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Biological control mitigates spread of vector-borne plant pathogens

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ABSTRACT

Diseases caused by vector-borne plant pathogens cause adverse impacts on yield resilience, food security, and farmer livelihoods, which are bound to aggravate under global change. Biological control is routinely discounted as a mitigation strategy for plant diseases, partially due to scarce and inconclusive empirical support. Here, using curated field survey data for 58 persistently or semi-persistently transmitted pathogens, we employ a multi-method approach to assess the role of resident (i.e., naturally occurring) biological control agents in these pathosystems. Our meta-analyses show how *in planta* pathogen incidence is strongly affected by vector abundance and infectivity. Meanwhile, biological control agent density negatively affects vector abundance and slows vector population build-up. Together, these relationships suggest that biological control lessens pathogen incidence by reducing vector abundance, though a paucity of data impedes direct, empirical demonstration of this effect. In particular, bipartite (mainly vector × pathogen) interactions have only been uncovered under field conditions for less than half of focal pathosystems. More so, just 5 % of studies simultaneously reported pathogen, vector, and biological control agent densities. Our study contests the long-standing dogma that arthropod-vectored pathogens cannot be mitigated through biological control, and accentuates how observational or manipulative field studies are imperative to grasp its full potential.

1. Introduction

Pests and pathogens jointly account for 20–30 % losses in global agrifood production, severely impacting food security and societal well-being (Savary et al., 2019). Viral, fungal, and bacterial pathogens cause disease epidemics fueled by climate change, global trade, and breakdowns of plant resistance (Gilbertson et al., 2015; Jones and Naidu, 2019). Vector-transmitted pathogens in particular cause severe impacts on global agriculture and associated livelihoods. For instance, citrus greening and olive quick decline cause multi-billion dollar losses for fruit growers in Western nations, while cassava mosaic geminiviruses compromise food security of millions in Africa (Gottwald, 2010; Jones and Naidu, 2019; Schneider et al., 2020). The management of plant disease is commonly addressed through insecticides aimed at vector control and plant varietal resistance (Perring et al., 1999). These measures often pose health or environmental risks, require protracted breeding efforts that may be challenged by climate change, can be impaired by resistance development or breakdown over a few months or years (McDonald and Linde, 2002; García-Arenal and McDonald, 2003), and may even favor disease progression, i.e., in the case of sublethal doses of chemical insecticides (Grilli and Holt, 2000), underlining a need to diversify management.

For transmission, vector-borne pathogens rely on arthropods. Phloem-feeding hemipterans such as aphids, whiteflies, leafhoppers and planthoppers, as well as mesophyll feeding thrips and mites, transmit viruses (Hogenhout et al., 2008; Gilbertson et al., 2015; Jones and Naidu, 2019). Leafhoppers, planthoppers and psyllids transmit phloem-limited bacteria, and sharpshooters and spittlebugs transmit xylem-limited bacteria (Weintraub and Beanland, 2006; Perilla-Henao and Casteel, 2016). Though often viewed in isolation, arthropod vectors are involved in a myriad of ecological interactions within and beyond crop boundaries that affect pathogens (Crowder et al., 2019; Clark et al., 2019). Models show predators, parasitoids, and entomopathogens affect pathogens by consuming vectors and by affecting vector behavior (Finke, 2012; Crowder et al., 2019). Yet, while some experiments show biological control agents reduce pathogen spread by lowering vector abundance, others unveil how they promote pathogens by increasing vector movement over comparatively short time-frames, small spatial scales and within simplified 'microworlds' e.g., laboratory or cage settings (Long and Finke, 2015; Tan et al., 2016; Clark et al., 2019; Lee et al., 2022). Such studies have spurred interest among epidemiologists to further assess the role of community structure in disease mitigation (Eigenbrode et al., 2018; Crowder et al., 2019; Lee et al., 2023).

Despite its bearing on disease, effects of biological control agents on vectors have not been extensively reviewed (Roudine et al., 2023). Consumptive effects are dependent on factors like predator density and attack rates (Finke, 2012), while non-consumptive effects involve behavioral, morphological, or physiological changes triggered by biological control agents (Ingerslew and Finke, 2020; Culshaw-Maurer et al., 2020). In particular, non-consumptive effects such as enhanced vector fitness, mobility, or probing frequency in response to 'landscapes of fear' can promote disease progression (Crowder et al., 2019; Lee et al., 2022). The 'landscape of fear' concept initially derived from observations that herbivores adjust their behavior in habitats or areas with an elevated risk of predation (Laundré et al., 2001; Culshaw-Maurer et al., 2020). Such fear-induced effects may even override those of predation-related reductions in vector survival (Long and Finke, 2015). In circumstances where biological control agents lower transmission efficiency, they are prone to slow disease spread (Crowder et al., 2019; Lee et al., 2021). This may be most likely in systems where transmission efficiency is low and prolonged vector residence times are required, such as with persistent pathogens (Eigenbrode et al., 2018; Roudine et al., 2023), which differ notably from pathogens transmitted in a non-persistent manner following comparatively short feeding bouts. Regardless of the above, biological control is routinely dismissed as a disease management strategy. This may relate to the fact that much plant pathology research is carried out in simplified, ecologically degraded and pesticide-intensive systems, where resident natural enemies are often unable to effectively regulate vector and pathogen populations (Dainese et al., 2019; Janssen and van Rijn, 2021). To complicate matters further, crop protection research tends to be reductionistic and is regularly performed in artificial settings or phenomenal 'microworlds' (Alrøe and Kristensen, 2002).

