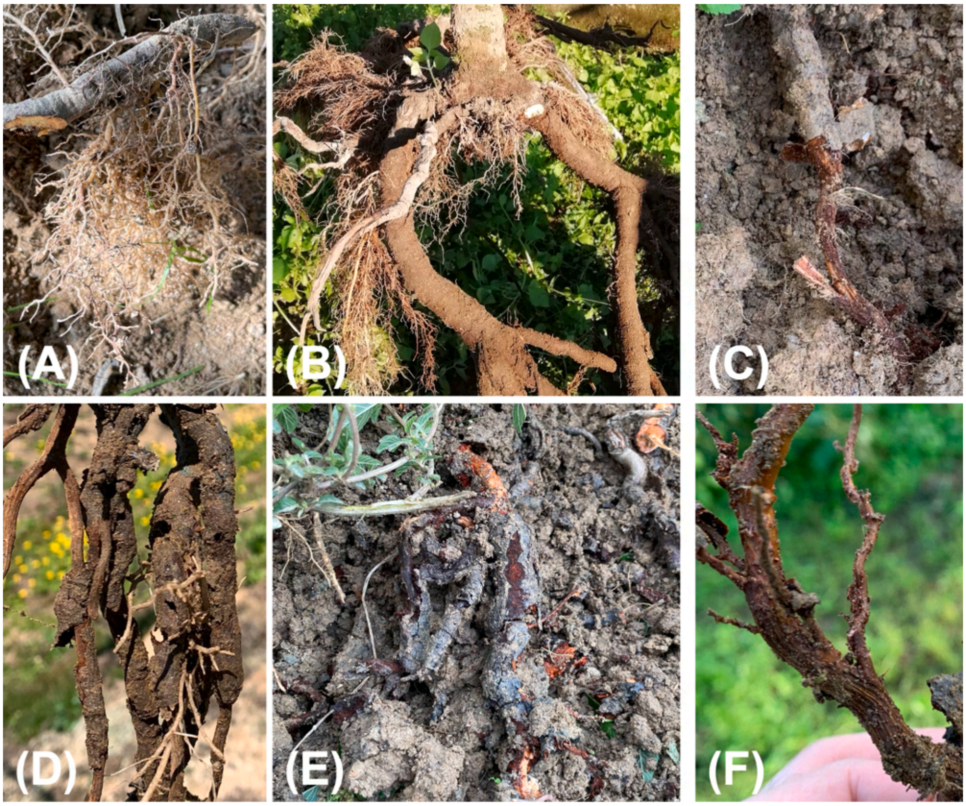

Fig. 2. Examples of healthy roots (A), compared to roots from plants showing the classical symptoms of Kiwifruit Vine Decline Syndrome (B-F).

3. Etiology of KVDS

3.1. Abiotic factors

The induction of KVDS is influenced by abiotic stressors, and excess of soil moisture and waterlogging have emerged as primary drivers, particularly in orchards established on poorly drained soils, in areas with high groundwater tables, or with inappropriate water management. Factors such as soil compaction, inappropriate irrigation scheduling, and imbalanced fertilization can increase the susceptibility of plants to KVDS. Indeed, kiwifruit plants are highly sensitive to root anoxia, elevated transpiration demand, and high soil temperatures due to the small intercellular spaces between adjacent cells, which restrict internal gas exchange and worsen symptoms of root asphyxia (Donati *et al.* 2020; Savé & Serrano 1986; Smith *et al.* 1989). Soil waterlogging, which often occurs when water is provided using surface irrigation practices or when heavy rainfalls occur, is a significant abiotic factor associated with KVDS (Spigaglia *et al.* 2020). Although abiotic stressors can compromise plant health, evidence suggests that they are not sufficient on their own to cause KVDS. Experimental work by Savian et al. (2020) demonstrated that kiwifruit plants grown in soil collected from a KVDS-affected orchard only developed symptoms when the soil was not sterilized, confirming the essential role of living soil microbial communities in inducing KVDS. In addition, field surveys have revealed that root damage can also occur in the absence of waterlogging (Tacconi *et al.* 2019). These findings support the view that KVDS arises from the interplay between abiotic stresses, which weaken plant defenses or create favorable environmental conditions, and biotic agents, which exploit these vulnerabilities to colonize roots and cause decline.

3.2. Potential pathogens

It is thus clear that KVDS cannot be attributed to abiotic stressors alone but rather emerges from their interaction with the soil microbial community. Besides evidence from microcosm experiments (Savian *et al.* 2020; Tacconi *et al.* 2015), several studies supported this theory through direct isolation of potential pathogens, pathogenicity trials, or metabarcoding approaches (Donati *et al.* 2020; Guaschino *et al.* 2024; Mosca *et al.* 2024; Prencipe *et al.* 2020; Savian *et al.* 2020, 2021, 2022). Different species of pathogenic organisms have been suggested to be involved (Table 1 and Fig. 3). In particular, oomycetes (species of *Phytopythium, Pythium* and *Phytophthora*) seem to play a major role in the induction of KVDS (Bardi 2020; Donati *et al.* 2020; Prencipe *et al.* 2020; Savian *et al.* 2021). Fungi (e.g., *Desarmillaria* spp., *Fusarium* spp.) and bacteria (genus *Clostridium*) have also been associated with the disease (Bardi 2020; Donati *et al.* 2020; Savian *et al.* 2021; Spigaglia *et al.* 2020). Although the involvement of biotic factors in determining KVDS has been confirmed by several independent studies and it is widely accepted by the scientific community, we are still far from precisely determining which microorganisms intervene in each specific situation and how they interact with each other and with abiotic factors to cause KVDS. It is important to note that the pathogenicity of some of the microorganisms potentially associated with KVDS has not been confirmed yet (Table 1 and Fig. 3). Understanding the identity, diversity, ecology, and epidemiology of these microorganisms is key to clarify the origin and spread of KVDS, and to move towards sustainable management solutions.

