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Environmental influences on long-term disease occurrence in viticulture: a holistic effect size-based analysis of vineyard, technology and soil domains

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ABSTRACT

Viticulture is constantly influenced by various environmental factors that create a complex production context, affecting grapevine conditions, crop yield, and quality. We can classify these environmental factors into three main groups: vineyard, technology, and soil domains. These three domains cover the factors that most significantly determine outcomes in grape production. Production-related factors within coexisting domains could neutralise each other. Therefore, to clarify the potential roles of environmental factors in the long-term occurrence of the main grape pathogens (*Botrytis cinerea*: BC, *Plasmopara viticola*: PV, *Erysiphe necator*: EN), we examined the overall effect linking long-term disease occurrence to relevant environmental variables, assessed pathogen-specific differences, and identified shared environmental features affecting disease dynamics using an effect size-based framework with heterogeneity assessment adapted from meta-analytic approaches. We found that the overall effect size of the complex growing context is low, with substantial heterogeneity and pathogen-specific patterns. Environmental variables had the most complex effects on BC, whereas PV and EN were only partially influenced by the growing environment. Thus, their infection risk varied according to specific, similar features of the environmental factors (i.e., spatiotemporal scales). Specifically, among the pathogens, BC was modified by the vineyard and soil domains, whereas we could not detect a significant impact of these conditions on PV and EN. These results suggested that the infections of these two pathogens were highly dependent on climatic variables. Our study highlighted that different results can be obtained by examining variables within complex systems rather than testing them independently.

1. Introduction

Agricultural systems are complex environments shaped by various factors that directly influence plant conditions, crop yield, and quality [1]. These systems can be objectively characterised by describing them according to the most important factors influencing production, thereby enabling comparison across these complex areas based on these environmental variables. Furthermore, these variables, rather than acting independently, operate simultaneously to produce a combined effect on crop production e.g., Refs. [2,3]. The purpose of production determines environmental complexity, along with crop type, associated plant management and technology used [4,5]. These effects are more pronounced and consistent in perennial plantations than in annual crops, because the same plants remain under the same growing conditions over a long period, with few opportunities to modify the overall growing environment [6,7]. Moreover, certain plantation characteristics are more closely related, sharing similarities, than others, based on their agrotechnical purposes, biological functions, and the level of flexibility in management control.

Viticulture has expanded worldwide, creating a complex production environment with diverse technologies applied [8]. Moreover, in viticulture, environmental and production-related factors have long-term, cumulative effects on plant performance over decades [4,9]. Therefore, understanding and categorising the production-related and environmental factors is essential for optimising grape production and management practices. Considering these aspects, these environmental factors in viticulture can be classified into three main 'domains'. The 'vineyard domain' includes variables related to vineyard characteristics,

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which are mostly determined when the vineyard is established (i.e., low modification level) [10]. The 'technology domain' refers to the specific agricultural technologies applied and production management strategies (i.e., high modification level) [11]. The 'soil domain' encompasses variables associated with soil properties, where some properties are fixed by regional conditions, while others can be gradually improved through management (i.e., moderate modification level) [12]. Together, these domains cover the primary sets of factors that shape and determine the production outcomes in grape production.

Healthy plants can yield the highest agricultural output; thus, producers endeavour to create ideal growing conditions [13,14]. There is strong evidence that certain vineyard properties can influence the health conditions of grapes. For example, inclination influences solar radiation in vineyards, with sloping areas receiving more, which favours the growing and ripening conditions, thus indicating a lower occurrence of *Plasmopara viticola* (Berk. and M.A. Curtis) Berl. and De Toni (PV hereafter), on a long-term basis [15]. The row orientation aligned with the prevailing wind direction could promote the dispersion of airborne spores of *Botrytis cinerea* Pers. (BC hereafter). Additionally, a vineyard surrounded by denser grape plantations increases the infection rates of BC and PV due to enhanced inoculum production from neighbouring plantations [16,17].

The applied technology of grape cultivation relied predominantly on chemical treatments. In addition to these solutions, agrotechnical practices indirectly help growers reduce pathogen pressure. For instance, a higher canopy wall increases the incidence of BC, as the self-shading effect shifts the microclimate [17,18]. Similarly, removing the front leaves from the cluster zone reduces the risk of infection by *Erysiphe necator* Schwein. (EN hereafter) leading grape pathogens [19,20]. Furthermore, appropriate inter-row management in vineyards can indirectly suppress the risk of pathogen infection by enhancing soil biological activity [21] and accelerating the decomposition of infected plant debris, the primary source of fungal inoculum [22,23].

The unique soil properties are crucial in shaping the region-specific characteristics and distinctive quality of a grape product, which is often known as one of the key elements of the 'terroir-concept' [15]. However, soil properties have also direct effects on the general health conditions of vineyards within the same growing region or climatic conditions [24–26]. Additionally, plantations are often located in the same place for an extended period, thereby their soil characteristics can directly affect the overall health of vineyards on a long-term basis, even within the same growing region or under similar climatic conditions [24–26]. For example, soil organic matter and nitrogen sources primarily supply nutrients for grape development, particularly for shoot and leaf biomass and tissue quality, thereby affecting the success of plant pathogen infection [27]. Furthermore, soil pH is one of the key factors modifying the nutrient availability and uptake efficiency. Thus, any deviations from the optimal range (in grapes: pH 6.0-7.0 [28]) can lead to nutrient deficiencies, which reduce plant growth and cause general deterioration in plant health [29]. To prevent overall decline, grape growers commonly use soil liming to adjust soil pH, which indirectly reduces the risk of pathogen infection through improved soil quality [30]. For suitable nutrient uptake, the soil's water-holding capacity is also crucial, which is strongly determined by particle size distribution. Soil with predominantly small mineral particles has a greater water-holding capacity than soil with predominantly larger particles, leading to more frequent plant diseases [25,31].

The interactions and contributions of vineyard, technology, and soil domains to long-term disease occurrence have rarely been comprehensively compared. However, individual interpretations of variables within or between domains in long-term disease occurrence may lead to incorrect conclusions, as these factors form a complex, growing environment that simultaneously influences disease occurrence. An illustrative example of this synergistic effect is soil warming, which depends on solar radiation and soil properties. This relationship is influenced by factors such as row orientation, vineyard inclination, and inter-row management, which contribute to earlier ripening, even in late varieties, exposing berries to a higher BC infection as sugar increases during ripening [15,17,32,33]. Consequently, susceptibility to plant pathogens creates a complex production context that cannot be explained by a single factor; thus, understanding environmental influences requires a comprehensive, transdisciplinary approach.

In grape production, there is an urgent need to understand the role of complex production contexts in the long-term occurrence of grape pathogens, alongside global technological and climatic challenges. Therefore, in this large-scale study, we examined the key factors influencing grape production, classified into three leading environmental domains: vineyard, technology, and soil. Our focus was on understanding how these factors affect the long-term occurrence of main grape pathogens, such as *Botrytis cinerea*, *Plasmopara viticola* and *Erysiphe necator*. Due to the complex and combined nature of the environmental variables throughout the vineyard, technology, soil, and their simultaneous presence, these factors can reinforce and weaken each other simultaneously. So, testing these interactive effects is particularly challenging because it is difficult to separate the effects of each factor on the other. Moreover, the domain concept categorises environmental factors into distinct categories, along with the scientific disciplines and practical approaches in viticulture. This discipline-specific classification approach facilitates a more interpretable transition from human-induced factors to natural conditions. Nevertheless, the domain-specific grouping can be oversimplified and rigid, overlooking other relevant aspects of grape production management. Thus, additional grouping factors (i.e., moderator variables) are necessary to address the overall complexity by considering plant health aspects, management perspectives, and spatiotemporal scales in the relationships between disease occurrence and environmental factors.

Therefore, we aimed to address three main objectives: 1) What is the overall effect on the relationships between long-term disease occurrence and relevant environmental variables? 2) Are there pathogen-specific differences in the overall effect size (ES, hereafter) and associated heterogeneity? 3) What type of environmental factors can affect disease occurrence in response to environmental factors in each grape pathogen? To analyse such complex effects and global patterns while maintaining biological interpretability across diverse data domains, we decided on an effect size-based analytical framework. This approach was chosen over a single global multivariate model to avoid potential overfitting and to ensure the comparability of heterogeneous variables on a standardised scale. This framework incorporates effect size estimation and heterogeneity assessment, drawing on concepts methodologically analogous to meta-analyses of multiple independent studies. Although our study is based on a single compiled dataset, this approach enables reliable, objective comparisons across diverse statistical outputs [34]. These statistical procedures provide an overall ES that describes the combined effect across associations, along with weighted ES values based on their sample sizes. Moreover, the procedure can also quantify the degree of heterogeneity, defined as the variance of the particular ES values [35]. Heterogeneity can arise from various environmental factors and from the way these variables are measured or assessed. Measurement processes and associated errors may be domain-specific, and environmental factors within the same domain often exhibit greater similarity than those across different domains. Accordingly, heterogeneity reflects the consistency of ES patterns within a domain. Overall ES and heterogeneity provide complementary information: ES represents the magnitude of the associations, and the heterogeneity indicates the variability of within-domain features. When individual effects within a domain differ in magnitude or direction, opposing influences may offset each other, yielding a low overall ES despite substantial underlying variability. Conversely, low heterogeneity indicates more consistent effects across variables. Detected heterogeneity may further suggest biologically meaningful mechanisms that structure these patterns, which can be examined using moderator variables in meta-regression.

Based on the joint interpretation of overall ES and heterogeneity, we

predicted six conceptual scenarios with distinct biological implications, as illustrated in Fig. 1. A high overall ES with low heterogeneity indicates that associations represent consistent, strong effects, with variables affecting the pathogen similarly and being significantly influenced by environmental factors (Fig. 1A). When both overall ES and heterogeneity are high, effects vary but remain mainly aligned, producing a systematic impact (Fig. 1B). A low overall ES with low heterogeneity suggests that small individual effects could offset each other over the long term, resulting in a small yet consistent combined effect (Fig. 1C). Conversely, a low overall ES with high heterogeneity indicates effects that vary in both magnitude and direction, so offsetting one another. Some variables may depend on location or variety, while others show inconsistency (Fig. 1D). The absence of a significant overall ES with low heterogeneity may indicate methodological constraints limiting detectability (Fig. 1E). Finally, high heterogeneity without a significant overall ES implies that associations differ greatly, suggesting a lack of a consistent, systematic pattern (Fig. 1F).

