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EXTERNAL SCIENTIFIC REPORT

Model framework for the assessment of EU climatic suitability for the establishment of organisms harmful to plants and plant products – CLIMPEST project (SLA/EFSA-JRC/2008/PLH/01)

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ABSTRACT

In the frame of the SLA a model framework was developed named ClimPest allowing the assessment of EU climatic suitability for the establishment of organisms harmful to plants and plant products and more specifically to estimate the weather suitability for potential infection by the citrus pathogen *Guignardia citricarpa* (common name Citrus Black Spot - CBS). The model framework Climpest can be re-used for other plant diseases and pests and it contains the following modelling solutions: ClimIndices (calculation of climatic indexes) and Potential Infection Model (calculation of the potential infections of foliar fungal pathogens on plants). The software has access to a remote database containing historical series of daily weather data with Europe spatial coverage on a 25 x 25 grid. Climate change scenarios for 2020 and 2050 are also made available related to the emission scenarios A1B and B1. The software was designed to be extended autonomously by third parties with diverse modelling solutions, other than the ones provided in this first version.

KEY WORDS

Model framework, potential infection model, BioMa, meteorological databases, climate change scenarios

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SUMMARY

The project ClimPest is a service agreement in the framework of the collaboration agreement between the European Commission Joint Research Centre (DG JRC) and the European Food and Safety Authority (EFSA), JRC.BLX.CA.31022-2008.

Within the project a model framework for foliar fungal pathogens simulation based on EU climate, crop/vegetation and biological characteristics of the organism has been developed and made available to EFSA. The model framework developed in the frame of the SLA is under the BioMa framework which is a software platform that allows launching the simulation of one of the modeling solutions deployed. The ClimPest version (ClimPest is-a BioMA) contains the following modeling solutions: ClimIndices (calculation of climatic indexes) and Potential Infection Model (calculation of the potential infections of pathogens on plants). The software has access to a remote database containing historical series of daily weather data with Europe spatial coverage on a 25 x 25 grid. Climate change scenarios are also made available centering 2020 and 2050, currently from one global circulation model (Hadley3), and related to the emission scenarios A1B and B1. Output data can be saved on resources chosen by the user.

Specific studies on simulation possibilities on other harmful organisms based on EU climate, crop/vegetation and biological characteristics of the organism have been conducted based on the JRC weather databases and the developed model framework contributing to following scientific opinions (the second cited based on preliminary work on model components, later included in the ClimPest platform):

Scientific Opinion of the Panel on Plant Heath on a request from the European Commission on the Plant health risk of *Thaumetopoea processionea* L., the oak processionary moth, for the EU territory. The EFSA Journal (2009) 491, 1-64. (Appendix A)

Scientific Opinion of the Panel on Plant Health on a request from the European Commission on *Guignardia citricarpa* K. The EFSA Journal (2008) 925, 1-108. (Appendix B)

Interpolated climatic data and newly derived climatic indicators for the EU establishment assessment of harmful organisms have been provided to EFSA to conduct further studies.

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BACKGROUND

The establishment of new organisms harmful to plants and/or plant products might have severe consequences on the food and feed chain, causing yield losses or affecting food and feed safety, e.g. by increases in plant protection products residues or in mycotoxins. The measures to prevent the introduction of organisms harmful to plants and/or plant products into the European Union are defined in the Council Directive 2000/29/EC. The International Plant Protection Convention (www.ippc.int/) and the International Standards for Phytosanitary Measures n. 2 and 11 (https://www.ippc.int/index.php?id=ispms&no_cache=1&L=0) outline the framework for the assessment of risk for phytosanitary purposes. The estimation of the probability of establishment is one of the key elements for the overall assessment of the risk posed by organisms harmful to plants and/or plant products. Establishment potential is influenced by several factors including the suitability of the environment, the availability and distribution of hosts, the potential for adaptation and reproductive strategy of the organism and the cultural practices and control methods applied. Climate is one of the major drivers for the estimation of the probability of establishment. Various models combining data on climate, plant host phenology and distribution, as well as on biology, ecology and epidemiology of the harmful organisms are available in literature. There is a need for parameterisation and use of these models and application to the European conditions. Moreover, climatic changes already occurred and future scenarios of climate changes need to be considered.

In this context JRC was asked to develop a model framework that would allow assessing EU climate suitability for the establishment of organisms harmful to plants and/or plant products..

TERMS OF REFERENCE

The terms of reference of this work are defined by the Service Level Agreement Nr. 31153-2008-11 TPW ISP between the European Community and the European Food Safety Authority as well as by the Collaboration Agreement JRC.BXL.CA.31022-2008 between the European Community and the European Food Safety Authority.