3.2.1. Bacteria

The characterization of bacterial isolates is limited compared to other groups of microorganisms. Isolates of *Clostridium bifermentans* and *Clostridium subterminale* from symptomatic plants were able to produce symptoms when inoculated in controlled conditions (Spigaglia *et al.* 2020). The same authors suggest that the anaerobic condition associated with the waterlogging could create the condition to foster growth and development of these two *Clostridium* species (Spigaglia *et al.* 2020), but to the best of our knowledge, this remains the only report of isolated bacterial pathogens. The use of metabarcoding did not help to clarify the potential role of bacteria in inducing KVDS. While several studies report

Table 1

List of potential pathogens associated with the Kiwifruit Vine Decline Syndrome identified by each study.

Study	Bacteria	Fungi	Oomycetes	Method used
Donati et al. (2020)		*Desarmillaria tabescens*	*Phytophthora megasperma,* *Phytophthora infestans* *Phytopythium* spp.	Isolation, pathogenicity assays
Savian et al. (2020)	—	*Fusarium solani*	*Phytopythium vexans* *P. chamaehyphon*	Isolation
Prencipe et al. (2020)	—	—	*Phytopythium vexans*	Isolation, pathogenicity assays
Spigaglia et al. (2020)	*Clostridium bifermentans* *Clostridium subterminale*	—	—	Isolation, pathogenicity assays
Savian et al. (2021)	—	—	*P. chamaehyphon*	Isolation, pathogenicity assays
Savian et al. (2022)	—	*Dactylonectria macrodidyma* *Thielaviopsis basicola*	*Phytophthora sojae-like* *Phytopythium* spp.	Metabarcoding
Mian et al. (2023a)	—	—	*Phytophthora* sp. *Globisporangium intermedium*	Metabarcoding
Manici et al. (2022)	—	*Dactylonectria* spp.	—	Metabarcoding
D'Ippolito et al. (2022)	—	*Ilyonectria vredenhoekensis* *Fusarium oxysporum* *Paraphaeosphaeria michotii*	—	Isolation
Guaschino et al. (2024)	—	—	*Phytopythium* sp.	Metabarcoding
Mosca et al. (2024)	—	—	*P. vexans* *P. litorale*	Isolation, metabarcoding
Sadallah et al. (2022)	—	—	Multiple *Phytophthora* spp.	Isolation, pathogenicity assays
Prencipe et al. (2023)	—	—	*P. vexans* *P. litorale* *P. chamaehyphon* *P. helicoides*	Isolation, pathogenicity assays
Cardacino et al. (2025)	*Ralstonia* sp.	*Fusarium* spp. *Ilyonectria* spp. *Thelonectria* spp.	*Phytophthora* spp. *Pythium* spp. *Globisporangium* spp.	Metabarcoding

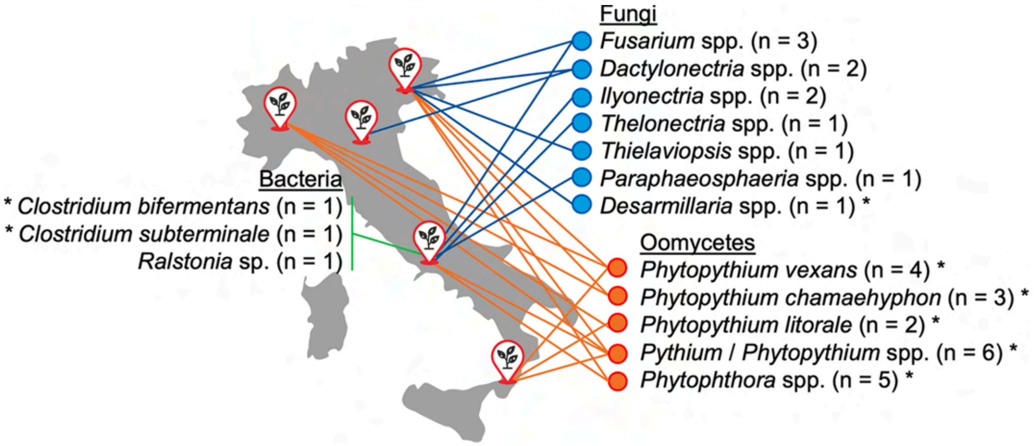

Fig. 3. List of pathogens (bacteria, fungi, and oomycetes) associated with the Kiwifruit Vine Decline Syndrome (KVDS) in Italy and geographical location where they have been identified. For each pathogen we report the number of studies that support their association with KVDS, and whether its ability to induce KVDS has been confirmed with pathogenicity assays (marked with an asterisk).

changes in plant or soil bacterial communities when comparing symptomatic and asymptomatic plants (Cardacino *et al.* 2025; Guaschino *et al.* 2024; Manici *et al.* 2022; Mosca *et al.* 2024), none of them clearly identified bacteria potentially involved in inducing the syndrome. More recently, Cardacino et al. (2025) reported a high prevalence of ASVs identified as *Ralstonia* spp. associated with symptomatic plants.

