

Article

Investigating the Susceptibility of Winter Wheat Varieties to Foliar Diseases Using Data-Driven Models

Oksana Yu. Kremneva ^{1,*} , Ksenia E. Gasiyan ¹ , Olga V. Doroshenko ²  and Mikhail V. Golub ² 

¹ Federal State Budgetary Scientific Institution «Federal Research Center of Biological Plant Protection», Krasnodar 350000, Russia; gasiyankkk@mail.ru

² Institute for Mathematics, Mechanics and Informatics, Kuban State University, Krasnodar 350040, Russia; oldorosh@mail.ru (O.V.D.); m_golub@inbox.ru (M.V.G.)

* Correspondence: kremenoks@mail.ru

Abstract

The objective of this study is to evaluate the potential of airborne spore monitoring for predicting the severity of foliar diseases in winter wheat by developing variety-dependent disease models that account for variety susceptibility and applying a statistical procedure that accommodates the hierarchical structure of panel data. The experiments were conducted in the fields of the FSBSI Federal Research Center of Biological Plant Protection on plots sown with five winter wheat varieties exhibiting varying susceptibility to foliar diseases, while the processing of the data was carried out in 2025–2026. The concentration of spores in the air was estimated using a portable spore trap. Along with air sampling, visual assessments of the development of major fungal pathogens on plants were performed. The hypothesis of variety-specific susceptibility was tested using moderation analysis. The analysis revealed a relationship between leaf disease severity and the number of detected spores, with the strength of correlation varying depending on the pathogen species and variety susceptibility. Using pairwise comparisons of regression slopes for each variety, it was demonstrated that the development of *Blumeria graminis* depends primarily on spore concentration levels and climatic conditions rather than on variety identity. In contrast, for *Puccinia striiformis*, *Puccinia triticina*, and *Pyrenophora tritici-repentis*, variety susceptibility/resistance was shown to exert a statistically significant influence on disease development. These findings will serve as the foundation for a novel phytosanitary monitoring methodology, which is essential for generating forecasts and informing decision-making regarding plant protection measures.

Keywords: prognosis; identification; spores; wheat disease; wheat variety; mixed effect model; *Blumeria graminis*; *Puccinia triticina*; *Puccinia striiformis*; *Pyrenophora tritici-repentis*



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1. Introduction

Stopping crop diseases in their early developmental stages within fields is significantly more feasible than managing established epidemics. However, detecting disease symptoms when their incidence is less than 1% remains a challenging task [1], particularly when relying on classical monitoring methods involving visual evaluation of symptoms and estimation of disease severity and prevalence. To address this challenge, plant protection specialists and agronomists typically employ two primary approaches. The first is a prophylactic strategy in which fungicides are applied according to the stages of phenological growth of the crop [2]. The second is a threshold-based strategy initiated when

disease development reaches the level of economic injury [3]. Specific threshold values are calculated to regulate the application of strategies for each disease in each phenological stage. Although these approaches are effective, they often lead to the irrational use of fungicides. In the prophylactic approach, fungicides may be applied long before infectious particles appear in the air or when their concentration is low. Therefore, the disease may not develop in the field at all under conditions unfavorable to the pathogen. In contrast, under the threshold-based approach, it may already be too late to stop disease progression, or multiple repeated fungicide applications could be required.

Plant disease diagnostics using air samplers have achieved significant advancements [4,5]. Various spore-trapping devices have already demonstrated that they can be effective in monitoring the progress of plant disease [6,7], specifically in wheat [8–10]. Numerous studies have focused on improving the efficiency of sampling technologies and simplifying the processing of obtained data [11–13]. There is a wide variety of designs, structures and installation techniques for spore trap devices as well as methods of analysis of data obtained using air samplers [14,15]. Information on the quantity of pathogen spores in the air during the early growing season can serve as a threshold value for preventative treatment, thereby ensuring crop protection during the initial stages of disease development. Alternatively, such information can be utilized to determine the progression of the disease within the crop at each specific phenological phase.

Wheat is a major global agricultural crop cultivated on approximately 219 million hectares with a production of more than 760 million tons per year [16]. However, it is highly susceptible to airborne foliar disease, most notably powdery mildew, yellow rust, brown rust, and tan spot [17–20]. The critical challenge in phytosanitary monitoring of these diseases is not merely detecting and identifying diseases after symptom manifestation but determining the presence of disease prior to symptom appearance or at the earliest stages of pathogen development. A key criterion for assessing the epidemic potential of disease pathogens is the species and quantitative composition of phytopathogen spores contained in the air space among agricultural crops.

However, accurately predicting disease progression based only on airborne spore levels is complex, as pathogen development in agricultural crops depends largely on both variety resistance and weather conditions. Several studies have demonstrated the influence of climatic conditions on the quantity of fungal spores in the air and the seasonality of their distribution under field conditions [21,22]. Some other works have demonstrated distinct differences in the manifestation and development of phytopathogens on varieties with varying resistance levels [23,24]. This varietal effect occurs since the same amount of inoculum during the early stages of vegetative development could result in varying disease severity under identical weather conditions, depending on the genetic resistance of the variety. In subsequent phenological phases, the infection load may, in turn, depend on how strongly the pathogen has established itself within the specific variety's stand. Therefore, it is essential to investigate the dynamic relationship between airborne spore levels throughout the growing season and disease development to develop a methodology capable of accurately predicting disease progression in the field, explicitly taking into account the characteristics of the wheat variety.

In order to transform raw spore count data into efficient predictive models of wheat leaf disease development, a statistical approach is required that can explicitly integrate biological data with variety-specific responses. Field phytopathological datasets are inherently complex, hierarchical, and are affected by environmental noise. Linear mixed-effects models (LMMs) are increasingly used to analyze such nested, repeated-measure data, allowing for the simultaneous estimation of fixed effects, such as the impact of spore concentration, and random effects, such as variation between years and phenological phases,

without losing statistical power [25–27]. Within this predictive framework, moderation analysis enables researchers to test whether the relationship between spore concentration and disease severity could be changed through dependence on a third variable such as variety [28,29].

Accordingly, the primary objectives of this study are:

1. To assess the impact of airborne phytopathogenic fungal spore concentration on the severity of foliar diseases in winter wheat;
2. To evaluate how varietal susceptibility moderates this relationship.

Our core hypothesis is that the spore–disease relationship is not constant, but is significantly modulated by host genetic resistance, i.e., variety-specific susceptibility. The interpretation of the conditional effects of spores for each variety allows us not only to establish the fact of moderation but also to qualitatively rank varieties according to their degree of susceptibility. Therefore, this study provides a data-driven framework for future decision-support systems in precision crop protection by integrating airborne spore monitoring data with variety-dependent disease modeling.

2. Materials and Methods

2.1. Experimental Data Acquisition

Over three years (2022, 2023 and 2024) experimental studies with five varieties of winter wheat were conducted in the test fields of the Federal State Budgetary Scientific Institution “Federal Scientific Center of Biological Plant Protection” (FSBSI FSCBPP), Krasnodar (45°2.413' N, 38°58.5598' E, 29 m above sea level), see Figure 1.

Weather conditions during the three years of the study varied in a different manner, as in Figure 1, where plots of average humidity, average temperature and precipitation are demonstrated. In 2022, precipitation was higher than the average value, which, being combined with relatively high humidity and low spring temperatures, resulted in favorable conditions for stripe rust. In 2023, although precipitation was lower than in 2022, relative humidity remained above long-term averages throughout the growing season, and spring temperatures exceeded both the previous season and long-term averages. The latter favored diseases such as powdery mildew, tan spot, and, later in the growing season, leaf rust. The warmest and driest conditions of the study period were observed in 2024: precipitation and relative humidity were below the long-term average, providing favorable conditions for rust diseases and tan spot.

Five winter wheat varieties with varying susceptibility to foliar diseases and preliminary investigations performed by various researchers were selected as study objects [23,30]:

1. Grom (susceptible to brown and yellow rusts, resistant to powdery mildew, moderately resistant to tan spot)
2. Svarog (resistant to brown and yellow rusts, moderately resistant to powdery mildew, moderately susceptible to tan spot)
3. Bezostaya 100 (resistant to brown rust and powdery mildew, moderately resistant to yellow rust, susceptible to tan spots)
4. Yuka (susceptible to brown rust, moderately susceptible to yellow rust and tan spot, resistant to powdery mildew)
5. Alekseich (resistant to brown rust, yellow rust, and powdery mildew, susceptible to tan spot)

The area of the experimental plot for each variety was 20 m².

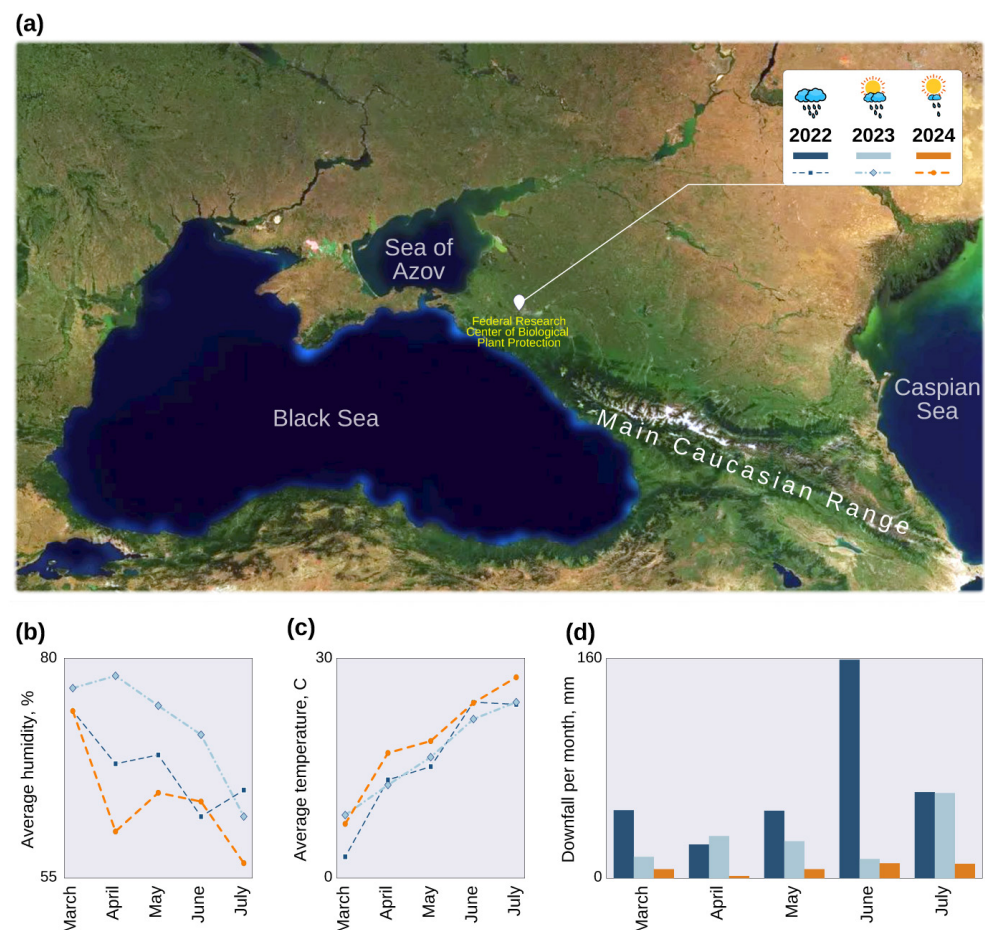


Figure 1. Map with point showing location of the agroecosystem where data were collected (a), average humidity (b), average temperature (c) and rainfall per month (d) for five months from March to July over three years (2022, 2023 and 2024).