Indeed, scientists' ability to detect relevant patterns concerning effects of biological control agents on plant pathogens has been impeded by reliance on simplified experiments with a narrow set of vectors and/or pathogens (Lee et al., 2023; Wyckhuys et al., 2023). Disease research may benefit, however, from including greater levels of complexity as revealed by field-level data in systems including multiple biological control agents, companion plants, or non-pest herbivores over longer time horizons (Long and Finke, 2015; Mauck et al., 2015; Clark et al., 2019; Chisholm et al., 2019; Roudine et al., 2025). Such observational or manipulative studies in actual farm settings could yield transformative insights to improve disease models and plant pathogen management (Lee et al., 2023; Roudine et al., 2025).

Here, we built a global database of observational studies to gauge the impact of resident microbial or invertebrate biological control agents on arthropod-transmitted pathogens in real-world crop settings. After screening the published literature for 58 persistent or semi-persistent pathogens, we used a multi-model approach to assess biological control agent impacts on field-level vector abundance, population dynamics, and disease progression. Overall, our observational 'systems approach' can be instrumental in unveiling the potential of biological control as a viable disease management strategy. It also identifies opportunities for advancing our understanding of the effects of natural enemies on plant disease control and spread.

2. Materials & methods

We compiled a list of 58 bacterial and viral pathogens transmitted in a persistent or semi-persistent fashion by arthropods, affecting a wide range of annual or perennial food, feed, and fiber crops (Supplementary Tables 1, 2). Bacteria included *Candidatus* Liberibacter spp., *Candidatus* Phytoplasma spp., *Spiroplasma* spp., and *X. fastidiosa*, transmitted by leafhoppers, psyllids, or spittlebugs. Additionally, 49 viruses were included that are transmitted by nine different families or superfamilies of vectors. Typically, a given pathogen has multiple vector species and affects more than one plant or crop (Supplementary Table 2). As a result, the initial list of 58 pathogens gave rise to a far larger set of pathosystems, which we defined as unique combinations of pathogens, hosts, and vectors at the species level (Eigenbrode et al., 2018). We only considered pathogens with medium to long inoculation and acquisition periods, between 2 and 48 h, and excluded pathogens transmitted in a non-persistent manner. Hence, stylet-borne pathogens transmitted with short feeding bouts lasting a few seconds were not considered. While non-persistently transmitted pathogens cause many economically important diseases in vegetables and fruit crops, their transmission often occurs when transient vectors land on and probe a plant, even when those vectors do not establish or reproduce (Fereres and Moreno, 2009). For such pathogens, biological control agents generally do not have enough time to interfere with pathogen spread (Roudine et al., 2023) and may even favor disease proliferation (Dáder et al., 2012).

Once focal pathosystems had been defined, a stepwise process was followed for literature screening, data extraction, database compilation, and analysis. For each pathosystem, the literature was screened using digital libraries or search engines (Web of Science or Google Scholar). For a given pathosystem, literature queries were designed to locate publications that reported a pathogen and its vector, a vector and one or more biological control agents, or all three organisms. Topic searches were composed of the focal crop, pathogen, or vector or any search terms that either referred to common natural enemies of a given vector, types of natural enemies, the ecosystem service of biological control, predation, or parasitism. Publications were only retained that reported on field or semi-field studies (mesocosm trials, and when absolute or relative abundance data were presented for at least two of the three interaction partners (i.e., vector, pathogen, and biological control agent). Through this process, a near-exhaustive literature search was performed for each of the pathosystems.

Data from publications were extracted into a common database. Studies were classified into one of two types: (i) those reporting a single ‘snapshot’ survey of at least two interaction partners and (ii) those where surveys were replicated at various times and reflected temporal dynamics. For all studies, the pathogen, vector, and biological control agent(s) were recorded at the finest resolution available. We logged the study country, crop age (days after planting), and field traits including the presence of inter- or cover-crops, degree of weediness, presence and exact composition of crop varieties (intraspecific diversification), and use of fertilizers or insecticides. Where reported, we logged any measures of crop productivity such as yield.

