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Stemphylium vesicarium: a rising threat to European horticulture

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Abstract *Stemphylium vesicarium* is an emerging multi-host fungal pathogen that increasingly threatens European and global horticulture. Initially recognized as the causal agent of brown spot of pear and Stemphylium leaf blight of onion, the pathogen is now associated with diseases of other economically important crops, including spinach. Its broad host range, host-specialized pathotypes, host-specific toxins, and widespread fungicide resistance make disease management particularly challenging, often resulting in severe yield losses. The epidemiology of *S. vesicarium* is shaped by its polycyclic nature and dual reproductive strategy, with sexual ascospores colonizing alternative hosts in early spring and asexual conidia acting as the primary source of inoculum. The pathogen overwinters associated to crop residues, woody tissues, and alternative weed hosts, and can also spread through infected seeds, transplants, and thrips. Multilocus phylogenetics and whole-genome sequencing have clarified taxonomic ambiguities within *Stemphylium*, revealing substantial genetic diversity and complex population structures. In Europe, favourable climatic conditions, limited chemical control, fungicide-insensitive populations, and the lack of resistant cultivars in many crops underscore the urgent need for integrated disease management strategies. This review aims to give a valuable insight into the current knowledge on taxonomy, epidemiology, genetic diversity, toxin-mediated pathogenicity, and management of *S. vesicarium*, and identifies key research gaps to support sustainable disease control in European horticulture.

Keywords Onion · Pear · Spinach · Epidemiology · Disease management · Sustainable cropping systems

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Introduction

Phytopathogenic fungi threaten crop productivity and quality worldwide. Among these pathogens, *S. vesicarium* is receiving increasing attention because of its broad host range, host-specific toxins, fungicide resistance, and economic impact across multiple cropping systems worldwide (Gazzetti et al., 2025; Hay et al., 2021; Stricker et al., 2021a). In the 1970s, *S. vesicarium* was first reported as the causal agent of brown spot on pear (BSP) on *Pyrus communis* L. in Italy, and of Stemphylium leaf blight on onion (SLB) in India and in Texas (USA) (Miller et al., 1978; Ponti et al., 1982; Rao & Pavgi, 1975). More recently, in 2021, the pathogen was also detected on spinach in Italy, and reports of new emerging diseases on multiple horticultural crops highlights its expanding host range and the dynamic threat it poses to global food security (EPPO, 2026; Gilardi et al., 2022).

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The epidemiology of *S. vesicarium* is characterized by a polycyclic disease cycle, multiple inoculum sources, and diverse dispersal pathways. Airborne ascospores released in early spring may saprophytically colonize crop residues or alternative hosts; conidia subsequently produced on this plant material constitute an important source of inoculum for crop infections, which are dispersed mainly by wind and rain splash (Gossen et al., 2021; Llorente & Montesinos, 2006; Rossi et al., 2005). In onion, conidia can also be transported over short distances by thrips and over longer distances through infected transplants and seed (Leach et al., 2019; Piñeros-Guerrero et al., 2026). *Stemphylium* spp. can be seed-transmitted in spinach and radish, while colonization and sporulation on dead non-host foliage may support its field persistence and environmental dispersal (Foster et al., 2019; Hay et al., 2021; Hernandez-Perez & du Toit, 2006; Rossi et al., 2005). Disease progression is strongly influenced by favourable temperatures, high humidity, prolonged leaf wetness, inoculum availability, and older or senescing tissues. Disease management is complicated by the occurrence of polycyclic epidemics, overwintering on crop debris, limited host resistance, restricted fungicide availability, and fungicide-insensitive populations (Foster et al., 2019; Gazzetti et al., 2025; Gossen et al., 2021; Spawton & du Toit, 2024a). Therefore, current management approaches are shifting from reliance on chemical fungicides toward integrated pest management (IPM) strategies that incorporate biological control agents (BCA), genetic resistance breeding, and optimized agronomic practices (Cavina et al., 2024). This review provides an updated synthesis of current knowledge on *S. vesicarium*, focusing on: (*i*) genetic diversity and population structure; (*ii*) its toxin arsenal and role in multi-host pathogenicity; (*iii*) host–pathogen molecular interactions; and (*iv*) available integrated management strategies for the most economically damaging diseases on onion, spinach and pear.

Pathogen taxonomy: from morphological identification to advanced genetic approaches

S. vesicarium is a necrotrophic to hemibiotrophic filamentous ascomycete belonging to the genus *Stemphylium* (family *Pleosporaceae*, order *Pleosporales*, class *Dothideomycetes*). *S. vesicarium* was first described by Persoon (1801) as *Sphaeria herbarum*. The currently accepted anamorph name is *Stemphylium vesicarium* (Wallr.) E.G. Simmons, based on Wallroth's (1833) basionym. More than a century later, Simmons (1969) provided a comprehensive description of the teleomorph *Pleospora allii* (Rabenh.) Ces. & De Not., which was subsequently reported in India by Rao and Pavgi (1975). Morphologically, conidia of *Stemphylium* spp. are typically rounded, whereas those of *Alternaria* spp. (also in the family of *Pleosporaceae*), are generally tapered into a conical or cylindrical beak. Despite this distinction, the two genera were frequently mistaken because both produce pigmented and multiseptate conidia. *S. vesicarium* can be further distinguished by its characteristic, apically percurrent conidiophores (Simmons, 1969), with conidia forming on both aerial and submerged hyphae (Chandel et al., 2024). However, morphological features are highly influenced by environmental conditions and culture characteristics, limiting reliable discrimination among *Stemphylium* species. Currently, *Stemphylium* species identification relies primarily on molecular phylogenetics. Sequencing of the ITS region is commonly used for preliminary identification, while the *gpdH, cmdA,* and *tef1-α loci* provide greater resolution for species delimitation and phylogenetic inference (Chandel et al., 2024). Indeed, these molecular analyses demonstrated that *S. herbarum, S. mali*, and *S. alfalfae* are conspecific with *S. vesicarium*, allowing unambiguous identification of isolates, whose morphological traits closely resemble those of other *Stemphylium* species (Woudenberg et al., 2017).

