Innovative approach to diagnosing the development of net blotch in winter barley

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Abstract. The article demonstrates the possibility of applying intelligent digital technologies to forecast the development of net blotch disease in winter barley caused by Pyrenophora teres. The obtained intelligent solution in the form of a binary decision tree has the ability to determine scenarios of net blotch development into three classes: depressive, moderate, and epiphytotic. To effectively train the model during the period from 2021 to 2023, field and laboratory experiments were conducted on the research sites of the Federal Research Center of Biological Plant Protection. The experiments collected data on the degree of leaf damage, the type of resistance of the variety, the growth phase at which primary infection occurred, and the average relative air humidity during the vegetation period in which infection occurred. The total sample size was 249 observations. The trained model demonstrated high classification accuracy on both the training and test sets, with an accuracy rate exceeding 0.96 and 0.92, respectively. The study shows that the innovative method discussed in the article for forecasting the development of net blotch in winter barley can be successfully integrated into the overall strategy of phytosanitary diagnostics of grain crops, including barley.

1 Introduction

The intensive development and widespread adoption of digital technologies in recent years have been transforming the landscape of key sectors in the economy and social sphere. The agricultural sector has not been an exception, and its transformation is aimed at addressing a range of global challenges, with a particular focus on combating diseases and pests affecting grain crops. The active development and spread of harmful organisms in agriculture are influenced by several global factors, including climate change, low genetic diversity in agricultural crops, and uncontrolled use of chemical protection and fertilizers. In these conditions, digital technologies become a reliable ally for farmers, offering broad

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opportunities not only for efficient management of production processes but also for the development of intelligent strategies to combat pathogens.

The most important grain crop for global agriculture is winter barley, widely used as both a feed and food crop, ranking fourth in global food production after maize, rice, and wheat [1]. Russia holds the top position in the world in the production of this grain crop, annually cultivating up to 8 million hectares and harvesting approximately 23 million tons. One of the diseases significantly impacting the yield of winter barley is net blotch, caused by the fungus Pyrenophora teres. According to data from the 1990s and 2000s, this pathogen has become dominant in the crop phytocenosis, both in southern Russia and worldwide [2]. Annual losses from net blotch on the leaves of winter barley are substantial, ranging from 15 to 50 percent. Epidemics occur approximately five times every ten years. Under favorable meteorological conditions, the prevalence of the disease on susceptible varieties can reach 100%, with a development rate of 50-90% [2, 3].

Modern integrated protection of barley crops from net blotch involves the application of various phytosanitary measures: cultivation of resistant varieties, agrotechnical methods, seed treatment, and field spraying with fungicides. However, many of these practices demonstrate low effectiveness in combating the disease. Among the barley varieties cultivated in Russia, there are very few with sufficient resistance to net blotch. Agrotechnical measures do not fully protect crops from the disease; certain practices can only slightly slow down its development. Seed treatment also proves to be less effective. Guaranteed crop preservation can only be ensured through plant spraying with fungicides that are effective against this particular disease. To make a timely decision on the advisability of applying fungicides against net blotch on barley leaves, it is necessary to assess the level of threat posed by the disease under specific conditions (variety, weather, growth phase). Undoubtedly, addressing the issue of predicting the degree of net blotch development in winter barley cannot be achieved today without transitioning to innovative methods, with artificial intelligence (AI) forming the basis of these methods.

Note that in previous articles [4-6], the authors considered and solved other types of diagnostic tasks related to diseases of cereal crops, including winter barley. Specifically, utilizing computer vision technologies has resulted in high diagnostic accuracy and effectiveness in tasks such as the classification and segmentation of diseases in winter barley.

The aim of this study is to substantiate the possibility of using digital intelligent technologies in predicting the development of net blotch in winter barley.

2 Materials and methods

The preparation of infectious material for winter barley plants was carried out in greenhouse complexes and laboratory conditions at the Federal Research Center of Biological Plant Protection, following approved methodologies and standardized procedures. For artificial plant infection, inoculation was performed in the juvenile phase. The cultivation of the fungal inoculum and plant inoculation in the adult plant phase under field conditions were conducted using standard methods [7]. In field conditions, monitoring was initiated from the first manifestation of the disease, with subsequent assessments carried out until the milky-waxy ripeness phase of the grain at intervals of 10-12 days.

During the implementation of the experiment to model the development of net blotch, the following input factors were taken into account:

- observed current disease development (%) – a parameter reflecting the current level of leaf infection by the disease;
- type of resistance of the variety (R = resistant / S = susceptible) – a factor characterizing the degree of susceptibility of the variety to the pathogen.
• stage development in which primary infection occurred – tillering, jointing, flag leaf emerging.
• average relative air humidity (%) – calculated for the vegetative phase in which infection occurred.

The target variable (forecast) is the degree of disease development at the early milk ripening stage with the following possible values: depression (D), moderate development (M), or epiphytoty (E).

The total volume of the obtained labeled dataset was 249 observations. To assess the model's performance, the dataset was split into two parts: 50 objects were randomly selected for training, and 199 for the final evaluation. The division of the dataset into training and testing sets is a crucial step in the machine learning methodology, aimed at testing the model's ability to generalize and accurately predict on new data not encountered during training.