The terms of reference of this work are defined by the Service Level Agreement Nr. 31153-2008-11 TPW ISP between the European Union and the European Food Safety Authority as well as by the Collaboration Agreement JRC.BXL.CA.31022-2008 between the European Union and the European Food Safety Authority.

The purpose of this work is to provide a framework for analysis and modelling of the probability of establishment of organisms harmful to plant and plant products using climatic data and biological requirements of the host plants and of the harmful organisms. The overall objective of the project is to analyse and report data on the EU environmental suitability (including climate and host plants) for the establishment of organisms harmful to plants and plant products and to support the activities of the EFSA Plant Health Panel by comparing methodologies for modelling the climatic suitability for establishment, by modelling for specific harmful organisms under study by the PLH Panel and by providing specific climatic data. The specific objectives of this project are: development of a model framework for foliar fungal pathogens based on EU climate, crop/vegetation and biological characteristics of the organism; studies on simulation possibilities on other harmful organisms based on EU climate, crop/vegetation and biological characteristics of the organism; provision of interpolated climatic data and newly derived climatic indicators for the EU establishment assessment of harmful organisms.

The product to be delivered as result of this service level agreement is a software platform for modelling climate suitability for assessing the establishment potential of organisms harmful to plants and plant products, BioMA-ClimPest. BioMA-ClimPest is a desktop application designed and developed for analyzing, parameterising and running modelling solutions based on biophysical models against a database which includes spatially explicit units. The application is based on independent components, for both the modelling solutions and the graphical user's interface. The component-based structure allows implementing in BioMA diverse modelling solutions targeted to specific modeling goals. The system allows also for adding new modelling solutions, the target being disease/pest models to be run against a spatially explicit weather database. The BioMA simulation environment includes integrated tools for Monte Carlo based sensitivity analysis (LUISA), and a solver framework

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(Optimizer) to assist in parameter calibration. Both LUISA and Optimizer can be used with each modelling solution made available in BioMA, and both can be extended: LUISA for sensitivity analysis engines, and Optimizer for solvers and objective functions, which can be based on either simple or composite indices.

ACKNOWLEDGEMENTS

This contract was awarded by EFSA to: Joint Research Centre, European Commission

Contract title: Model Framework for the assessment of EU climatic suitability for the establishment of organisms harmful to plants and plant products

Contract number: SLA/EFSA-JRC/2008/PHL/01

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INTRODUCTION AND OBJECTIVES

INTRODUCTION

The establishment of organisms harmful to plant and plant products from outside the EU has a prerequisite the suitability of weather conditions in the variety of environments of member states. The evaluation of potential infection by such organisms requires as key inputs series of weather data in the areas which can be identified as at risk for a specific crop or perennial. Such data are used as inputs both for static, statistical models and for process based bio-physical models. The latter often require a time resolution of one hour, rather than a day, to simulate cohorts of either pests or diseases, and also require variables not commonly available such as leaf wetness.

JRC-IES AGRI4CAST maintains a database of weather data with a resolution of 25 x 25, which contains daily data from 1982. Actual weather stations are distributed irregularly on the EU-27 surface. Data from such stations are used to build the data grid, which provides a source of data uniformly distributed.

The main components of a framework to estimate potential infection by diseases or pests can hence be described with the components of Figure 1.

The framework is targeted at allowing estimates of potential infection considering mainly weather, and, in some cases, also agricultural management and phenology/growth of hosts. A new model component simulating the various phases of a disease population development is also being implemented.

Applications were developed to estimate derived meteorological variables (e.g. vapor pressure deficit, leaf wetness, simple and composite weather indices), and to simulate biophysical processes (e.g. crop development and growth, diseases infection). Some simulations (e.g. pests and diseases epidemics) require a finer temporal resolution for weather data, for instance deriving hourly values. Because of the infrastructure described, simulating the potential infection of a disease or the potential epidemics of a pest can be done by running diseases or pests models on the grid cells where the crop/perennial of interest is grown (or on all cells). This involves the use of either available models or the implementation of specific ones.

An added feature is the possibility of running simulations using climate change scenarios as downscaled from IPCC (Intergovernmental Panel on Climate Change); different time frame (centered on 2020 or 2030), two realizations of the scenario A1B, HadleyCenter3 and ECHAM5. New emission scenarios and realizations will become available to BioMA-CLIMPEST users.