Host range and main hosts

S. vesicarium has been reported on more than 500 plant species, including horticultural crops, cereals, legumes, and ornamentals (Hay et al., 2022; Köhl et al., 2009). Regarding alternative hosts, few studies have investigated common weed species growing near onion fields and pear orchards, such as redroot pigweed (*Amaranthus retroflexus* L.), purslane (*Portulaca oleracea* L.), bull thistle (*Cirsium vulgare* L.), curly dock (*Rumex crispus* L.), willowherb (*Epilobium* spp.), sow-thistle (*Sonchus* spp.), field horsetail (*Equisetum arvense* L.), can also serve as alternative hosts. On these weeds the pathogen may invade, colonize, and sporulate on dead (but

not living) tissues, contributing to inoculum persistence within production landscapes (Köhl et al., 2009; McDonald et al., 2023). Major horticultural hosts include onion (*Allium cepa* L.), garlic (*A. sativum* L.), leek (*A. porrum* L.), shallot (*A. cepa* L. var. *aggregatum*), spinach (*Spinacia oleracea* L.), asparagus (*Asparagus officinalis* L.), European pear (*Pyrus communis* L.), lucerne (*Medicago sativa* L.), mango (*Mangifera indica* L.), tomato (*Solanum lycopersicum* L.), radish (*Raphanus sativus* L.), sunflower (*Helianthus annuus* L.), parsley (*Petroselinum crispum* (Mill.) Fuss), wheat (*Triticum aestivum* L.), hazelnut (*Corylus avellana* L.), chilli pepper (*Capsicum annuum*), buckwheat (*Fagopyrum esculentum* Moench), sugar beet (*Beta vulgaris* L.), and soybean (*Glycine max* (L.) Merr.) (EPPO, 2026; Hay et al., 2021): on such crop plants the impact of the disease varies depending on the host and affected plant organ. Despite foliar infections can significantly reduce productivity by diminishing photosynthetic area in crops such as onion and tomato, the disease could be even more severe in leafy vegetables like spinach, and in fruit crops such as pear, where symptomatic leaves or fruits become unmarketable (Bhattarai et al., 2025; Rossi et al., 2005). Therefore, the following sections focus on three different key pathosystems: SLB (onion), BSP (pear), and Stemphylium leaf spot on spinach (SLS), highlighting features on their host–pathogen interactions and impact on European crop production.

Stemphylium leaf blight of onion

Onion (*Allium cepa* L.) is one of the most important vegetable crops worldwide and is highly susceptible to a wide range of diseases affecting yield and bulb quality. *S. vesicarium* was first reported on onion during the 1970s and initially regarded as a secondary foliar pathogen. However, SLB has recently emerged as one of the most destructive foliar diseases of onion in major production regions globally, with yield losses reaching 80%–90% under favourable conditions (Cortiello et al., 2023). Symptoms generally develop 7–14 days after infection, typically on older or outer leaves. Early symptoms consist of characteristic "dirty tips" (Fig. 1A), followed by yellowish-brown, spindle-shaped to elongated lesions that progressively enlarge (Fig. 1B). As the disease advances, lesions become necrotic, with dark centres and abundant sporulation (Fig. 1C) (Chandel et al., 2022; Hay et al., 2022). Severe infections accelerate leaf senescence, reduce photosynthetic area, and decrease bulb size and marketability (Hay et al., 2021; Rao & Pavgi, 1975). Overlap of symptoms can lead to confusion between SLB and purple blotch caused by *Alternaria* spp., the latter typically producing lesions

Fig. 1 Symptoms of Stemphylium Leaf Blight: dirty tip (**A**), oval shaped, whitish lesions (**B**), that coalesce and become necrotic due to the production of conidia (**C**)

with purple margins and dark sporulating centres (Hay et al., 2022). In addition to visible symptoms, SLB induces significant physiological and metabolic alterations. Infected plants exhibit reduced chlorophyll and carotenoid contents together with increased phenolic compounds, indicating activation of stress and defence responses (Zapata-Sarmiento et al., 2020). Metabolomic analyses revealed decreases in sucrose, citric acid, succinic acid, and several amino acids, whereas pyruvic acid accumulated in infected tissues (Medina-Melchor et al., 2022). Because pyruvate is a central substrate in respiratory metabolism, its increase may reflect pathogen-induced metabolic reprogramming that favours fungal growth and colonization. However, given its role in plant stress responses, a contribution to host defence cannot be excluded (Chandel et al., 2022; Medina-Melchor et al., 2022). In addition, the pathogen may utilize 4-aminobutyrate (GABA) as a nitrogen source, accounting for its decline in infected tissues (Medina-Melchor et al., 2022).

Stemphylium leaf spot of spinach

Spinach (*Spinacia oleracea* L.) is cultivated worldwide for both fresh-market and processing use. Although Europe contributes a relatively small proportion of global fresh spinach production, countries such as Denmark play a key role in the international spinach seed industry, since their long photoperiods and mild summer temperatures favour flowering and seed set. Production systems, characterized by dense plantings and frequent overhead irrigation, create a humid microclimate with prolonged leaf wetness, thus promoting several foliar diseases, including downy mildew (*Peronospora effusa*), anthracnose (*Colletotrichum spinaciae*), Cercospora leaf spot (*Cercospora beticola*), white rust (*Albugo occidentalis*), and Stemphylium leaf spot (SLS) (Liu et al., 2020). Traditionally attributed to *S. botryosum* based solely on morphology, through multilocus phylogenetic analyses SLS is now known to be caused by *S. vesicarium* and *S. beticola* (Liu et al., 2020). Although both pathogens induce similar symptoms, *S. vesicarium* predominates in warmer spinach-growing regions, whereas *S. beticola* is more frequently associated with cooler environments, particularly in seed-production systems (Spawton & du Toit, 2024a, b). Symptoms caused by *S. vesicarium* appear as small (1–3 mm), circular white-to-brown lesions with a sunken centre, distinct brown margin, often surrounded by a chlorotic halo within 8 days (Gilardi et al., 2022) (Fig. 2). SLS development is fostered by warm temperatures, high humidity, prolonged leaf wetness, and host water stress. A genome-wide association study has identified several genomic regions associated with quantitative resistance to SLS among spinach germplasm, strengthen the importance of resistance breeding programs as a promising

Fig. 2 Symptoms of Stemphylium Leaf Spot on spinach leaves

component of integrated disease management (Bhattarai et al., 2025).