3.2.2. Fungi

Fungal genera like *Fusarium, Desarmillaria, Ilyonectria*, and *Dactylonectria* have also been reported to be associated with KVDS. *Desarmillaria tabescens*, a known threat to many horticultural crop plants (Mihail *et al.* 2002), was found exclusively in the roots of symptomatic kiwifruit plants (Donati *et al.* 2020), and its virulence is reported to be exacerbated by climate change and waterlogging (Klopfenstein *et al.* 2009; Sturrock *et al.* 2011). Fungi belonging to the *Cylindrocarpon/Ilyonectria* complex were isolated or detected from roots showing KVDS symptoms (Tacconi *et al.* 2015), in particular the species *Cylindrocarpon paucisepticum* was identified by Tosi et al. (2015). Fungi belonging to the genus *Ilyonectria* were isolated from symptomatic plants (D'Ippolito *et al.* 2022), and their association with KVDS was also confirmed by metabarcoding analysis (Savian *et al.* 2022). Before the emergence of KVDS, *Ilyonectria* spp., together with *Cylindrocarpon* spp., were reported to be responsible for root rot in kiwifruit orchards in Türkiye (Erper *et al.* 2013). Using metabarcoding, ASVs identified as *Dactylonectria* spp. were found in 50 % of the plants from KVDS-affected orchards in Emilia Romagna (central Italy) (Manici *et al.* 2022). *Dactylonectria* spp. were isolated from roughly 30 % of the plants in a survey conducted in Friuli-Venezia-Giulia (northeastern Italy), results confirmed by follow-up metabarcoding analyses (Savian *et al.* 2020, 2022). In Piemonte (northwestern Italy), *Dactylonectria* was identified as the most represented fungal genus in KVDS-affected plants using metabarcoding, with an average relative abundance ~20 % (Guaschino *et al.* 2024).

Species of *Fusarium* were highly represented among isolates in northern (Savian *et al.* 2020) and central Italy (D'Ippolito *et al.* 2022). However, *Fusarium solani* was found to cause crown rot on kiwifruit plants only when it was forcefully introduced into the tissues through wounding, and was unable to cause fine root decay when roots were submerged in a suspension of hyphae and conidia (Savian *et al.* 2020). *Fusarium solani* was reported as a secondary invader, accelerating fine root decay when associated with oomycetes, since it was unable to cause root rot by itself (Savian *et al.* 2020).

3.2.3. Oomycetes

Since the first reports of KVDS, oomycetes (Fig. 4) have been constantly associated with this syndrome and, in particular, four genera of oomycetes have been most frequently isolated and/or detected: *Phytopythium, Pythium, Globisporangium,* and *Phytophthora* (Donati *et al.* 2020; Savian *et al.* 2020). In symptomatic plants, the relative abundance of these oomycetes drastically increases compared to healthy plants (Donati *et al.* 2020; Mian *et al.* 2023a; Mosca *et al.* 2024; Prencipe *et al.* 2023; Savian *et al.* 2022).

Among the species of *Phytopythium*, the greatest interest goes to *Phytopythium vexans*, an oomycete that was shown to be associated with KVDS through direct isolation (Bernardini *et al.* 2024; Donati *et al.* 2020; Mosca *et al.* 2024; Özkan Kahraman & Yıldız 2024; Polat *et al.* 2017; Prencipe *et al.* 2020; Savian *et al.* 2021) and metabarcoding (Guaschino *et al.* 2024; Mosca *et al.* 2024). When isolating oomycetes directly from roots, *P. vexans* occurred in about 55 % of the symptomatic plants (Savian *et al.* 2020), and represented around 50 % of the isolates obtained with the baiting technique (Bernardini *et al.* 2024; Mosca *et al.* 2024). While two metabarcoding studies showed a lower relative abundance of this oomycete in symptomatic plants (Mian *et al.* 2023a; Savian *et al.* 2022), three others showed that *P. vexans* is the most abundant organism in soil, rhizosphere, and roots of symptomatic plants (Guaschino *et al.* 2024; Mian *et al.* 2025; Mosca *et al.* 2024). In northwestern Italy, diseased roots showed a relative abundance of ~70 % of *P. vexans* within the oomycete community, compared to ~16 % of healthy plants (Guaschino *et al.* 2024). Similarly, in Calabria (southern Italy), *P. vexans* was highly abundant in KVDS-affected roots and frequently isolated using baiting (Mosca *et al.* 2024). For *P. vexans*, Koch's postulates were widely fulfilled in independent studies conducted in controlled conditions both in Türkiye and Italy (Polat *et al.* 2017; Prencipe *et al.* 2020; Türkkan *et al.* 2022). A recent study developed a quantitative qPCR detection method for *P. vexans* based on the *cytochrome oxidase subunit I* (COI) mitochondrial gene (Guaschino *et al.* 2025). While *P. vexans* has been the most common and the most studied oomycete in all the KVDS-affected areas, other species, such as *Phytopythium litorale* and *Phytopythium chamaehyphon*, were isolated and characterized from orchards where KVDS was spreading (Mosca *et al.* 2024; Prencipe *et al.* 2023; Savian *et al.* 2020). The pathogenicity of both *P. litorale* and *P. helicoides*, together with *P. chamaehyphon*, was demonstrated in independent studies (Prencipe *et al.* 2023; Savian *et al.* 2020, 2022).

Species of the genus *Pythium*, and the closely related genus *Globisporangium*, were isolated both in Türkiye and Italy from diseased plants (Bernardini *et al.* 2024; Savian *et al.* 2020; Türkkan *et al.* 2022), including *Globisporangium intermedium, Globisporangium sylvaticum, Globisporangium heterothallicum*, and *Pythium dissotocum. Globisporangium sylvaticum* and *G. intermedium* were isolated using the baiting technique (Bernardini *et al.* 2024), through direct isolation from symptomatic roots (Savian *et al.* 2020), and identified using metabarcoding (Mian *et al.* 2023a).