To measure the concentration of spores in the air around winter wheat, which are related to foliar disease pathogens, a portable spore trap developed in FSBSI FSCBPP by Kremneva et al. [8] was used to determine the level of contamination of the plants. The device operates as an impactor, containing a microscope slide coated with a retainer compound (petroleum jelly), onto which phytopathogenic fungal spores settle as rectangular impressions with an area of 100 mm²; for more details on the spore trap device see [8]. A photograph of the spore trap device during the experimental test is presented in Figure 2a. Each sampling was performed during a 1 min exposure of the spore trap, which allows spores to be collected from an approximately 1 m² area of the experimental plot in five independent replicates. A photograph of an example of a sample, with nine stripes corresponding to nine different exposures, is shown in Figure 2b. For the identification and quantitative measurement of phytopathogenic fungi, the samples obtained were examined under a light microscope with an objective magnification of 10× [15]. The methodology and technical aspects of the procedure of calculating the number of spores in the spore trap samples are described in detail by [8,15]. It should be also mentioned that molecular confirmation was not performed in this study.

The spore trap device was used along with an evaluation of disease development in the considered varieties of crops using standard phytopathological methods in five replicates. The Peterson scale [31] was used to assess rust diseases, the Saari–Prescott scale [32] was applied to evaluate tan spots, and specialized scales developed by the International Maize and Wheat Improvement Center (CIMMYT) were used for the evaluation of powdery mildew [33]. Wheat growth stages are reported according to the Zadoks scale [34].

Assessments were conducted from the resumption of spring wheat vegetation until the onset of physiological desiccation, when the development of foliar disease could no longer be evaluated.

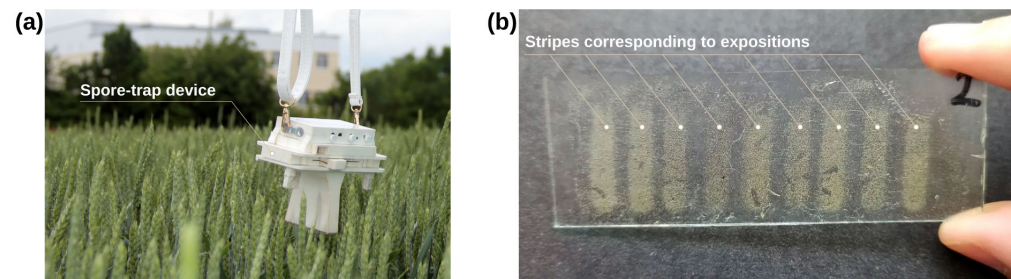


Figure 2. Photograph of spore trap device (a) and a sample used in the spore trap device (b).

Therefore, the number of spores detected in each of the five replicates ($i = \overline{1, 5}$) taken on a certain day within the k -th measurement or phenological phase ($k = \overline{1, 8}$) during the three-year study ($j = \overline{1, 3}$) will be designated as $spore_{ijk}$. The following phases were counted for each of the three years from 2022 to 2024: Z_{30} , Z_{31} , Z_{32} and Z_{37} for the stem elongation principal growth stage, Z_{47} corresponding to flag leaf sheath opening, Z_{51-59} for the inflorescence emergence principal growth stage, Z_{61-69} for the anthesis principal growth stage and Z_{75} corresponding to medium milk. The level of disease development will correspondingly be designated as $disease_{ijk}$.

During the three-year study period, all four target winter wheat foliar diseases were detected. The scatter plot in Figure 3a shows a positive near-linear relationship between the foliar disease severity and the number of spores detected (on a log-scale), however this differs between the pathogens. For example, a small number of spores is enough for foliar disease to begin developing in *P. tritici-repentis*, whereas in *B. graminis*, the number of spores must exceed a certain threshold before the disease begins to develop rapidly. The box plot shown in Figure 3b depicts that *B. graminis* and *P. tritici-repentis* are the most consistently observed pathogens, while *P. striiformis* and *P. triticina* exhibit a large number of outliers. The reason for this is that, in some cases, disease symptoms were not visually observed on wheat leaves, even though the crops were generally infected.

Differences in pathogen spore concentration across plots are determined by the biological characteristics of the pathogens and host variety traits. Variety susceptibility influences not only disease development but also sporulation intensity: the infection process is inhibited on genetically resistant varieties, which reduces the production of urediniospores or conidia even in the presence of primary infection. The sporulation process varies among pathogens; for example, *B. graminis* sporulation occurs continuously under favorable conditions, whereas new conidia generations of *P. tritici-repentis* are formed discretely at intervals of 7–20 days.

2.2. Hierarchy of Data Structure

The collected data describe the spatiotemporal dynamics of the considered observations of winter wheat crops over three growing seasons (2022–2024), which can be reflected in a hierarchical structure, which is illustrated by Figure 4. In the proposed hierarchy, two interrelated levels of temporal and spatial characteristics are assumed, where the temporal one has three sub-levels.

The spatial level of the hierarchy consists of data obtained from individual experimental plots that contain specific wheat varieties with different resistances to foliar diseases. Since these varieties were pre-selected according to their genotypes, the spatial level of the hierarchical structure reflects controlled experimental conditions.

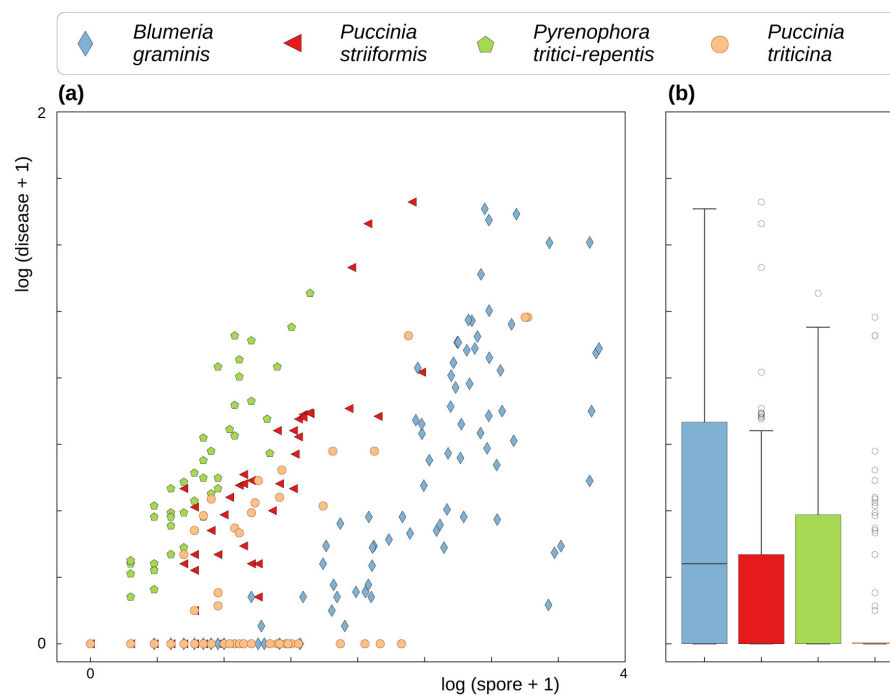


Figure 3. Scatter plot of foliar disease severity $disease_{ijk}$ and number of detected $spore_{ijk}$ (a) and box plots of foliar disease severity $disease_{ijk}$ (b) for four kinds of pathogens considered.