Next, we logged data for each interaction partner. For the vector, we recorded its canopy-level abundance on a per-plant basis or as individuals per leaf, tiller, sweep sample, square meter, meter of row, or trap. When population counts were disaggregated by life stage, we omitted eggs as they do not directly affect pathogen transmission. We logged the percentage of infectious vectors, host plant occupancy (% plants harboring the vector), and a measure of vector mobility consisting of relative abundance of dispersive stages over immobile ones (e.g., whitefly adults over nymphs or winged over alate aphids). For hemipteran vectors, we recorded the presence or absence of ant tending as it can influence vector populations. For pathogens, we logged disease incidence as either the % of symptomatic plants or the % of plants with positive pathogen titers. If titers of multiple co-infecting pathogens were assessed, and overall disease prevalence was not reported, the titer of only one pathogen was entered into the database. As such, interactive effects of pathogens were discounted (Eigenbrode et al., 2018). For microbial or invertebrate biological control agents, we extracted data on prevalence (% vectors infected / killed), absolute abundance of predators, or parasitism rate. Where feasible, counts were converted to a per plant basis to allow for comparisons. For studies reporting time-lagged or population dynamics data, each of the above variables was recorded multiple successive time steps i.e., T1, T2. The time step was specified as either days after planting or the number of days after onset of the experiment, ranging from a few days or weeks for annual crops to several months or a year for perennials.

2.1. Statistical analysis

For ‘snapshot’ studies and (where relevant) time-lagged studies, relationships between pathogen incidence and vector was assessed using the following equation:

$$y_{i,j} \quad \sim \quad \beta_i * x_{i,j} + C_i + \quad \varepsilon_{i,j} \tag{1}$$

where $y_{i,j}$ is *in-planta* pathogen incidence for study *i* at site *j*, $x_{i,j}$ is either the abundance or infectivity of vectors; β_i is the coefficient of x on the response y; and C_i and $\varepsilon_{i,j}$ are the model intercept and residual. The same equation (Eq.1) was used to investigate the relationship between vector and biological control agents, where $y_{i,j}$ is the abundance of vectors and $x_{i,j}$ is the abundance of predators or parasitoids. Due to a paucity of data, relationships between biological control agents and pathogens were not assessed. All data were transformed by the z-score standardization method, and studies with less than five sites or observations were excluded and those with zero or near-zero variance were also filtered. We used meta-analysis to compute an overall effect size of the coefficient β, based on the restricted maximum likelihood (REML) method and accounting for between-study variance, with study as a random effect. R package “meta” was used for this meta-analysis (Schwarzer, 2015). Function nearZeroVar() from the Package “caret” was used for near zero variance filtering (Kuhn et al., 2020).

For studies reporting time-lagged patterns, we computed the relative growth rate of vector, pathogen, or biological control agent populations between successive observations. By using relative growth ratios, we aimed to standardize changes over time and allow for comparisons across pathosystems with varying initial abundances. In addition, predator/prey ratios accurately capture biological control services and carry value as a universal metric in comparative studies (Liu and Lu, 2025).However, as this approach may conflate autoregressive effects, we conducted additional analyses using explicit lagged variables. To do this, we used the same approach as in the “snapshot” analysis. That is, we firstly applied the Eq.1 to obtain the regression coefficient between the vector (abundance) at T2 ($y_{i,j}$) and natural enemies at T1 ($x_{i,j}$), and the pathogen incidence at T2 ($y_{i,j}$) with vector abundance at T1 ($x_{i,j}$). Then we used meta-analysis to compute an overall effect size of the coefficient β. Next, we assessed relationships between population growth ratios of vectors vs. pathogens, vectors vs. biological control agents, and pathogens vs. biological control agents using a linear mixed model (LMM), with study as a random factor. We further investigated whether biological control agent type (predator, parasitoid or entomopathogen) affected population growth ratios of different partners. In addition, a LMM was used to assess how relative biological control agent abundance (biological control agent: vector ratio) changed between time steps, or how relative vector abundance (vector: pathogen ratio) changed between time points. Lastly, LMMs were applied to assess how pathogen incidence, vector abundance, or biological control agent abundance varied between time points. In all models, study was a random factor and package “nlme” (Pinheiro et al., 2014) was used. Data analysis was conducted using R (R Core Team, 2012).

3. Results

We assessed effects of (i) vectors on plant pathogens, (ii) biological control agents on vectors, and (iii) biological control agents on pathogens with a meta-analysis of 81 'snapshot surveys' and 61 'time-lagged surveys' where quantitative data were reported on at least two interaction partners. These covered 26 and 17 different pathosystems, respectively (Supplementary Fig. 1). The most 'snapshot surveys' were focused on (carrot) yellows, citrus greening (Huanglongbing disease), and corn stunt spiroplasma. For time-lagged patterns, the most studies focused on Huanglongbing disease and barley yellow dwarf virus. For both 'snapshot surveys' and 'time-lagged surveys', only a single study was found for 35 % of pathosystems (Supplementary Fig. 1).