Another genus that seems related to root rot in kiwifruit plants is *Phytophthora*, which includes devastating plant pathogens that cause significant economic and ecological damage worldwide (Brasier *et al.* 2022). Previous studies have reported the presence and the pathogenicity of some *Phytophthora* species in kiwifruit plants with root rot in California (Conn *et al.* 1991), France (Baudry *et al.* 1991), New Zealand (Stewart & McCarrison 1992), Korea (Lee *et al.* 2001) and Chile (Latorre 1991). Among them, the most frequent isolated was *Phytophthora cryptogea. Phytophthora citrophthora, Phytophthora cryptogea, Phytophthora megasperma*, and *Phytophthora palmivora* were isolated from plants showing symptoms similar to KVDS in Türkiye (Akilli *et al.* 2011; Çiftçi *et al.* 2016; Kurbetli & Ozan 2013). Some studies have proved the pathogenicity of *P. citrophthora* (Akilli *et al.* 2011), *P. palmivora* (Çiftçi *et al.* 2016) and *P. cryptogea* (Kurbetli & Ozan 2013) on 8-month-old to 1-year-old kiwifruit plants. In Italy, the role of *Phytophthora* species is controversial as its presence was not reported in some areas, such as Calabria and Piemonte (Guaschino *et al.* 2024; Mosca *et al.* 2024), while in northeast Italy several studies reported the presence of *Phytophthora* spp. associated with symptomatic plants (Bernardini *et al.* 2024; Donati *et al.* 2020; Sadallah *et al.* 2022; Savian *et al.* 2022; Tacconi *et al.* 2015). In addition, a previous study showed the presence of *Phytophthora infestans* and *Phytophthora megasperma* in the secondary roots of both symptomatic and asymptomatic plants (Donati *et al.* 2020). In northeastern Italy, different species of *Phytophthora* (*P. acerina, P. nicotianae, P. plurivora, P. citrophthora, P. cinnamomi, P. palmivora*) were isolated using baiting and used to perform pathogenicity assays (Sadallah *et al.* 2022). Based on the symptoms observed in the greenhouse experiment, the least aggressive species were *P. nicotianae and P. citrophthora*, while the most aggressive ones were *P. acerina* and *P. cinnamomi* (Sadallah *et al.* 2022). Interestingly, in northeastern Italy, a metabarcoding approach showed the constant association of KVDS with a phylotype closely related to *Phytophthora sojae* (Mian *et al.* 2023a; Savian *et al.* 2022). Nevertheless, except for the constant association with KVDS, pathogenicity and more detailed information on the species are not yet

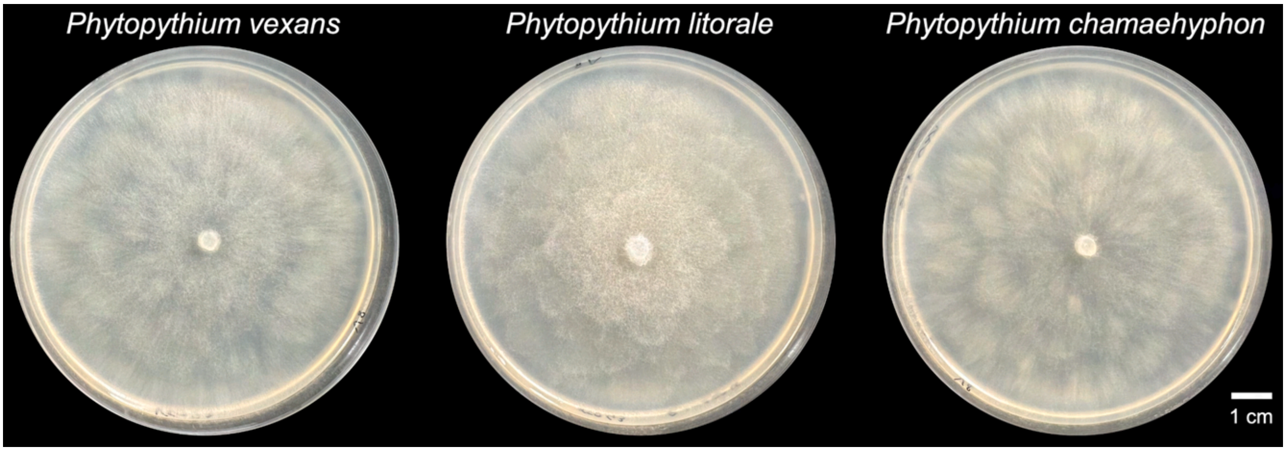

Fig. 4. Example of oomycete morphotypes isolated using a baiting approach from plants symptomatic to the Kiwifruit Vine Decline Syndrome.

available, since, even after several attempts, *Phytophthora sojae*-like isolates have never been obtained.

3.2.4. Oomycete communities

While traditional isolation techniques have played a crucial role in identifying key microbial groups associated with KVDS, they only reveal a limited fraction of the microbial diversity present in plant-associated environments. To overcome this limitation, recent studies have adopted culture-independent approaches, such as metabarcoding, which allows for a profiling of the entire microbial community including unculturable and low-abundance taxa.