Brown spot of pear

Pear (*Pyrus communis* L.) is an economically important fruit crop cultivated worldwide. In Italy, once the second-largest global producer, pear production has markedly declined in recent years, with the loss of approximately 10,800 ha of orchards between 2018 and 2024, with a 1.7-fold reduction in production volume (FAO, 2024). This decline has been associated with multiple factors, including prolonged summer periods of extreme heat (35–40 °C), the increasing disease incidence of fire blight (*Erwinia amylovora*) and pear scab (*Venturia pyrina*), pest pressure, such as the brown marmorated stink bug (*Halyomorpha halys*) and pear psyllids (*Cacopsylla pyri* and *C. pyricola*). Among the major phytosanitary constraints affecting European pear production, *S. vesicarium* is one of the most economically damaging pathogens, with estimated losses of up to 90% on susceptible cultivars under highly favourable conditions (Montorsi et al., 2025). BSP symptoms develop on leaves, shoots, and fruits as expanding necrotic lesions (Fig. 3). On fruitlets, necrotic spots frequently develop at the calyx end, whereas on mature fruits lesions are predominantly located along the equatorial region (Llorente et al., 2012). Frequently, fruit symptoms are enhanced during 3–7 months of cold storage, leading to significant post-harvest losses. Disease onset generally occurs in late spring, and infection, symptoms progression and disease severity are strongly influenced by environmental conditions, such as temperature, humidity, leaf wetness duration, and host susceptibility (Llorente et al., 2012; Moragrega et al., 2021).

Fig. 3 Symptoms of Brown Spot of Pear on a fruit and leaves of cv. Abbé Fétel

Epidemiology and sources of inoculum

S. vesicarium can be transmitted to its host plants horizontally, and colonises the host tissue by means of its germinating spores that originate from infected leaves, twigs, fruits, and from crop residues of numerous plant families; alternatively, it is vertically transmitted, from within the parent plant to the offspring via the seed, as reported for onion and spinach (Hay et al., 2021; Spawton & du Toit, 2024a, b) (Fig. 4A and B). *S. vesicarium* is both seed-borne and seed transmitted, due to its ability to infect both the pericarp and the embryo of seeds (Hernandez-Perez & du Toit, 2006). Such evidence aligns with the broader recognition that seed transmission significantly contributes to global dispersal of *S. vesicarium* and facilitates its introduction into new production areas. In onion, transplant-mediated dissemination represents another key epidemiological factor, emphasizing the value of pathogen-free propagation material to prevent long-distance spread of the fungus among production regions (Piñeros-Guerrero et al., 2026).

Epidemiology of *S. vesicarium* is driven by the production of both sexual ascospores (teleomorph: *Pleospora allii*) and asexual conidia (anamorph: *S. vesicarium*). Overwintering structures include mycelium and pseudothecia formed on infected plant debris such as fallen leaves, senescent tissues, and weeds. The efficient formation of pseudothecia on crop residues is further supported by the homothallic nature of *S. vesicarium*. Recent evidence showed that isolates of *S. vesicarium* recovered from spinach field residues carried both MAT1-1 and MAT1-2 mating-type idiomorphs within a single genome, consistent with self-fertility (Spawton & du Toit, 2024a, b). Due to this genetic configuration,