Overall, vector × pathogen interactions were the most reported relationship. In snapshot surveys, vector abundance (66 studies), pathogen incidence (61), and vector infectivity (36) were routinely reported. Variables such as host occupancy, % winged morphs, or ant tending were only reported in 2–3 studies each. Biological control received little attention in snapshot surveys, with 7, 3, and 2 studies reporting predators, parasitoids and entomopathogens, respectively, and only four studies (5 %) reporting data on all three interaction partners. In time-lagged surveys, vector abundance (58 studies) and pathogen incidence (27) were commonly reported, while vector infectivity, host occupancy, or % winged morphs were reported in only 4–10 studies each. Further, 19 and 16 studies reported predators or parasitoids, but only one had entomopathogen biological control agents. Three time-lagged studies (5 %) covered all three interaction partners.

Meta-analyses yielded a significant positive effect size (β) of 0.21 ± 0.1 (P = 0.037, number of studies n = 16) for vector abundance on *in planta* pathogen incidence (Fig. 1A), and 0.52 ± 0.2 (P = 0.01, n = 5) for vector infectivity on pathogen incidence (Fig. 1B). As such, pathogen incidence was consistently determined by the field abundance or infectivity of its vectors. For the interaction between biological control agents and vector abundance, meta-analysis yielded a significant negative effect size β of −0.16 ± 0.07 (P = 0.016, n = 51) (Fig. 2). However, due to data scarcity, no analyses were performed on the interaction between biological control agent abundance and *in-planta* pathogen incidence or vector infectivity.

For time-lagged surveys, we did not uncover strong relationships between the population growth ratios of vectors vs. pathogens (P = 0.14, n = 16), vectors vs. biological control agents (P = 0.14, n = 37), or pathogens vs. biological control agents (Supplementary Fig. 2a). When relating the population growth ratio of vectors to biological control agents, effects of predators vs. parasitoids were not statistically distinguishable (Supplementary Fig. 2b). Yet, relative biological control agent abundance (agent: vector ratio) at one time step negatively affected vector abundances at the subsequent time-step (β = −0.17 ± 0.04; LMM, P < 0.001, n = 41) (Fig. 3A) and relative vector abundance at one time step negatively affected pathogen incidence at the subsequent time (β = −0.34 ± 0.10; LMM, P = 0.001, n = 16) (Fig. 3B). High relative biological control agent abundance thus dampened vector population growth. Yet, counterintuitively and in contrast to results from the meta-analysis, vector abundance seems to reduce pathogen incidence (β = −0.24 ± 0.09; LMM, P = 0.001, n = 16). When assessing explicit lags in the independent variables, biological control agent abundance at one time-step negatively affected vector abundance at a subsequent one (β =-0.27 ± 0.12, P = 0.017, n = 15), whereas vector abundance at T1 strongly and positively affected pathogen incidence at T2 (β =0.51 ± 0.11, P < 0.001, n = 7) (Supplementary Fig. 3a, b). Lastly, LMMs revealed how pathogen incidence, vector abundance, or biological control agent abundance at one time point strongly and positively explained their respective values at a subsequent time-step (β = 0.81 ± 0.08, P < 0.001, n = 21; β = 0.51 ± 0.05, P < 0.001, n = 88; β = 0.63 ± 0.05, P < 0.001, n = 39, respectively; Fig. 4).

