Potential Response of Soil-Borne Fungal Pathogens Affecting Crops to a Scenario of Climate Change in Europe

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Abstract: A study was carried out on the potential response of soil-borne pathogens causing crop yield losses under a climate change scenario in Europe. A controlled chamber set of experiments was carried out to quantify pathogen response to temperature using pure colonies of three soil-borne fungi, representative of low (*Fusarium nivale*), medium-high (*Athelia rolfsii*) and high (*Macrophomina phaseolina*) temperature requirements. A generic model to simulate fungal growth response to temperature based on these experiments was developed and linked to a soil temperature model component, and to components to simulate soil water content accounting for crop water uptake of potential hosts. Pathogens relative growth was simulated over Europe using the IPCC A1B emission scenario as realization of the Hadley-CM3 global climate model, available from the European Commission and processed for use with biophysical models. The simulations resulting from using the time span centred on 2030 were compared to the baseline, centred on the year 2000, using a sample of 30 years of daily weather. The general trend of soil-borne pathogens response to the scenario of climate change is a relative increase in growth in colder areas of Europe, as a function of their temperature requirements. Projections of *F. nivale* in the future indicate a relative increase of this winter pathogen of wheat in Northern European countries. *A. rolfsii* and *M. phaseolina*, two soil-borne pathogens typical of warmer agricultural areas, could find more favourable conditions in areas of the Central Europe, but they differentiated in Southern Europe where *A. rolfsii* resulted affected by summer soil temperatures above optimum.

Keywords*:* modelling crop diseases, BioMA platform, wheat foot rot, charcoal rot, southern blight.

1   INTRODUCTION

Soil borne fungal pathogens are the causal agents of root rot in herbaceous and fruit tree crops, and represent the main biotic components of yield decline in intensively cultivated areas. Those pathogens survive on organic residues in soils and cause root rot with impact ranging in severity from decreased growth rates to the death of the plant, depending on the host susceptibility and/or on environmental conditions [Redman et al. 2001]. The most common soil borne pathogens are *Pythium* spp., *Rhizoctonia solani*, *Rhizoctonia* spp., *Fusarium* spp., *Phoma* spp., *Cylindrocarpon* spp. and *Sclerotinia sclerotiorum*. Some of the more relevant pathosystems as economic return are: *Sclerotinia sclerotiorum*/sunflower [Purdy 1979], *Colletotrichum* coccodes/potato [Lees and Hilton 2003], *Pythium tracheiphylum*/lettuce [Gonzalez et al. 2004]; *Macrophomina phaseolina*/sunflower; *Cochliobolus sativus*/wheat and barley [Mathre et al. 2003]; although many soil-borne pathogens can attack several hosts, the most representative is *Pythium* spp. (*Pythium ultimum* or *Pythium irregulare* and others), agents of damping-off of many

herbaceous and woody crops [CAB 1990]. Furthermore, crop yield losses are due in several cases to a complex of pathogens such as the case of black root rot of strawberry [Manici et al. 2005]; apple replant disease [Mazzola 1998]; common root rot and Fusarium foot rot of wheat [Wegulo and Klein 2010].

According to the Intergovernmental Panel on Climate Change [IPCC 2007], predictions for the 21th century indicate a generalized increase of air temperature. Such increment will potentially impact on soil temperature regimes; consequently soil borne pathogens may increase their biological pressure on crops, causing higher yield losses, and may experience a shift in their target hosts range.

The epidemiology of soil borne pathogens is affected by several biological and physiochemical factors which increase the complexity in formalizing their behaviour in process-based biophysical models. However, as most of fungal pathogens causing root rot can survive in soil and colonize roots of host crops in the mycelium state, it is possible to explore in controlled conditions via pure cultures, their growth response to temperature [Pettitt et al 1996]. Soil temperature is in fact the main driving force of their development and the key physiochemical factor of their ecology, being water often non limiting in presence of crops. Therefore an *in vitro* set of experiments on mycelia growth rate in response to temperature was carried out, aiming at developing a model to reproduce the response of some soil borne pathogens which has been successively applied to scenarios of climate change.