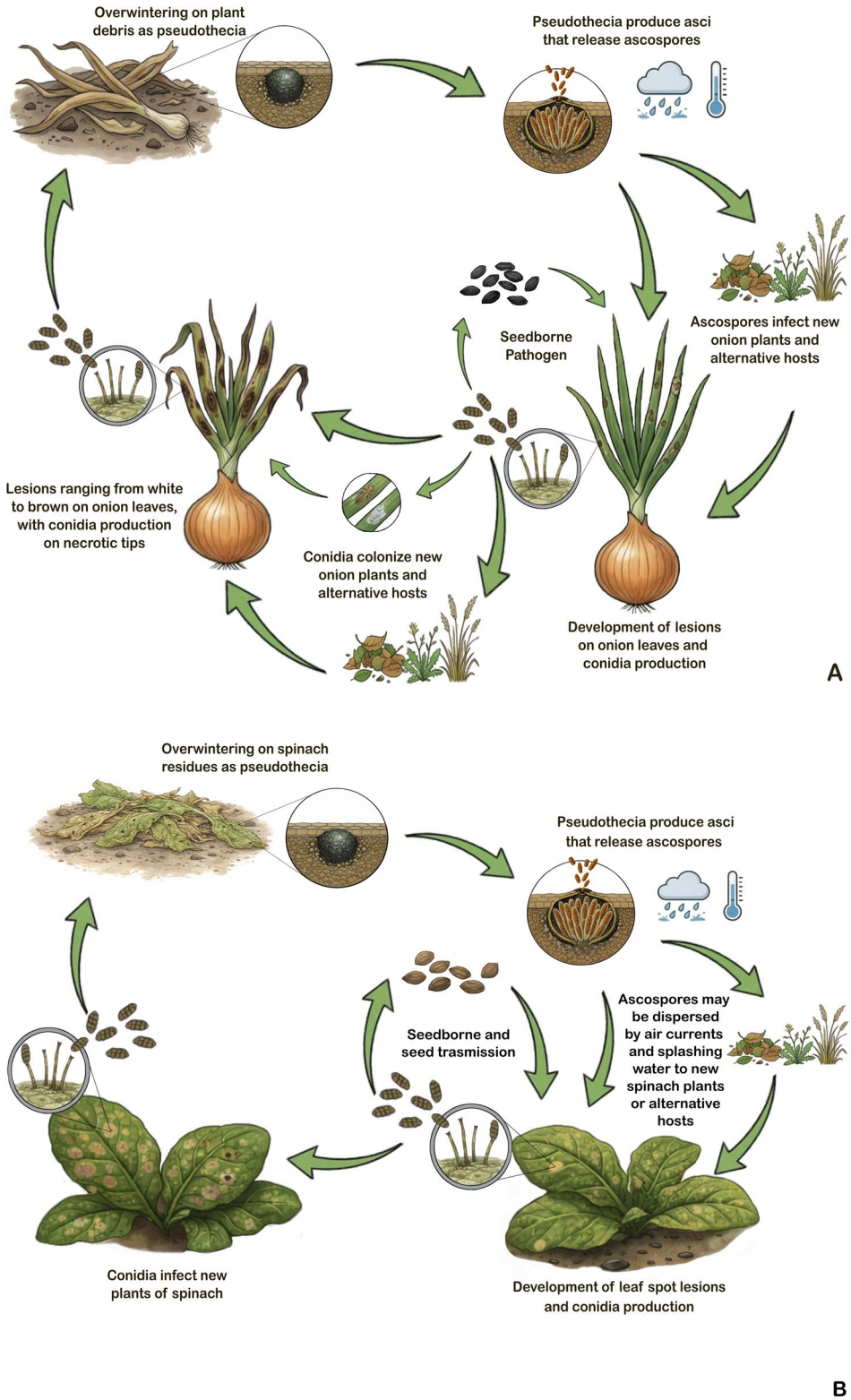

Fig. 4 Life cycle of Stemphylium vesicarium on: **A** onion, **B** spinach and (**C**) pear

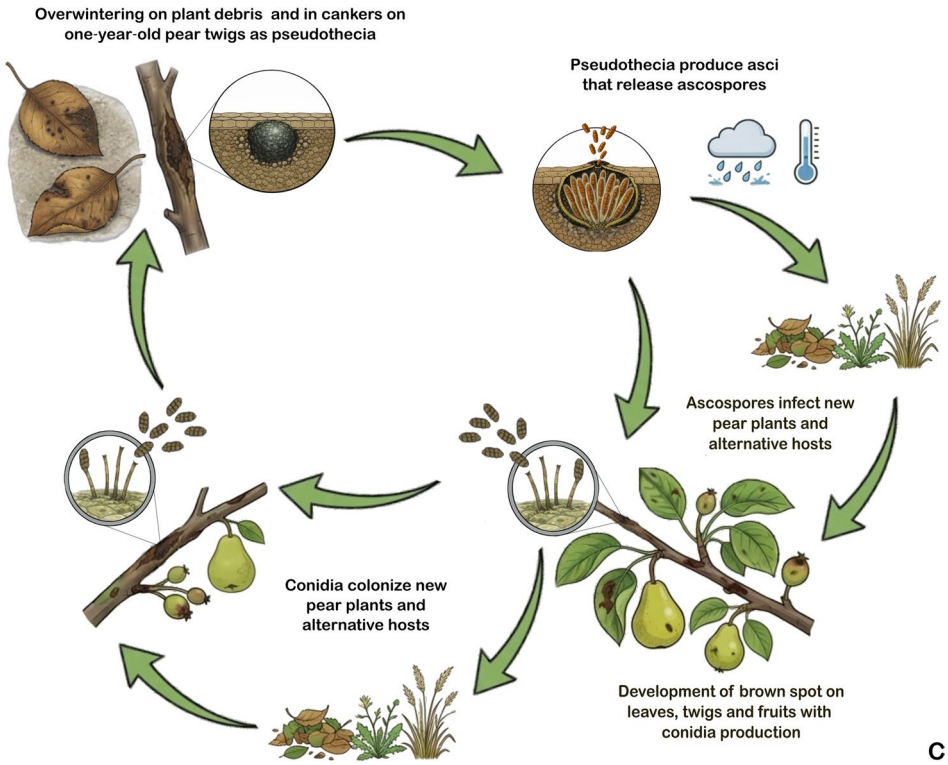

Fig. 4 (continued)

the fungus can complete sexual reproduction and produce overwintering pseudothecia without requiring a compatible mating partner. This reproductive strategy likely enhances the rapid and abundant production of pseudothecia on infected residues, facilitating long-term survival and ascospore-mediated inoculum carryover between cropping seasons (Spawton & du Toit, 2024a, b). Ascospores discharged by overwintering pseudothecia saprophytically colonize plant debris and alternative hosts on the orchard/field floor. Subsequent generations of conidia produced on this colonized debris constitute a crucial source of primary *inoculum* in several cropping systems (Hay et al., 2021; Koike et al., 2013). A brief wetting period followed by drying favours ascospore discharge, whereas prolonged or intense rainfall may reduce airborne concentrations through washout or flooding of pseudothecia (Gossen et al., 2021). Alternative weed hosts can consequently sustain the pathogen between cropping cycles and facilitate local or interfield spread (McDonald et al., 2023) (Fig. 4A, B and C). The temporal patterns of ascospore release vary among crops and agrosystems, but their early occurrence supports this mainly saprophytic role (Gossen et al., 2021; Llorente & Montesinos, 2006). In pear orchards, pseudothecia and viable ascospores also develop in cankers on one-year-old twigs, identifying woody tissues as an additional overwintering substrate and supporting removal of infected pruning residues (Cavina et al., 2024) (Fig. 4C). During the cropping season, conidia produced on colonized residues and infected leaves, fruits and twigs drive secondary spread. Wind, rain splash and irrigation disperse conidia over short to medium distances, sustaining polycyclic epidemics (Hay et al., 2022). In onion, *Thrips tabaci* can passively transfer conidia within and among plants, although at low rates; feeding injuries may also facilitate infection and contribute to patchy SLB epidemics (Leach et al., 2019). Moreover, soil-related stresses, including soil compaction, may further increase disease severity, underscoring the complex interplay between environmental conditions and pathogen aggressiveness (Hay et al., 2021).