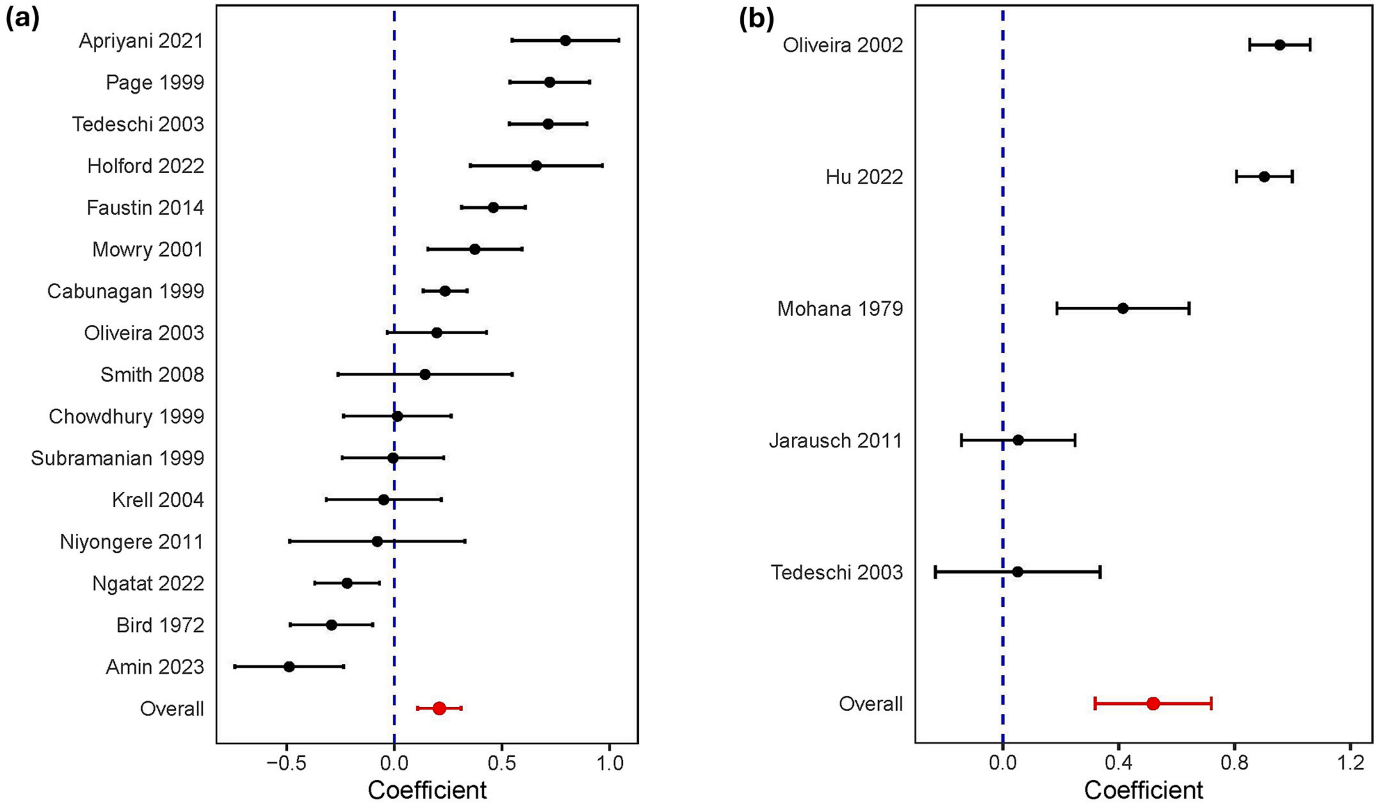

Fig. 1. Effect sizes for the relationship between *in-planta* pathogen incidence and vector abundance (a) or vector infectivity (b). Patterns are drawn from a meta-analysis of 'snapshot' surveys for 26 pathosystems (references in Supplementary Table 3). Effect sizes are indicated per study and overall. Error bars refer to standard error.

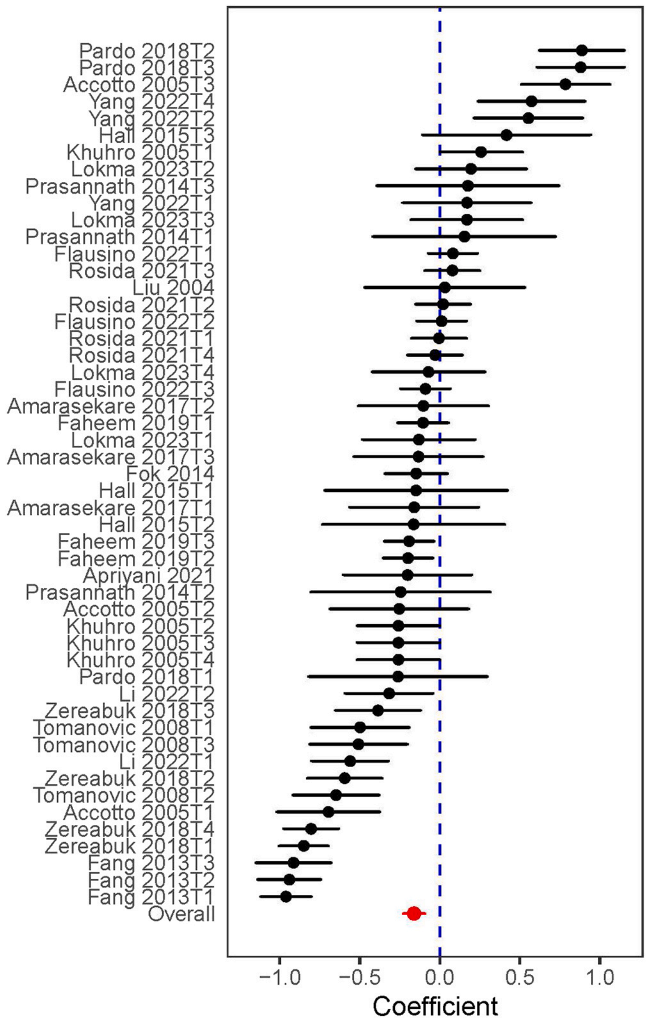

Fig. 2. Effect sizes for the relationship between natural enemy abundance and vector abundance. Patterns are drawn from a meta-analysis of 18 'snapshot' and 'time-lagged' surveys. For time-lagged surveys, data reported under a given time-step i.e., T1–5 are treated separately. Effect sizes are shown per study (references in Supplementary Table 3) and overall. Error bars refer to standard error.