Savian et al. (2022) applied a metabarcoding approach to profile oomycete communities in the root endosphere and rhizosphere of healthy versus symptomatic kiwifruit plants sampled in northeastern Italy. The study identified a *Phytophthora sojae*-like taxa as the most abundant species in diseased samples and detected several *Phytopythium* species, including *P. chamaehyphon* and *P. citrinum* (the latter not previously linked to KVDS). The results from Savian et al. (2022) align with those from Guaschino et al. (2024), who similarly reported a highly skewed community structure in KVDS-affected orchards, with *P. vexans* accounting for over 50 % of the oomycete community in the rhizosphere and soil of diseased kiwifruit plants, compared to less than 20 % in healthy counterparts. These findings suggest a strong association between oomycete community composition and disease status, with oomycetes emerging as key biotic indicators of KVDS in soil, rhizosphere, and roots. Notably, *Phytophthora* spp. were consistently rare (<1 % relative abundance) across all sample types, challenging previous assumptions about their role in the disease. Mian et al. (2023a) found that genotypes exhibiting resistance to KVDS, such as *A. macrosperma* accessions Ma176 and Ma183 and *A. arguta* cv. Miss Green, harbored distinct oomycete profiles compared to susceptible genotypes like *A. polygama* and *A. chinensis* var. *deliciosa* cv. Hayward. *Phytophthora* spp. were predominantly detected in sensitive genotypes, while *Globisporangium intermedium* was more abundant in asymptomatic plants. Mosca et al. (2024) used a combination of metabarcoding and targeted isolation to investigate the microbiomes associated with symptomatic and asymptomatic kiwifruit plants. While their results did not indicate strong shifts in overall microbial diversity, they confirmed a consistent association of *Phytopythium vexans* with KVDS symptoms. This species was significantly enriched in both root and soil samples from symptomatic plants, matching sequences of the isolates obtained from baiting. Similar results were also obtained by Cardacino et al. (2025), who found taxa identified within the genera *Phytophthora, Pythium* and *Globisporangium* as major components of the soil and root endosphere oomycete communities associated with symptomatic kiwifruit plants.

Together, the studies described above show that the community of oomycetes is a very important factor in the induction of KVDS. Thus, we used the publicly available data from three studies with compatible design and markers (Guaschino *et al.* 2024; Mosca *et al.* 2024; Savian *et al.* 2022) to perform a meta-analysis using an approach similar to Hopkins et al. (2025) as detailed in the Supplementary Materials, with the goal of generalizing results across the three different locations (northeast, northwest, and southern Italy). Our results show that in soil from plants symptomatic to KVDS, the community of oomycetes in soil is more diverse (Chao1 index) and less dominated (Fig. 5 A) compared to soil collected from asymptomatic plants. No effects were recorded on α- or β-diversity metrics in roots (Fig. 5 A). We also used two different approaches (LEfSe and Random Forest analyses, Fig. 5 B) to identify marker species associated with plants symptomatic to KVDS. Both approaches identified the same pool of species, *P. vexans, P. terrestris, P. helicoides*, and *P. sojae*. While they were all identified as marker species in root samples, only *P. vexans* and *P. helicoides* were identified in soil samples. It is important to note that while *P. vexans* was identified in all three studies, a *P. sojae*-like phylotype was only identified in Savian et al. (2022). Taken together, these results further support the idea that species of *Phytopythium* and *Phytophthora* can be the main biotic agents behind KVDS.

4. Management strategies

4.1. Agronomic management

The growing evidence that KVDS results from the interplay between soilborne pathogens and abiotic stresses urges to consider disease management in a holistic framework. While pathogens can directly damage kiwifruit roots, their establishment and virulence are strongly influenced by environmental conditions such as waterlogging, soil compaction, rising temperatures and vapor pressure deficit. Thus, agronomic practices aimed at reducing plant stress represent the first line of defense against KVDS. Soil compaction, often consequence of repeated treatments against *Pseudomonas syringae* pv. *actinidiae*, can reduce soil porosity and favor waterlogging, one of the major factors promoting the induction of KVDS (Nari & Vittone 2017). Excessive irrigation, often exceeding 80–100 L/day per plant, can further contribute to soil saturation, creating conducive conditions for KVDS (Nari & Vittone 2017). Current strategies mainly aim to reduce root stress through agronomic practices such as adding organic matter, preparing raised beds to improve aeration and reduce flooding damage. Soil

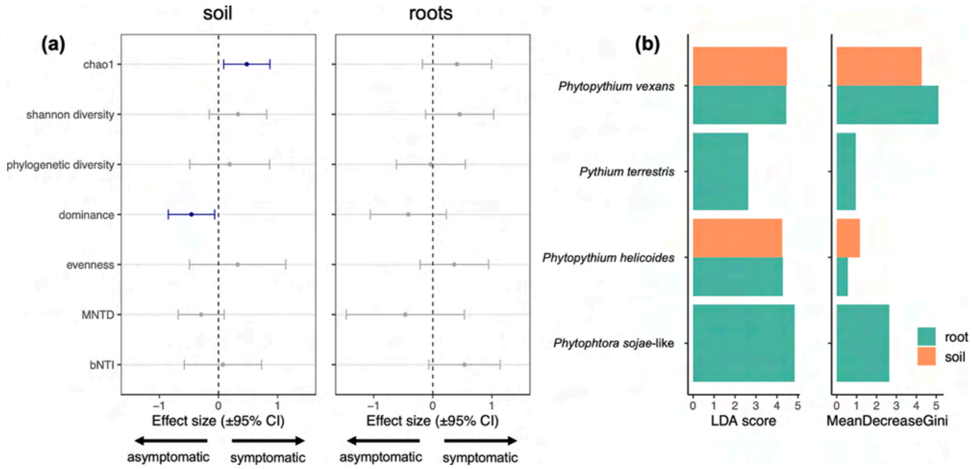

Fig. 5. (A) Effect size (±95 % CI) of the Kiwifruit Vine Decline Syndrome (KVDS) on the diversity of oomycete communities in soil (left) and roots (right). Bars in blue represent variables with effect size significantly different from zero. (B) Species of oomycetes significantly associated with KVDS using two different approaches, LEfSe (left) and Random Forest (right).

ridging showed to be effective in reducing KVDS symptoms and in improving plant growth, but it did not prevent the induction of KVDS (Bardi *et al.* 2020). Shading nets are an additional tool to reduce the plant evapotranspirative stress and potentially limit the impact of KVDS (Mandalà *et al.* 2025; Nari *et al.* 2023). These measures alone are not sufficient to prevent KVDS, and careful irrigation management and the use of tolerant rootstocks remain among the most promising strategies (Bardi 2021). Effective management therefore requires tailored irrigation guided by soil moisture monitoring.