Genetic diversity, virulence, and toxin-mediated pathogenesis in *Stemphylium vesicarium*

S. vesicarium displays substantial genotypic and allelic diversity, and isolates may form host-specific pathotypes with marked different virulence profiles, even from the same host species and genotype, requiring tailored disease-management strategies (Heck et al., 2023; Köhl et al., 2009). Because morphology do not reliably distinguish closely related taxa, species identification requires multilocus analyses of the most informative genomic regions (*i.e.,* ITS, *gpdH*, *cmdA*, and *tef-1 loci*), as discussed in section "Pathogen taxonomy: from morphological identification to advanced genetic approaches". More recently developed microsatellite markers (SSRs) further enable analysis of the spatio-temporal genetic structure of pathogen populations (Heck et al., 2023). However, despite these groupings, morphological features and even DNA sequences at certain *loci* (*e.g., gpdH*) may remain indistinguishable among *S. vesicarium*, *S. herbarum*, and *S. alfalfae* (Koike et al., 2013). Indeed, Woudenberg et al. (2017) synonymized the latter two species with *S. vesicarium*. This combination of genetic variability and host specialization highlights the complexity of *S. vesicarium* epidemiology and reinforces the need for management approaches tailored to specific pathogen populations. Whole-genome sequencing (WGS) has provided additional insights into the molecular determinants of pathogenicity. The pear isolate 173-1a13FI1M3 contains genes associated with fungicide resistance, plant cell-wall degradation, and secondary metabolism, including candidates potentially involved in virulence and toxin biosynthesis (Gazzetti et al., 2019).

Host-specific toxins (HSTs) are important pathogenicity determinants in necrotrophic fungi, although their role in *S. vesicarium* is best established in the pear pathosystem and remains uncertain in onion and spinach (Singh et al., 1999, 2000; Stricker et al., 2021b). *S. vesicarium* produces toxins in apoplastic fluids that may facilitate early colonization. During germination, conidia form appressoria, while toxins alter plasma-membrane permeability, causing electrolyte leakage and ultrastructural changes that promote penetration and infection (Singh et al., 2000). These phytotoxins induce chlorosis, necrosis, and foliar lesions (Hay et al., 2021). From culture filtrates of pear-derived isolates, the two toxins SV-I and SV-II have been isolated, purified and characterised (Singh et al., 1999), along with additional metabolites including stemphylin, stemphyperylenol, stemphyloxin, and stemphol, all recognized as host-specific toxins (Stricker et al., 2021b). Pear-pathogenic *S. vesicarium* isolates produce SV-1 and SV-2, which selectively induce necrosis of leaf veins in susceptible European pear cultivars. SV-1 is highly active at 0.01–0.1 µg ml^{-1}, whereas resistant cultivars and non-host plants such as onion and tomato remain insensitive even at 1,000 µg ml^{-1}, demonstrating host-dependent rather than general phytotoxicity (Singh et al., 1999). During active foliar and fruit infection, germinating conidia are thought to release SV-1 and SV-2 into host tissues. SV-1 acts early on the plasma membrane of susceptible cells, causing dose-dependent electrolyte leakage and rapid loss of membrane integrity. Ultrastructural alterations, including plasmalemmal invaginations near plasmodesmata, occur within hours of toxin exposure (Singh et al., 1999, 2000). The resulting ion leakage, cellular dysfunction, and localized cell death produce characteristic veinal necrosis and may facilitate early fungal colonization. SV-2 probably complements SV-1 by reinforcing membrane damage and symptom development. Detection of SV-toxins in intercellular fluids and the induction of lesions by non-pathogenic spores supplied with small toxin quantities further support their direct contribution to pathogenicity (Singh et al., 1999). Other secondary metabolites have been identified, but their specific contributions to disease remain less clearly established. Variation in toxin production may explain host specialization and cross-infectivity. Some *S. vesicarium* isolates infect asparagus and multiple *Allium* hosts, whereas parsley isolates infect related *Apiaceae* but not leek, onion, spinach, or tomato (Foster et al., 2019; Koike et al., 2013). Future studies should identify the genes controlling SV-toxin biosynthesis, clarify interactions between SV-1 and SV-2, and determine how toxin profiles shape host range, virulence, and cultivar susceptibility.

Disease management on onion, pear and spinach

Integrated Pest Management (IPM) strategies for *S. vesicarium* affecting onion, spinach and pear aim to combine preventive and curative measures, and

include agronomic practices (*e.g.,* seed sanitation and certification, residue management by burying or destroying crop debris immediately after harvest, crop rotation, soil sanitation, weed control, optimal fertilization), targeted fungicide applications, use of disease forecasting models, and, where feasible, use of BCAs. These approaches mirror strategies widely applied to other fungal pathogens.