2. Materials and methods

2.1. Data collection

To accomplish the analyses, we collected data from each domain using different methods and approaches based on the following general framework. Data about the infection severity and variables regarding the vineyard and technology domains were collected from grape growers using a citizen science research approach via questionnaire, while for the variables related to the soil domain, we queried data from a national database. The following sections provide detailed descriptions.

2.2. Citizen science approach

To explore the effects of a complex growing environment, a citizen science approach was used, following the research design of previous studies [17,36]. The advantage of the widely used methodology is the large amount of data collected from both professional and non-professional volunteers across a broader geographical area, thus making it suitable for revealing general correlations in several topics at a large spatial scale [37,38]. We collected geo-referenced data, including more than 22 grape varieties on the grey mould (*Botrytis cinerea*, BC), downy mildew (*Plasmopara viticola*, PV), and powdery mildew (*Erysiphe necator*, EN) long-term disease severity from Hungary, which is a traditional wine- and grape-producing country in Europe (area: 93, 030 km^2, 9.7 million inhabitants). Data were surveyed using an online, semi-quantitative questionnaire between July 2020 and March 2023 based on [17]. Around 5000 participants were reached via e-mail, on different social media platforms and personally at professional and educational events for grape and wine producers (professional and

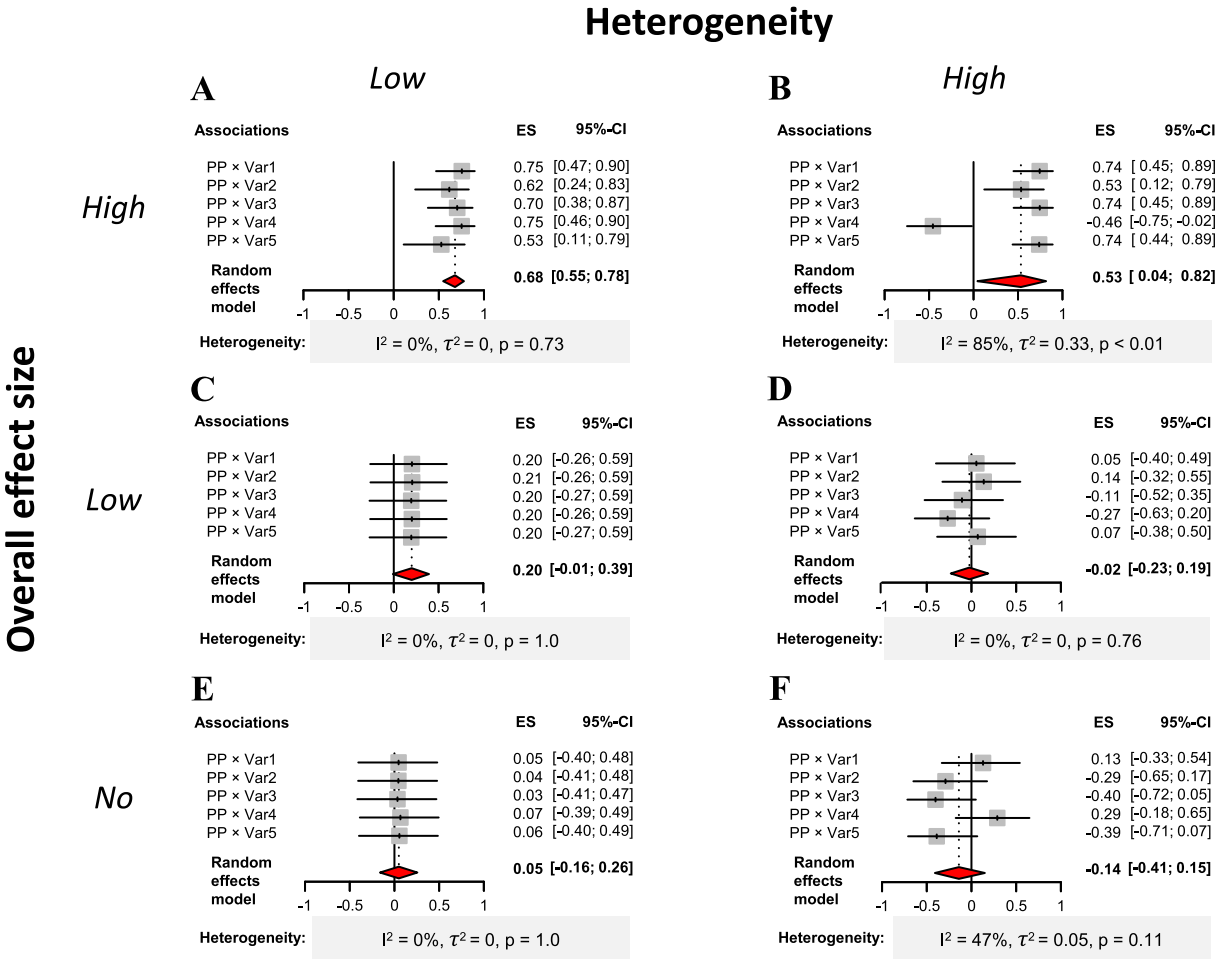

Fig. 1. Mini-forest plots illustrate our predictions about varying overall effect sizes and their heterogeneity, based on simulated data.
A grey square indicates the effect size (ES) of an association between plant pathogen infection (PP) and an environmental variable (e.g., Var1) with the associated confidence interval (CI 95%, horizontal line). The distance from zero reflects the magnitude of the ES, and the ES was considered significant when its CI did not include zero. The red diamond indicates the overall ES value (with CI 95%, diamond length) calculated by the Random effects model. Predictions can be formulated with varying biological implications based on combinations (A-F) of overall ES magnitudes (i.e., High, Low, No) and levels of heterogeneity (i.e., Low, High). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

non-professional) held in Hungary. The questionnaire was completed by 181 volunteers, 112 of whom were qualified in plant protection (61.87 %) and gained independent observations (N = 239 vineyards). Farmers provided data on the average plant health conditions of vineyards based on the preceding five years, average cultivation technology, the most relevant growing environment properties [17] and vineyard position (i.e., geographic coordinates of the vineyard or its nearest location). Consequently, the overall multi-year crop protection effects and trends could be quantified, and the long-term relationships between factors influencing pathogen infestation could be explored. Within the citizen science method, the surveyed variables belonged to three main sections: infection evaluation, vineyard and technology domains. The surveyed variables are briefly described below.

2.3. Infection evaluation

Our study was explicitly designed to investigate long-term infection tendencies rather than year-specific or within-year infection dynamics. Accordingly, long-term infection status was evaluated using two infection variables, both referring to averages over the previous five years. The infection ratio (numeric-discrete) was defined as the ratio of the infected vines within the focal vineyard for BC, PV, and EN separately. Infection ratio values were classified into five ordered categories ranging from absent (or very low) to high infection (0-5 %, 6-20 %, 21-50 %, 51-80 % and 81 % or higher). Infection severity (numeric-discrete) reflected the infection level of the cluster (in BC) or canopy (in PV and EN) of an average vine for each pathogen separately. Similarly, severity values were classified into five ordered classes, ranging from absent (or very low) to high infection (0-20 %, 21-40 %, 41-60 %, 61-80 % and 81 % or higher).

Citizen science surveys, including infection data, spanned several years, and the five-year periods partially overlapped across observations. Year-specific normalisation was applied to harmonise differences in temporal framing and ensure comparability among records. Prior to statistical analyses, a general pathogen-specific infection occurrence index was first constructed by averaging the infection ratio and infection severity values. Then, a min-max normalisation method was applied to these pathogen-specific infection occurrence indices separately for each year. For this procedure, we used the following Eq. (1):

$$x' = \frac{x - x_{\min}}{x_{\max} - x_{\min}} \quad (1)$$

where x represented the general infection occurrence index, and the x_{min} and x_{max} were the yearly minimum and maximum infection values, respectively. Consequently, all infection data were brought to a standard, continuous range between 0 and 1, where 0 means no infection occurrence, and 1 represents a heavy infection event. These pathogen-specific infection occurrence (hereafter infection occurrence) variables were used in further statistical analyses.

2.4. Tested variables

Variables for the vineyard domain, volunteers provided data on the most relevant vineyard properties, such as the grape variety, which was used for expressing the ripening category ('Ripening', numeric-discrete; 0, 1, 2 as early, medium and late, respectively). The plantation age ('Age', numeric-continuous) was calculated by the difference between the vineyard plantation and the survey year. Furthermore, farmers provided information on slope of the plantation ('Inclination', numeric-discrete; 0, 1, 2, as plain: <5 %, gently slope: 5-12 % and sloping: 12 % or higher, respectively) and the row orientation ('Orientation', factor; North-South, NorthEast-SouthWest, East-West and SouthEast-NorthWest, abbreviated as N-S, NE-SW, E-W and SE-NW, respectively, hereafter). The ratio of the surrounding vineyards ('Surrounding vineyards', numeric-discrete) around the focal vineyard within a 1 km radius was also classified into four numeric categories as 0, 1, 2 and 3, labelling none (0-5 %), scattered (6-50 %), many (51-80 %) and high (81 % or higher) classes, respectively.

The growers shared information on the technology applied, which belongs to the technology domain. The number of pesticide applications ('Treatments', numeric-discrete; as no or reduced: <6, moderate or high: 6≤, respectively) described the average number of crop protection treatments applied in a single growing season based on the last five years. The height of the canopy wall described the vertical isolation distance between the ground surface and the canopy leaves at the lowest position, whose values were expressed in centimetres ('Distance', numeric-continuous). The inter-row management ('Inter-row'; numeric-discrete was classified into two categories: no (i.e., bare soil surface) and yes, if the inter-rows were covered by cover plants (e.g., mown grass) or organic materials (e.g., grass clippings, straw, mulches). Removing the leaves from the cluster zone ('Leaf removal', numeric-discrete) was surveyed, whether it is applied (yes) or not (no), during the fruit development period.

Finally, to characterise the corresponding soil conditions, data of the soil domain were provided by the renewed soil spatial data infrastructure: Digital Optimised Soil Related Maps and spatial Information (DOSoReMI.hu; https://dosoremi.hu/en/) for each vineyard position [39,40]. Soil data derivation was supported by land use information [40]. We compiled site-specific soil data as rootable depth ('Rootable depth', numeric-continuous), organic matter content ('Organic matter', numeric-continuous), $CaCO_3$ content ('Lime content', numeric-continuous), pH ('pH', numeric-continuous), clay- ('Clay content', numeric-continuous), silt- ('Silt content', numeric-continuous), and sand ('Sand content', numeric-continuous) content. Estimated soil parameters, such as organic matter content, lime content, pH, and the particle size distribution, were available for different soil layers (0-30 cm, 30-60 cm, 60-100 cm, and 100-200 cm). However, the soil quality can be highly varied among the vertical soil profiles, and the root biomass is also unevenly distributed across the different vertical layers of soil [41,42]. So, we calculated a weighted mean for each soil parameter, considering the weights (0.15, 0.55, 0.25, and 0.05, respectively) based on the biomass proportion of the root system among the soil vertical profile provided by previous studies [41,42]. Moreover, the estimation accuracy of the provided soil properties could vary based on the size of the corresponding vineyard (i.e., data from a smaller vineyard is more accurate). Therefore, we provided data regarding the size of the area for further statistical analyses to incorporate this variable into the models as a statistical correction.