4. Discussion

So far, the role of biological control in mitigating vector-borne plant pathogens has chiefly been examined in studies performed under simplified contexts (e.g., Lee et al., 2023). We addressed this knowledge gap by analyzing field-level observations on vector-pathogen-biological control agent interplay for 58 semi-persistent or persistent pathogens. Our work unveiled how disease incidence is tied to vector infectivity and vector abundance, which in turn, is negatively affected by biological control agent density. Time-lagged patterns also showed how biological control agent populations at initial time-steps reduce the subsequent vector population build-up. However, our study reveals that field-level data on some epidemiological variables are sparse. Bipartite interactions were only assessed under real-world conditions for 29–45 % of pathosystems – with 35 % represented by a single study. Lastly, most studies neglected parameters like vector mobility or plant occupancy and included at most one individual species of natural enemy. Despite these limitations, our work provides support for inclusion of biological control as an integral component of disease mitigation programs.

When examining disease through a community lens, the epidemiological equation contains variables indicative of at least four organisms: plant, vector, pathogen, and biological control agent (Finke, 2012; Crowder et al., 2019). Among those, transmission efficiency has often been posited as a core determinant of disease spread (Crowder et al., 2019). Yet, its assessment in the field is not straightforward and rarely performed. Our work shows how, for persistently and semi-persistently transmitted pathogens, vector abundance or infectivity may be valid proxies for disease risk. This contrasts with studies of more limited scope in which diseases proliferate despite declines in vector abundance, which led scientists to put forward alternative measures such as host plant occupancy or movement as better predictors of disease risk (Lee et al., 2023). Yet, consumptive and non-consumptive effects in laboratory microcosms often differ markedly from the field (McKemey et al., 2003; Hatano et al., 2010). Thus, a sole consideration of these dynamics under simplified contexts deprived of a community perspective may make them prone to yield artifactual results (Polis, 1991). Meanwhile, our findings align with studies suggesting biological control agents exert the strongest impacts on pathogens by suppressing vectors (Clark et al., 2019) and that vector abundance may mirror disease spread (Kersch-Becker and Thaler, 2015; Claflin et al., 2017). These observations have also been made independently in various pathosystems including cassava geminiviruses (Fauquet and Fargette, 1990), grapevine leafroll disease (Cooper et al., 2018), maize stunt disease (de Oliveira et al., 2023) or *Xylella fastidiosa* (Mizell et al., 2017). Whereas vector abundance provides the demographic end-point of biological control agents' effects, field work must ascertain the extent to which vector abundance captures biological control agent-mediated impacts on disease spread.

Time-lagged patterns revealed how initial biological control agent or vector abundance mediated subsequent rates of vector population or disease development. Though immediate biological control agent impacts on disease spread cannot often be ascertained due to data shortages, our findings hint at a key role of biological control. Our findings correspond with analyses showing that biological control agents reduce pest densities by 73–130 % - as compared to control groups - and increase mortality by 159 % across crops and agroecological contexts (Stiling and Cornelissen, 2005; Boldorini et al., 2024). They also align with observations that early-season natural enemies slow disease build-up in the field (Landis and Van der Werf, 1997). Equally, risk cues associated with foraging biological control agents can impede vector settling and delay transmission (Lee et al., 2021; Fereres and Moreno, 2009). In turn, vector population growth may offer an effective lens to assess consumptive and non-consumptive effects of biological control agents (Kersch-Becker and Thaler, 2015) and the often-elusive interaction modifications that accrue over time (Clark and Crowder, 2021). Hence, though direct evidence cannot be brought to bear due to data shortages, abundant biological control agent communities are prone to slow vector population build-up, which in turn appears to exert a dampening effect on disease progression.

As scientists increasingly attempt to incorporate complexity into experiments, few studies have considered more than one species of natural enemy and rarely treat them in combination (Northfield et al., 2012; Long and Finke, 2015; Dupont et al., 2020). The same abstraction is evident in our analyses, as many studies only reported a single biological control agent. Further, nearly all field censuses report BCAs from the same agroecosystem stratum and trophic guild. Ample attention is paid to large-bodied diurnal predators such as coccinellids (8.6–31.1 % of studies in snapshot or time-lagged surveys, respectively) or parasitoids (3.7–26.2 %), while entomopathogens (1.6–2.5 %) are largely overlooked. Yet, different biological control agent taxa or guilds vary in the type and magnitude of their consumptive and non-consumptive effects (Long and Finke, 2015; Northfield et al., 2012; Ong et al., 2018). For instance, leafhoppers cease phloem feeding in the vicinity of active hunters but not in the presence of ambush predators (Tholt et al., 2018). Further, due to complementary resource use or habitat partitioning, the impact of multiple biological control agents regularly surpasses the sum of each species alone (Northfield et al., 2012; Dainese et al., 2017). Yet, when only single biological control agents are considered, these