Crop management methods

Management strategies to control the diseases caused by *S. vesicarium* should be adapted to the host, agricultural environment, and epidemiological context. Crop rotation represents an excellent suggestion for annual crops, such as onion and spinach, but not for pear and other perennial crops. Management should also account for differences between protected and open-field systems, particularly in inoculum sources, environmental conditions, or availability of fungicides and their dosage (phytoiatric treatments might be different as active substance and/or dosage). Cultivar choice plays an important role in disease management: indeed, the use of resistant or tolerant varieties may significantly reduce disease incidence and severity, although market requirements may restrict growers to popular susceptible cultivars. In onion, only a limited number of genotypes show moderate resistance to SLB, indicating that useful resistance exists but remains scarce (Chandel et al., 2022). Spinach germplasm shows greater variability, with 11%–27% of tested cultivars classified as resistant and 29%–48% as moderately resistant to SLS (Spawton & du Toit, 2024a). Susceptibility may also vary with crop stage and production system, including baby-leaf versus mature spinach and open-field versus tunnel cultivation. In pear, 'Passe Crassane', 'Abbé Fétel', 'Alexandrine', and 'Conference' are highly susceptible to BSP, whereas 'Williams' ('Bartlett'), Max Red Bartlett (red-skinned bud mutation/sport of 'Williams'), Blanquilla, Beurre Hardy, Louis Bonne, Grand Champion, Highland and Ercolini are regarded as having low susceptibility (Llorente & Montesinos, 2006). A major QTL associated with BSP susceptibility, designated 'SV susceptibility', was identified on Linkage Group 15 of 'Abbé Fétel' using the cross 'Abbé Fétel' × Max Red Bartlett (Cappai et al., 2018). The use of certified or sanitized seed and healthy transplants is recommended for onion and spinach, although infected seed alone may not generate severe disease outbreaks (Hay et al., 2021, 2022; Spawton & du Toit, 2024a, b). When pathogen contamination is low and mainly confined to the pericarp, inoculum can be reduced using 1.2% sodium hypochlorite (NaOCl) for 60 min or hot-water treatments at 50 °C for up to 30 min or 60 °C for up to 10 min (Liu et al., 2020; Spawton & du Toit, 2024a, b). Crop rotation can delay disease onset and development in onion and spinach, but rotation species must be selected carefully, since *S. vesicarium* can infect cereals, including wheat and barley, which may become inoculum reservoirs (Farag et al., 2022). Reducing overwintering inoculum is therefore essential. Infected crop residues should be removed, buried, or destroyed, and weeds controlled because they can harbour the pathogen, sometimes without symptoms. Weed removal also improves aeration and shortens leaf-wetness periods (Hay et al., 2021; McDonald et al., 2023). In pear orchards, nutritional and orchard-floor sanitation measures can complement fungicide-based BSP management. Soil application of calcium chloride ($CaCl_2$) at bloom may protect developing fruit by increasing calcium concentration; reduced BSP symptoms were observed in 'Abbé Fétel', particularly when fruit calcium exceeded 1,000 mg kg^{-1} dry weight (Toselli et al., 2012). Post-season sanitation should include removal of infected fallen leaves and fruit mummies, which support pseudothecia and ascospore production. This strategy can be reinforced by orchard-floor applications of calcium cyanamide ($CaCN_2$), a slow-release nitrogen fertilizer with liming, transient biocidal, and microbial-modulating effects; by accelerating residue decomposition, $CaCN_2$ may reduce the availability of overwintering substrates for pseudothecia development, thereby lowering inoculum carry-over between cropping seasons (Šušek, 2008). Pear leaf litter, ground-cover litter, and cankered twigs represent additional inoculum sources. Pseudothecia and viable ascospores have been detected on one-year-old twigs, suggesting that cankered material and pruning residues should be removed where feasible (Cavina et al., 2024). However, pruning should be balanced against potential yield losses because pear fruiting structures develop on older branches. Finally, practices that shorten leaf wetness can limit infection and conidial dispersal. Appropriate plant spacing and canopy management improve ventilation and rapid leaf drying: the preferred row orientation

remains (possibly) the North–South, despite the prevailing winds. In spinach and onion, irrigation should be scheduled early in the day, and overhead irrigation should be minimized where possible. Drip irrigation is preferable in pear orchards because it limits canopy wetness, reduces water use, and avoids conditions favourable to BSP and other diseases (*e.g.*, fireblight).

Fungicide applications

Chemical control of *S. vesicarium* is not an easy task for several reasons: host range, limited crop-specific registrations, epidemiology, and capacity to develop fungicide resistance. Treatments must also be coordinated with programmes targeting other pathogens, *e.g. Venturia pyrina* for pear, *Peronospora* spp. and *Botrytis* spp. for onion and spinach. Management relies on fungicides from FRAC groups 2, 3, 7, 9, 11, and 12, selected according to crop, disease risk, and pathogen sensitivity (FRAC, 2025). In pear orchards, applications begin at petal fall and may be repeated every 7–14 days without forecasting systems. Severely affected orchards may require up to 25 annual treatments, highlighting the limited sustainability of chemical control (Cavina et al., 2024). Under standard disease pressure, however, fungicide timing is guided by forecasting models to optimize application times and reduce chemical inputs. Despite their effectiveness, resistance in *S. vesicarium* populations from onion, spinach and pear has been detected both *in vitro* and in field conditions against several active compounds. In onion, reduced sensitivity or resistance has been reported to DMIs (FRAC 3), SDHIs (FRAC 7), anilinopyrimidines (FRAC 9), and QoIs (FRAC 11), with possible emerging insensitivity to fludioxonil (FRAC 12) (Stricker et al., 2021b). In pear, control failures involve dicarboximides (FRAC 2), DMIs, SDHIs, QoIs, and, rarely, fludioxonil. Recent SDHI resistance has been linked to the SDHB P230L and SDHC H134R mutations (Gazzetti et al., 2025). In spinach, resistance mainly affects the QoIs azoxystrobin and pyraclostrobin and is associated with the G143A mutation in the cytochrome *b* gene (Spawton & du Toit, 2024a). Repeated chemical fungicide applications, rapid asexual reproduction, and multiple infection cycles favour resistance selection. Fungicide stewardship should therefore combine forecasting-based timing with rotation or mixtures of products having different modes of action (Gossen et al., 2021; Stricker et al., 2021a). Several dithiocarbamates have been withdrawn in the European Union, further restricting available options. In organic systems and countries with few registered products, management may depend on sulphur or copper compounds. Environmental concerns associated with copper use support the need to integrate cultural practices, resistant cultivars, forecasting systems, and biological control agents (BCAs) into sustainable management programmes (Moragrega et al., 2021).