2.5. Statistical analysis

All statistical analyses were run in the R environment (version 4.4.3., R Development CoreTeam 2019).

2.5.1. Calculating effect-size

An ES value describes the direction and magnitude of the corresponding relationship, enabling consistent quantitative comparisons. In the present study, we applied two approaches for calculating ES that describe the focal relationships between infection occurrence and environmental variables. In both approaches, we conducted full pairwise comparisons, where the dependent variable was always the infection and the explanatory variable was one of the environmental variables.

First, we used Spearman's rank correlation, a robust nonparametric test. Second, we applied a more sophisticated approach, using a parametric Generalized Linear Mixed Model. The application of different approaches required getting a more comprehensive picture of the infection patterns driven by environmental factors. However, both statistical methods are suitable for analysing the magnitude and direction of the relationship between two variables, and they are based on different methodological foundations, assuming divergences in the

calculation of ES between the two statistical approaches. Regarding the diversity of tested variables, their data can have different types and resolutions, and an integrated analysis may not be able to deal with them uniformly. An important addition is that a mixed model can account for random and non-independent systematic effects (e.g., repeated sampling, Variety), can handle differences in non-normal distributions, incorporate statistical corrections for different data quality by weighting (e.g., size of vineyard), and allow spatial autocorrelation for spatial non-independence. A possible disadvantage of mixed models is that the application of excessive statistical corrections can obscure existing biological correlations, which is not the case with Spearman's correlations.

In Spearman's rank correlation, the ES were directly converted from the deterministic coefficients (i.e., the rho of Spearman's correlation), identifying the relationships between pathogen-specific infection indexes and the domain variables.

To analyse the relationships between the pathogen-specific infection occurrence index and the environmental factors (regarding the leading domains), we applied a Generalized Linear Mixed Model (GLMM) using Template Model Builder (TMB) ('glmmTMB', hereafter) implemented by the 'glmmTMB' package [17,43]. The glmmTMB models were run using the following general frameworks. The constructed mixed models were run separately for BC, PV and EN, where the response variable was the pathogen severity, while the predictor variable was the single focal domain variable that was tested separately. Models incorporated their domain-specific adjustments, which were applied constantly along variables belonging to the same domain. The random effects were incorporated to account for non-independence in the data. In all models, the dependent variable was log-transformed to improve normality and stabilize the variance, and the explanatory variables were scaled (by the 'scale' function) before running the model to facilitate standard comparison of the calculated ES. The response variable was modelled using a gaussian family distribution ('gaussian'). The model was weighted by the plantation age to give older plants more influence [17]. Model assumptions were assessed through residual diagnostics and goodness-of-fit measures. The glmmTMB models were run using the following model specifications outlined in Table 1.

Calculating the ES of a given relationship from a mixed model structure is challenging due to the random structures. Therefore, we calculated the marginal R^2 (R-squared) value that quantifies the proportion of variance only of the fixed effects (without the random effects) in the corresponding mixed-effects models. The marginal R^2 explains the magnitude of the variance attributed to the fixed effects alone, on a scale between 0 and 1, where higher values reflect a greater proportion of variance. We applied the function of 'r2_nakagawa' from the 'performance' package.

The marginal R^2 values were considered as ES for each focal relationship based on the theoretical framework of Cohen [44]. To preserve the correct direction of the relationship described by marginal R^2, we signed the calculated marginal R^2 values according to the sign of the t-values of the corresponding focal variable (signed marginal R^2, hereafter).

We run paired t-tests to compare possible differences in the extraction method of ES values obtained from Spearman correlation and GLMM for each pathogen.

2.5.2. Moderator variables

The domain concept organises environmental factors into three classes based on viticulture disciplines. The vineyard group is a collective category that describes the biological and environmental context of the vineyard. The technology group includes production-related variables that refer to cultivation and management interventions in the vineyard. The soil group encompasses variables that describe the physical, chemical, and biological properties of the soil, which are largely determined by natural conditions. Due to the artificial nature of the domain classification, we created four additional moderator variables, including 'Temporal dynamics', 'Spatial scale', 'Plant health', and 'Pathogen appearance', which consider other relevant aspects. A comprehensive summary of environmental variables and their corresponding scores for each moderator variable is presented in Table 2.

The 'Temporal dynamics' refer to the temporal stability of an environmental factor in a vineyard, and the extent to which it can be flexibly changed through direct farming interventions. These levels were scored on a scale of 0 to 3. Stable (0): Factors that remain constant and fixed during the cultivation period, showing no temporal variation. These factors determine the cultivation process and cannot be altered at the farmer level. Limited flexibility (1): Change can be expressed on a decadal scale. Factors associated with plantation establishment, the extent of which is not entirely constant. The potential for change exists, but it requires strong intervention to achieve modest improvements. Moderate flexibility (2): Change is detectable over the years, influenced by growers' decisions or occurring steadily due to natural processes. Fully flexible (3): Change occurs quickly and flexibly within a year during the growing season, often linked to direct operational management decisions.

The 'Spatial scale' indicates the geospatial level at which an environmental factor is present and how its effects can be observed in the vineyard. Vine (0): This level is related to individual plants or small

Table 1
General descriptive table of the glmmTMB model structures for the vineyard, technology, and soil domain variables to analyse the relationships between the infection and specific domain variables.[1] In the model, only one variable was selected from this column at a time in each domain. In each domain, we provided all combinations of dependent and explanatory variables.[2] The random factors were included in the models to account for potential systematic variation among observations from individual Producer s (i.e., 'Producer ') and grape varieties ('Variety'), identifying data points sourced from the exact same location or grower and grape variety, respectively. Thus, we were able to address repeated observations from the same location in the statistical analyses due to their statistical non-independence.[3] Vineyard age: If the vineyard was 5 years old or older, the weight was set to 1. For vineyards younger than 5 years, the weight was calculated by dividing the plant's age by 5 [17]. Vineyard size: The soil properties of smaller vineyards are estimated with greater accuracy than those of larger ones. This calculation method normalizes the weight data by setting the minimum value (80 ha) to 1 and progressively down-weighting larger values using the ratio of the logarithm of the minimum area size and the logarithm of the area size.

Domain	Dependent Variables[1]	Explanatory Variables[1]	Mixed model approach (glmmTMB)			
			Type	Random factor[2]	Weights[3]	Spatial correction
Vineyard	BC PV EN	Inclination, Orientation, Surrounding vineyards, Plant age, Ripening	glmmTMB	Producer + Variety	Vineyard age	no
Technology	BC PV EN	Treatments, Distance, Inter-row, Leaf removal	glmmTMB	Producer + Variety	Vineyard age	no
Soil	BC PV EN	Rootable depth, Organic matter, Lime content, pH, Clay content, Silt content, Sand content	glmmTMB	Locality	Vineyard size	yes (Locality)

Table 2
Comprehensive table of the environmental factors for each moderator variable. See text for the detailed description of each moderator variable and its factor levels. Numbers in parentheses indicate the scores used for performing meta-regressions.

Environmental factors	Moderator variables				
	Domain	Temporal dynamics	Spatial scale	Plant health	Pathogen appearance
Inclination	Vineyard	Stable (0)	Landscape (2)	No or weak indirect (0)	Strong (2)
Orientation	Vineyard	Limited flexibility (1)	Plantation (1)	Moderate direct (2)	Strong (2)
Surrounding vineyards	Vineyard	Stable (0)	Landscape (2)	No or weak indirect (0)	Critical (3)
Age	Vineyard	Moderate flexibility (2)	Vine (0)	Conditionally indirect (1)	Moderate (1)
Ripening	Vineyard	Limited flexibility (1)	Vine (0)	Moderate direct (2)	Critical (3)
Treatments	Technology	Fully flexible (3)	Plantation (1)	Strong direct (3)	Critical (3)
Distance	Technology	Limited flexibility (1)	Plantation (1)	Moderate direct (2)	Strong (2)
Inter-row	Technology	Moderate flexibility (2)	Plantation (1)	Conditionally indirect (1)	Strong (2)
Leaf removal	Technology	Fully flexible (3)	Vine (0)	Strong direct (3)	Critical (3)
Rootable depth	Soil	Stable (0)	Plantation (1)	No or weak indirect (0)	No or mild
Organic matter	Soil	Limited flexibility (1)	Plantation (1)	Conditionally indirect (1)	Moderate (1)
Lime content	Soil	Stable (0)	Landscape (2)	Conditionally indirect (1)	No or mild
pH	Soil	Limited flexibility (1)	Plantation (1)	Conditionally indirect (1)	Moderate (1)
Clay content	Soil	Stable (0)	Landscape (2)	No or weak indirect (0)	Strong (2)
Silt content	Soil	Stable (0)	Landscape (2)	No or weak indirect (0)	Moderate (1)
Sand content	Soil	Stable (0)	Landscape (2)	No or weak indirect (0)	No or mild

groups of plants. Plantation (1): This level reflects the properties or other differences within a plantation (i.e., blocks or parts of the plantation). Landscape (2): This factor level determines the entire area or region, which includes several plantations.

The 'Plant health' reveals the production-related factors that directly and immediately impact the overall health condition of the vine. No or weak indirect (0): There is no direct effect, or the effect is weak and only indirect, influenced by multiple factors. Conditionally indirect (1): The effect is mostly indirect but can become significant under extreme environmental conditions or threshold situations. Moderate direct (2): It has a direct and moderate effect on the health of the plant occurring within the season. Strong direct (3): It has an immediate, direct effect on the plant condition or on the pressure of plant pathogens.

