



Prediction of Sclerotinia Spore Release in Oilseed Rape Fields in the United Kingdom

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Abstract

A set of experiments to measure the presence of Sclerotinia spores in oilseed rape fields was undertaken in a specially sown field in the Rothamsted Research centre (just north of London). Spores were measured by assessing the Sclerotinia DNA present on wax tapes retrieved from Burkard spore trapping devices. The corresponding weather data was taken from a climate monitoring station less than 1 kilometre away.

Sclerotinia sclerotia were deliberately buried in a small square inside the Oilseed Rape field and naturally conditioned over the winter and early spring months to produce sporulation structures (apothecia) in the spring. In the early spring spore trapping devices were placed in the centre of the small square to continuously record daily concentrations of airborne spores by impaction onto wax-coated tapes, which were removed and replaced weekly. Upon removal, the wax tapes were taken away for quantitative PCR analysis in the laboratories of Rothamsted Research.

Using the measured weather data and also information about the Rothamsted site such as soil composition and field crop rotations a prediction was made of the likelihood of spores being released according to the Raiso-Sclero model which was originally developed primarily for prediction of Sclerotinia infection in France. The Raiso-Sclero model was able to correctly predict nearly all of the major spore releases. Depending on the threshold chosen there was either one major false positive, one major false negative or one minor false positive and one minor false negative.

The results of the analysis support the use of the Raiso-Sclero model in Oilseed Rape fields in the United Kingdom to predict the likelihood of a large-scale release of ascospores during the spring flowering season. Further experimental work to take place this year and next at multiple locations to provide additional validation.

Keywords: Sclerotinia, Oilseed Rape, Ascospores, Raiso-Sclero model, Quantitative PCR analysis.