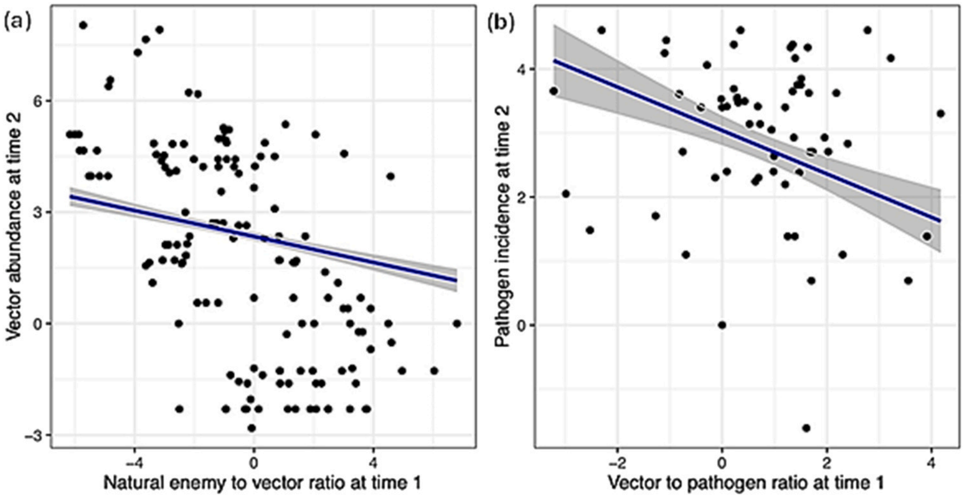

Fig. 3. Early-season biological control agent or vector (relative) abundance explains respective vector abundance (a) or pathogen incidence (b) at subsequent times. Ratios shown are the biological control agent to vector abundance or vector abundance over pathogen incidence. Patterns are shown for 17 pathosystems for which time-lagged field data were available. Lines and shades show regressions and 95 % CI from linear mixed models (number of studies = 41 and 16 for a, b, respectively). All data are log transformed.

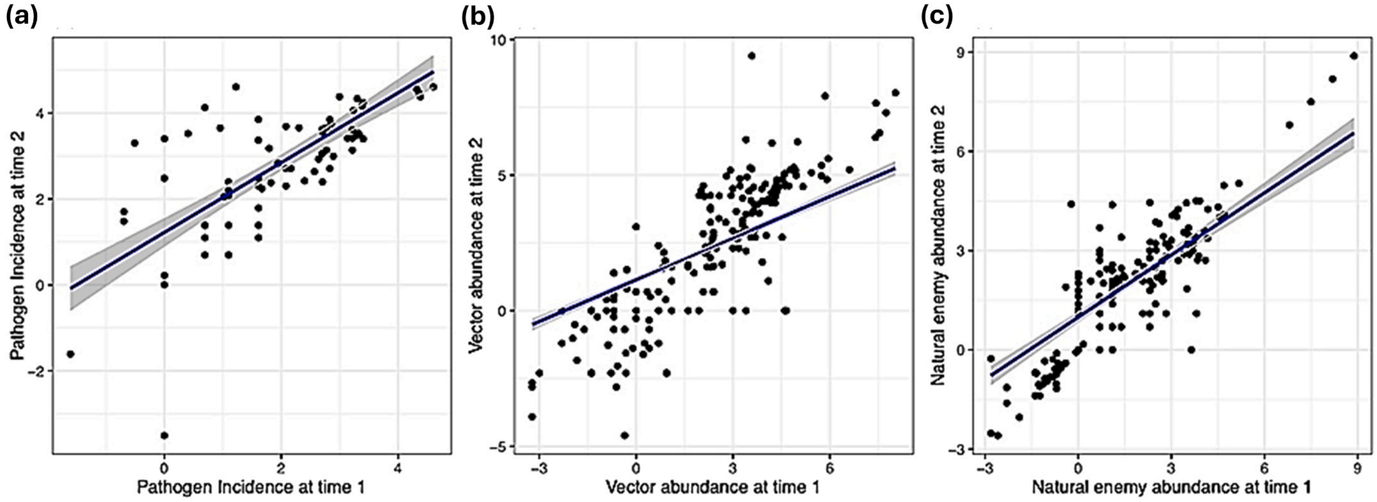

Fig. 4. Pathogen incidence (a), vector abundance (b), or abundance of biological control agents (c) at one time step are positively related to their respective values at a subsequent time. Patterns are plotted for 17 pathosystems for which time-lagged field data were available. Lines and shades show regressions and 95 % CI from linear mixed models (number of studies = 21, 88, 39 for a, b, and c, respectively). All data are log transformed.

phenomena remain invisible and the effects of biological control communities with many species are impossible to detect.