2   MATERIALS AND METHODS

The work was carried out in three phases: a) a controlled chamber set of experiments to quantify pathogens response to temperature using an in vitro test with pure culture of three reference soil borne pathogens; b) the development of a generic model to simulate growth response to temperature; and c) the application of the model in spatialized simulation runs to test pathogen responses to soil temperature over Europe, comparing future scenarios to a baseline weather.

2.1   Soil-borne pathogens response to temperature

Three reference soil borne pathogens: *Fusarium nivale* (*Microdochium nivale*) (FN), *Athelia rolfsii* (AR) and *Macrophomina phaseolina (MP)* were chosen for this pilot experiment on basis on their different temperature requirement and for rising interest of their impact on the crops. *Fusarium nivale* (*Microdochium nivale*) (FN) is the main agent of Fusarium patch or foot rot of cereals in cold season; *Athelia rolfsii* (AR) and *Macrophomina phaseolina* (MP) are two facultative pathogens causing yield losses on a large range of crops in warm season, respectively agent of Southern blight (or Athelia wilt) and Charcoal rot, which have been recently reported to cause damage also in warm temperate areas. Three Petri plates (dia. 9 cm) containing 10 mL of Potato Sucrose Agar, a conventional growing media for filamentous fungi, were inoculated in the centre with a 4mm agar disk taken from the pure colonies of each of isolates labelled F_niv04, Sc_rol09 and MAC184 in the culture collection of CRA-CIN Agronomy [Manici 2012]. Inoculated plates were incubated at 8-10 different temperatures ranging from 4°C to 45°C, according to the temperature requirements of the pathogens, in a Binder KBW 400 growth chamber (from 8 to 45°C) and in a ventilated cooled (from 1 to 9°C) chamber. For each testing temperature, the minor and major radii of each colony were measured at the beginning and end of working day for temperatures close to the expected optimum, and daily for other temperatures, until each colony reached the edge of the Petri plate, or the 7th day of incubation was reached. Response was expressed as growth rate (mm day^{-1}), as resulting as average of the daily average increase of the radii. Growth tests were repeated twice for each temperature regime, and the average value of two replicates was used in this study. The controlled chamber experiment was carried out during spring 2011. Other soil-borne species were grown in the controlled chamber but the results are not presented here.

2.2   Modelling temperature response

Growth rates were normalized by dividing the observed response to a given temperature by the maximum growth rate measured for a given pathogen. This approximation (i.e., slightly higher maximum rates could have been measured at the real optimum temperature, possibly not tested) was used instead of selecting the maximum of the fitted rate; new controlled chamber experiments are being run to enrich measured responses and models will be re-fitted. However, the current, exploratory fitting on the data available captures the essential diversity of thermal responses among the pathogens considered. The function proposed by Yan and Hunt [1999] was used to fit the response to temperature. The curve is based on the three cardinal temperatures: T_{min}, minimum temperature for growth (below this temperature there is no observable growth), T_{opt}, optimum temperature for growth, and T_{max}, maximum temperature for growth (above this temperature the growth ceases). The function is:

$$f(T) = \left(\frac{T_{max}-T}{T_{max}-T_{opt}}\right)\left(\frac{T-T_{min}}{T_{opt}-T_{min}}\right)^{\left(\frac{T_{opt}-T_{min}}{T_{max}-T_{opt}}\right)} \tag{1}$$

The function was chosen primarily because of the biological meaning of its parameters, and also because of its flexibility (it changes shape from a parabola to a curve including a flex point according to the ratio of the distance T_{max} - T_{opt}, and T_{opt} - T_{min}). Parameters were optimized using the Microsoft Excel Solver to minimize the sum of squares of differences estimated-observed growth rates. The constraint imposed to the optimization was setting T_{min} to the known value from literature, given that the optimization would yield biologically unacceptable low results without such bound, with a negligible gain in minimizing the error (the curve used would have approached asymptotically T_{min}).