4.2. Resistant rootstocks

While research on breeding programs to identify new varieties resistant to KVDS is still ongoing, rootstocks represent a pivotal strategy in mitigating the deleterious effects of soil-borne diseases (Augstein & Melnyk 2025). In Italy, a few years after the appearance of KVDS, Mian et al. reported the first empirical observations of a KVDS-resistant genotype *A. macrosperma* Bounty71 (syn. SAV1) used as rootstock (Mian *et al.* 2022a). Also, rootstock Z1, a hybrid of *A. chinensis* var. *deliciosa* (P1) and *A. arguta* 'Gemma', with good grafting affinity with green and yellow flesh varieties, showed a promising tolerance to KVDS. An additional study identified three genotypes of *A. macrosperma* (Ma176, Ma183, and Bounty71) as highly tolerant to KVDS, while *A. polygama* and *A. chinensis* var. *deliciosa* ('Hayward') were highly susceptible, showing significant root decay and plant mortality (Mian *et al.* 2022b).

The selection of appropriate rootstock genotypes is crucial to allow the cultivation of susceptible plant varieties in conducive soils. In addition to *A. macrosperma*, there is a wider set of genetic diversity that can be explored to breed new kiwifruit varieties tolerant or resistant to KVDS. For example, the rootstock 'Miliang' is one of the most widely used rootstocks in Chinese commercial orchards due to its high resistance to soil-borne diseases and its ability to promote early flowering and increased vigor in grafted cultivars (Liu *et al.* 2009). Among the wild *Actinidia* species, the rootstock KR5 (*A. valvata*) showed greater tolerance than 'Hayward' (*A. chinensis* var. *deliciosa*) under waterlogging stress, and transcriptomic analysis identified some key genes involved in this tolerance mechanism (Li *et al.* 2021). However, the survival of *A. valvata* genotypes under waterlogging conditions may depend on root system configuration and regeneration capacity, similar to other flood-tolerant plants, showing variability of this trait in *A. valvata* genotypes (Li *et al.* 2020). This diversity offers significant potential for the exploration of germplasm to identify genotypes resilient to KVDS.

4.3. Biofumigation

Biofumigation is an environmentally sustainable pest and disease management strategy that involves the use of biologically active plant-derived compounds to suppress soil-borne pathogens. Given the growing restrictions on synthetic fumigants, biofumigation represents a promising tool for integrated disease management, despite reports of some pathogens exhibiting tolerance (Alderley *et al.* 2022). Mian et al. (2023b) studied in vitro the inhibitory effects of leaf extracts from seven *Eruca vesicaria* subsp. *sativa* (rocket) cultivars, along with their bioactive compounds (glucosinolates and their derived metabolites), on the mycelial growth of three oomycetes associated with KVDS: *P. chamaehyphon, P. vexans*, and *P. citrophthora*. Across all three pathogens, mycelial growth was suppressed by approximately 67 % after 15 days. In a follow-up study, the same authors tested the potential efficacy of biofumigation in microcosms under controlled conditions, growing plants on soil from a field with active spread of KVDS (Mian *et al.* 2025). Additionally, plants were co-cultivated with rocket to examine whether intercropping could similarly mitigate disease symptoms. Both approaches significantly reduced KVDS severity by 70–80 % in treated plants compared to controls. Yet, to better understand the underlying mechanisms, a metabarcoding analysis was performed on the rhizosphere microbiome, revealing that both rocket-based treatments influenced the community of oomycetes, including a reduction in the relative abundance of *P. vexans*. These findings suggest that rocket-based treatments, either through extract application or intercropping, could serve as an effective, environmentally friendly strategy for KVDS management, with potential scalability for field applications.

4.4. Biocontrol agents

Interest in controlling soil-borne diseases using biological control agents, mainly bacterial and fungal strains, has recently increased due to the social demand for environmentally friendly alternatives to chemical pesticides (Niu *et al.* 2020). Although several beneficial microbial strains have demonstrated excellent efficacy against pathogens in vitro or under controlled greenhouse conditions, examples of successful application of biological control agents under field conditions are rare (Mazzola & Freilich 2017). Biocontrol agents are currently being investigated to evaluate their ability to reduce the impact of KVDS. In particular, an experimental trial was conducted on potted *A. chinensis* var. *deliciosa* ('Hayward') plants transplanted in soil from a KVDS symptomatic orchard (Ermacora *et al.* 2024). Kiwifruit plants were treated with a selection of commercial products: Amylo-X® LC (*Bacillus amyloliquefaciens* D747), Remedier (*Trichoderma gamsii* ICC 080 and *Trichoderma harzianum* ICC 012), Micosat F® (a microbiological consortium), and with *Pseudomonas asplenii* strain Pa4A7 (isolated as endophyte of kiwifruit plants). Commercial formulations did not reduce the incidence of the syndrome while isolate Pa4A7 proved very effective in preventing the appearance of KVDS symptoms on treated plants (Ermacora *et al.* 2024). Additional biocontrol agents being investigated include *Beauveria bassiana* and strains of *Bacillus amyloliquefaciens* (Sofo *et al.* 2024).