Disease forecasting models

Disease forecasting models were developed to optimize fungicide timing, reduce unnecessary pesticide applications, and improve disease management by integrating environmental parameters and *S. vesicarium* epidemiology to identify conditions conducive to infection and recommend appropriate application timing, thereby reducing costs and minimizing the risk of resistance development without compromising yield or quality. For SLB, several forecasting systems originally developed for other pathosystems have been evaluated, including TOMcast, developed for *Septoria lycopersici* and *Colletotrichum coccodes* on tomato, and BOTcast, developed for *B. squamosa* on onion. Although some forecasting-based schedules reduced disease severity in specific years while lowering the number of fungicide applications, none of them consistently outperformed conventional programmes across environments and seasons (Stricker et al., 2021b). This limited operational success of this forecast models likely reflects the epidemiological complexity of the onion-*S. vesicarium* pathosystem. Models developed for other diseases may fail to capture key components of SLB epidemics, including early or cryptic infections, rapid polycyclic conidial spread, toxin-associated leaf dieback, and reduced fungicide sensitivity (Gossen et al., 2021; Stricker et al., 2021b). Consequently, current evidence highlights the need for onion-specific forecasting systems. To date, no specific weather-based forecasting model has been developed or validated for SLS. In pear, forecasting models play a central role in BSP management. BSPcast, developed in Spain, predicts infection risk based on leaf wetness duration and temperature during wet periods (Montesinos et al., 1995). The model has been implemented or tested in Catalonia (Spain), Emilia-Romagna (Italy), Portugal, Belgium, and the

Netherlands as a decision-support tool for fungicide scheduling. Under low-to-moderate disease pressure, BSPcast-guided programmes can reduce fungicide use by approximately 30%–40% while maintaining disease control comparable to conventional spray schedules (Llorente et al., 2000, 2012). BSPcast calculates cumulative infection risk from daily wetness and temperature data and has been reported to substantially reduce fungicide applications compared with calendar-based programmes (Llorente & Montesinos, 2006). The additional model PAMcast, forecasts pseudothecia maturation and ascospore release by integrating winter temperature and humidity data, thereby supporting prediction of primary inoculum availability in pear orchards (Llorente et al., 2006).

Biological control: current research and commercially available biopesticides

Biological control represents a promising complement or alternative to fungicides for managing *S. vesicarium*, particularly where fungicide efficacy is declining or resistance is widespread. Biopesticides include microbiological control agents (*m*BCAs) and botanicals (*e.g.,* plant extracts, essential oils), which suppress pathogens through multiple modes of action such as competition, antibiosis, hyperparasitism, and induction of plant defences (ISR). A systematic literature search was carried out to summarize the progress and the current research trends on identifying and testing BCAs against *S. vesicarium* on onion, pear and spinach.

On onion, promising *m*BCAs have been identified: *Pseudomonas fluorescens* reduced mycelial growth *in vitro* and lowered SLB severity under greenhouse conditions (Hussein et al., 2007). Similarly, *Trichoderma asperellum* reduced mycelial growth, conidial production, and disease severity, while improving plant physiological *status* in field trials (Zapata-Sarmiento et al., 2020).

Several biocontrol strategies have also been investigated for pear. *Trichoderma*-based products have been shown to suppress conidial production on leaf litter and ground-cover residues and to reduce ascospore release from overwintering pseudothecia (Moragrega et al., 2021). Other antagonists, including *Bacillus* and *Pseudomonas* species, have demonstrated strong inhibitory activity against *S. vesicarium in vitro* and on detached pear fruits (Montorsi et al., 2025). However, despite encouraging laboratory and detached-fruit results, the direct application of *m*BCAs to pear canopies has generally been unsuccessful under commercial orchard conditions. The establishment and persistence of antagonists in the pear phyllosphere and carposphere are strongly influenced by environmental conditions, resulting in inconsistent disease control (Llorente et al., 2012; Moragrega et al., 2021). Consequently, biocontrol strategies targeting overwintering inoculum on orchard-floor residues may provide a more reliable approach than attempts to protect aerial tissues directly. To date, no published studies are available on biological control of *S. vesicarium* in spinach, highlighting an important area for future research.

Commercial biopesticides

Despite growing interest in biological control, relatively few biopesticides have been marketed for the management of *S. vesicarium*, and their availability varies among countries and crops. Nevertheless, several commercial products based on *Bacillus*, *Pseudomonas*, and *Trichoderma* species have been developed following promising research results against this pathogen. Commercially available biocontrol products against this pathogen on onion, pear and spinach are listed in Table 1, together with trade names and web links, targeted crops, active substance, modes of action and geographical markets. In both the EU and North America, commercial formulations are mainly based on *Bacillus amyloliquefaciens*, *B. subtilis*, *B. mycoides*, *Pseudomonas chlororaphis*, and *Trichoderma* spp., targeting onion, pear, and spinach. Representative products are characterized by different modes of actions, such as: (*i*) competition, antibiosis and ISR, provided by Serenade ASO®, Amylo-X®, Taegro®2, Serifel®, AVIV®, Botrybel®, Monobac® and Howler EVO®; (*ii*) competition and ISR, provided by Rhapsody® and Companion®; (*iii*) ISR, provided by LifeGard® and finally through (*iv*) antibiosis by AmyloShield™ and Guarda®. They are available as liquid concentrates, wettable powders, or granules and can be applied trough different methods (*i.e.,* ground spray on turf, aerial spray, chemigation) during the entire cropping season of onion, pear or spinach.

Table 1 A broad description of some commercial biopesticides applied in the control of *Stemphylium vesicarium* on pear, onion and spinach

Category	Commercial Name	Host plant	Active substance	Mode of Action	Geographical markets
EOs	Guarda®	Onion (Bulb and Green)	Thyme oil, Thymol chemotype	Antibiosis	USA
*m*BCAs	Botrybel®	Onion	*Bacillus amyloliquefaciens AH2*	Competition, ISR, Antibiosis	EU
*m*BCAs	Monobac®	Onion	*Bacillus amyloliquefaciens AH2*	Competition, ISR, Antibiosis	EU
*m*BCAs	Serifel®	Onion	*Bacillus amyloliquefaciens* MBI 600	Competition, ISR, Antibiosis	USA, EU
*m*BCAs	AmyloShield™	Fruits, Vegetables	*Bacillus amyloliquefaciens* PTA-4838	Antibiosis (cyclic lipopeptides)	USA; Canada
*m*BCAs	Amylo-X®	Pear	*Bacillus amyloliquefaciens* subsp. *plantarum* D747	Competition, ISR, Antibiosis	USA, EU
*m*BCAs	LifeGard®	Spinach	*Bacillus mycoides* isolate J	ISR	USA
*m*BCAs	Rhapsody®	Pear	*Bacillus subtilis* QST 713	Competition, ISR, Antibiosis	USA, EU
*m*BCAs	Serenade ASO®	Pear	*Bacillus subtilis* QST 713	Competition, ISR, Antibiosis	USA, EU
*m*BCAs	AVIV®	Onion (Bulb and Green)	*Bacillus subtilis* IAB/BS03	Competition, ISR, Antibiosis (Foliar; ground)	USA
*m*BCAs	Howler EVO®	Onion	*Pseudomonas chlororaphis* AFS009	Competition, ISR, Antibiosis	USA
*m*BCAs	Remedier®	Pear	*T. asperellum* ICC012 + *T. gamsii* ICC080	Hyphal parasitism; metabolite activity (treatments on turfgrass)	EU
*m*BCAs	TELLUS WP®	Pear	*T. asperellum* ICC012 + *T. gamsii* ICC080	Hyphal parasitism; metabolite activity	EU
*m*BCAs	Vitanica® TC Protect	Pear	*T. asperellum* ICC012 + *T. gamsii* ICC080	Hyphal parasitism; metabolite activity	EU