The model was implemented as a new software component adopting the architecture presented by Donatelli and Rizzoli [2008]. Modelling solutions for simulating soil temperature were tested [Donatelli et al. 2012a] and have become available in the BioMA platform [BioMA 2012]. BioMA (Biophysical Models Applications) is a software framework designed and developed for analysing, parameterizing and running modelling solutions based on biophysical models against a database which includes spatially explicit units, in this case cells of 25 x 25 km. The framework uses framework-independent components, both for the modelling solutions and the graphical user's interface. The component-based structure allows BioMA to implement diverse modelling solutions targeted to specific modelling goals. This framework allows for an easy extension of modelling solutions, hence simplifying the use of the component implemented in a spatially explicit context. Consequently, the soil-borne model component was linked to other components to simulate crop water limited growth and development, soil erosion and runoff, soil water dynamics into the soil profile, and finally soil temperature. All these models, as implemented in such software components, were needed to simulate soil water balance, being soil water content a needed input to estimate soil temperature. Most of the software components used are available for download [Components 2012], and a deployment of the platform accessing weather data via web service is planned for release in the second half of 2012 (allowing running also other modelling solutions). Daily values of soil temperature, at reference depths of 0.05 and 0.1m were then linked as input to the soil-borne pathogens component to simulate the relative growth rates of the tested fungi; the average response was used as response to soil temperature.

2.3   Simulating pathogen response over Europe

A dataset of weather data on scenarios of future climate, suitable for use with biophysical models has recen tly become available from the European

Commission, derived from the ENSEMBLE scenarios, and covering Europe with a grid of 25 x 25 km. ENSEMBLE data were post-processed to make the data set usable with crop models as described by Donatelli et al. [2012b]. Two time spans were chosen as climate inputs for the simulation experiment: the baseline, representing a sample of 30 years of daily weather centred on the year 2000, and the IPCC emission scenario A1B centred on 2030. Average differences between 2030 and 2000 time series are shown for temperature (Figure 1) and rainfall (Figure 2), referring to summer and winter periods.
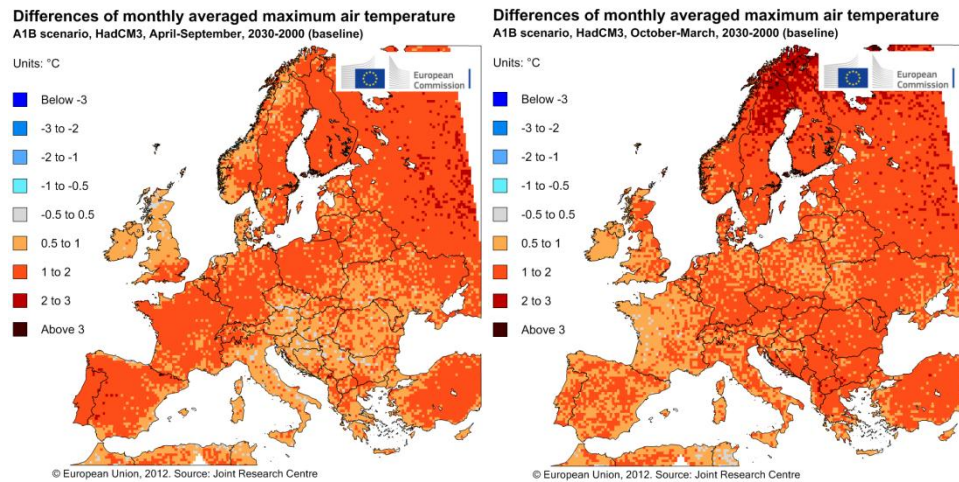
Differences of monthly averaged maximum air temperature
A1B scenario, HadCM3, April-September, 2030-2000 (baseline)

Units: °C

- Below -3
- -3 to -2
- -2 to -1
- -1 to -0.5
- -0.5 to 0.5
- 0.5 to 1
- 1 to 2
- 2 to 3
- Above 3

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Differences of monthly averaged maximum air temperature
A1B scenario, HadCM3, October-March, 2030-2000 (baseline)

Units: °C

- Below -3
- -3 to -2
- -2 to -1
- -1 to -0.5
- -0.5 to 0.5
- 0.5 to 1
- 1 to 2
- 2 to 3
- Above 3