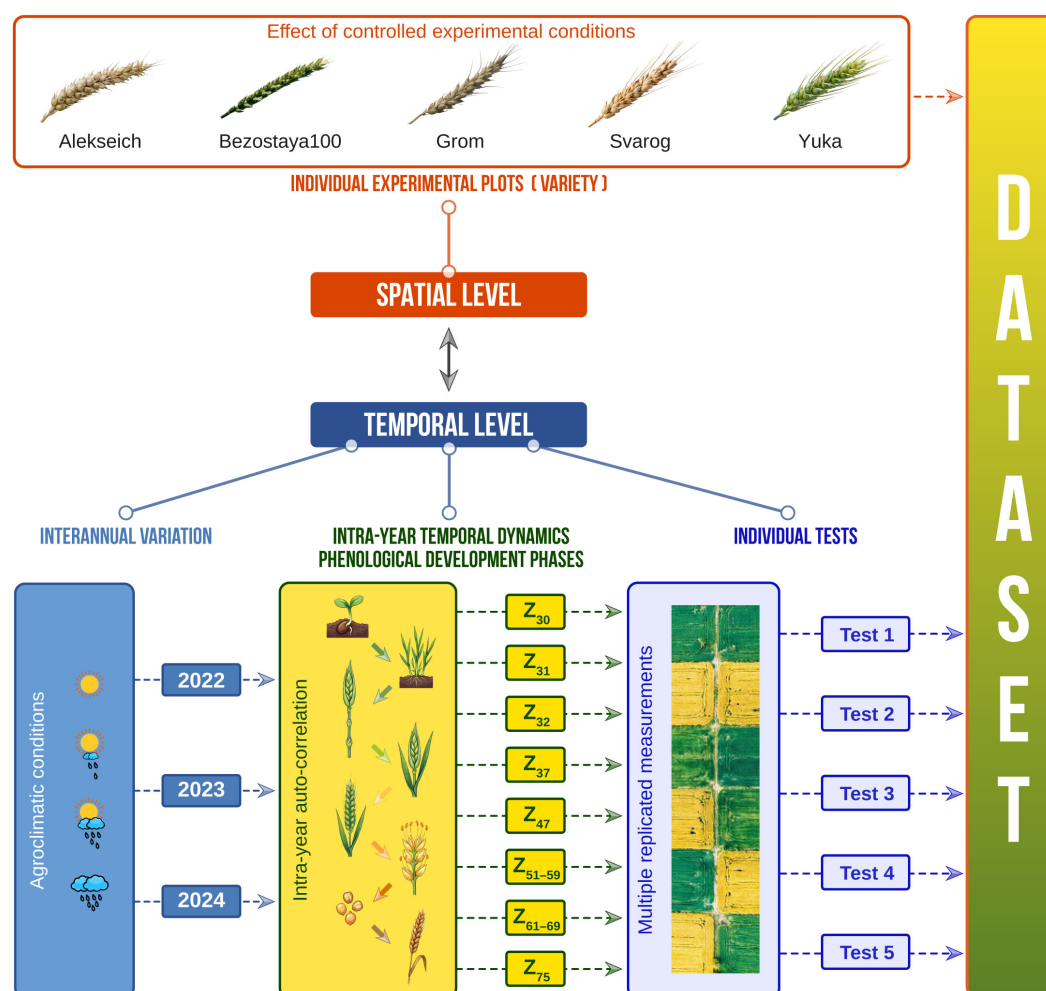


Figure 4. Hierarchical structure of the composition of the considered dataset.

The first temporal level of the hierarchy reflects the interannual variation in experimental conditions driven by differences in meteorological factors influencing both the pathogen sporulation dynamics and the development of foliar diseases. Direct inclusion of detailed weather covariates into the model at this stage is impractical due to the risk of overparametrization and multicollinearity. Instead, interannual differences are indirectly accounted for through a categorical year variable, with aggregates the combined effect of uncontrolled environmental factors.

The second temporal level of the hierarchy describes the temporal dynamics within a year, represented by the wheat phenological phase or date of measurement. This level reflects the cumulative development of the pathogen during the growing season. Repeated observations on the same plot at different phases are not statistically independent and may exhibit temporal auto-correlation, which must be taken into account when constructing the model.

The third temporal level of the hierarchy includes multiple replicated measurements conducted within combinations $year \times plot \times phenological\ phase$. To eliminate pseudo-replication and reduce the influence of random measurement error, the replicated measurement values for each factor were aggregated into a single representative value (median) for each experimental unit. Consequently, the final unit of analysis corresponds to a unique combination of year, plot and phenological phase.

The described hierarchical structure informs the choice of a statistical approach that allows for the simultaneous assessment of the influence of controlled experimental factors while taking into account stochastic variation at different levels of data aggregation.

2.3. Models

The hierarchical structure of the experimental data, being characterized by nested levels of repeated measurements ($year \rightarrow experimental\ plots \rightarrow phenological\ phase/date \rightarrow aggregated\ samples$), involves statistical dependence between observations. In this case, the employment of classical generalized linear regression such as the ordinary least squares (OLS) method violates the fundamental assumption of error independence. This leads to pseudo-replication and underestimation of standard errors, which increases the likelihood of false-positive conclusions. Linear mixed-effects models (LMMs) take into account this nested structure by introducing random effects to simulate unaccounted heterogeneity at each hierarchical level [25,26].

The model specification is based on four interrelated hypotheses. First, a fixed positive relationship is assumed to exist between the pathogenic spore concentration and the severity of leaf damage. Furthermore, the model takes into account a lag in the effect of spore concentration influence on foliar disease incidence. Secondly, the strength of this relationship can be modified by the genetic resistance of specific wheat varieties [28]. The latter is formalized by introducing a moderator variable of the variety as a fixed effect. Thirdly, the model must account for significant inter-annual variability in meteorological conditions. Year can be included as a fixed factor to control for specific environmental realizations or as a random effect to describe the variance of a sample from the distribution of possible climate scenarios. Fourthly, the temporal dynamic within a year represented by successive days potentially contains autocorrelation between repeated measurements, allowing testing of the phase as a potential random effect.

Based on the biological incubation period of the pathogens under study and weekly observations, it is assumed that the manifestation of disease symptoms occurs at least one stage after the detection of spores in the air. This assumption more accurately describes the causal relationship between spore infection and disease development. The incubation periods of the studied pathogens range from 4 to 21 days. As observations were conducted

during 7–10 day intervals corresponding to a single phenological stage, a one-stage lag is the minimum resolvable time step required to detect the transition from infection to visible symptoms. From a statistical perspective, a longer introduction or pathogen-specific lag structure is impractical as additional lags would result in data loss and a reduction in statistical power. Therefore, the quantitative evaluation of foliar disease severity $disease_{ijk}$ is considered in the i -th replicate, j -th year, and k -th phenological phase, while the relation with the number of spores $spore_{ij,k-1}$ in the $(k - 1)$ -th day corresponding to a certain phenological phase is considered.

The following subsection outlines the process of incorporating random components (*year* and *phase*) and the algorithm for including moderating effects into the final model. The choice of the best model (LMM and OLS) is based on an assessment of the informativeness of random effects and the convergence of model specifications.

2.3.1. Year Effect Parametrization: Fixed Versus Random Formulations

The inter-annual variability in the dependence of foliar disease severity on spore concentration can be explained by two specifications: a random effect or a fixed effect. The choice between the two parameterizations of the model is determined by both the biological interpretation of the features and the statistical properties of the data.

The model describing the dependence of foliar disease severity on spore concentration with a random year effect (Model 1) is defined as follows:

$$disease_{ijk} = \beta_0 + \beta_1 \cdot spore_{ij,k-1} + u_j + \varepsilon_{ijk}. \quad (1)$$

Here β_1 is the fixed slope of the averaged population dependence of disease development on spore concentration, $u_i \sim N(0, \sigma_{year}^2)$ describes the random year effect, representing the deviation of j -th year from the general average, and $\varepsilon_{ijk} \sim N(0, \sigma^2)$ is the residual error.

The model for the dependence of foliar disease severity on spore concentration with a fixed year effect (Model 2) is defined as follows:

$$disease_{ijk} = \beta_0 + \beta_1 \cdot spore_{ij,k-1} + \gamma_j \cdot I(year = j) + \varepsilon_{ijk}. \quad (2)$$

$I(year = j)$ is a variable encoding the years considered. The estimation of the coefficient γ_j determines the bias of β_0 for the j -th year relative to the base level. In this specification, years are considered fixed rather than stochastic conditions of the experiment. The model estimates the differences between years without assuming that they belong to the same general population. This approach is preferred if the research focuses on monitoring meteorological events that occurred during the field seasons.

Competing models are ranked using the Akaike's information criterion corrected (AICc), which is adjusted for small sample size, and the Bayesian information criterion (BIC). The AICc of a model is calculated as

$$AICc = -2\ell + 2k + \frac{2k(k+1)}{n-k-1},$$

where ℓ are the logarithms of the likelihoods, where k is the number of parameters and n is the sample size. In the presence of a random effect, the exact value of k is not uniquely determined. In practice, the approximation $k = p + q$ is used, where p is the number of fixed parameters and q is the number of estimated variance components [26]. If $\Delta IC = IC_{M1} - IC_{M2} > 2$, where IC is AICc or BIC, the model with the smaller value is considered to have significant support in the data. Regardless of the value of $\Delta AICc$, the estimate $\hat{\sigma}_{year}^2$ is tested. If the estimate is close to zero, the random specification is considered inadequate even if IC is formally better.

2.3.2. Random Phase Effect

The third model (Model 3) accounts for potential intra-annual autocorrelation in the observations arising from repeated measurements across successive phenological phases via the introduction of a random phase effect:

$$disease_{ijk} = \beta_0 + \beta_1 \cdot spore_{ij,k-1} + C(year_j) + \omega_k + \varepsilon_{ijk}. \quad (3)$$

Here $\omega_k \sim N(0, \sigma_{phase}^2)$ describes the random effect related to k -th day/phenological phase, which reflects the stochastic variability of pathogen development at different stages of the growing season, whilst $C(year_j)$ represents the effect (fixed or random) of year depending on the results of the comparison described in Section 2.3.1. The rest of the terms are kept in the model as in (2) and the distribution of the residual error ε_{ijk} remains unchanged. In the absence of statistical evidence for a random phase effect, the relationship is described by the base model M_{base} (Model 1 or Model 2).

The hypothesis that including phase as a random effect is necessary is tested at the boundary of the parameter space:

$$H_0 : \sigma_{phase}^2 = 0 \quad \text{vs} \quad H_1 : \sigma_{phase}^2 > 0. \quad (4)$$

The test is performed using the likelihood ratio test (LRT):

$$LRT = -2(\ell_{M3} - \ell_{M_{base}}), \quad (5)$$

where ℓ_{M3} and $\ell_{M_{base}}$ are the log-likelihoods for the random effects phase model and the corresponding base model, given that Model 3 is nested in M_{base} (or equivalent to it for $\sigma_{phase}^2 \rightarrow 0$).

Since the null hypothesis lies at the boundary of an acceptable range of variance ($\sigma_{phase} \geq 0$), the asymptotic distribution of LRT (5) does not follow the standard chi-squared distribution. For an objective hypothesis test, a parametric bootstrap procedure with $B = 10^3$ iterations is used to generate an empirical distribution of the LRT statistic [35,36]. The empirical p -value is proportional to the bootstrap samples in which the LRT statistic exceeded the observed value:

$$p_{emp} = \frac{1}{B} \mathbb{I}(LRT_{bootstrap} > LRT). \quad (6)$$

If $p_{emp} > 0.05$, the random phase effect is excluded.