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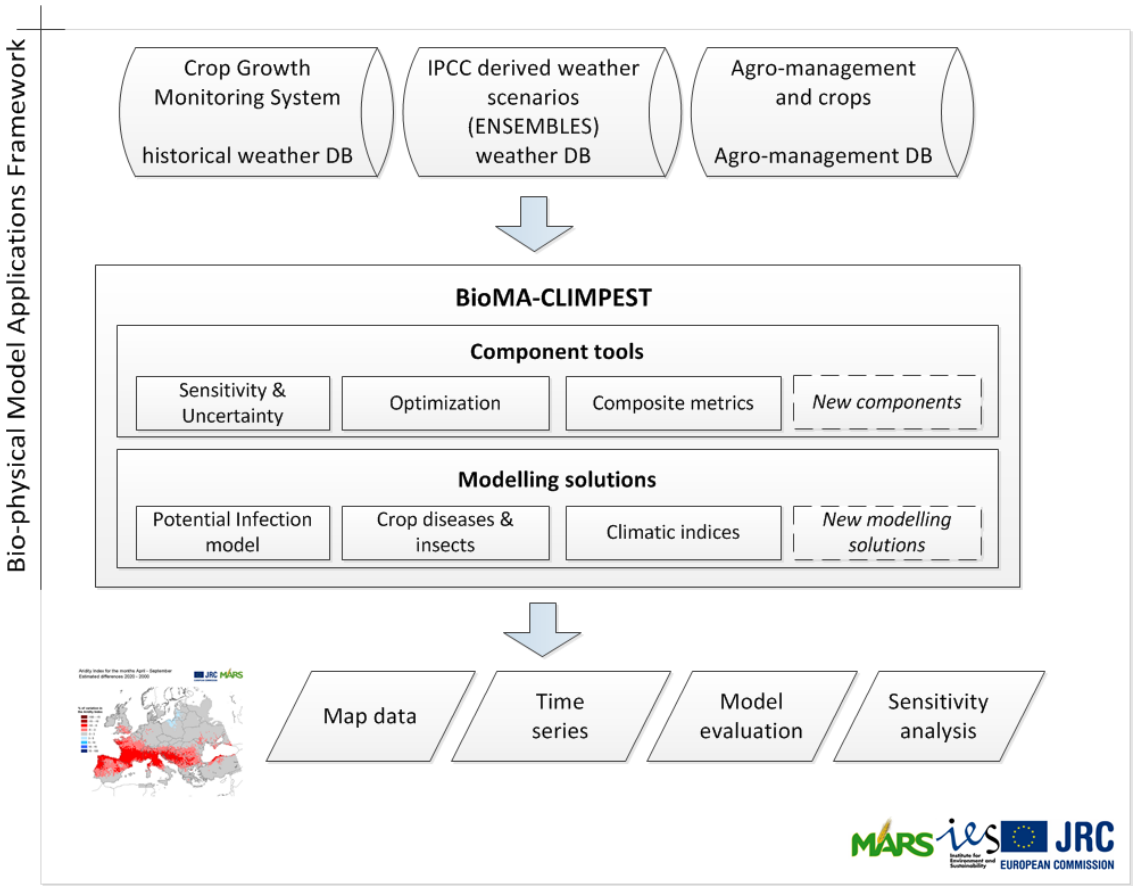

Figure 1. Component diagram of ClimPest. The input database sources are on a JRC server, whereas the application runs on the local machine (as in the default deployment).

One features which is not visible using the software is however a key aspect of it: as mentioned the software is made to allow extensibility autonomously by third parties. This means that EFSA or any other user can extend its functionalities to target new modelling problems, or to use new modelling options.