European Commission

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Figure 1. Difference of monthly averaged maximum temperature (HadCM3, A1B, 2030-2000) for April-September (left) and October-March (right), from Donatelli et al. 2012b.
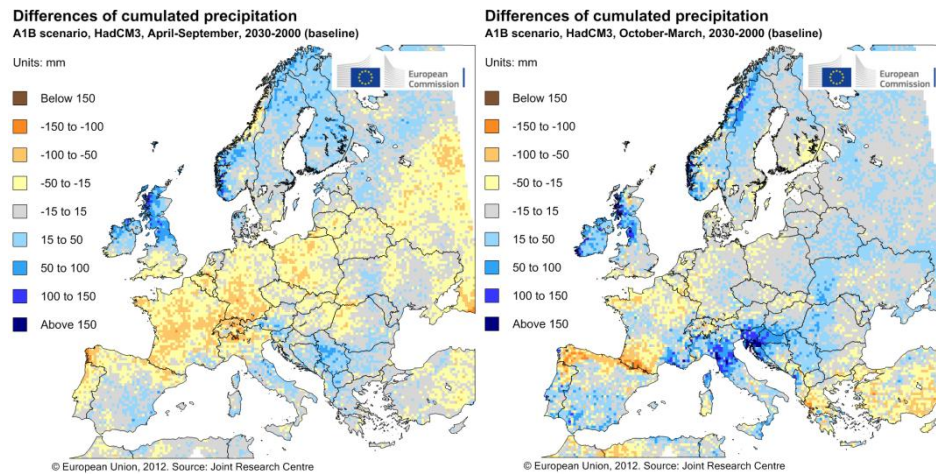
Differences of cumulated precipitation
A1B scenario, HadCM3, April-September, 2030-2000 (baseline)

Units: mm

- Below 150
- -150 to -100
- -100 to -50
- -50 to -15
- -15 to 15
- 15 to 50
- 50 to 100
- 100 to 150
- Above 150

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Differences of cumulated precipitation
A1B scenario, HadCM3, October-March, 2030-2000 (baseline)

Units: mm

- Below 150
- -150 to -100
- -100 to -50
- -50 to -15
- -15 to 15
- 15 to 50
- 50 to 100
- 100 to 150
- Above 150

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Figure 2. Difference of cumulated precipitation (HadCM3, A1B, 2030-2000) for April-September (left) and October-March (right), from Donatelli et al. 2012b.

The realization of the A1B scenario originated from runs of the Hadley-CM3 global circulation model from the UK Met Office Hadley Centre for Climate Change.

The aim of this study was to estimate potential growth of soil-borne pathogens in the future temperature regime compared to current conditions. A daily time step simulation was run for *F. nivale* (FN), *A. rolfsii* (AR), and *M. phaseolina* (MP), given the heterogeneity of their temperature responses, hence representing a broad range of thermal requirements of the pathogens evaluated. In order to estimate crop water uptake, impacting on the water balance in conditions close to the real pathosystems, simulations of FN were run coupled with the simulation of a winter wheat crop, whereas the simulations of SR and MP were run simulating sunflower. The multi-model crop library CropML [Confalonieri et al. 2012], was used, selecting growth functions of the model CropSyst [Stöckle et al., 2003]. No biotic impact on

crops yield was simulated; crop growth was driven by weather variables and soil water availability, assuming no other limitation. Only one synthetic soil profile, representing a loam soil in flat land, was simulated in this analysis. Crops were simulated according to crop masks used in the CGMS (Crop Growth Monitoring System) of the Joint Research Centre – Monitoring Agricultural Resources unit. White cells in the maps indicate that the value for crop presence in crop mask used is null. Agro-management was simulated limited to planting and harvest, according to the CGMS database.

3   RESULTS AND DISCUSSION

Relative growth rates vs. temperature are shown together with the modelled responses (Figure. 3). The estimated parameter values are reported in Table 1.