2.3.3. Moderation by Varietal Traits

In this section, the testing of an a priori hypothesis concerning the differential susceptibility of different wheat varieties to pathogens is considered. As the experiment involves a fixed set of genotypes of independent research interest, the varietal identity is specified as a fixed factor. One variety ('Alekseich') is adopted as the reference level and the remaining four varieties are coded as dummy variables according to the following rule:

$$I(sort = m) = \begin{cases} 1, & \text{sort} = m \\ 0, & \text{otherwise} \end{cases}, \quad m \in \{2, 3, 4, 5\}$$

The basic model (Model 4) describing the relationship between the severity of foliar disease and spore concentration while accounting for the effects of year, phase and variety is defined as follows:

$$disease_{ijk} = \beta_0 + \beta_1 \cdot spore_{ij,k-1} + \sum_{m=2}^K \alpha_m \cdot I(sort = m) + C(year_j) + \delta \cdot \omega_k + \epsilon_{ijk}. \quad (7)$$

Here β_1 is the overall slope of the reference variety, α_m is the fixed intercept shift for the m -th variety, and $C(year_j)$ and ω_k correspond to the effects of year and day/phenological phase. The specifications of the model are described in the previous stages of model verification (δ is equal to 0 or 1 depending on the presence of the phase random effect in the model).

To test the hypothesis that variety resistance manifests itself through differential susceptibility to infection, terms that describe the interaction between spore concentration and variety identity are introduced in addition to the terms used in (7). The final moderator model (Model 5) is specified as follows:

$$disease_{ijk} = \beta_0 + \beta_1 \cdot spore_{ij,k-1} + \sum_{m=2}^K \alpha_m \cdot I(sort = m) + \sum_{m=2}^K \theta_m \cdot spore_{ij,k-1} \cdot I(sort = m) + C(year_j) + \delta \cdot \omega_k + \epsilon_{ijk}. \quad (8)$$

where θ_m are the moderator coefficients, reflecting changes in the regression slope for the m^{th} variety relative to the reference variety. The variety-specific slope is calculated as $\beta^{(m)} = \beta_1 + \theta_m$.

Therefore, the statistical significance of the moderation effect is tested under the null hypothesis of the joint absence of interaction:

$$H_0 : \theta_1 = \theta_2 = \dots = \theta_K = 0 \quad \text{vs} \quad H_1 : \exists m \in \{2, 3, 4, 5\}, \theta_m \neq 0.$$

Nested models are compared by taking into account their stochastic nature as defined in previous steps. If Model 4 (7) contains a confirmed random effect (e.g., year or phase), the comparison is performed using the LRT. If random effects are excluded and the model is reduced to an OLS regression, the joint significance of the four added interaction terms is tested using the F -test

$$F = \frac{(RSS_{\text{main}} - RSS_{\text{int}}) / (K - 1)}{(RSS_{\text{int}} / (n - 2K - 2))} \sim F(K - 1, n - 2K - 2),$$

where RSS_{main} is the residual sum of squares for Model 4 without the interaction described by (7), RSS_{int} is the residual sum of squares for Model 5 with the interaction described by (8), K is the number of varieties, and n is the number of observations.

2.4. Comparison of Varietal Susceptibility

As the aim of the study is to confirm the presence of different varietal resistances rather than construct a precise predictive equation, the subsequent analysis focuses on assessing the variety-specific slopes and their statistical significance.

Let us denote $\beta_1^{(m)}$ the slope of the $disease \sim spore$ relationship for the m -th variety ($m = 1, \dots, 5$). Therefore, the coefficient $\beta_1^{(ref)} = \beta_1^{(1)} = \beta_1$ is used for the reference variety, and the conditional effects of the other varieties are calculated as $\beta_1^{(m)} = \beta_1 + \theta_m$. The standard error (SE) for the coefficient $\beta_1^{(m)}$ is calculated using the formula:

$$SE(\hat{\beta}_1^{(m)}) = \sqrt{\hat{\sigma}^2(\hat{\beta}_1) + \hat{\sigma}^2(\hat{\theta}_m) + 2 \cdot Cov(\hat{\beta}_1, \hat{\theta}_m)},$$

where the dispersion and covariation of the regression coefficients are determined through the corresponding elements of the estimated covariance matrix of the regression coefficients.

The hypothesis that the coefficient $\beta_1^{(m)}$ equals zero is tested by considering 95% confidence intervals

$$CI^{(m)} = \hat{\beta}_1^{(m)} \pm t(\alpha, n - p) \cdot SE(\hat{\beta}_1^{(m)}) \quad (9)$$

and the presence of zero in this interval does not reject this hypothesis.

To test the hypothesis of equal varietal resistance, including a comparison with the reference variety, a direct pairwise comparison of the variety-specific slopes is performed. For each of the ten pairs of varieties *A* and *B*, the null hypothesis is formulated:

$$H_0^{(AB)} : \beta_1^{(A)} - \beta_1^{(B)} = 0 \quad \text{vs} \quad H_1^{(AB)} : \beta_1^{(A)} - \beta_1^{(B)} \neq 0 \quad (10)$$

The linear contrast $\hat{L}_{AB} = \hat{\beta}_1^{(A)} - \hat{\beta}_1^{(B)}$ is calculated based on the vector of fixed effects estimates $\hat{\beta}$.

$$SE(\hat{L}_{AB}) = \sqrt{\hat{\sigma}^2(\hat{\theta}_A) + \hat{\sigma}^2(\hat{\theta}_B) - 2 \cdot Cov(\hat{\theta}_A, \hat{\theta}_B)}$$

The test statistic is

$$t_{AB} = \frac{\hat{L}_{AB}}{SE(\hat{L}_{AB})}.$$

Since all pairwise contrasts for a single factor are tested simultaneously, Tukey's honestly significant difference (HSD) correction is applied to control for false positives. Adjusted 95% confidence intervals for the slope difference are calculated using the following formula:

$$CI_{Tukey}^{(AB)} = \hat{\delta}_{AB} \pm \frac{q}{\sqrt{2}} \cdot SE(\hat{\delta}_{AB}), \quad (11)$$

where $q = q(\alpha, K, df)$ and $df = n - p$ is the critical value of the studentized range distribution.

The null hypothesis is rejected if zero is not included in the adjusted interval. A significant difference is interpreted as statistical confirmation of the different responses of wheat varieties to infection.

3. Results

3.1. Experimental Data Processing

The experimental data obtained during the three-year study period require were preliminary processed. First, the results of replicate experiments conducted within a single day for each plot were aggregated. It is known that the use of a sample mean leads to biased estimates if the data represented by this sample belong to an asymmetric distribution. Therefore, the coefficient of variation was analyzed to determine the homogeneity of the intra-day experimental data. The analysis revealed that 26.5% of the replicate samples obtained using the spore trap showed high variability, while the replicate experiments to determine the severity of the foliar disease showed only 10% variability. Consequently, averaging for both types of experimental samples was performed using median values. Note that aggregating of replicates to a single median value affects variance estimation. However, the analysis of the coefficient of variation (CV) shows that intra-replicate variability for disease severity is relatively low. Therefore, the loss of within-group variance data does not critically impact variance estimation at higher hierarchical levels. For spore count, where variability is higher, the median is used to ensure robustness against extreme outliers, which could introduce systematic bias into regression model estimates.

The next question to address is whether the results obtained during all three years (2022–2024) could be considered as random samples from a single general population. Although approximately 350 experiments were conducted each year, this resulted in small sample sizes (7–8 observations) as they include data for each pathogen depending on the affiliation of the variety. It should also be noted that pathogens are not necessarily observed every year.

Figure 5 exhibits twelve plots of the number of spores $spore_{ijk}$ detected using the spore trap device during days D₁–D₈ corresponding to phenological phases Z₃₀–Z₇₉ for all years (2022–2024) and pathogens. Figure 6 presents plots similar to Figure 5 where the level of foliar disease development caused by pathogens is analyzed according to the Peterson scale [31] for *P. striiformis* and *P. triticea*, the Saari–Prescott scale [32] for *P. tritici-repentis*, and the specialized CIMMYT scale [33] for *B. graminis*. These plots allow us to investigate the dynamics of pathogen spores during the active flight period, where a complete absence or statistically low amounts of pathogen spores can be observed in certain years.

