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Modelling the effects of climate on the incidence of the nut rot of chestnuts caused by *Gnomoniopsis castanea*

Guglielmo Lione, Luana Giordano, Fabiano Sillo, Paolo Gonthier

Department of Agricultural, Forest and Food Sciences, University of Torino, Grugliasco, ITALY
guglielmo.lione@unito.it

Gnomoniopsis castanea is an emerging fungal pathogen causing nut rot on chestnut trees. In order to model the incidence of *G. castanea* as a function of climate a Partial Least Squares Regression (PLSR) analysis was performed in four steps: I) assessment of the pathogen incidence, II) pre-selection of predictors, III) models fitting, IV) external validation.
I) 40 to 120 ripe nuts were sampled in each of 12 sites located in the north-west of Italy in 2011. The incidence of *G. castanea* in each site was assessed by determining the amount (in %) of infected nuts. The diagnosis of the pathogen was performed with both isolation trials and molecular analyses. The incidence ranged from 20% to 93% depending on site.
II) Geostatistical analyses involving the Ripley's function, the Nearest Neighbor Hierarchical Clustering (NNHC) and the spatial autocorrelation index of Moran revealed that, despite the geographical clustering of sites ($P<0.05$), the incidence of *G. castanea* was not spatially autocorrelated ($P>0.05$). This finding suggests an influence of site-dependent factors on the disease. A Principal Coordinates Analysis (PCoA) followed by a Hierarchical Cluster Analysis (HCA) on maximum, mean and minimum temperatures and on rainfalls showed that warmer temperatures were associated to a significant increase of the incidence (+10.4%; $P<0.05$).
III) The temperatures of the months before nut harvesting were selected as predictors for the fit of PLSR models on the logit transformed values of *G. castanea* incidence. Cross-validation and bootstrap analyses were carried out to perform models selection.
IV) External validation performed on data collected from sites not used for models fitting showed the good predictive abilities of the models ($\rho>0.70$; $P<0.05$).
All the above findings demonstrate that there is a relation between the climate and the incidence of *G. castanea*, providing statistical tools to forecast the incidence of the disease at site level.