Table 1. Model parameters

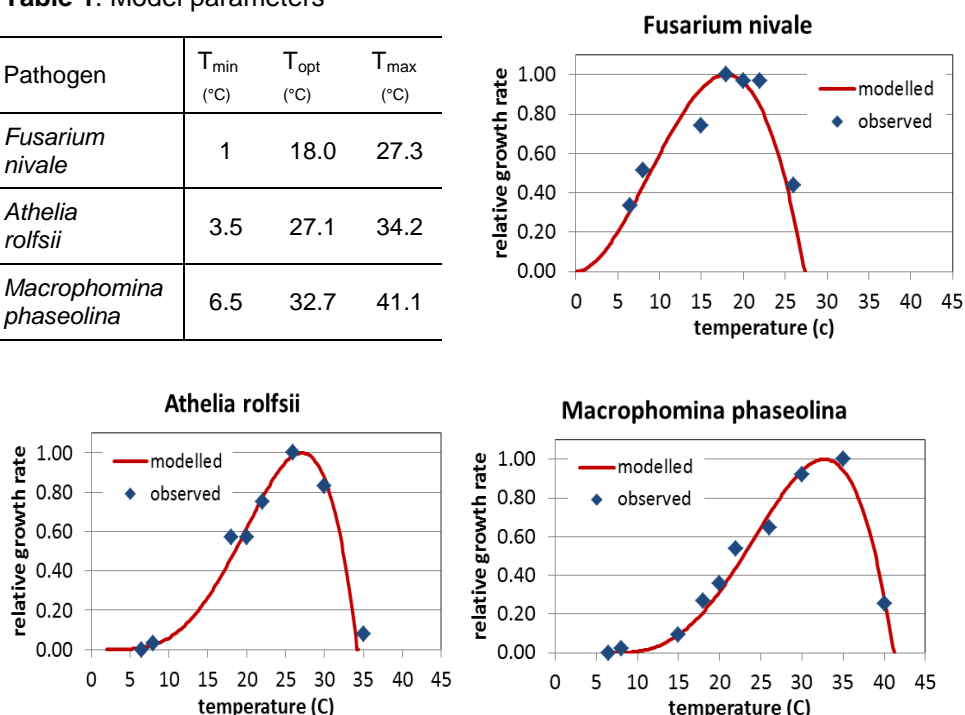| Pathogen	T_{min} (°C)	T_{opt} (°C)	T_{max} (°C)
Fusarium nivale	1	18.0	27.3
Athelia rolfsii	3.5	27.1	34.2
Macrophomina phaseolina	6.5	32.7	41.1

Figure 3 Observed and modelled normalized growth rates of the three soil borne pathogens tested, *F. nivale, A. rolfsii and M. phaseolina*.

3.1   *F. nivale* response to scenarios of climate change

Data are presented as percentage difference of cumulative relative growth comparing the future scenario to the reference weather. Positive values indicate increased potential growth.

The simulation across the winter period (October-March) of FN on wheat, a soil borne pathogen representative of low temperature requirement, shows an overall increase of growth rate of the fungus in the future scenarios compared to current conditions. This increase ranges from 10 to 40%, with peaks of differences of relative growth rate in soils of the colder agricultural areas of the Northern Europe, especially in United Kingdom, Ireland, Denmark, Finland, Norway and in the continental areas of Central Europe (Figure . 4). This trend is due to an increase of soil temperature during winter in the colder areas of Europe and to the consequent reduction of limiting conditions for the fungus, characterized by a T_{min} and T_{opt} of 1°C and 18°C, respectively (Table 1, Figure1). Agreement between temperature

requirements inferred from *in vitro* study and the outbreaks of foot rot symptoms was observed by Pettitt et al. [1996] in a study about the impact of FN, based on 4 year-data of disease records in Scotland, attributed to an increased soil temperature regime of the years under evaluation. This supports the findings of this study which estimates a noticeable increase of dynamics of the potential biological pressure with respect to the realization of the A1B scenario centred on 2030 in Europe.
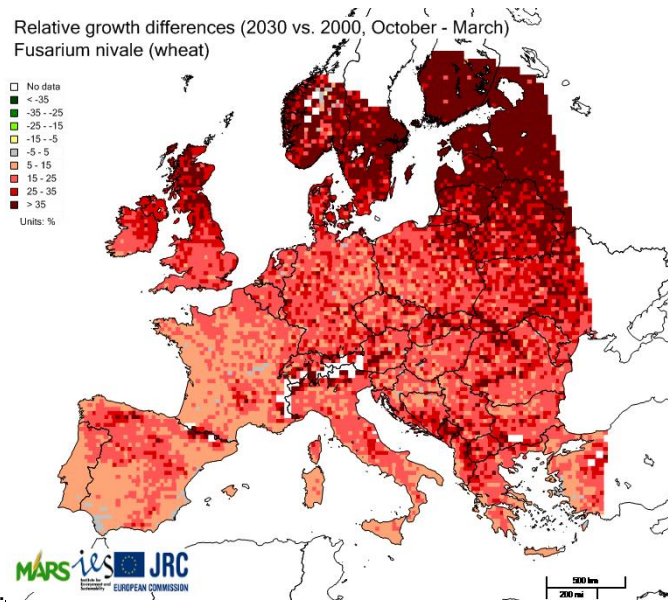

Figure 4 Relative growth differences of *F. nivale* (FN), agent of Fusarium patch or foot rot of cereals, between the winter periods of 2030 and current climatic conditions.