The 'Pathogen appearance' indicates how much an environmental factor contributes to the potential for infection and the spread of pathogens in viticulture. No or mild (0): The related environmental factors cannot directly influence the appearance of pathogens. Their effects are only indirect, long-term, or highly influenced by other factors. Moderate (1): This level includes factors which may contribute to the risk of infection but are less important on their own. Their effects are indirect and moderately influence the living conditions of pathogens. Strong (2): This level incorporates factors which effectively modify the living conditions of pathogens or the circumstances of infection. While their effects are more direct and significant, they are not sufficient on their own, so they usually contribute to the emergence of pathogens in combination with other factors. Critical (3): The factors at this level play a key role in the emergence of pathogens. Their effect is immediate, direct, and influential, and they are often capable of either causing or preventing an epidemic on their own.

2.5.3. Meta regression and testing heterogeneity

We performed ES-based analyses using '*meta*' [45] and '*metafor*' [46] packages. We applied the '*rma.mv*' function to provide meta-regression models and '*metacor*' function to deliver heterogeneity statistics and visualizations. In all meta-analytic random-effects models, ES estimates were transformed using Fisher's z transformation ('*escalc*' function) before conducting the analyses. During model fitting, we used restricted maximum-likelihood estimator methods ('REML'). For each research objective, we utilized the same model structure and database subsets for both types of ES estimates, which were calculated by Spearman's rank correlation or glmmTMB, and these models were tested separately during the statistical analyses.

First, to calculate the average ES across the ES estimates and quantify the total heterogeneity (Obj. 1), we fitted a meta-analytic random-effects model, including all pathogens ($k = 48$) without entering any moderator variables.

Second, to identify the pathogen-specific differences in the overall effect and assess the level of heterogeneity (Obj. 2), we made slight modifications to the initial model. We created a pathogen-specific subset of the ES estimates and ran separate analyses for each pathogen species ($k = 16$ for each species).

Third, to investigate how different moderators influence the relationships between disease occurrence and environmental factors (Obj. 3), we fitted multivariate meta-analytic random-effects models, each including a single moderator variable. We tested each moderator individually, applying separate analyses for each pathogen species ($k = 16$ for each species).

This study interpreted the magnitude of the overall ES and heterogeneity values based on the following benchmarks. The ESs, calculated by both Spearman's rank correlation or glmmTMB approaches, for a given environmental factor, such as $r < 0.05$, 0.05-0.1, 0.1-0.2, 0.2-0.3, 0.3-0.4, >0.4, were considered 'Negligible', 'Very small', 'Small', 'Medium', 'Large', and 'Very large' effect categories, respectively [44,47]. The degree of heterogeneity was described by Cochran's Q, I^2, τ^2 and τ. An I^2-value reflects the proportion of total variation due to heterogeneity attributed, which can be estimated within a range between 0 and 100, using the traditional benchmarks for interpretation as follows: 25%, 50%, and 75% values referred to as low, moderate and high heterogeneity, respectively [48]. We also tested the statistical difference of the heterogeneity from being zero. To calculate the amount of true heterogeneity, we calculated τ^2 and τ (the square root of τ^2), which indicate the variance of the ES parameters across the correlation structures tested and describe the variance of the true ES [34].

3. Results

3.1. Overall effect of environmental variables on long-term disease occurrence

The overall ES of all pathogens was found to be negligible, similarly in both ES calculation approaches (Table 3). However, ES estimates calculated by Spearman's rank correlation revealed significant effects, while the GLMM approach was slightly below the detection threshold. The heterogeneity estimates associated with both calculation methods showed consistently moderate levels.

3.2. Pathogen-specific differences in effect sizes and heterogeneity

To identify the role of each pathogen species in the variations of the overall effect, we assessed the pathogen-specific overall ES separately

Table 3
The overall and pathogen-specific effects on the relationship between long-term disease occurrence and production-related environmental factors in vineyards. The table presents a summary of the fitted meta-regressions to estimate the overall effects for both overall and pathogen-specific null models. The statistical tests were run separately for each model. Abbreviations: ES calculation refers to the method of the calculation of ES estimates, parameter estimates (β) with their standard errors (SE), z-values, 95% confidence intervals (CI) and p-values. Significant results are highlighted in bold. The asterisks indicate the level of significance of the given predictor (*p < 0.05, **p < 0.01, ***p < 0.001). Each model is based on 16 ES values.

ES calculation	Predictor	β	CI (lower, upper)	SE	z-value	p-value
ALL pathogen						
Spearman	**Intercept**	**0.029**	**0.010, 0.047**	**0.009**	**3.030**	**0.002** **
GLMM	Intercept	0.013	−0.006, 0.031	0.009	1.355	0.175
Botrytis cinerea						
Spearman	Intercept	0.022	−0.01, 0.054	0.016	1.345	0.179
GLMM	Intercept	0.006	−0.026, 0.038	0.016	0.366	0.715
Plasmopara viticola						
Spearman	**Intercept**	**0.038**	**0.006, 0.07**	**0.016**	**2.327**	**0.020** *
GLMM	Intercept	0.019	−0.013, 0.051	0.016	1.172	0.241
Erysiphe necator						
Spearman	Intercept	0.026	−0.006, 0.058	0.016	1.575	0.115
GLMM	Intercept	0.013	−0.019, 0.045	0.016	0.809	0.419

for each species (Table 4). The pathogen-specific overall ES values were negligible and positive, but only PV (Spearman) showed a significant difference from zero. The associated heterogeneity estimates varied considerably across pathogens, ranging from low to high levels, indicating high pathogen-specific variances. The BC exhibited the highest heterogeneity, the PV showed a moderate level, but only in the case of the Spearman calculation. Furthermore, the heterogeneity of EN was negligibly low.

Regardless of the type, the ES calculation procedure yielded highly consistent results across the model statistics for the meta-regressions and their associated heterogeneity tests. However, the Spearman approach provided slightly larger ES estimates and indicated stronger effects than the GLMM approach; we found no statistically significant differences between the ES calculation procedures for either focal pathogen (BC: $t(15) = 1.03$, $p = 0.317$, mean diff. with $CI_{95.} = 0.016$ [−0.017, 0.049]; PV: $t(15) = 1.29$, $p = 0.217$, mean diff. with $CI_{95.} = 0.019$ [−0.012, 0.05]; and EN: $t(15) = 1.93$, $p = 0.073$, mean diff. with $CI_{95.} = 0.013$ [−0.001, 0.026]).

3.3. Environmental moderators of disease occurrence across grape pathogens

We found high variations in the effects of moderators across pathogen species.

In BC, we found that all moderator variables significantly or marginally contributed to explaining the observed heterogeneity (Fig. 2, Table 5). However, none of them could completely account for the residual heterogeneity (i.e., QE values, Table 6). Additionally, based on the model estimates and the model fit statistics (i.e., BIC values) of the meta-regressions, it was indicated that pathogen appearance (increase) and domain were the most informative predictors with the strongest impact. The pathogen's appearance or risk of infection increased the ES estimates. Within the domain, the soil-related variables showed a detectably lower association compared to vineyard factors, which increased the ES estimates. Technological factors had similarly marginally lower, yet still positive, effects than vineyard factors. Consequently, we identified significant differences among the domain subgroups in their within-group heterogeneities (Table 7). Soil and vineyard groups exhibited moderate and high levels, respectively, while the technology group reflected a moderate amount, but only in the GLMM type of ES calculation. Furthermore, temporal dynamics showed a modestly significant positive effect on the occurrence of disease through environmental factors. Plant health showed a significant positive effect, suggesting that more direct interventions against plant pathogens or enhancements to plant health conditions could have a greater impact on the relationship between disease and environmental factors. In contrast, spatial scale had limited explanatory power, showing a negative, marginally significant trend that indicated increasing spatial scales reduced the impact on the ES estimates.

In PV, we were unable to detect any significant moderator variables that could explain the variance in the ES estimates (Fig. 3). Accordingly, the associated heterogeneity estimates were insignificant in both the Spearman and GLMM approaches. However, in the Spearman ES calculation, we observed detectable residual heterogeneity in all models that the moderators could not account for (Table 5, Table 6). When testing the within-group heterogeneity of the domain moderator

Table 4
Summary of heterogeneity estimates for overall and pathogen-specific models. The table presents the relevant heterogeneity estimates calculated from the random-effects models without moderator variables, for all pathogens and for each pathogen separately. Abbreviations: ES calculation refers to the method of the calculation of ES estimates, Q: Cochran's Q statistics for assessing heterogeneity, p-value: corresponding p-value, $\tau 2$: estimated amount of total heterogeneity, τ: the square root of the $\tau 2$, I2: degree of heterogeneity expressed in percent, df: corresponding degree of freedom, CI: corresponding confidence intervals. Significant results are highlighted in bold. The asterisks indicate the level of significance of the given predictor (*p < 0.05, **p < 0.01, ***p < 0.001).

ES calculation	Predictor	BIC	Q (df) p-value	τ^2 CI (lower, upper)	τ CI (lower, upper)	I^2 (%) [CI lower, upper]
ALL pathogen						
Spearman	**Intercept**	−50.56	**115.70 (47) <0.001** ***	**0.006 [0.003, 0.012]**	**0.079 [0.055, 0.111]**	**59.4 [44.2, 70.4]**
GLMM	**Intercept**	−67.00	**99.72 (47) <0.001** ***	**0.005 [0.002, 0.010]**	**0.069 [0.045, 0.100]**	**52.9 [34.5, 66.1]**
Botrytis cinerea						
Spearman	**Intercept**	21.96	**73.50 (15) <0.001** ***	**0.017 [0.007, 0.047]**	**0.131 [0.086, 0.217]**	**80 [68.4, 87.4]**
GLMM	**Intercept**	16.41	**68.15 (15) <0.001** ***	**0.015 [0.006, 0.043]**	**0.124 [0.08, 0.207]**	**78.3 [65.3, 86.5]**
Plasmopara viticola						
Spearman	**Intercept**	−23.32	**28.29 (15) 0.0198** *	**0.004 [0, 0.015]**	**0.062 [0.013, 0.123]**	**47.5 [6.2, 70.6]**
GLMM	Intercept	−37.18	14.58 (15) 0.482	0 [0, 0.006]	0 [0, 0.075]	0 [0, 52.3]
Erysiphe necator						
Spearman	Intercept	−38.22	13.39 (15) 0.5724	0 [0, 0.005]	0 [0, 0.071]	0 [0, 52.3]
GLMM	Intercept	−36.02	15.74 (15) 0.400	0 [0, 0.006]	0.014 [0, 0.08]	4.5 [0, 54.5]

