

4th INTERNATIONAL MEETING AGRISCIENCE & PRACTICE (ASP 2024)

Development of hypothetical infection model based on environmental variables for *Plasmopara viticola* (Berk. & M.A. Curtis) Berl. & De Toni

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Introduction

A hypothetical infection model for *P. viticola* was created in this study using field data. This model utilizes average temperature and wetness duration as inputs, and its findings are compared with actual disease development data. This process provides an overview of how theoretical and scientific assumptions align with real field observations.

Material and Methods

The exploration was conducted from May 29, 2023, until July 3, 2023, in a vineyard located at Smilica, near Kavadarci, Republic of North Macedonia (41°42'71.4" N, 22°0'10.75" E), planted with the Vranec variety. The vines were double cane pruned and vertically trained (double Guyot). The IBM® SPSS® Statistics software was used for regression analysis environmental variables between (average temperature; wetness duration; mean dew point temperature, and minimum temperature) and disease severity. The process involved data collection, linear regression analysis (Equation1), and quadratic polynomial regression for nonlinear relationships (Equation2). A hypothetical infection model (Equation 3) for *P.viticola* was developed based on field conditions, with coefficients calculated from regression equations. The control variant consisted of 90 vines, where downy mildew was monitored on the leaves. At the vineyard, the control was treated just once with active ingredient folpet on 20 May 2023. The software tool ImageJ uses fuzzy logic techniques for the analysis of a disease severity which calculates the ratio between infected and healthy tissue (Figure 1).

Results and discussion







Figure 2. An overview of climatic factors contributing to dew point formation is crucial for the onset, progression, and decline of *P. viticola* infection. Data were obtained from the ERA5 ag dataset provided by the European Centre for Medium-Range Weather Forecasts (ECMWF).

Hypothetical Infection Model Building

Linear model calculation:

 $\hat{y} = \beta o + \beta 1(x) = -8,879 + 13,249 \times 3,8 = 41,5 \log(0.415) \approx -0.38 = -(-0.38) = 0,38 \pm 0,03 = 0,35$ is the coefficient representing W in equation 3

Quadratic model calculation:

$$x$$
-vertex = $-\frac{b}{2a} = -\frac{77.4}{2\times(-1.7)} = 26,78201 \approx 26,8; \frac{26.8}{100} = 0,268$
 $log(0.268) \approx -0.57187 = -(-0.57187) = 0,57$ is the coefficient representing B in equation 3; A- is a probability (P^) where we have two conditions on the field that can occur in case of favorable external conditions for the development of *P.viticola* and that an infection may or may not happen, so according to that

 $P^{\wedge} = \frac{1}{2} = 0.5$; t- research duration is expressed in days



Figure 1. A- The original image of the diseased leaf; B- The selected diseased area on a leaf

 $\hat{y} = \beta o + \beta 1(x)$...Equation 1 $y = ax^2 + bx + c$; x-vertex = $-\frac{b}{2a}$... Equation 2 $H = A^{-bt} \times cos (Bt + Wt)$...Equation 3



Research duration is expressed in days

Figure 3. Visualization of Data Obtained from Hypothetical Infection Model Building

Conclusion

The hypothetical infection model shows that it detects the moment when the infection reaches its maximum, which is a positive aspect. However, when the curve shows decreasing values, it tends to overpredict. Furthermore, as the infection gains momentum, it becomes less predictable.

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