3.2   *A. rolfsii and M. phaseolina* response to scenarios of climate change

Spatialized simulations of AR and MP referred to summer period suggest an overall increase of more suitable conditions for these pathogens in the future in the Mediterranean and Central European countries. These two pathogens, representative of medium-high and high temperature requirements, respectively, (AR: T_{max}=34.2°C; T_{opt}=27.1°C; MP: T_{max} = 41.1°C; T_{opt} = 32.7 °C, Table 1, Figure 1), are estimated to respond to future weather conditions with a generalized relative higher growth rate within the continental areas of Mediterranean (i.e. Italy, Spain and France) and with a marked homogeneity in the countries of Central Europe (Figure 5 and 6).

The projections made on 2030 time frame (Figure 5 and 6), suggest that these two soil-borne pathogens, which in the current conditions are adapted to the Mediterranean agro-environmental conditions, could shift and expand their areals towards relatively colder areas of the Central Europe. However, AR differs as it shows the suboptimal response due to too high soil temperatures in Southern Europe. In those conditions, the potential relative growth may be unchanged or slightly higher, whereas MP would take full advantage of the higher soil temperature pattern. This trend has been already observed in the last five-ten years with respect to several soil-borne pathogens typical of the warmer agricultural areas, which were found to be the main cause of depletion of the yields in temperate areas in which their impact on production levels was substantially negligible and where they were only occasionally isolated. In particular, AR, has been reported to cause damage in warm temperate areas of the US and Europe [Xu et al. 2008]; whereas MP, originally adapted to extensive crops such as soybean, cotton, sunflower and sorghum in the past [Wrather et al. 1995], has

become agent of root rot on several horticultural crops in 2000 decade [Aegerter et al. 2000; Avilés et al. 2008].
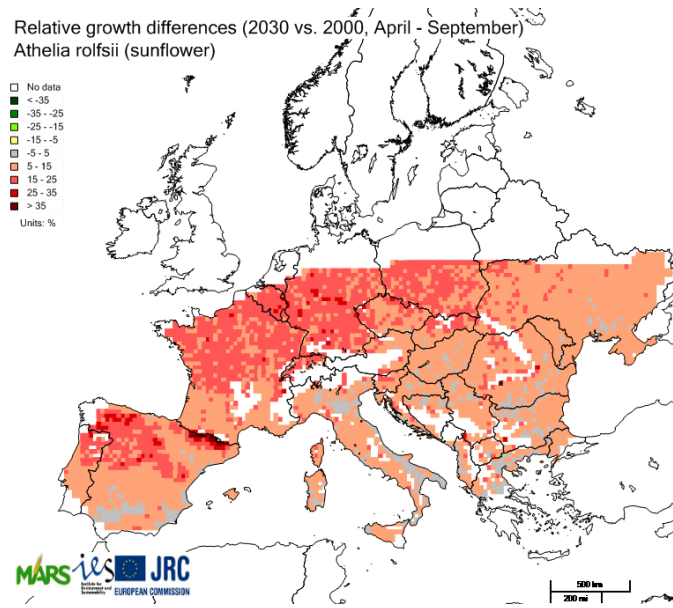
Figure 5 Relative growth differences of *A. rolfsii* (AR), agent of southern blight or Athelia wilt on a wide range of cultivated plant species, between the summer periods of 2030 and current climatic conditions.
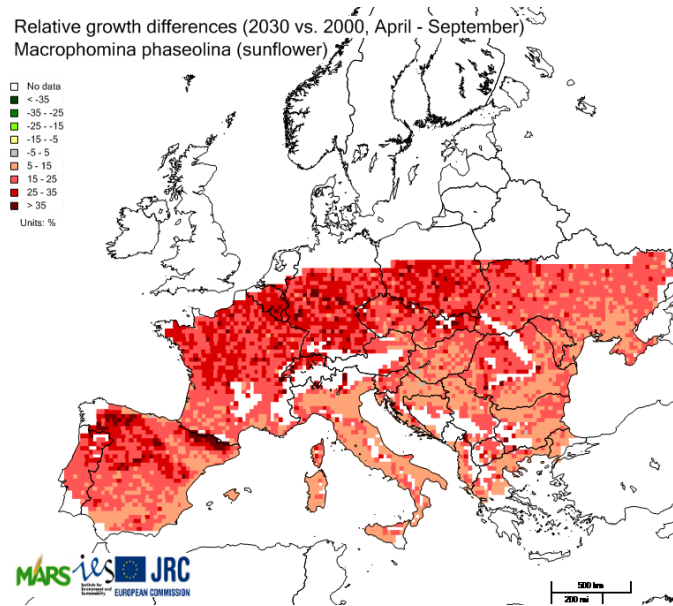
Figure 6 Relative growth differences of *M. phaseolina* (MP), agent of charcoal rot, between the summer periods of 2030 and current climatic conditions.