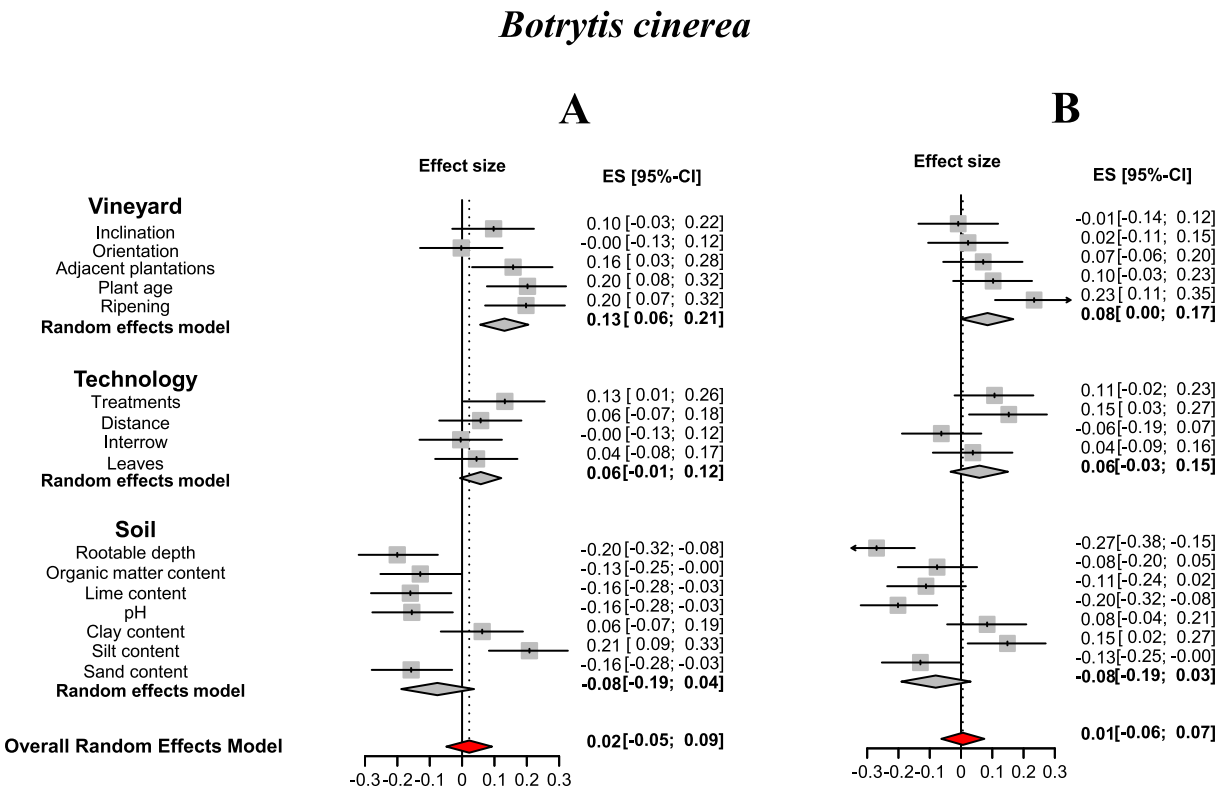

Fig. 2. The overall effects of tested domains in *Botrytis cinerea*
The figure shows the overall effect sizes (ES) of tested domains (vineyard, technology, soil) from Spearman's rank correlation (A) and Generalized Linear Mixed Model (B) on *Botrytis cinerea* (N = 237). A grey square indicates the ES (based on Fisher's z transformation) within moderator variables with the associated confidence intervals (CI 95%, horizontal line). The distance from zero reflects the magnitude of the ES, while the corresponding ES was considered significant when the corresponding CI did not include zero. The grey diamonds represent the ES values for the corresponding domain, while the red diamond indicates the overall ES value calculated by the Random effects model. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

(Table 7), only the soil (in Spearman-type) and the vineyard (in GLMM-type) groups showed high and moderate levels of heterogeneity, respectively.

Regarding EN, we found that spatial scale completely explains the observed heterogeneity by demonstrating a significantly negative impact on the relationships between disease occurrence and environmental factors (Fig. 4). Temporal dynamics could also contribute to understanding this heterogeneity, showing a significant positive impact (i.e., insignificant QE, significant QM values; see Tables 5 and 6). This effect was visible in the Spearman approach; the same trend was only partially detectable using the GLMM approach. We observed a marginally significant positive impact of plant health. Moreover, domain moderators also exhibited a marginally detectable impact on the ES estimates. Only the technology subgroup exhibited moderate within-group heterogeneity in the domain moderator (Table 7).

4. Discussion

4.1. General patterns: overall ES and heterogeneity

In this study, we report a large-scale citizen science project that examined the relationships between complex growing conditions and plant health in vineyards using an ES-based analytical framework. Although the overall effect of environmental factors on pathogen occurrence was generally weak, the actual ES varied significantly among different focal plant pathogens and moderators, with both positive and negative effects repeatedly recorded, which generates considerable heterogeneity.

For all pathogen species, the overall ES values consistently displayed negligible, positive values. However, the associated heterogeneity values obtained very significant species-specific effects, indicating high, moderate, and low heterogeneity levels in BC, PV, and EN, respectively. The degree of heterogeneity in the strength of the relationships between disease occurrence and environmental variables reflects the degree of exposure of the given pathogen to the combined effects of environmental factors. High heterogeneity, as assessed in BC, suggests that environmental variables have the most complex effect on the pathogen's infection processes, making them the most difficult to understand. In contrast, pathogens with medium or low heterogeneity (in PV and EN, respectively) are only partially influenced by the growing environment concerning their infection processes and long-term prevalence, so their infection risk varies depending on one or a few specific factors.

The low overall ES, along with the varied pathogen-specific heterogeneity, may be attributed to specific environmental variables having either small positive or negative impacts on disease occurrence when considered individually. These opposing factors can counterbalance each other's effects over time, leading to a low overall ES. Furthermore, when ES remains low despite increasing heterogeneity, it suggests that potentially more meaningful factors may be acting in opposing directions, reducing or neutralising the overall impact. In such cases, identifying one or more specific moderator variables that account for the variance in the total heterogeneity can help us better understand the pathogen-specific patterns of disease occurrence in relation to environmental factors.

As a final remark on the general patterns, we highlight the critical importance of the ES estimation in meta-analytic studies. To avoid potential bias and ensure consistent results, we applied two different approaches. We found that the procedure for ES calculation yielded highly consistent results across model statistics for the meta-regressions and their associated heterogeneity tests, regardless of the calculation method

Table 5
The effect of moderator variables on the relationship between long-term disease occurrence and production-related environmental factors in vineyards. The table presents a summary of the fitted meta-regressions to test the effect of moderator variables on the relationship between long-term infection occurrence and environmental factors (Predictor). The statistical tests were run separately for moderator variables in each pathogen (*Botrytis cinerea*, *Plasmopara viticola*, *Erysiphe necator*). We report parameter estimates (β) with their standard errors (SE), z-values, 95% confidence intervals (CI) and p-values. Significant results are highlighted in bold, while the marginally significant effects ($0.05 < p \leq 0.1$) are in italics. The asterisks indicate the level of significance of the given predictor (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$). Each model is based on 16 ES values.

Model	Predictor	Spearman					GLMM				
		β	CI (lower, upper)	SE	z-value	p-value	β	CI (lower, upper)	SE	z-value	p-value
Botrytis cinerea											
Domain	**Intercept (Domain: Vineyard)**	**0.132**	**0.074, 0.189**	**0.029**	**4.5**	**<0.001*****	**0.084**	**0.027, 0.141**	**0.029**	**2.882**	**0.004****
	Domain: Technology	−0.074	−0.16, 0.012	0.044	−1.688	0.0915	−0.025	−0.111, 0.06	0.044	−0.577	0.564
	Domain: Soil	**−0.208**	**−0.283, -0.133**	**0.038**	**−5.438**	**<0.001*****	**−0.164**	**−0.238, -0.089**	**0.038**	**−4.296**	**<0.001*****
Temporal dynamics	Intercept	−0.01	−0.053, 0.034	0.022	−0.435	0.6639	−0.025	−0.068, 0.018	0.022	−1.124	0.261
	Temporal dynamics	**0.034**	**0.003, 0.065**	**0.016**	**2.122**	**0.0339***	**0.033**	**0.002, 0.064**	**0.016**	**2.07**	**0.038***
Spatial scale	Intercept	0.065	0.003, 0.126	0.031	2.066	0.0388*	0.054	−0.008, 0.115	0.031	1.716	0.086.
	Spatial scale	*−0.036*	*−0.08, 0.008*	*0.023*	*−1.6*	*0.1097*	*−0.04*	*−0.084, 0.004*	*0.022*	*−1.788*	*0.074.*
Plant health	Intercept	−0.004	−0.05, 0.042	0.023	−0.179	0.8576	−0.044	−0.09, 0.002	0.023	−1.885	0.059.
	Plant health	0.025	−0.006, 0.056	0.016	1.553	0.1204	**0.047**	**0.016, 0.078**	**0.016**	**2.979**	**0.003****
Pathogen appearance	**Intercept**	**−0.123**	**−0.182, -0.064**	**0.03**	**−4.094**	**<0.001*****	**−0.135**	**−0.193, -0.076**	**0.03**	**−4.505**	**<0.001*****
	Pathogen appearance	**0.089**	**0.059, 0.12**	**0.016**	**5.751**	**<0.001*****	**0.086**	**0.056, 0.117**	**0.015**	**5.606**	**<0.001*****
Plasmopara viticola											
Domain	Intercept (Domain: Vineyard)	0.023	−0.034, 0.08	0.029	0.795	0.4267	0.032	−0.025, 0.089	0.029	1.088	0.277
	Domain: Technology	0.061	−0.025, 0.146	0.044	1.386	0.1659	0.016	−0.069, 0.101	0.044	0.366	0.714
	Domain: Soil	−0.001	−0.076, 0.074	0.038	−0.026	0.9793	−0.038	−0.112, 0.037	0.038	−0.995	0.32
Temporal dynamics	Intercept	0.022	−0.021, 0.065	0.022	0.995	0.3197	0.009	−0.034, 0.052	0.022	0.412	0.68
	Temporal dynamics	0.017	−0.014, 0.048	0.016	1.077	0.2815	0.011	−0.02, 0.042	0.016	0.676	0.499
Spatial scale	Intercept	0.074	0.013, 0.135	0.031	2.364	0.0181*	0.047	−0.014, 0.108	0.031	1.496	0.135
	Spatial scale	−0.03	−0.074, 0.014	0.022	−1.349	0.1775	−0.023	−0.067, 0.021	0.022	−1.037	0.3
Plant health	Intercept	0.015	−0.031, 0.061	0.023	0.651	0.5148	0.016	−0.03, 0.062	0.023	0.679	0.497
	Plant health	0.021	−0.01, 0.052	0.016	1.348	0.1777	0.003	−0.028, 0.034	0.016	0.191	0.848
Pathogen appearance	Intercept	0.07	0.011, 0.129	0.03	2.332	0.0197*	0.032	−0.027, 0.09	0.03	1.069	0.285
	Pathogen appearance	−0.02	−0.05, 0.011	0.015	−1.27	0.2039	−0.008	−0.038, 0.022	0.015	−0.514	0.607
Erysiphe necator											
Domain	Intercept (Domain: Vineyard)	0.043	−0.015, 0.1	0.029	1.461	0.144	0.047	−0.01, 0.104	0.029	1.605	0.108
	Domain: Technology	0.029	−0.057, 0.114	0.044	0.654	0.5128	−0.011	−0.096, 0.075	0.044	−0.25	0.802
	Domain: Soil	−0.055	−0.13 0.02	0.038	−1.443	0.1489	−0.07	−0.145 0.004	0.038	−1.848	0.065.
Temporal dynamics	Intercept	−0.005	−0.049, 0.038	0.022	−0.241	0.8095	−0.011	−0.054, 0.032	0.022	−0.479	0.632
	Temporal dynamics	**0.033**	**0.002, 0.064**	**0.016**	**2.087**	**0.0369***	0.025	−0.006, 0.056	0.016	1.601	0.109
Spatial scale	**Intercept**	**0.088**	**0.027, 0.149**	**0.031**	**2.811**	**0.0049****	**0.077**	**0.016, 0.138**	**0.031**	**2.471**	**0.013***
	Spatial scale	**−0.052**	**−0.096, -0.008**	**0.022**	**−2.332**	**0.0197***	**−0.054**	**−0.098, -0.01**	**0.022**	**−2.401**	**0.016***
Plant health	Intercept	−0.006	−0.052, 0.04	0.023	−0.26	0.795	−0.006	−0.051, 0.04	0.023	−0.24	0.81
	Plant health	*0.03*	*−0.001, 0.061*	*0.016*	*1.888*	*0.059.*	0.018	−0.013, 0.049	0.016	1.118	0.263
Pathogen appearance	Intercept	−0.011	−0.069, 0.048	0.03	−0.353	0.7242	−0.014	−0.073, 0.044	0.03	−0.473	0.636
	Pathogen appearance	0.022	−0.008, 0.053	0.015	1.442	0.1494	0.017	−0.013, 0.047	0.015	1.089	0.276