5. The economic impact of KVDS

According to data from the Food and Agriculture Organization of the United Nations (FAOSTAT), the global area dedicated to kiwifruit cultivation has reached approximately 286,104 hectares in 2022, representing a significant increase compared to previous years. In fact, the cultivated area has grown by about 63 % since 2011, when it stood at 175,801 hectares. Among the countries with the largest areas under kiwifruit cultivation, China leads by a wide margin, accounting for around 70 % of the global total. It is followed by Italy (8.4 %), New Zealand (5.1 %), and Greece (approximately 4.7 %). Together, these four countries represent about 87.8 % of the world's total kiwifruit cultivation area. In terms of global production, the total output in 2022 reached 4 539,471 tons (FAO, 2024). The top producers were China with 2,380,304 tons, New Zealand with 603,522 tons, Italy with 523,120 tons, and Greece with 320,270 tons.

A detailed analysis of trends in kiwifruit cultivation and production in Italy over the past decade (ISTAT, 2024) reveals a fluctuating pattern, with an overall decline in both cultivated area and production volume (Fig. 6). This downward trend is particularly evident in the cultivated area, which peaked in 2018 at approximately 26,700 hectares, before falling to 25,219 hectares in 2023 (a decrease of 5.5 %). At the regional level, the decline in cultivated area has been more pronounced in certain production zones, particularly in north-eastern Italy. This reduction has been partially offset by an expansion of kiwifruit cultivation in southern regions of the country. The primary cause of this decline might be associated with the emergence of KVDS. By 2020, according to Tacconi (2020), the area affected by this disease was estimated at 6,560 hectares, representing approximately 25 % of the national kiwifruit cultivation area. Regarding exports, data from the Italian Institute of Services for the Agricultural and Food Market (ISMEA, 2023) indicate that Italy exports an average of 275 million kilograms of kiwifruit annually (based on the 2020–2022 three-year average). About 63 % of this production is sold within the European Union, while the remaining 37 % is exported to non-EU countries. With an average export price of €1.75 per kilogram, Italian kiwifruit exports generate an estimated annual revenue of €483

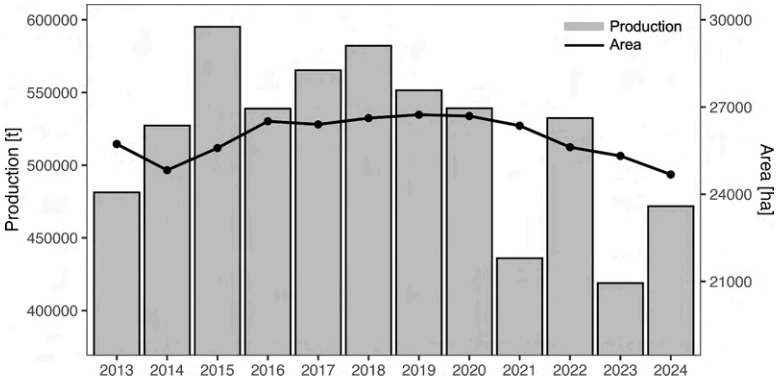

Fig. 6. Kiwifruit cultivation area and production in Italy 2013– 2024 (Source: ISTAT).

million.

We assessed the economic impact of KVDS using data from "*Rete di Informazione Contabile Agricola*" (RICA, https://rica.crea.gov.it/ accessed on 10 November 2024) and the partial balance method, a widely used tool for estimating the economic impact of pest or disease outbreaks (Breukers *et al.* 2008) and one of the methods suggested by the International Plant Protection Convention (IPPC) (FAO, 2017). During the stable production phase, data indicate that with an average price of €0.77 per kilogram and a yield of 16,800 kg per hectare, the Total Gross Production (TGP) amounts to €13,011 per hectare, while the Gross Saleable Production (GSP) is €12,956 per hectare. Specific costs, which include inputs directly related to cultivation (e.g., fertilizers, pesticides), total to €2,815 per hectare. The Gross Margin (GM), calculated by subtracting specific and general crop-related costs from the GSP, is €10,196 per hectare. The Operating Margin (OM), obtained by deducting labor and machinery costs from the GSP, is €7,232 per hectare. Based on these figures, the economic loss associated with the 6,560 hectares currently affected by KVDS is estimated at €85 million in terms of GSP and €47 million in terms of OM. These estimates are based on a relatively modest average yield of 16,800 kg/ha; however, in some regions, current yields reach up to 25,000 kg/ha, suggesting that actual losses could be significantly higher.

The decline in profitability could also result in job losses, particularly among skilled laborers specialized in kiwifruit cultivation. According to ISMEA (2025), one hectare of kiwifruit orchards requires approximately 500 labor hours. For the 6,560 hectares affected by KVDS, this translates to a total of 3.28 million labor hours at risk. Beyond production losses, there is also a decline in land value. Vanneste et al. (2017) reported that the value of orchards impacted by *Pseudomonas syringae* pv. *actinidiae* damage in New Zealand dropped from NZ$450,000/ha to NZ$70,000/ha.