4   CONCLUSIONS

The general trend of soil-borne pathogen response to future weather scenario, as outlined by this study, clearly estimates a marked increase of potential relative growth rate in the colder areas of Europe, as a function of the more favourable soil temperature regimes. Projections of FN in the future indicate a relative increase of this winter pathogen of wheat in the Northern European countries. Similarly, AR

and MP*,* two soil-borne pathogens typical of warmer agricultural areas, could find more favourable conditions in relatively colder areas of central Europe under the future summer temperature regimes. However, AR would experience soil temperatures at times too high, hence leaving the pathogen response unchanged in the warmest areas. Generalizing this type of response, to be further investigated with other pathogens with slightly lower than AR temperature requirements, might confirm that such pathogens may be impacting heavily in Central and Northern Europe, but not in the warmest areas of the South. Ongoing work includes a second controlled chamber experiment including the same fungi to improve the estimate of temperature responses, and the extension of the weather input to the ECHAM5 realization of the A1B emission scenario, available as described by Donatelli et al. [2012b].

The approach adopted in this study, even if not including the simulation of yield levels and quality decline of herbaceous and woody crops, opens further perspectives for the application of biophysical models in predicting response to climate change of a large number of soil fungal pathogens, of agricultural and forest interest**.** The modelling solution can be further developed to match with greater detail the phenology of specific hosts with respect to their sensitivity to pathogens. This would allow more specific estimates of the potential damage in future scenarios, thus reproducing with more accuracy the complex interactions of the specific pathosystems. Such an improved modelling solution could be easily imported in to the BioMA platform allowing an easy re-run of the simulations with different pathogens, and by including other key aspects of the agricultural systems such as estimates of impacts on crops.

ACKNOWLEDGMENTS

REFERENCES

Aegerter, B.J., T.R. Gordon, and R.M Davis, Occurrence and pathogenicity of fungi associated with melon root rot and vine decline in California. *Plant Disease, 84*, 224-230, 2000.

Avilés, M., S. Castillo, J. Bascon, T. Zea-Bonilla, P. Martín-Sánchez, and R. Pérez-Jiménez, First report of *Macrophomina phaseolina* causing crown and root rot of strawberry in Spain. *Plant Pathology, 57*, 382, 2008.

BioMA http://bioma.jrc.ec.europa.eu/bioma/help/ [verified May 4, 2012]

Commonwealth Agricultural Bureau (CAB) *Description of Pathogenic Fungi and Bacteria N1-1000 from January 1064 to March 1990*. Cab international Mycological Institute. Kluwer Acc Pub., 1990.

Components http://bioma.jrc.ec.europa.eu/components/ [verified May 5, 2012], http://agsys.cra-cin.it/tools/ [verified May 5, 2012].

Confalonieri R., M. Donatelli, S. Bregaglio, T. Stella, G. Negrini and M. Donatelli, An extensible, multi-model software library for simulating crop growth and development, paper presented at International Environmental Modelling and Software Society (iEMSs) 6th International Congress, Leipzig, Germany, July 1-5, 2012.

