Effects of pathogen sexual reproduction on the evolutionary and epidemiological control provided by deployment strategies for two major resistance genes in agricultural landscapes

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EXPLOITING SIMILARITIES WITHIN PHYLOGENETIC CLADES OF COLLETOTRICHUM SPP. TO DEVELOP A MECHANISTIC, WEATHER-DRIVEN MODEL FOR ANTHRACNOSE DISEASES

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Text
Fungi of the genus Colletotrichum cause serious pre- and post-harvest losses to several agricultural crops worldwide. A systematic literature review was conducted to retrieve the metadata on the influence of temperature on four biological processes: (mycelial growth, conidial germination, infection by conidia, and sporulation) for seven Colletotrichum clades (acutatum, graminicola, destructivum, dematium, gloeosporioides, and orbiculare) and the singleton species, C. coccodes. The metadata was first analyzed to define inter- and intra-clades similarities and differences, and then used to develop temperature-dependent equations representing the effect of temperature on the biological processes for the different clades. This clade-based approach was used to develop a mechanistic, weather-driven model for Colletotrichum anthracnose diseases, able to predict anthracnose progress during the growing season on the aerial organs of different herbaceous and fruit tree crops. The model was evaluated against the disease progress of fungi belonging to five clades on six different hosts by using data from epidemics occurred in Italy, the USA, Canada, and Japan. Results showed high concordance between model predictions and field data, with overall concordance correlation coefficient of 0.928. After further validation, the model could be used to support decision-making for crop protection in a wide range of cropping systems.

C5.1-4

EFFECTS OF PATHOGEN SEXUAL REPRODUCTION ON THE EVOLUTIONARY AND EPIDEMIOLOGICAL CONTROL PROVIDED BY DEPLOYMENT STRATEGIES FOR TWO MAJOR RESISTANCE GENES IN AGRICULTURAL LANDSCAPES

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Text
Resistant cultivars are of value for protecting crops from disease, but can be rapidly overcome by pathogens. Several strategies have been proposed to delay pathogen adaptation (evolutionary control), while maintaining effective protection (epidemiological control). Resistance genes can be *i*) combined in the same cultivar (pyramiding), *ii*) deployed in different cultivars sown in the same field (mixtures) or in different fields (mosaics), or *iii*) alternated over time (rotations). The outcomes of these strategies have been investigated principally in pathogens displaying pure clonal reproduction, but many pathogens have at least one sexual event in their annual life cycles. Sexual reproduction may promote the emergence of superpathogens adapted to all the resistance genes deployed. Here we improved the spatially explicit stochastic model *landsepi* to include pathogen sexual

reproduction, and then investigated the effect of sexual reproduction on evolutionary and epidemiological outcomes across deployment strategies for two major resistance genes. Sexual reproduction favours the establishment of a superpathogen when single mutant pathogens are present together at a sufficiently high frequency, as in mosaic and mixture strategies. However, sexual reproduction did not affect the optimal strategy recommendations for a wide range of mutation probabilities, associated fitness costs, and landscape organisations.

C5.1-5

A SPATIALLY EXPLICIT NETWORK MODEL TO ASSESS THE EFFECTIVENESS OF WITHIN- AND BETWEEN-SITE TREATMENT ON EPIDEMIC SPREAD ACROSS A LANDSCAPE

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Text
The relevance of networks for improved understanding and control of plant disease epidemics has gained prominence in plant pathology in the last two decades. Disease spread between nodes in a network has been a central topic and limited attention has been given to within-node dynamics. We develop a spatially explicitly network model to establish relative effectiveness of implementing within-node treatment (protectant or curative fungicide and roguing) and between-node treatment (quarantine, trade) on epidemic spread of an aerially dispersed pathogen. The dynamic component of the model is captured by the number of host units that are either Susceptible (S), Protected (P), Exposed (E), Infected (I), Treated (T) or Removed. Within-node dynamics modeled using rates at which, I infect others, E becomes infectious, I loses infectivity, and fungicide effectiveness parameters. Spread between nodes is modeled using a power-law dispersal kernel and the rate of trade between nodes. Surveillance time is drawn from a uniform random number and when disease is detected, a node is treated as described above. Simulations are run with the model, representing experiments with three network structures [small-world, random, and scale-free] of 200 nodes with varying sizes with three different levels of connectivity for network sizes of 200, 400 and 800. Results of the simulations will be discussed and we plan to avail the model in an open-source environment for use by interested researchers.

C5.1-6

MODELING THE AIRBORNE INOCULUM OF POLYSTIGMA AMYGDALINUM FOR IMPROVING THE CONTROL OF ALMOND RED LEAF BLOTCH

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