In addition to quantifiable economic losses, there are environmental damages related to the loss of ecosystem services. Permanent tree crops, like kiwifruit, contribute to climate regulation, air quality improvement, and erosion control (Ali *et al.* 2021). Another critical issue is the cost of orchard removal. Indeed, kiwifruit orchards involve substantial infrastructure (poles, wires, and concrete foundations) making the conversion to another crop significantly more expensive. From a strategic standpoint, given Italy's well-established kiwifruit supply chain, the reduction in production volume poses a serious threat to market share, potentially opening the door for competing countries to fill the gap.

6. Future outlook and conclusions

Over a decade of research has established KVDS as a multifactorial syndrome, best understood through an integrative model that connects environmental stressors, host physiology, soil microbial communities, and orchard-scale interactions. KVDS provides not only an urgent challenge for kiwifruit production but also a broader model for studying other decline syndromes in horticultural systems worldwide. Our KVDS model (Fig. 7) integrates different components: (i) predisposing environmental conditions that induce root hypoxia and stress; (ii) host physiological breakdown; (iii) biotic invasion by oomycetes and opportunistic pathogens; and (iv) orchard-scale amplification driven by soil hydrology, management practices, and climate change. This multifactorial perspective moves beyond a single-pathogen framework and identifies KVDS as a possible emergent disease induced by shifts of plant–environment–microbiome interactions under global change pressures.

Despite significant advances, fundamental knowledge gaps remain in the mechanistic basis of KVDS. The precise sequence of physiological breakdown requires greater clarification. Similarly, the interactions between stress-induced host vulnerability and the soil microbiome remain poorly defined. While *P. vexans* and other oomycetes are consistently associated with symptomatic roots, the role of viruses, nematodes, fungi, bacteria, and broader soil microbiome shifts is still unresolved (Mosca *et al.* 2024). The challenge ahead lies in determining which pathogens act as primary drivers, which are opportunistic invaders, and how these roles shift under varying environmental contexts. Bridging these mechanistic gaps will require integrative approaches that combine plant physiology, soil ecology, and microbiome science.

Current management practices focus on alleviating plant stress, with partial success. Soil ridging, shading, improved irrigation strategies, and organic amendments can mitigate but not prevent KVDS. Sustainable strategies such as biofumigation and the use of biocontrol agents show promise but remain at early stages of testing. In particular, the use of microbial consortia tailored to reshape rhizosphere communities and suppress putative pathogens could provide long-term resilience. However, scaling these interventions to orchard level and across diverse environments remains a key challenge. Perhaps the most durable path forward lies in breeding and rootstock innovation, and it can be pursued without a definitive knowledge of the etiology of the syndrome. Preliminary trials suggest that certain *Actinidia* genotypes, including *A. macrosperma, A. arguta*, and *A. valvata*, exhibit partial resistance or tolerance to KVDS, with superior root development and greater resilience under waterlogging. Incorporating these genotypes into breeding programs or using them directly as rootstocks offers a realistic strategy for restoring productivity in affected regions. Advances in genomics and transcriptomics can accelerate the identification of key tolerance traits, enabling marker-assisted selection and informed deployment of resilient planting material.

Ultimately, the path forward requires an integrated disease management framework that combines soil health restoration, irrigation optimization, shading technologies, biotechnological tools, and resistant rootstocks. Given the rapid spread of KVDS across Italy and the risk of emergence in other Mediterranean regions, proactive surveillance is essential. Equally important is the integration of stakeholders' knowledge and socio-economic considerations, ensuring that solutions are

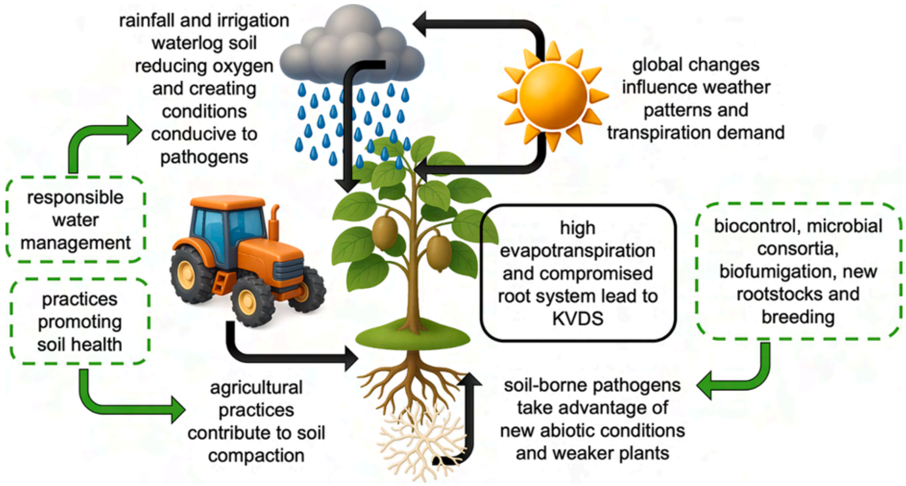

Fig. 7. Model explaining the multi-factorial nature of the Kiwifruit Vine Decline Syndrome (KVDS), together with potential solutions (green boxes and arrows). Individual graphic elements were generated using GPT-5.

practical, scalable, and cost-effective. This challenge calls for the need of transdisciplinary approaches, where plant pathology, plant physiology, agronomy, soil science, and climate research converge. KVDS thus serves as a timely model for how global change is reshaping plant health, highlighting the need for integrated frameworks that go beyond traditional single-pathogen paradigms (Francomano *et al.* 2026). By embracing this integrated vision, the kiwifruit industry can not only mitigate KVDS but also enhance resilience to future decline syndromes in an era of accelerating climate change.

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CRediT authorship contribution statement

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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.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.stress.2026.101298.

Data availability

Data used for the meta-analysis is publicly available. Accession numbers are available from the original articles.

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