Donatelli, M., S. Bregaglio, R. Confalonieri, R. De Mascellis and M. Acutis, Comparing modelling solutions at submodel level: a case on soil temperature simulation. *Environmental Modelling and Software, submitted*, 2012a.

Donatelli, M., D. Fumagalli, A. Zucchini, B. Baruth and R.L. Nelson, A EU 27 database of derived daily weather data from climate change scenarios for

use with crop simulation models, paper presented at International Environmental Modelling and Software Society (iEMSs) 6th International Congress, Leipzig, Germany, July 1-5, 2012b.

Donatelli, M., and A. Rizzoli, A design for framework-independent model components for biophysical 3 systems, paper presented at International Environmental Modelling and Software Society (iEMSs) 4th International Congress, Barcellona, Spain, July 7-10, 727-724, 2008.

Gonzalez, A.J., J.C. Tello, and M.L. Herrero, First report of *Pythium tracheiphilum* causing wilt and leaf blight on lettuce (*Lactuca sativa*) in Spain. *Plant Disease, 88*, 138, 2004.

Intergovernmental Panel on Climate Change (IPCC), *Climate Change 2007: Synthesis Report*. Contribution of Working Groups I, II and III to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change. Core Writing Team, Pachauri, R.K., and A. Reisinger (Eds.) IPCC, Geneva, Switzerland, pp. 104, 2007.

Purdy, L.H., *Sclerotinia sclerotiorum*: history, diseases and symptomatology, host range, geographic distribution, and impact. *Phytopathology, 69*, 875-880, 1979.

Lees, A.K., and A.J. Hilton, Black dot (*Colletotrichum coccodes*): an increasingly important disease of potato. *Plant Pathology, 12*, 1-12, 2003.

Mathre, D.E., R.H. Johnston, and W.E. Grey, Diagnosis of common root rot of wheat and barley. *Plant Management Network*, 2003. http://www.plantmanagementnetwork.org/pub/php/diagnosticguide/2003/rootrot/

Manici, L.M., Micoteca http://www.cra-cin.it/isciTC/Micoteca_web/index.html, [verified May 5, 2012]

Manici, L.M., F. Caputo, and G. Baruzzi, Additional experiences to elucidate the microbial component of soil suppressiveness towards strawberry black root rot complex. *Annals of Applied Biology, 146*, 421-430, 2005.

Mazzola, M. Elucidation of the microbial complex having a causal role in the development of apple replant disease in Washington. *Phytopathology, 88* (9), 930-938, 1998.

Pettitt, T.R., D.W. Parry, and R.W. Polley, Effect of temperature on the incidence of nodal foot rot symptoms in winter wheat crops in England and Wales caused by *Fusarium culmorum* and *Microdochium nivale*. *Agricultural and Forest Meteorology, 79*, 233-242, 1996.

Redman, R.S., D.D. Dunigan, and R.J. Rodriguez, Fungal symbiosis: from mutualism to parasitism, who controls the outcome, host or invader? *New Phytologist, 151*, 705-716, 2001.

Stöckle C.O., M. Donatelli, and R.L. Nelson, 2003. CropSyst, a cropping systems simulation model, *European J. Agronomy,* 18, 289-307.

Wegulo, S.N., and R.N. Klein, Common Root Rot and Fusarium Foot Rot of Wheat, University of Nebraska–Lincoln Extension, http://www.ianrpubs.unl.edu/pages/publicationD.jsp?publicationId=1260, 2010.

Wrather, J.A., A.Y. Chambers, J.A. Fox, W.F. Moore, and G.L. Sciumbato, Soybean disease loss estimates for the southern United States, 1974 to 1994. *Plant Disease, 7*, 1076-1079, 1995.

Yan, W., and L.A. Hunt, An equation for modelling the temperature response of plants using only the cardinal temperatures. *Annals of Botany, 84*, 607-614, 1999.

Xu, Z., M.L. Gleason, D.S. Mueller, P.D. Esker, C.A. Bradley, J.W. Buck, D.M. Benson, P.M. Dixon and J.E.B.A. Monteiro, Overwintering of *Sclerotium rolfsii* and *S. rolfsii* var. *delphinii* in Different Latitudes of the United States. *Plant Disease, 92*, 719-724, 2008.