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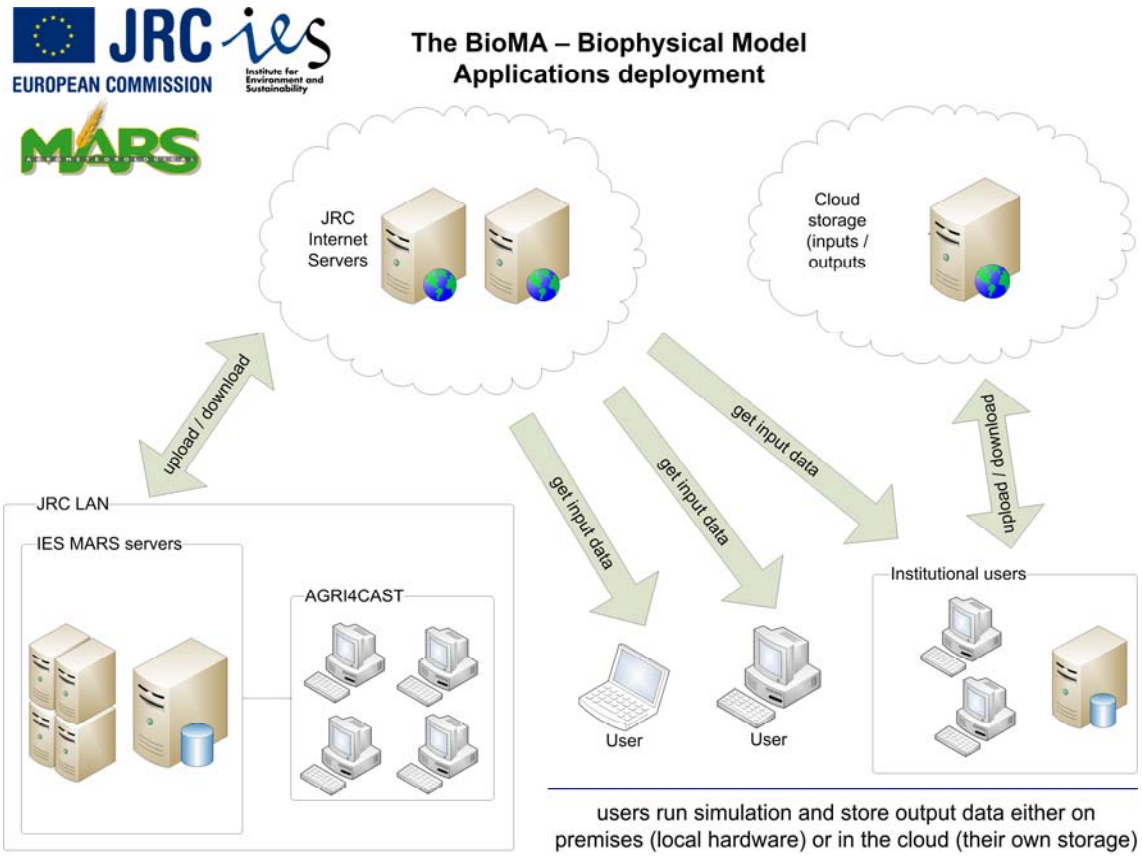

Figure 2b. Example deployment of BioMA-CLIMPEST

OBJECTIVES

The objectives of the service agreement are:

The development of a model framework for foliar fungal pathogens simulation based on EU climate, crop/vegetation and biological characteristics of the organism

Studies on simulation possibilities on other harmful organisms based on EU climate, crop/vegetation and biological characteristics of the organism

Provision of interpolated climatic data and newly derived climatic indicators for the EU establishment assessment of harmful organisms

MATERIALS AND METHODS

The analysis which will be carried out will estimate the climate suitability with respect to potential infection. Other aspects which impact on infection establishment and epidemiology will not be considered. The prosed methodologies have been implemented under the CLIMPEST model framework.

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1. Deriving weather and weather related variables

The JRC maintains a database of daily values. Some daily variables currently not stored can be generated/estimated, and hourly variables are always estimated/generated according to specific needs as described below.

1.1. Hourly values

For the simulation of a couple of processes there is a need to obtain hourly meteorological values, for instance one of the more significant problems related to the modeling of leaf wetness, which is shared by both empirical and process based ones, is the need of hourly meteorological data as inputs.

The availability of hourly data is often a limiting factor for operational use, because of their scarce availability. In fact, meteorological stations commonly record air temperature, solar radiation, relative humidity, rainfall, wind speed, and wind direction with the standard suite of sensors with a daily time step. Hourly values of these variables are collected by a growing percentage of weather stations, but still the coverage of such stations is not complete. Furthermore, process based models require as inputs not only these common-measured variables but also other ones related to them (e.g. dew point temperature, actual vapor pressure, vapor pressure deficit, slope of the vapor pressure curve, saturation vapor pressure, latent heat of vaporization, atmospheric density and others) that mostly cannot be measured directly. This limitation strongly affects the operational use of models.

JRC and CRA have developed a reusable and extensible software library of software components called *CLIMA* (Donatelli et al., 2005), that is a synthetic weather estimator/generator. *CLIMA* includes 5 main subcomponents: including estimation/generation functions for each relevant weather variable. These basic model components are:

AirT: air temperature generation;

ET: reference evapotranspiration estimation;

GSRad: solar radiation estimation/generation;

Rain: precipitation generation;

Wind: wind speed generation;

LeafWetness: leaf wetness estimate.

Each of the components offers a wide range of alternative methods to perform estimates and data generation.