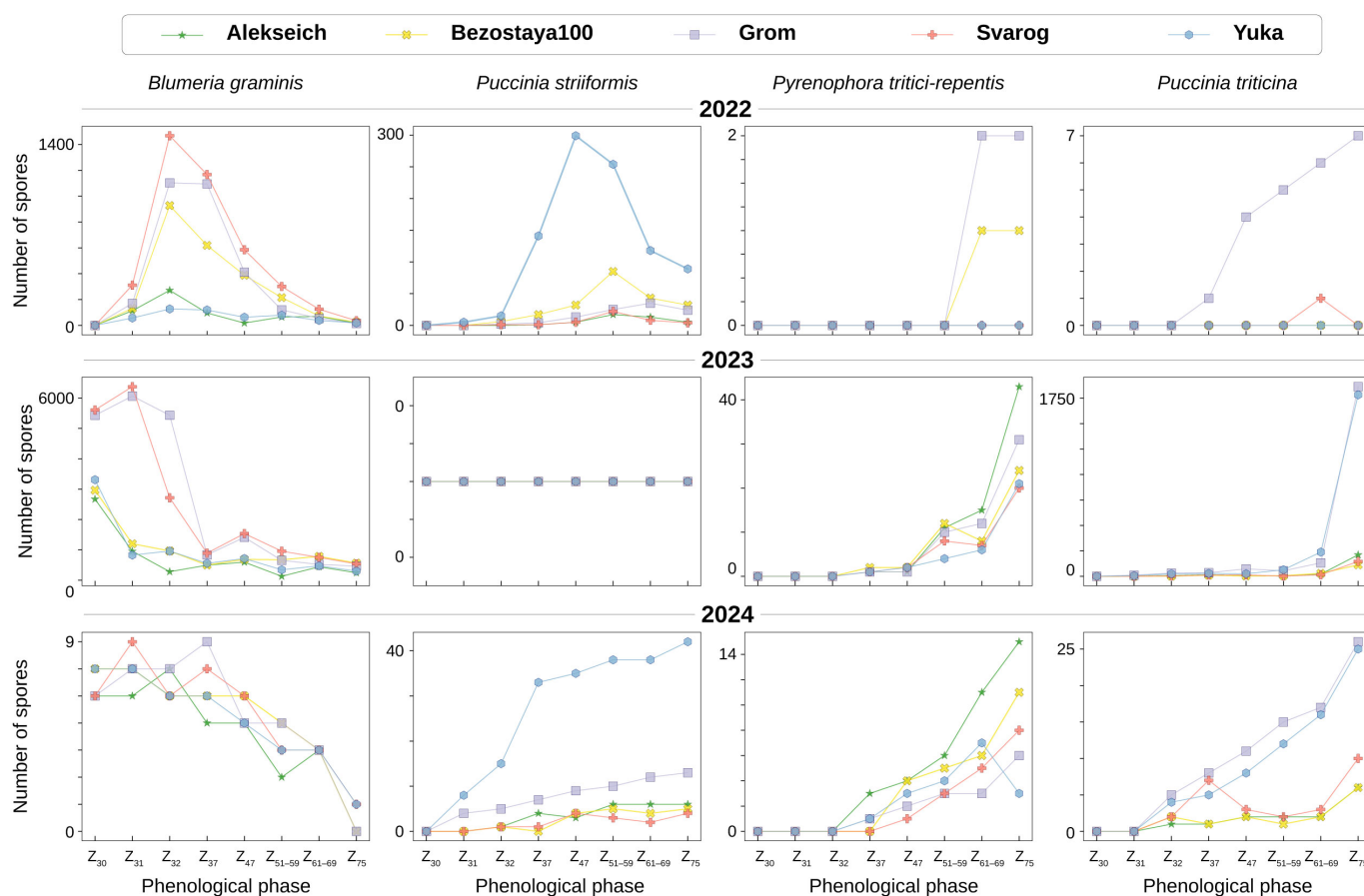


Figure 5. The number of spores $spore_{ijk}$ detected by the spore trap device during phenological phases Z₃₀–Z₇₉ in 2022–2024 for five varieties (calculated as a median of the number of spores identified in five replicates).

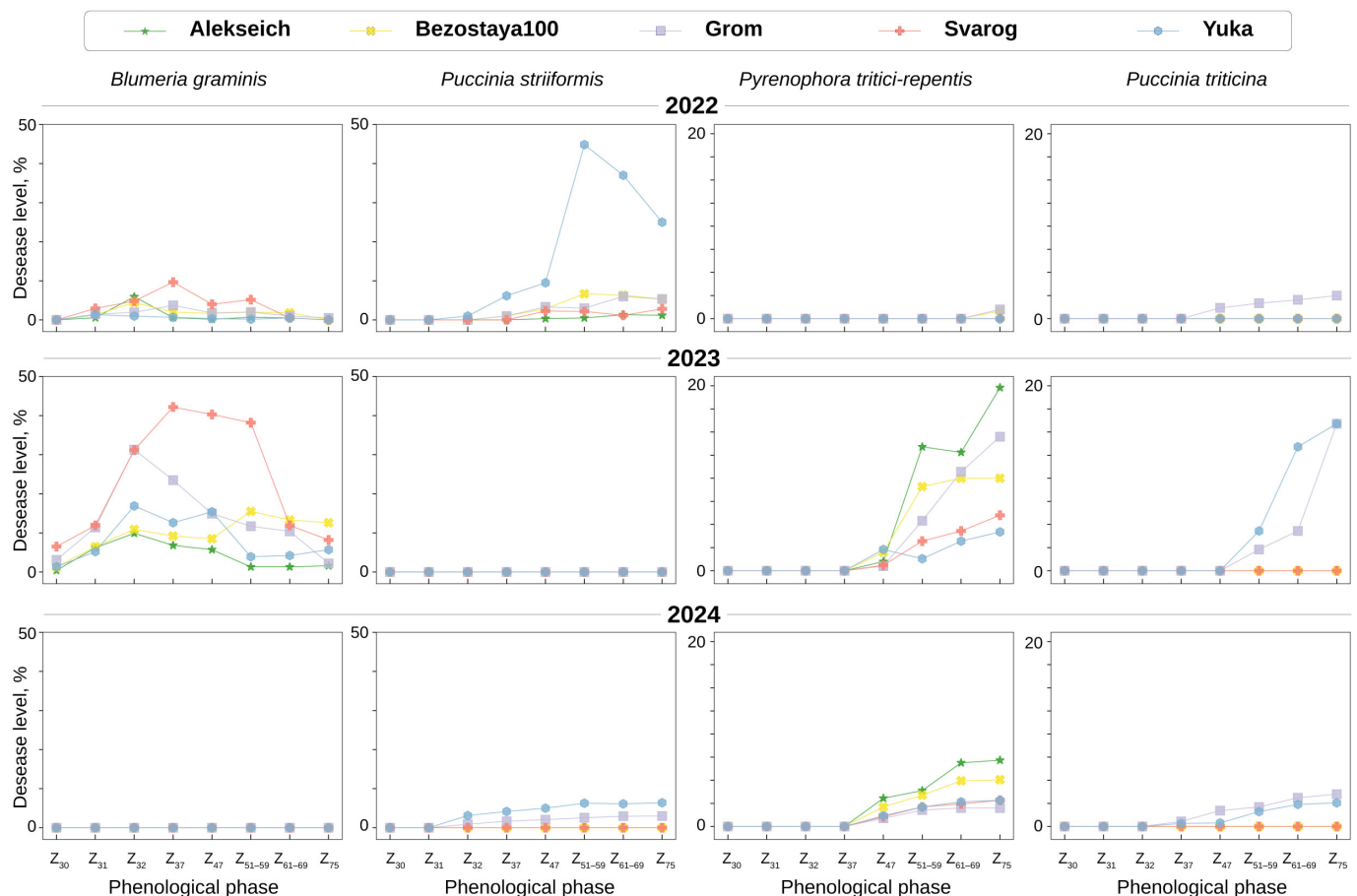


Figure 6. The degree of disease development on different wheat varieties in phenological phases Z_{30} – Z_{79} in 2022–2024 calculated according to the Peterson scale [31] for *P. striiformis* and *P. triticina*, the Saari–Prescott scale [32] for *P. tritici-repentis*, and the specialized CIMMYT scale [33] for *B. graminis*.

The results of the pathogen presence/absence analysis by year are presented in Figure 7 (crosses and ticks in the case of absence and presence respectively). Based on these results, the years suitable for further analysis are determined. For each pathogen, there is at least one year in which the pathogen is not observed. However, years in which a particular pathogen is absent are not represented by zero values. Instead, analysis of each pathogen is limited to the years in which it is present. This approach is chosen to prevent the influence of unsuitable climatic condition, which results in the pathogen not being observed, from affecting the assessment of varietal resistance. Accordingly, each pathogen is analyzed only over a two-year period, and the analysis included all five studied varieties (Grom, Svarog, Bezostaya 100, Yuka, and Alekseich) for all four pathogens. The specific years and the final number of aggregated observations n for each pathogen are as follows:

- *B. graminis*: 2022 and 2023, $n = 75$;
- *P. striiformis*: 2022 and 2024, $n = 75$;
- *P. triticina* and *P. tritici-repentis*: 2023 and 2024, $n = 80$.

Analysis of Figures 5 and 6 also reveals that experimental values can differ by several orders of magnitude over years, indicating heteroskedasticity in the variance around annual mean values. Ives [37] demonstrated that logarithmic transformation of the data combined with linear models provides robust statistical significance testing. Therefore, the data are logarithmically transformed here and in the subsequent analysis using the formula $\tilde{x} = \lg(x + 1)$ to stabilize the variance.

Pathogen	Observation	2022	2023	2024
Blumeria graminis	spores	low level		
	disease	low level		
Puccinia striiformis	spores			low level
	disease			
Pyrenophora tritici-repentis	spores	low level		
	disease	low level		
Puccinia triticina	spores			
	disease			

Figure 7. Table with results of observation of spores showing presence or absence of pathogens.

The feasibility of combining data across years can be assessed by testing the homogeneity of correlations between disease severity and pathogen spore counts. Figure 8 presents Spearman correlation coefficients and bootstrap-derived confidence intervals (based on 1000 resamples), calculated separately for each pathogen by year [38].

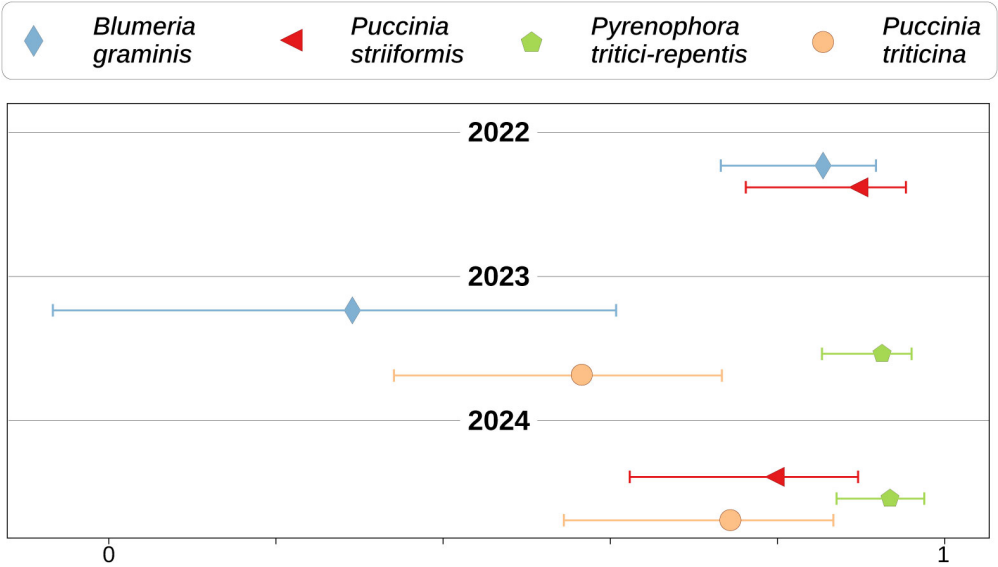


Figure 8. Spearman correlation coefficients and bootstrap-derived confidence intervals between disease severity and pathogen spore counts.