Two aspects of our study deserve added emphasis. First, our analyses did not consider non-persistently transmitted pathogens, which are numerous and linked to debilitating diseases such as potato virus Y (PVY) or cucumber mosaic virus (CMV). Their transmission occurs very fast i.e., within seconds by transient vector species that land and probe briefly on a plant, but generally do not colonize the crop (Fereres et al., 2017). These (aphid) vectors tend to be highly responsive to predator or parasitoid presence and risk cues, exhibiting dropping behavior and/or increased reproduction to varying extent and in an adaptable, species- or context-dependent manner (Nelson and Rosenheim, 2006; Humphreys et al., 2021). Their propensity to move between plants combined with rapid pathogen transmission limits the mitigation potential of biological control (Roudine et al., 2023). As such, our findings likely cannot be extrapolated to this group of pathogens. Second, while there is an overall negative relationship between natural enemy numbers and vector abundance, many studies have non-significant or even positive effects. This is not unexpected, as our study treated all biological control agents with available field data equivalently. This regardless of guild, life history or foraging strategy, dietary breadth and feeding preferences, attack mode and rates, or them being subject to 'donor control' (Hawkins, 1992). Yet, more often than not, only a small complement of species within a diverse natural enemy community are responsible for effective biological control (Hawkins et al., 1999; Wyckhuys et al., 2024a). Meanwhile, sustaining a diverse set of agents with varying response modes and roles is crucial to uphold functional integrity and service supply (Dainese et al., 2017, 2019), and such also applies to the regulation of insect vector populations (Losey and Denno, 1998).

To ascertain the contribution of biological control to disease dynamics, there is an urgent need for large-scale and/or replicated field evaluations that simultaneously consider all three-partite interactions (Lee et al., 2023; Roudine et al., 2023). So far, studies of all interaction partners under real-world conditions have been inordinately sparse (Lee et al.,2022; Landis and Van der Werf, 1997; Roudine et al., 2025). Future work should thus be geared towards consolidating a critical body of three- or even four-party (plant, biological control agent, vector, and pathogen) co-occurrence data. Exciting, new research further shows that crop diseases can only be effectively mitigated by accounting for the broader ecological context, including pollinators (Mhlanga et al., 2024) or landscape-level weed diversity (Susi and Laine, 2021). Our analyses demonstrate how simple measures such as predator: vector abundance ratios have considerable explanatory power, and experimental data can also be reconciled with structural equation (or food web) modeling (Clark et al., 2019) and a more effective tapping of so-called 'biological dark data' (Upham et al., 2021). There is also room for next-generation approaches such as high-throughput infectivity or gut content screening of vectors or biological control agents (Furlong, 2015; Trollip et al., 2023). For many pathogens, baseline insights on vector biology and ecology also are needed before accurate inferences can be made on biological control (Eigenbrode et al., 2018). Lastly, disciplinary silos need to be dismantled. To serve society better, plant pathologists, entomologists, biological control scientists and growers have to meaningfully team up and jointly embark upon 'systems science' (Jactel et al., 2020; Wyckhuys et al., 2023).

Biological control features poorly within today's disease management toolbox, and its role is regularly dismissed even where vectors are comparatively inefficient. In particular, a central dogma in plant pathology even posits that resident or released natural enemies are unable to control vector-borne plant pathogens (Way and Heong, 1994). Instead, our work underlines that its mitigation potential may be substantial and can possibly be fortified by bundling it with other compatible measures across scales (Okamoto and Amarasekare, 2012; Wyckhuys et al., 2024b). For example, biological control impacts often even supersede those of plant quality (Asiimwe et al., 2013), while its relative contribution is greatly attenuated by 'full' host plant resistance (Kersch-Becker and Thaler, 2015). Habitat management through the establishment of intercrops, flower strips or hedgerows or a progressive phasedown of pesticide use might also enhance biological control agent abundance and diversity, which, in turn defines biological control outcomes (Landis et al., 2000; Perovic et al., 2018; Roudine et al., 2023). These approaches are slowly but surely being integrated in management toolkits for high-profile diseases such as citrus greening (Patt et al., 2020; Irvin et al., 2024; Cortez-Madrigal, 2024). Yet, interdisciplinary science is imperative to gauge the practicality, efficacy, and viability of habitat management in disease mitigation and to ensure their uptake with growers (Roudine et al., 2023; Chaplin-Kramer et al., 2019). More broadly, our findings call for a comprehensive re-assessment of biological control as a viable disease mitigation strategy. Given the societal impacts of plant disease, the need for collaborative science and integrative 'systems' approaches to advance this field of inquiry is more urgent than ever.

CRediT authorship contribution statement

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Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Maged Elkahky reports financial support was provided by European Commission. KAGW is the chief executive officer of Chrysalis Consulting – a firm which provides tailored support to nature-friendly farming and biological control. If there are other authors, they 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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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.agee.2025.109683.

Data availability

I have uploaded all data in a repository & provided a link in the manuscript file.

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