

Digital Processing of Light Microscopy Images in Plant Pathogen Diagnostics

Abstract

In addition to molecular composition, macroscopic symptoms, and host specificity, microscopic investigation remains an indispensable method in the recognition process of the causal agents of plant diseases. Although electron microscopy is a powerful technique for such purposes, it is not always necessary. We utilize digital processing of light microscopy images to distinguish between asexual stages of downy mildews (*Peronosporaceae*, *Oomycetes*).

The morphological structures appropriate for their classification include the pattern of conidiosporangiothecium branching (dichotomous, monopodial, sympodial), the length and type of branches, the shape of tips (presence/absence of swelling), the number of sterigmata, and the shape of conidiosporangium. For the case study, representatives of five genera with morphological features relatively developed from the biological point of view and with frequent occurrence in Central Europe were used: *Bremia lactucae* (lettuce downy mildew), *Plasmopara viticola* (grapevine downy mildew), *Peronospora destructor* (onion downy mildew), *Pseudoperonospora cubensis* (downy mildew of cucurbits), and *Phytophthora infestans* (potato late blight).

The goals were to 1/ pre-process raw light microscopy images in order to measure pre-selected features; 2/ determine variances in the anamorphic state of downy mildews and select a group of features convenient for the purpose of pattern classification; 3/ develop a proper classification method with appropriate sensitivity. Convenient image processing and pattern recognition methods were utilized.

According to the results, the five examined species of crop pathogens could be well discriminated using the selected features as the method preserved differences among closely relative genera. Future perspective is to test whether the method may be used for diagnosis of the species within a genus. As the automatic structure recognition, feature selection and pattern classification is based on software specifications, the defined characteristics of biological taxons may stand a limitation to suitability of the proposed method.