Table 6
Summary of heterogeneity estimates for all models with moderators. The table presents the relevant heterogeneity estimates calculated from the random-effects models with moderator variables provided for each pathogen separately. The statistical tests were run separately for moderator variables in each pathogen. Abbreviations: Spearman and GLMM terms refer to the method of the calculation of effect sizes, BIC: Bayesian Information Criterion, QE: degree of residual heterogeneity, QM: degree of moderator heterogeneity, df: corresponding degree of freedom, p-value: corresponding p-value. Significant results are highlighted in bold, while the marginally significant effects ($0.05 < p \leq 0.1$) are in italics. The asterisks indicate the level of significance of the given predictor (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$). Each model is based on 16 ES values.

Model	Spearman			GLMM		
	BIC	QE (df) p-value	QM (df) p-value	BIC	QE (df) p-value	QM (df) p-value
Botrytis cinerea						
Null	21.96			16.41		
Domain	3.02	**42.34 (13) <0.001** ***	**31.17 (2) <0.001** ***	6.69	**46.17 (13) <0.001** ***	**21.97 (2) <0.001** ***
Temporal dynamics	23.65	**69.00 (14) <0.001** ***	**4.50 (1) 0.034** *	18.33	**63.86 (14) <0.001** ***	**4.29 (1) 0.038** *
Spatial scale	25.59	**70.94 (14) <0.001** ***	2.56 (1) 0.110	19.42	**64.95 (14) <0.001** ***	*3.20 (1) 0.074.*
Plant health	25.74	**71.09 (14) <0.001** ***	2.41 (1) 0.12 0	13.74	**59.27 (14) <0.001** ***	**8.87 (1) 0.003** **
Pathogen appearance	−4.93	**40.42 (14) <0.001** ***	**33.08 (1) <0.001** ***	−8.81	**36.72 (14) 0.001** **	**31.43 (1) <0.001** ***
Plasmopara viticola						
Null	−23.32			−37.18		
Domain	−13.73	**25.64 (13) 0.019** *	2.64 (2) 0.267	−26.96	12.56 (13) 0.483	2.02 (2) 0.364
Temporal dynamics	−18.28	**27.13 (14) 0.019** *	1.16 (1) 0.282	−31.44	14.12 (14) 0.441	0.46 (1) 0.499
Spatial scale	−18.95	**26.47 (14) 0.023** *	1.82 (1) 0.177	−32.06	13.50 (14) 0.487	1.08 (1) 0.3
Plant health	−18.94	**26.47 (14) 0.023** *	1.82 (1) 0.178	−31.02	14.54 (14) 0.410	0.04 (1) 0.848
Pathogen appearance	−18.74	**26.68 (14) 0.021** *	1.61 (1) 0.204	−31.24	14.31 (14) 0.427	0.26 (1) 0.607
Erysiphe necator						
Null	−38.22			−36.02		
Domain	−30.68	8.69 (13) 0.796	*4.70 (2) 0.096.*	−27.83	11.68 (13) 0.554	4.06 (2) 0.131
Temporal dynamics	−36.38	9.03 (14) 0.829	**4.36 (1) 0.037** *	−32.38	13.18 (14) 0.513	2.56 (1) 0.109
Spatial scale	−37.46	7.95 (14) 0.892	**5.44 (1) 0.020** *	−35.58	9.98 (14) 0.764	**5.76 (1) 0.016** *
Plant health	−35.59	9.82 (14) 0.775	*3.56 (1) 0.059.*	−31.07	14.49 (14) 0.414	1.25 (1) 0.263
Pathogen appearance	−34.11	11.31 (14) 0.662	2.08 (1) 0.149	−31	14.55 (14) 0.409	1.19 (1) 0.276

Table 7
Estimates of the subgroup heterogeneity within domain moderator for each pathogen. The table presents the relevant heterogeneity estimates of the subgroups within the domain moderator calculated from the random-effects models provided for each pathogen separately. The statistical tests were run separately for each pathogen. Abbreviations: Spearman and GLMM terms refer to the method of the calculation of ES estimates, k: number of the tests combined in the current statistical analysis, τ^2: estimated amount of total heterogeneity, τ: the square root of the τ^2, Q: Cochran's Q statistics for assessing heterogeneity, I^2: degree of heterogeneity in percent, p-value: significance level of the heterogeneity. Significant results are highlighted in bold, while the marginally significant effects ($0.05 < p \leq 0.1$) are in italics. The asterisks indicate the level of significance of the given predictor (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$).

Pathogen	ES calculation	Domain subgroups	k	τ^2	τ	Q	I^2 (%)	p-value
Botrytis cinerea	Spearman	Vineyard	5	0.003	0.059	7.21	44.5	0.125
		Technology	4	0	0	2.29	0	0.514
		Soil	**7**	**0.020**	**0.141**	**33.86**	**82.3**	**<0.001** ***
	GLMM	*Vineyard*	*5*	*0.005*	*0.070*	*8.52*	*53.0*	*0.074*
		Technology	*4*	*0.005*	*0.068*	*6.25*	*52.0*	*0.100*
		Soil	**7**	**0.019**	**0.136**	**32.14**	**81.3**	**<0.001** ***
Plasmopara viticola	Spearman	Vineyard	5	0	0	0.66	0	0.956
		Technology	4	0	0	2.21	0	0.530
		Soil	**7**	**0.012**	**0.110**	**23.04**	**74.0**	**<0.001** ***
	GLMM	Vineyard	5	0	0	2.74	0	0.602
		Technology	4	0.002	0.043	4.28	29.8	0.233
		Soil	7	0	0	5.44	0	0.489
Erysiphe necator	Spearman	Vineyard	5	0	0	2.53	0	0.640
		Technology	4	0.004	0.059	5.45	44.9	0.141
		Soil	7	0	0	0.89	0	0.989
	GLMM	Vineyard	5	0	0	3.92	0	0.418
		Technology	4	0.004	0.065	5.97	49.8	0.113
		Soil	7	0	0	1.78	0	0.939

used. Despite this, the overall ES values were similar across pathogens, and forest plots showed some variable-specific variation (Figs. 2–4). The ES estimates calculated from Spearman's rank correlation were often larger and indicated stronger effects in the meta-regressions, whereas the corresponding estimates from the GLMM approach yielded moderate effects (e.g., compare Silt content in BC, Fig. 2). However, these were not large enough to affect the overall pattern. A possible explanation for this variance is that a GLMM model is highly adjusted statistically, considering more parameters than the calculation of Spearman's rank correlation. Moreover, the GLMM approach is a parametric test, calculated with the original raw data. Thus, we can account for differences in data distributions, and every tested relationship can be corrected sophisticatedly for different parameters (e.g., as random factors); however, the effects may be enhanced or reduced due to possible overfitting of multiple parameters. In contrast, Spearman's correlation is a nonparametric test that considers two variables simultaneously; thus, the additional sources of variation in the raw data are neglected and remain hidden.