Correlations can be deemed homogeneous here if the correlation coefficients are statistically significant and their confidence intervals overlap. Based on these results, it can be concluded that the data for *P. striiformis*, *P. tritici-repentis* and *P. triticina* can be pooled across the years of observation for subsequent analysis. In the case of *B. graminis*, a statistically significant correlation is observed in 2022 but not in 2023; this discrepancy may be attributed to inter-annual differences in climatic conditions conducive to the development of *B. graminis*.

3.2. Specification of the Basic Dependency Model

The first step of the analysis is the verification of the structure of the base model, which describes the dependence of the degree of leaf damage *disease* on the pathogen spore concentration *spore*. Since inter-annual variability in meteorological conditions can influence the epidemiological dynamics, two kinds of parametrization of the year factor are compared: a random effect reflecting the stochastic variance between years described by (1) and a fixed effect model described via (2). The comparison is performed for four pathogens (*B. graminis*, *P. striiformis*, *P. tritici-repentis*, *P. triticina*) using the information criteria AICc and BIC as well as assessment of the variance components.

The results of the comparison are presented in Table 1. Model 2 with a fixed year effect demonstrates significantly lower information criterion values for all four pathogens. The difference in AICc varies from 4.46 (*P. tritici-repentis*) to 9.53 (*B. graminis*), and the difference in BIC values varies from 6.71 to 11.71. According to the accepted criteria for interpretation, a difference in information criteria greater than 2 indicates an advantage of the model with the lower value. Additionally, for most pathogens, the estimated variance of the random year effect $\hat{\sigma}_{year}^2$ is close to zero (less than 0.005), which indicates the absence of stochastic inter-annual variability. Though the variance is positive for pathogen *B. graminis* ($\hat{\sigma}_{year}^2 = 0.027$), the fixed parametrization provides the best balance between goodness of fit and model complexity, too.

Table 1. The results of the comparison of Model 1 and Model 2.

	Model	<i>B. graminis</i>	<i>P. striiformis</i>	<i>P. tritici-repentis</i>	<i>P. triticina</i>	
$\hat{\beta}_1$	value	1	0.434	0.568	0.913	0.387
		2	0.359	0.558	0.908	0.402
	<i>p</i> -value	1	$1.43 \cdot 10^{-9}$	$3.18 \cdot 10^{-52}$	$1.93 \cdot 10^{-69}$	$1.62 \cdot 10^{-14}$
		2	$5.22 \cdot 10^{-5}$	$2.54 \cdot 10^{-22}$	$1.35 \cdot 10^{-26}$	$1.21 \cdot 10^{-11}$
$\hat{\sigma}_{year}^2$	2	0.027	0.002	0.0003	0.0043	
$\hat{\gamma}_j$	2	0.412 (<i>j</i> = 2023)	−0.109 (<i>j</i> = 2024)	−0.064 (<i>j</i> = 2024)	0.159 (<i>j</i> = 2024)	
<i>p</i> -value		$1.92 \cdot 10^{-7}$	0.027	0.122	0.008	
AICc	1	18.72	−26.86	−41.99	−4.59	
	2	9.18	−32.95	−46.45	−11.60	
BIC	1	27.42	−18.17	−33.00	4.40	
	2	15.70	−26.43	−39.71	−4.85	
Δ	ΔAICc	9.53	6.08	4.46	7.01	
	ΔBIC	11.71	8.25	6.71	9.25	

It should be emphasized that the estimate of the core coefficient $\hat{\beta}_1$, which reflects the strength of the relationship between spore concentration and foliar disease severity, remains stable and statistically significant ($p < 0.05$) when moving from Model 1 to Model 2 for all pathogens. This confirms the robustness of the main finding that disease development depends positively on spore concentration, regardless of how inter-annual variability is accounted for. The coefficient describing the fixed effect of year $\hat{\gamma}_j$ is insignificant only for *P. tritici-repentis* ($p = 0.122$), which suggests that the weather conditions in 2023 and 2024 had a similar effect on the development of this disease. For the remaining pathogens, the year fixed effect is significant, indicating that inter-annual differences in weather conditions manifested as a deterministic shift in the baseline disease level. Weather

conditions were more favorable for *B.graminis* development in 2023 than in 2022 ($\hat{\gamma}_{2023} = 0.412, p = 1.92 \cdot 10^{-7}$), and weather conditions were better for *P.triticina* development in 2024 than in 2023 ($\hat{\gamma}_{2024} = 0.159, p = 0.008$). On the contrary, unfavorable weather can be observed for *P. striiformis* in 2024 compared to 2022 ($\hat{\gamma}_{2024} = -0.109, p = 0.027$). Based on this analysis, Model 2 is selected for further analysis.

The characteristics of Model 3 (3), incorporating a random effect of phenological phase and a fixed effect of year, are presented in Table 2. The null hypothesis (4) is tested using a parametric bootstrap for the LRT statistic (5). For all four pathogens, the empirical p -value (6) exceeds the significance threshold ($p_{emp} = 0.79$ for *B. graminis*, 0.27 for *P. striiformis*, 0.61 for *P. tritici-repentis*, and 0.49 for *P. triticina*), while the obtained LRT statistic values do not reach the corresponding 95% empirical critical values. In addition, the variance estimates for the random phase effect are close to zero for *P. striiformis* and *P. tritici-repentis*. The variances calculated for the other pathogens are positive but still rather small. This results in the elimination of the random phase effect from the final specification, and Model 2, which includes a fixed year effect without stochastic components, is adopted as the base model for the subsequent varietal susceptibility analysis.

The transition from mixed-effect modeling to the final OLS specification is data-driven and based on diagnostic testing of statistical assumptions. Due to the heteroscedasticity observed in the raw data, a logarithmic transformation is applied to stabilize variance and median aggregation of replicates is used as a robust measure against outliers. The assumption of independence of residuals is tested by estimating a random phase effect. Non-significant results of the LRT confirm the absence of temporal auto-correlation and justify the exclusion of the random phase component. Therefore, since the variance of the random effects of year and phase is statistically indistinguishable from zero, mixed-effects models can be mathematically reduced to the OLS.

Table 2. The characteristics of Model 3 and the results of the comparison with Model 2.

	<i>B. graminis</i>	<i>P. striiformis</i>	<i>P. tritici-repentis</i>	<i>P. triticina</i>
$\hat{\sigma}_{phase}^2$	0.0174	0.0067	0.0057	0.013
LRT	7.26	1.54	5.39	6.87
LRT _{95,emp}	22.05	7.65	24.48	16.63
p_{emp}	0.79	0.27	0.61	0.49

3.3. Moderation by Varietal Susceptibility

In this subsection, the hypothesis that wheat varietal susceptibility to foliar disease depends on the pathogen species and weather conditions is tested. The base specification for this stage is described by Model 2, given by (2), which includes a fixed effect for year and is estimated using the OLS method. Within this framework, Model 4, given by (7), and Model 5, given by (8), are compared. Model 4 incorporates the effects of spore concentration, variety and year, while Model 5 additionally contains interaction terms between the spore concentration variable and the variety indicator variables. The joint significance of the four additional interaction terms, θ_m , is evaluated using the traditional F -test for nested models.

The results of the comparison of Model 4 and Model 5 are presented in Table 3. Both specifications demonstrate high statistical significance: the overall F -test rejects the null hypothesis of a lack of explanatory power of the models ($p < 0.05$ for all pathogens and both models). A statistically significant improvement in the quality of the fit is found for three out of four considered pathogens if the moderator interaction term is included. The moderation effect manifests itself clearly in the case of *P. triticina*: the introduction of the interaction terms increases the adjusted coefficient of determination R_{adj}^2 by 0.116 points

(from 0.523 to 0.639), decreases the value of the information criteria, and yields a statistically significant result for the joint test of the parameters θ_m ($p = 0.0004$). For *P. striiformis*, this introduction leads to a significant increase in R^2_{adj} (from 0.881 to 0.910) and a decrease in the information criteria values, whereas the F -test rejects the null hypothesis of the absence of moderation at the $p = 0.0007$ level. For *B. graminis* and *P. tritici-repentis*, the addition of the interaction term does not improve the model. The F -test does not reject the null hypothesis ($p = 0.5719$ and $p = 0.5789$ correspondingly), and the information criteria values worsen, indicating a lack of statistical basis for assuming differential varietal responses to spore concentration for this pathogen.

Table 3. The results of the comparison of Model 4 and Model 5.

	Model	<i>B. graminis</i>	<i>P. striiformis</i>	<i>P. tritici-repentis</i>	<i>P. triticina</i>	
R^2_{adj}	4	0.721	0.881	0.820	0.523	
	5	0.729	0.910	0.817	0.639	
AIC	4	6.71	−58.40	−43.77	−13.13	
	5	8.21	−73.01	−39.12	−29.11	
BIC	4	21.93	−43.18	−28.03	2.61	
	5	32.13	−49.10	−14.39	−4.38	
F	statistic	4	28.57	79.77	53.53	13.62
		5	18.21	65.35	31.84	13.19
	p -value	4	$1.27 \cdot 10^{-15}$	$3.55 \cdot 10^{-26}$	$7.13 \cdot 10^{-23}$	$7.67 \cdot 10^{-10}$
		5	$5.87 \cdot 10^{-14}$	$1.58 \cdot 10^{-26}$	$3.79 \cdot 10^{-20}$	$9.56 \cdot 10^{-12}$
H_0	F_{nested}	1.42	5.62	0.72	6.03	
	p -value	0.2403	0.0007	0.5789	0.0004	

The results of the moderation analysis revealing the effect of a significant interaction between variety and spore concentration are visualized as slope plots and scatter plots in Figure 9. Each subplot shows the relationship between foliar damage severity *disease* and spore concentration *spore* for the five wheat varieties and four pathogens with the year effect averaged for clarity (the variables are considered on a logarithmic scale).