The decision trees were chosen as the base model family. The selection of decision trees for predicting the development of net blotch in winter barley is justified by several factors that make these algorithms an attractive choice as the basic model for analysis.

1) Decision trees have a high degree of interpretability. With a structure resembling an acyclic graph, the decision-making process involves traversing the graph from the initial (root) node to the corresponding leaf (terminal) node.

2) Decision trees handle categorical data well, which is often encountered in the agricultural sector (two out of the four features describing the obtained data are categorical variables).

3) Decision trees are capable of detecting and modeling nonlinear dependencies between input features and the target variable. This is important given the complexity of interactions between various factors in agriculture.

4) Training decision trees usually do not require extensive computational resources, making them accessible for application in various conditions, including agriculture.

3 Results

The recursive machine learning procedure used in the study for building decision trees is called Induction of Decision 3 (ID3). This procedure iteratively divides objects into two or more groups at each stage. The algorithm begins constructing the tree with the root node and at each level selects the predicate (splitting condition) that best determines the current dataset. The process is recursively repeated for each obtained subgroup. During tree construction, the choice of the best predicate is made by optimizing the branching information criterion, which is a specific metric. This metric enables the algorithm to understand which feature is best suited for efficiently dividing the data at each tree level.

In our study, we utilized the widely used and commonly applied Gini criterion (1). This criterion measures how many pairs of objects belonging to the same class will simultaneously end up in the left or right child node of the tree (assuming their predicate values match).

\[
Gini(\beta, X) = \#(x_i, x_j): y_i = y_j, \beta(x_i) = \beta(x_j)
\]

where \(X\) is the training dataset, \(x_i, x_j\) – are features (factors) of objects in the training dataset, \(\beta\) – predicate, \# – is an operator counting the number of pairs satisfying the condition.

As a result of applying the ID3 procedure, a decision tree was formed, as shown in Fig. 1. At each internal node of the tree, a split is made based on one of the four features. Categorical variables were subjected to the "one-hot encoding" procedure [8]. Thus, variables initially having two levels of categories were binary-encoded using labels 0 and 1. In this work, an example of such a variable is "susceptibility of the variety" (susceptible = 1, resistant = 0). In cases where a feature had more than two categories, a separate binary feature was created for each category. For example, if the «stage development» feature had categories A,
B, C, then after encoding, three new binary features would appear, each reflecting the presence or absence of the corresponding category.

This procedure allows for the consideration of the influence of categorical variables when building a decision tree, making it more flexible and capable of taking into account various factors in the data. Thus, the decision tree becomes more adaptive to different types of variables, enhancing its generalization ability.

To assess the predictive performance of the trained algorithm, matrices confusion of the models were calculated for the training set (fig. 2) and the test set (fig. 3). From fig. 2, it can be seen that out of 199 objects in the training set, the model made exactly 7 mistakes, confusing the class of moderate disease development with epiphytotic. For the test (holdout) set, which was not used in the training process, the number of errors was 4 out of 50. Thus, the accuracy metric (the proportion of correct algorithm predictions) on the training and test data is 0.96 and 0.92, respectively, which is a sufficiently high-quality indicator.

Fig. 1. Decision tree classifying scenarios of net blotch development
4 Discussion

The innovative method discussed in the article for forecasting the development of net blotch in winter barley can be successfully integrated into the overall strategy of phytosanitary diagnostics for cereal crops, including barley.

In the first stage of the strategy, computer vision technologies based on convolutional neural network architectures are applied for disease identification. Two types of tasks are addressed here: multi-class and multi-label classification. In the first case, each object corresponds to one class, and in the second case, to multiple classes, allowing for the possibility of the combined impact of various diseases.

After identifying the pathogen, the next stage involves determining the current level of disease development. For this task, it is recommended to use a semantic segmentation model built on the U-Net architecture. This model preserves spatial information during resolution enhancement and performs upsampling more smoothly.

The results of the first two blocks, along with expert information on the growth phase and meteorological data, are input into the third model – a decision tree. This model forecasts the development of the disease, enabling farmers to make informed decisions regarding management and disease control in agriculture.

Fig. 2. Confusion matrix of the model on the training set  
Fig. 3. Confusion matrix of the model on the test set

Fig. 4. Strategy for phytosanitary diagnostics of winter barley
5 Conclusion

The paper proposes an innovative approach to forecasting the development of the harmful disease in winter barley – net blotch caused by the fungus Pyrenophora teres. The approach is based on the use of digital intelligent technologies implemented in the form of binary decision trees, classifying possible scenarios of disease development into three categories: depressive, moderate, and epiphytotic development. Decision trees possess several advantages, including interpretability, handling of categorical features, and the ability to model nonlinear dependencies, which motivated the choice of this model family. It is demonstrated that the trained model shows high classification quality (accuracy on training and testing data is 0.96 and 0.92, respectively). Considering the balanced nature of the original dataset, the accuracy metric confirms the effectiveness of the trained model. Thus, the innovative approach to forecasting the development of net blotch in winter barley presented in this work has significant potential for integration into the overall strategy of phytosanitary diagnostics for cereal crops.

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