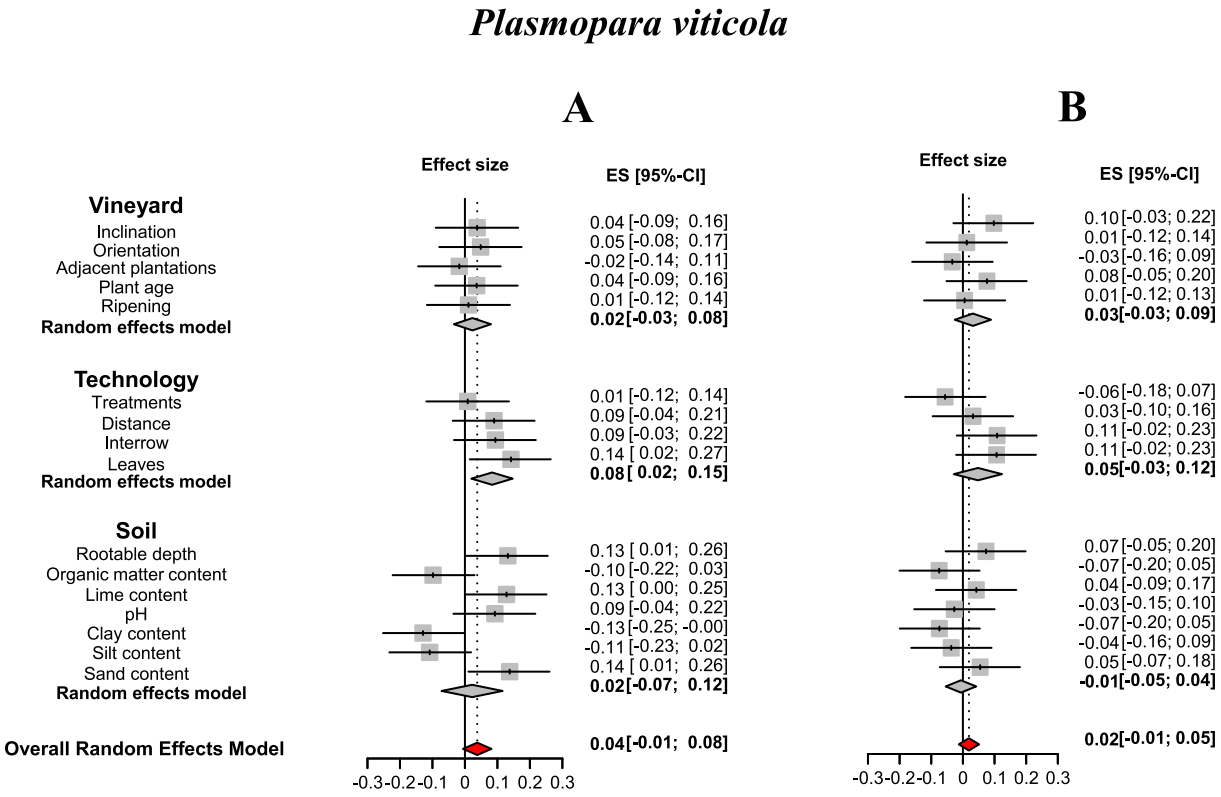

Fig. 3. The overall effects of tested domains in *Plasmopara viticola*
The figure shows the overall effect sizes (ES) of tested domains (vineyard, technology, soil) from Spearman's rank correlation (A) and Generalized Linear Mixed Model (B) *Plasmopara viticola* (N = 238). A grey square indicates the ES (based on Fisher's z transformation) within moderator variables with the associated confidence intervals (CI 95%, horizontal line). The distance from zero reflects the magnitude of the ES, while the corresponding ES was considered significant when the corresponding CI did not include zero. The grey diamonds represent the ES values for the corresponding domain, while the red diamond indicates the overall ES value calculated by the Random effects model. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

4.2. Effects of moderators

By testing moderator variables in meta-analytic analyses, we can gain a deeper understanding of the biological or functional mechanisms underlying heterogeneity in ES estimates [34]. Individual environmental factors have distinct impacts on pathogen pressure, but these effects act jointly [17]. Therefore, the complex influence of the growing environment should be broken down into separate domains or analysed using relevant moderators. Our results revealed high pathogen-specific heterogeneity in the ES estimates, which complexity was explained by moderators that varied significantly in terms of degree and explanatory power. These findings supported our hypothesis that the same or similar regulating factors shift the strength of relationships on disease occurrence in the same direction, thereby shaping the overall impact. However, the domain concept (i.e., grouping production-related factors into discipline categories) offers a suitable approach but cannot fully explain the within-domain heterogeneity patterns. This is because the environmental variables within the domain groups differ in several aspects, such as acting on different spatial or temporal scales (Table 2) and influencing the long-term appearance of pathogens while modifying their effects in a manner characteristic of the specific pathogen species.

We found that BC showed the most complex and heterogeneous picture among the pathogens tested. Both the domain and the other numeric moderators played a significant or partial role in explaining the observed heterogeneity; nevertheless, none fully accounted for the residual heterogeneity, as indicated by the QE values. Our results demonstrated the high relevance of the domain concept, as we identified it as a strong moderator, but the relevance of subgroups showed high variability, producing a counterbalancing effect. Vineyard- and technology-related factors tended to increase the positive impact of environmental factors on BC occurrence, while soil factors contributed to reducing it. These opposing effects explain the low overall ES values. Our findings illustrate how the effects of domain groups neutralise each other's opposing effects, although strong effects are evident when environmental factors are tested individually on disease occurrence. Supplementing the general results regarding the domain, other moderators helped to better understand the heterogeneity associated with BC.

Among the numeric moderators, pathogen appearance was among the strongest, describing a positive gradient along environmental factors that contributed to the potential for infection and the spread of BC in vineyards. This indicates that environmental factors, which have a greater direct and more immediate impact on the living conditions of pathogens or the circumstances of infection, and cause or prevent an epidemic (i.e., ‘strong’, ‘critical’ classes), have a stronger influence on the long-term occurrence in BC, while opposing factors with zero or less direct impacts (‘No or mild’ or ‘Moderate’) tended to reduce the BC occurrence.

According to our findings, pathogen occurrence in BC is primarily influenced by cultivation technology and specific plantation characteristics. Among the factors we examined, several are particularly relevant to pathogen appearance. Fungicide treatments are essential in grape production [49] due to the short incubation period of BC, which allows infection to progress rapidly [50]. These treatments also help prevent infection following unfavourable climatic events [51]. However, resistance to chemical fungicides could compromise the effectiveness of these implementations, regardless of the treatment frequency [52]. Additionally, pathogen appearance can depend on the susceptible phenological stage, which is determined by the timing of ripening based on the variety selection [53–55]. Furthermore, other key factors also contribute, particularly the conidial pressure from surrounding

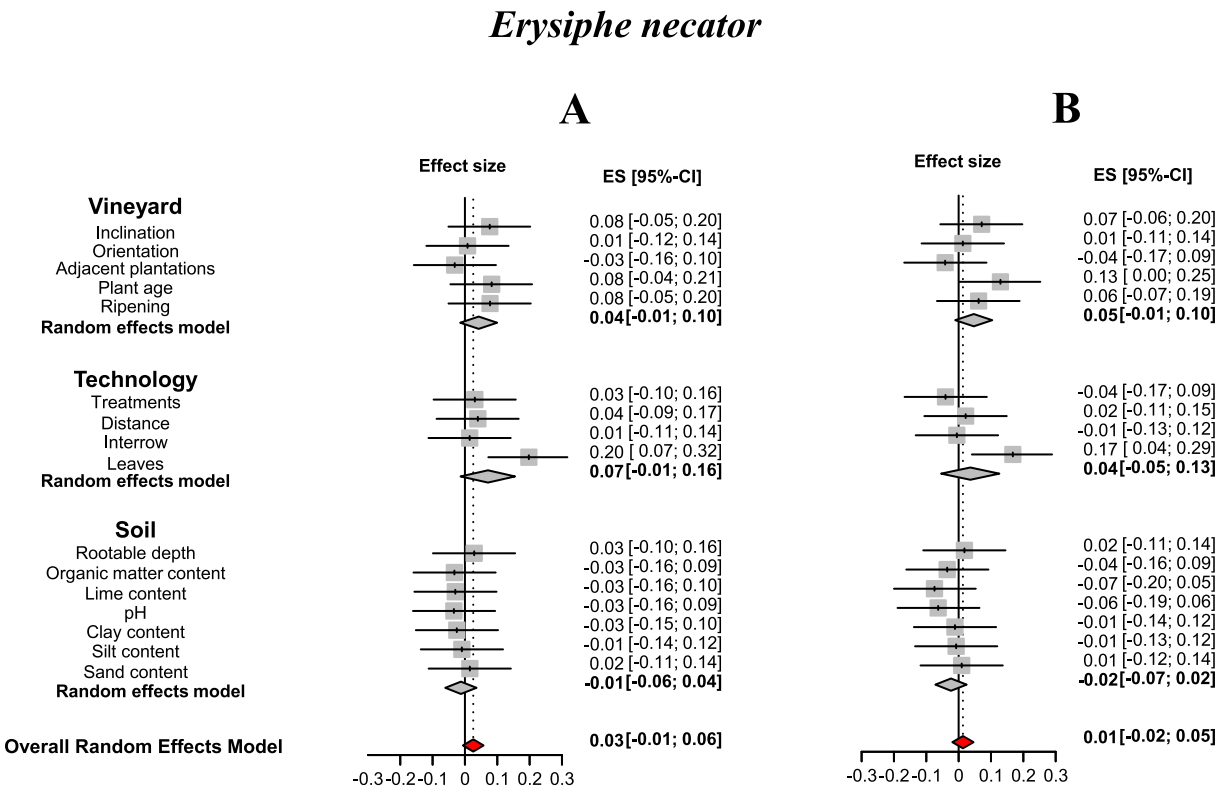

Fig. 4. The overall effects of tested domains in *Erysiphe necator*
The figure shows the overall effect sizes (ES) of tested domains (vineyard, technology, soil) from Spearman's rank correlation (A) and Generalized Linear Mixed Model (B) *Erysiphe necator* (N = 237). A grey square indicates the ES (based on Fisher's z transformation) within moderator variables with the associated confidence intervals (CI 95%, horizontal line). The distance from zero reflects the magnitude of the ES, while the corresponding ES was considered significant when the corresponding CI did not include zero. The grey diamonds represent the ES values for the corresponding domain, while the red diamond indicates the overall ES value calculated by the Random effects model. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

vineyards [56], and climatic conditions affecting the plantation, such as solar exposition and air circulation within the canopy [57]. In contrast, soil properties that promote the removal of excess water, such as sandy soils [31], help reduce pathogen occurrence. Thus, the technologies applied in viticulture directly impact infection potential by reducing conidia prevalence and preventing early infections during susceptible phenological stages, while plantation-related factors indirectly affect the growing environment, shaping infection processes by modifying conditions that are less ideal for the pathogen.

Our study emphasises the crucial role of the temporal dimension in viticulture. Accounting for these temporal dynamics is essential for understanding how disease occurrence associates with environmental factors over longer timescales. We found that temporal dynamics showed a modestly significant positive effect on disease occurrence, shaped by environmental factors, indicating that systematic modifications to the plantation environment can create a cumulative impact over time. These findings underscore the strong need for flexible, responsive management decisions to mitigate damage caused by plant pathogens or other undesirable events [58,59]. Additionally, current plant management can influence the long-term presence and severity of pathogens through decisions that modify specific environmental and technological factors, which have different temporal consequences and can affect outcomes within a single season or over the span of years or decades. For instance, at the establishment of a plantation, vineyard structure and landscape can determine several environmental conditions that can be advantageous or not [15,17,60]. These results also emphasise the importance of timing and the effectiveness of the management decisions over time. Addressing these aspects is crucial for shaping viticulture to adapt to a climate-resilient growing environment, such as mitigating unwanted abiotic stresses and the increasing emergence of pathogens [61].