3.4. Analysis of the Influence of Variety on the Susceptibility of Wheat Leaves to Fungal Infections

To quantitatively assess varietal differentiation in susceptibility to foliar diseases, 95% confidence intervals are calculated for the variety-specific slope $\beta_1^{(m)}$ of Model 5 according to (9). The slopes observed in Figure 10 characterize the intensity of the response of leaf damage severity to increasing spore concentrations for each of the four pathogens. Slopes whose confidence intervals do not include zero are considered statistically significant and indicate a reliable positive correlation between infection level and disease development for a given wheat variety. The results of the pairwise comparisons of the variety-specific slopes corrected using Tukey's method (11) are presented in Table 4 (if the interval does not include zero it is marked as bold).

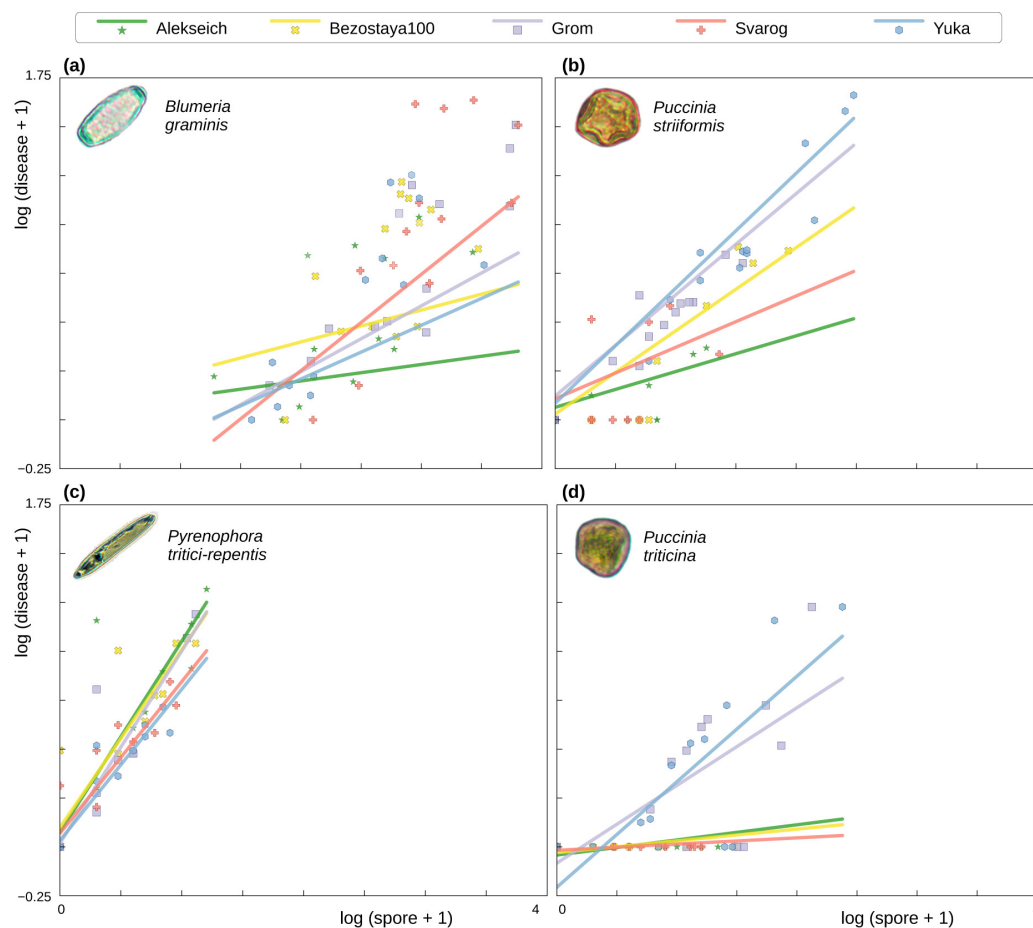


Figure 9. Varietal-specific slopes of relation between foliar damage severity *disease* and spore concentration *spore* for *B. graminis* (a), *P. striiformis* (b), *P. tritici-repentis* (c) and *P. triticina* (d).

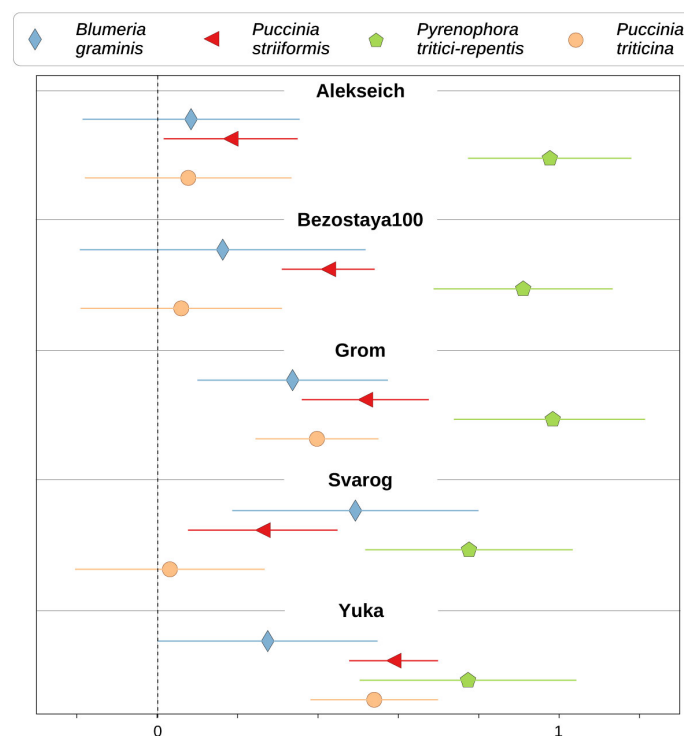


Figure 10. Confidence intervals (95%) for the effect of variety on the severity of foliar diseases, expressed in variety-specific slopes using Model 5.

Table 4. Confidence intervals of the pairwise comparison of variety-specific slopes.

Sort A	Sort B	Statistic	Pathogen			
			<i>B. graminis</i>	<i>P. striiformis</i>	<i>P. tritici-repentis</i>	<i>P. triticina</i>
Alekseich	Bezostaya100	$\hat{L}$	0.0789	0.2429	0.0664	0.0174
		c_{left}	−0.4949	−0.0371	−0.3551	−0.4662
		c_{right}	0.6527	0.5229	0.4879	0.5011
Alekseich	Grom	$\hat{L}$	0.2526	0.3349	0.0072	0.3201
		c_{left}	−0.2063	0.0149	−0.4393	−0.0842
		c_{right}	0.7114	0.6549	0.4536	0.7244
Alekseich	Svarog	$\hat{L}$	0.4087	0.0800	0.2010	0.0456
		c_{left}	−0.1147	−0.2672	−0.2588	−0.4324
		c_{right}	0.9322	0.4272	0.6609	0.5237
Alekseich	Yuka	$\hat{L}$	0.1907	0.4055	0.2035	0.4626
		c_{left}	−0.2855	0.1289	−0.2684	0.0556
		c_{right}	0.6670	0.6821	0.6755	0.8696
Bezostaya100	Grom	$\hat{L}$	0.1737	0.0920	0.0736	0.3375
		c_{left}	−0.3831	−0.1796	−0.3899	−0.0619
		c_{right}	0.7305	0.3636	0.5371	0.7370
Bezostaya100	Svarog	$\hat{L}$	0.3298	0.1629	0.1346	0.0282
		c_{left}	−0.2797	−0.1365	−0.3414	−0.4454
		c_{right}	0.9394	0.4623	0.6106	0.5018
Bezostaya100	Yuka	$\hat{L}$	0.1118	0.1626	0.1371	0.4800
		c_{left}	−0.4563	−0.0524	−0.3524	0.0774
		c_{right}	0.6799	0.3776	0.6266	0.8826
Grom	Svarog	$\hat{L}$	0.1562	0.2549	0.2082	0.3657
		c_{left}	−0.3467	−0.0856	−0.2896	−0.0211
		c_{right}	0.6590	0.5953	0.7060	0.7526
Grom	Yuka	$\hat{L}$	0.0619	0.0706	0.2107	0.1424
		c_{left}	−0.3937	−0.1973	−0.3005	−0.1547
		c_{right}	0.5175	0.3386	0.7219	0.4396
Svarog	Yuka	$\hat{L}$	0.2180	0.3255	0.0025	0.5082
		c_{left}	−0.3007	0.0279	−0.5204	0.1175
		c_{right}	0.7367	0.6230	0.5254	0.8989

3.4.1. *B. graminis*

A statistically significant positive slope was demonstrated for the pathogen *B. graminis* by the varieties Svarog ($\hat{\beta}_1^{(4)} = 0.493$; $CI^{(4)} = [0.188; 0.798]$), Grom ($\hat{\beta}_1^{(3)} = 0.337$; $CI^{(3)} = [0.102; 0.572]$) and Yuka ($\hat{\beta}_1^{(5)} = 0.275$; $CI^{(5)} = [0.003; 0.547]$) in Figure 10. However, for variety Yuka, the confidence interval lies close to the zero boundary, and, therefore, only varieties Svarog and Grom show susceptibility to this pathogen.

According to the results of the linear contrast comparison in Table 4, the variety-specific slopes are statistically comparable. The latter is consistent with the previously obtained non-significant result from the varietal moderation test ($p = 0.2403$). The Model 2 specification shows that the main effect of spore concentration (β_1) is positive and statistically significant. It also indicates that the year coefficient (γ_{2023}) has a significant positive value, which reflects higher infection levels and disease severity in 2023 compared to 2022. Therefore, it can be concluded that the development of wheat disease caused by the pathogen *B. graminis*

can only occur under favorable wheather conditions for this pathogen, and only for the Svarog and Grom varieties.

3.4.2. *P. striiformis*

Three out of the five varieties demonstrate statistically significant positive slopes in Model 5 for the pathogen *P. striiformis* (see Figure 10), which indicates a clear response to the infection load: Yuka ($\hat{\beta}_1^{(5)} = 0.588$), Grom ($\hat{\beta}_1^{(3)} = 0.518$), Bezostaya100 ($\hat{\beta}_1^{(2)} = 0.426$). For the Alekseich and Svarog varieties, the confidence interval does not formally include zero, but its lower limit is close to zero: $CI^{(1)} = [0.018; 0.348]$ and $CI^{(4)} = [0.078; 0.447]$ respectively.