Future perspectives

Although substantial progress has been made in understanding the biology, epidemiology, and management of *S. vesicarium*, important knowledge gaps continue to limit the durability as sustainability of management strategies. Its recent transition from a secondary pathogen to a priority pest in European horticulture demonstrates its remarkable adaptability and capacity to expand into new regions and across hosts (EPPO, 2026). Integrating population genomics, phylogeographic analyses, and epidemiological modelling will be essential to determine how climate change, host adaptation, movement of plant material, and fungicide selection shape pathogen emergence and population structure. Given the broad host range of *S. vesicarium* that includes several non-crop plants, further investigation on minor or alternative hosts and reservoir plants is required: indeed, as demonstrated for other pathosystems, weeds and volunteer hosts may act as significant inoculum sources, thus suggesting that their epidemiological relevance in *S. vesicarium* outbreaks is likely underestimated. The development of predictive models that incorporate climate projections and intensification of cropping systems, supported by epidemiological studies linking environmental conditions to infection risk in foliar pathogens, would enhance risk assessment and support more anticipatory, evidence-based management. Another priority is elucidating toxin-mediated pathogenicity. Although SV-1 and SV-2 are established pathogenicity factors in susceptible pear cultivars, the genes regulating their biosynthesis, their interactions during infection, and the molecular basis of host sensitivity

remain poorly understood. Comparative genomics, transcriptomics, metabolomics, and functional validation of candidate genes could determine how toxin profiles influence virulence, host specialization, and cross-infectivity. Similar studies are required to establish whether toxins contribute to its pathogenic success. *S. vesicarium* management mostly relies on the intensive use of fungicides (FRAC, 2025): however, the reduced sensitivity to multiple fungicide classes has been documented in the pathogen populations worldwide, demonstrating the need to diversify control strategies. Moreover, coordinated resistance surveillance supported by molecular diagnostics and genomic tools is also needed to track fungicide-resistance alleles, relate laboratory sensitivity to field efficacy, and guide crop-specific rotation and mixture programmes that reduce dependence on repeated fungicide applications.

Strengthening host resistance to *S. vesicarium* is equally important. QTLs associated with susceptibility in pear and variation in onion and spinach tolerance/resistance provide useful starting points for marker-assisted selection, QTL validation across diverse genetic backgrounds, and functional genomics to accelerate the development of cultivars combining durable resistance with commercially important traits.

Biological control offers complementary opportunities, but both development and commercialization of BCAs are constrained by formulation difficulties and inconsistent field performance. Protective mBCA applications to pear canopies have been largely unsuccessful under orchard conditions; therefore, future research should pivot toward orchard-floor and leaf-litter microbiome engineering to suppress primary inoculum. Targeting overwintering residues to reduce conidial production, pseudothecia development, and ascospore release may be more reliable than direct protection of aerial tissues (Moragrega et al., 2021). Innovative formulation technologies aimed at improving microbial stability, shelf life and reliability under field conditions will be critical for the future deployment of effective *m*BCAs. Further refinement and regional validation of disease-forecasting systems will also contribute to reducing chemical inputs, without affecting disease control. In particular, the inconsistent performance of TOMcast- and BOTcast-derived spray schedules for onion SLB suggests that future research should move beyond the adaptation of models developed for other pathosystems and focus instead on the development of native, onion-specific forecasting frameworks. Such models should incorporate key epidemiological components of *S. vesicarium*, early-season inoculum dynamics, conidial pressure, leaf wetness, host phenological stage, and fungicide sensitivity. Given the strong influence of climate variability on disease dynamics, forecasting frameworks integrating climate-change scenarios should be incorporated into long-term IPM planning. Their broader adoption will depend on robust multi-year validation, standardisation of epidemiological thresholds and seamless integration with precision-agriculture technologies.

Conclusions

The ascomycete *S. vesicarium* has emerged as a complex, multi-host pathogen of increasing economic relevance in European horticultural systems. Its broad host range, its ability to produce multiple infection cycles in a single season, its capacity for overwintering in diverse reservoir plants, and the progressive development of fungicide resistance collectively challenge traditional management approaches and underscore the limitations of single-measure control strategies.

In this review, we described the hosts of *S. vesicarium,* its epidemiology and common symptoms in different host crops. We particularly focused on three major diseases: SLB on onion, BSP on pear and SLS on spinach, due to their current economic impact in Europe. Sustainable management of *S. vesicarium,* therefore, requires an integrated approach that combines epidemiological knowledge, resistance breeding, optimized fungicide use, and innovative control strategies within a robust IPM framework. Limitation in using synthetic fungicides under increasingly restrictive regulatory regimes, and the ever-increasing development of *S. vesicarium* populations presenting low sensitivity to some classes of fungicides support their replacement with new effective and sustainable control strategies. Indeed, IPM policies drive towards non-chemical treatments as the applications of BCAs, when the disease pressure is low, or in combination with synthetic fungicides.

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Declarations

Conflict of interest On behalf of all authors, the corresponding author states that there is no conflict of interest.

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