Traditional grape and wine production relies on regional quality specifications and standards, highlighting its unique characteristics tied to a specific terroir brand [15]. Systematic spatial differences in grape infections may suggest a possible role for large-scale background mechanisms, along with variations related to macroclimatic, topographic, and soil conditions [31,62,63]. In contrast, our large-scale study found that spatial scale had limited explanatory power of spatial scale. Specifically, we revealed a negative, marginally significant trend that indicated increasing spatial scales reduced the impact on ES estimates. This may indicate that larger scales can compensate for local variability, making spatial scale less relevant in predicting disease occurrence at the landscape level.

A healthier plant has a more effective defence system against pathogens than a plant with a deteriorated physiological condition as a consequence of exposure to biotic and abiotic stressors [64]. Therefore, establishing and maintaining an optimal growing environment for grapes is crucial, not only for producing a high-quality product but also for ensuring effective plant protection [13,14]. More direct interventions against plant pathogens or improvements to plant health could have a greater impact on the relationship between disease and environmental factors [19]. Aligning with this, we identified a significant positive effect of the plant health moderator. Moreover, these results are consistent with studies showing that BC is more likely to infect weakened or stressed tissues rather than healthy ones [65,66]. Therefore, management practices aimed at maintaining or enhancing ideal growth conditions, such as balanced soil nutrient compositions and other properties [27,30] and structural factors of the vineyard landscapes [15,17,22,23], can help reduce abiotic stresses to lower the risk of pathogen infections indirectly.

Although most moderators contributed significantly to clarifying the sources of heterogeneity, none could fully explain the total heterogeneity observed. This pattern indicates that complex, multifactorial processes regulate the infection and epidemic spread of BC. These processes are primarily determined by environmental factors related to vineyard properties and soil, and only secondarily by the technological components of grape production. Identifying the combined effect of environmental factors on disease occurrence through the domain variables is especially challenging due to their complex interactions, which vary across temporal and spatial scales. However, future research that utilizes a comprehensive transdisciplinary approach could enhance our understanding of this complexity.

In the case of PV, explaining the role of moderators is challenging because none of them had a detectable effect. Additionally, the heterogeneity of the ES estimates was particularly low and showed a consistent pattern. The only exceptions to this were detected within certain domain subgroups, such as soil and vineyard (in Spearman and GLMM, respectively), suggesting that some technology-related features may affect disease occurrence. Although specific fungicide treatments can control or mitigate the severity of damage [67], rather than other plantation-related factors examined, it is more likely that PV occurrence is better determined by current climatic and microclimatic conditions [68]. Moreover, these environmental factors provide a stable background with only minimal or indirect influence on climatic conditions, which exhibit little to no fluctuation during the season or over the years, thereby, only the current climatic conditions can limit the spread of PV [69]. In this study, climatic factors were not examined and therefore cannot be captured by the moderators examined. However, the tested environmental factors may directly or moderately impact the microclimatic conditions within the plantation. For instance, applying leaf removal in the cluster zone promotes solar exposure and reduces humidity [20,70], while the use of cover plants in the inter-row can increase humidity [71,72]. Additionally, previous studies have demonstrated that species-specific features of PV, such as genetic adaptation, wide tolerance to environmental conditions, and other life-history traits, can promote its widespread occurrence in vineyards [73,74]. Consistently, our results indicate that predicting the long-term PV occurrence is less effective when relying solely on simple environmental or cultivation technology variables. This suggests that future comprehensive studies should incorporate factors that directly affect microclimatic conditions, with an emphasis on flexible, climate-dependent predictors, as static variables contributed little to reducing infections.

The overall heterogeneity of EN was very low. However, this was only fully explained by moderators related to spatial and temporal scales. Concerning spatial scale, factors with extensive spatial representation tend to weaken the identified relationships between disease occurrence and environmental factors. This suggests that processes occurring at the vine level primarily drive the long-term emergence of the pathogen. Conversely, the positive effect of temporal dynamics indicates that more rapidly and flexibly controllable environmental factors had the greatest influence on the emergence of ES estimates through environmental factors. The impact of other axes, described by the domain and plant health moderators, was minimal, but the technology subgroup displayed moderate internal heterogeneity. This aligns with earlier observations that spatiotemporal aspects show the most flexibly controllable factors are mainly linked to grape production technologies, such as defoliation of the cluster zone and fungicide applications. In addition to fungicide treatments, defoliation effectively reduces humidity and enhances UV exposure, creating a less favourable microenvironment for EN infection [20,70]. Therefore, our findings indicate that EN damage is mainly regulated by rapid and flexible technological applications at the vine level, rather than by less affected static or slowly changing soil or plantation characteristics. The results are consistent with the fact that EN infection and epidemic spread mainly originate from inoculum accumulating on the vine and its microenvironment [75], rather than the lesser influence of surrounding plantations. Both EN and PV are mainly affected by climatic conditions, which may similarly shape their infection and spread [68,75]. However, most tested environmental factors had little or no direct impact on microclimate regulation. We observed a less pronounced effect on long-term EN occurrence, indicating that the widespread presence of EN in vineyards is likely to persist, emphasising the importance of regular fungicide management. Future research should focus on environmental variables that significantly influence the microclimate of grapevines and on factors reducing inoculum sources.

Our citizen science study, employing an ES-based analytical approach, highlights that vineyards, as production environments, are shaped by complex interactions among vineyard features, management practices, and soil properties, which collectively determine plant health and the potential risk of pathogen infection. The pathogen's occurrence showed a species-specific variance according to the environmental conditions. Environmental factors play distinct functional roles and impacts; however, similar factors may lead to similar pathogen responses through their impacts on similar functional roles in the pathogen's life cycle. Treating the impact of unique environmental traits separately can be misleading, as grapevine health emerges from the complex interactions of multiple factors within the growing environment. Using moderator variables provided a valuable framework to distinguish these traits and better understand their roles within a broader production context. The present study demonstrated that the responses of the three pathogens to the moderators differed significantly, reflecting their specific ecological requirements and the environmental factors that influence infection. BC was shaped by a complex, multicausal set of factors, with no single moderator fully explaining the variance. In contrast, PV was less predictable based on static environmental factors, indicating a stronger influence of microclimate and current climatic events. In EN, spatial and temporal environmental patterns were evident and could be better incorporated comprehensively into large-scale studies in the future.

These pathogen-specific differences emphasise that grapevine diseases cannot be controlled according to uniform schemes, but management decisions require pathogen-specific strategies that reflect their ecological and environmental embeddedness. Practically, identifying moderators also allows for targeted plant protection interventions and identifying environmental factors that predict damage caused by particular pathogens. For example, in BC, more sophisticated data collection and multivariate models could improve prediction accuracy by accounting for ecological variables and plantation structure. For PV, models that include weather-dependent and microclimatic factors are necessary, while for EN, appropriate spatial monitoring and defoliation decisions require further attention. Ignoring this complexity risks underestimating or overemphasising certain factors, whereas recognising their combined effects allows for more precise and adaptive plant protection.

Beyond these pathogen-specific insights, our study also demonstrates the value of large-scale observation obtained under real growing conditions, which complements controlled experimental approaches. Citizen science is a particularly useful approach when combining the valuable experience of vine growers with scientific methods, offering opportunities for data collection at broad spatial and temporal scales. However, we identified some important methodological trade-offs: balancing data resolution with participant engagement, as response rates decreased with the complexity of the questionnaires; furthermore, self-reported surveys may introduce interobserver variability and potential bias due to varying levels of expertise. To increase the robustness of our study, we implemented several methodological interventions, such as surveying only the clearly identifiable grape pathogens to minimise misidentification, applying standardised categorical scales with visual guidance to mitigate potential interobserver variability, and statistical handling of the varying expertise of contributors in disease recognition by weighting data based on the level of expertise.

Additionally, maximising sample size by involving a large number of volunteers was essential to support data reliability. In addition, the current study's scope did not account for certain relevant biological and environmental factors. Our study focused on three main grapevine pathogens under Hungarian growing conditions; consequently, caution is necessary when extrapolating these findings to other viticultural regions with different climatic regimes. Therefore, future studies should extend this framework to broader spatial scales and explicitly integrate other drivers (e.g., high-resolution meteorological data) to improve the generalizability of long-term infection risk assessments. Combining citizen science observations with independently validated environmental and climatic datasets offers a promising way to enhance model generalizability and applicability in future research, especially as autonomous sensors and AI-supported IT platforms become increasingly available. Overall, our findings emphasise that grapevine diseases exhibit varying ecological and technological embeddedness, underscoring the need for differentiated, adaptive, and pathogen-specific management strategies in viticulture.

5. Conclusion

Vineyards are permanently extended to various environmental factors in the shared biophysical context. These factors encompass vineyard features, soil characteristics and crop management practices, which collectively establish the plant health. The separate interpretation of the impact of the unique characteristics could lead to incorrect conclusions, as the vine health is the result of a dynamic synergism given by the growing context. As an agricultural outcome of the neglected effect of a complex growing environment, the role of some environmental factors could be underestimated, while others could be overemphasised. These results highlighted how different results could be retrieved by examining variables within complex systems instead of testing them independently. Our study revealed that the long-term occurrence of grape primary pathogens originated in the cooperation of various interdisciplinary variable groups, called domains. We detected vineyard and soil domains as the main drivers of long-term disease occurrence, while in a complex analysis, the crop management domain did not have a determining role. Moreover, our large-scale research is based on observation of real growers from real growing conditions, thus *in vivo* testing the concepts of previous research. We are committed to benefit more from the citizen science research approach, which enables combining the valuable experience of vine growers with the methodological knowledge of researchers. This offers an excellent opportunity for further research to complement the knowledge gap on the role of climatic conditions in a complex growing context.

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CRediT authorship contribution statement

Gábor Markó: Conceptualization, Formal analysis, Funding acquisition, Investigation, Methodology, Supervision, Visualization, Writing – original draft, Writing – review & editing. **László Pásztor:** Investigation, Methodology, Writing – review & editing. **Annamária Laborczi:** Investigation, Methodology, Writing – review & editing. **Marietta Petróczy:** Methodology, Visualization, Writing – review & editing. **Ivett Kocsis:** Conceptualization, Investigation, Methodology, Project administration, Writing – original draft, Writing – review & editing.

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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Data availability

Data will be made available on request.

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