Taking into account the comparability of the slopes for these varieties ($\hat{L}(\text{Alekseich-Svarog}) = 0.08$), the significant differences (among varieties such as Grom, Bezostaya100 and Yuka), and the results listed in Table 4, it can be concluded that there is no dependence of the development of the disease on the concentration of spores for the Alekseich and Svarog varieties. Conversely, the linear contrasts of the Grom, Bezostaya100 and Yuka varieties are statistically non-significant, but the coefficients $\beta_1^{(m)}$ are statistically significant; that is to say, the correlation between the development of wheat leaf disease caused by *P. striiformis* and spore concentration is positive and the same for all these varieties. One noteworthy observation is the confidence interval for the linear contrast between the Yuka and Bezostaya100 varieties, with the left-hand boundary of the Yuka variety close to zero (-0.052). Together with the statistically significant negative coefficient (γ_{2024}) in Model 2, this suggests that the Yuka variety is more susceptible to the pathogen *P. striiformis* under favorable weather conditions.

3.4.3. *P. tritici-repentis*

For *P. tritici-repentis*, all five varieties exhibited high and statistically significant slopes ($\hat{\beta}_1^{(m)}$ from 0.773 to 0.984) and confidence intervals that not only excluded zero but also lay far from it (see Figure 10). This suggests that pathogens induce a strong response to leaf damage. Table 4 shows that there is no differentiation between varieties in response to the influence of the pathogen spores. As the coefficient γ_{2024} in Model 2 is statistically comparable to zero (i.e., weather conditions were similar for the development of this pathogen), it is possible that subtle variety susceptibility differentiation could not be detected experimentally.

3.4.4. *P. triticina*

For *P. triticina*, varietal differentiation was found, with two varieties, Grom ($\hat{\beta}_1^{(3)} = 0.398$) and Yuka ($\hat{\beta}_1^{(5)} = 0.540$), exhibiting statistically significant positive slopes, and in contrast, for Alekseich ($\hat{\beta}_1^{(1)} = 0.078$), Bezostaya100 ($\hat{\beta}_1^{(2)} = 0.060$) and Svarog ($\hat{\beta}_1^{(4)} = 0.032$), the confidence intervals include zero. This is consistent with the statistically significant result of the moderation test ($p = 0.0004$). Furthermore, the linear contrasts are equal in the Alekseich, Bezostaya100 and Svarog variety group ($\hat{L}(\text{Alekseich} - \text{Bezostaya}_{100}) = 0.017$, $\hat{L}(\text{Alekseich} - \text{Svarog}) = 0.046$, $\hat{L}(\text{Bezostaya}_{100} - \text{Svarog}) = 0.028$), as well as in the Grom and Yuka variety group ($\hat{L}(\text{Grom} - \text{Yuka}) = 0.142$). There is differentiation observed between the groups. For the Yuka variety, a statistically significant response to infection has been confirmed that differs from those of the Alekseich, Bezostaya100 and Svarog varieties. Such strict statistical significance is not achieved for the Grom variety, but all confidence intervals for the corresponding linear contrasts have left limits close to zero (-0.08 to -0.02). It can therefore be concluded that, for the Alekseich, Bezostaya100 and Svarog varieties, the relationship between wheat disease development caused by the P.

tritici pathogen is statistically insignificant, while, for the Grom and Yuka varieties, the relationship is positive and identical.

3.5. Summary of Statistical Modeling Analysis

To provide a comprehensive overview of the statistical modeling results, the key findings for each pathogen are summarized in Table 5. It should be noted that the moderation analysis presented in Section 3.3 does not reveal a statistically significant interaction between spore concentration and variety for *B. graminis* and *P. tritici-repentis*. However, to enable direct comparison among all pathogens, variety-specific slopes have been estimated using Model 5. The results of the pairwise comparison given in Table 4 confirm that the moderation effect is non-significant and that the slopes for these pathogens are statistically comparable across all varieties.

Table 5. Summary of the final statistical models.

Pathogen	Final Model	Moderation Effect	Differentiation
<i>B. graminis</i>	Model 4	Not significant	No
<i>P. striiformis</i>	Model 5	Significant	Yes
<i>P. tritici-repentis</i>	Model 4	Not significant	No
<i>P. tritici</i>	Model 5	Significant	Yes

4. Discussion

4.1. Statistical Associations and Biological Interpretations

Statistically, the moderation analysis confirmed the hypothesis that the relationship between airborne spore concentration and foliar disease severity is non constant, but significantly moderated by varieties identity for certain pathogens. Among the considered pathogens, three (*B. graminis*, *P. striiformis*, *P. tritici*) are biotrophic [18,39], while *P. tritici-repentis* is a hemibiotrophic pathogen [40]. Statistically, all the considered varieties have shown a significant positive correlation with hemibiotrophic pathogen *P. tritici-repentis*. Biologically, such a response could be explained by a distinct infection process driven by the production of specific protein toxins (e.g., ToxA, ToxB, ToxC, etc.) [23].

A clear differentiation of varieties by resistance level is observed for biotrophic pathogens. Genetically resistant varieties have demonstrated a statistically insignificant relationship between spore concentration and disease development, whereas susceptible varieties exhibited a statistically significant relationship. Comparison of the obtained statistical results with the previous investigation on varietal resistance [23,41] revealed a high degree of consistency for *P. tritici*, whereas sufficient discrepancies have been observed for *B. graminis* and *P. striiformis* [23,41]. The main findings and comparison with studies performed by Volkova and Izvarina [42] related to varietal susceptibility are the following:

- For *B. graminis*, the variety Svarog, classified in literature as moderately resistant, exhibit susceptibility according to the models comparable to the variety Grom. This discrepancy may be attributed to inter-annual weather variability. Thus, in 2023, which is favorable for powdery mildew development, even moderately resistant varieties exhibit increased susceptibility under high infectious load [43].
- For *P. tritici*, statistical models for resistance classification are consistent with the literature data. True resistant varieties (Svarog, Bezostaya 100, and Alekseych) show no statistically significant relationship with spore concentration, while susceptible varieties (Grom and Yuka) reveal a positive correlation.
- For *P. striiformis*, the models reveal a significant positive relationship indicating susceptibility for the varieties Grom, Yuka, and Bezostaya 100. The variety Yuka, classified in

the literature as moderately susceptible, show the highest susceptibility compared to other varieties according to the models. Similarly, the variety Bezostaya 100, generally considered as moderately resistant to yellow rust, exhibits significant positive slope in models. These discrepancies may be due to the specific weather conditions in the years analyzed (2022 and 2024). Meanwhile, the resistant varieties Svarog and Alekseich demonstrate statistically insignificant dependence on spore concentration.

- For *P. tritici-repentis*, the lack of variety differentiation in the models, despite literature data on resistance differences, is likely related to the limited range of weather conditions in the analyzed years (2023–2024), which did not provide contrasting conditions for the manifestation of genetic resistance differences. Furthermore, conidial generation cycle of this pathogen ranges from 7 to 20 days, which cannot be fully considered by the one-phenological stage lag interval used in the constructed models and might be masked subtle varietal differences. This also explains that the Alekseich variety, which according to the experimental data exhibited a higher degree of susceptibility to disease than the other varieties (see Figure 6), does not have varietal differentiation.

4.2. Methodological Aspects and Model Limitations

In this study, foliar disease severity was assessed using different standardized scales: the Peterson scale for rusts [31], the Saari–Prescott scale for tan spot [32], and the CIMMYT scale for powdery mildew [33]. Although all these scales aim to quantify the percentage of damaged leaf area, they were developed specifically to account for the distinct symptomatology and infection types of each pathogen. Because of these methodological differences in scale design and pathogen biology, the regression slopes cannot be directly compared across different pathogens and it can be only concluded that variety identity moderates the spore–disease relationship. Therefore, the obtained results could have practical significance for developing precision crop protection strategies. Namely, the established variety-specific slopes indicate that spore concentration thresholds for initiating fungicide treatment could be differentiated depending on variety in the future.

Several limitations of the current study should be acknowledged. A limitation of this study is the use of “year” as a proxy for environmental variation, which prevents the interpretation of specific weather effects. Future research will focus on the integration of specific climatic covariates such as temperature, humidity and precipitation into the models to disentangle these complex interactions and identify conditions under which genetic resistance is realized most effectively.

A broader methodological limitation of this study is the assumption that disease symptoms appear exactly one phenological stage after spore detection. Since the temporal duration of phenological stages is not fixed and biological incubation periods vary significantly among pathogens (ranging from 4 to 21 days), this fixed one-stage lag is a certain simplification. Although this structure is empirically justified by model fit comparisons and data constraints, it may affect the precision of estimates for pathogens with longer or more variable infection cycles. Further studies with higher-frequency temporal sampling should explore alternative and biologically informed lag structures.

5. Conclusions

This study investigates the relationship between airborne spore concentration and foliar disease severity in winter wheat, testing the core hypothesis that susceptibility of variety can significantly moderate this relationship. It is demonstrated that the obtained statistical moderation models are highly effective in differentiation of the epidemiological behavior of pathogens. For biotrophic pathogens (*P. striiformis* and *P. triticina*), genetic resistance successfully reduced the influence of spore concentration on the disease sever-

ity, confirming the critical role of variety selection in mitigating epidemic risks [24,30]. Conversely, the hemibiotrophic *P. tritici-repentis* exhibited a consistent response across all varieties, potentially due to toxin-mediated infection mechanisms and a relatively brief incubation period of 3–7 days. [23].

Furthermore, our findings demonstrate that combining airborne spore monitoring with variety-specific statistical modelling offers a robust framework for early disease risk assessment. This supports the growing view that aerobiological data has the potential to facilitate the transition from calendar-based to precision crop protection strategies [1,8]. However, since disease severity is assessed using different standardized scales, direct cross-pathogen comparison of association strength remains limited. Future studies must integrate specific climatic covariates in order to transit these statistical associations into operational decision-support systems.

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Abbreviations

The following abbreviations are used in this manuscript:

FSBSI FSCBPP	Federal State Budgetary Scientific Institution “Federal Scientific Center of Biological Plant Protection”
LMMs	Linear mixed models
CIMMYT	International Maize and Wheat Improvement Center
AICc	Akaike’s information criterion corrected
BIC	Bayesian information criterion
LRT	likelihood ratio test
HSD	honestly significant difference
CI	confidence intervals
OLS	ordinary least squares

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