1.2. Modelling leaf wetness

Leaf wetness is recognized as a very important weather parameter for plant disease epidemiology (Pedro, 1980; Huber and Gillespie, 1992; Gleason et al., 1994; Kim et al., 2002). For these reasons, the time when free water remains on the surface of plant tissues, termed leaf wetness duration, is a driving variable for the forecasting of plant epidemics because it strongly influences many processes such as the start of fungal pathogens active life cycle, the penetration of them through the leaves, and the occurrence of primary and secondary infections during the same season.

The estimate and use of this variable is then essential in the development of a model for the simulation of the inner processes related to the development rates of plant diseases caused by fungal pathogen and, consequently, to the yield losses caused by them.

Because leaf wetness duration is not widely measured, several methods have been developed to estimate it from weather data (Sentelhas et al., 2008). These methods, that are adopted by the existing leaf wetness models, can be divided into two broad categories, empirical (Gleason et al., 1994; Rao et al., 1998; Kim et al., 2002) and process-based (Pedro and Gillespie, 1982; Bass et al., 1991; Luo and Goudriaan, 2000; Magarey et al., 2006; Sentelhas et al., 2006).

Among the models used to estimate leaf wetness duration, some consider physical principles of dew formation and dew and/or rain evaporation, hence simulation physical processes. They have shown good portability and

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sufficiently accurate results, but their complexity is a disadvantage for operational use. Alternatively, empirical models simulate leaf wetness duration by using simple relationships of this variable with parameters measured at standard agro-meteorological stations. Their success depends on the accuracy of the weather data used as inputs and they are more site-specific than physical models (Huber and Gillespie, 1992; Kim et al., 2005).

In this context, JRC and CRA have developed a reusable and extensible software component, called LeafWetness (Bregaglio et al, 2011), written in C#, implementing in the current version 5 models to estimate hourly values of leaf wetness. The software component is available for download, inclusive of documentation and sample projects to illustrate re-use in custom developed applications. The models vary from process based to fully empirical, as described in the previous paragraph.

They are:

SWEB (Surface Wetness Energy Balance) (Magarey et al., 2006),

LWR (Leaf Wetness Reference) (Sentelhas P.C., Gillespie J., Gleason L. C., Monteiro B.M., Pezzopane M., Pedro Jr. J., 2006),

DP (Dew Parametrization) (Garratt, J. R., Segal, M., 1988),

CART (Classification And Regression Tree) (Kim, K. S., Taylor S. E., Gleason, M.L., Koehler, K.J., 2002)

ET (Extended Threshold) (Witchink Kruit J., Addo W., van Pul J., Jacobs F.G., Heusinkveld G.).

The working experience so far as identified SWEB as the most robust choice when reference data for calibration are missing, hence SWEB will be the model used in this project unless additional evidence will demonstrate one of the other models more accurate.

1.3. Interaction between CLIMA and LeafWetness

The minimum set of daily inputs needed by CLIMA for the generation of all the hourly inputs used by LeafWetness are minimum and maximum temperature, rain, and wind. The availability of daily maximum and minimum relative air humidity, and of solar radiation, improves the accuracy of the estimate of hourly values. A complete list of hourly values of the variables generated by CLIMA and used by the LeafWetness component is shown in table 1, with the name of the modeling approach (implemented as a *class*) used.

Table 1. Models to estimate/generate hourly weather data from daily values. Rainfall and wind hourly values are generated from daily values, other variables are estimated.

Name of the model (class)	***Name of the variable***
HAirAndDewTemperature	HourlyAirTemperature HourlyDewPointTemperature
HAirRelativeHumidity	HourlyRelativeHumidity
HVPDFAO	HourlyActualVaporPressure HourlyVaporPressureDeficit
HSVPDAsae	HourlySlopeVaporPressure
HLHVHarrison	HourlySaturationVaporPressure HourlyLatentHeatOfVaporization
HADAsae	HourlyAtmosphericDensity
HGSRGlobalSolarRadiationHourly	HourlyGlobalSolarRadiation
HNRFAO	HourlyNetRadiation

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	HourlySoilHeatFlux
HWMitchell	HourlyWindSpeed
HRMeteotest	HourlyRain
HPsychrometricConstant	HourlyPsychrometricConstant
HARFAO	HourlyAerodynamicResistance

2. Estimating potential infection

The JRC actions to estimate climate suitability with respect to potential infection will be of two types:

the extraction of monthly means from the database for subsequent CLIMEX analysis. The CLIMEX model/software requires monthly values of several weather variables to allows estimating the matching between two sites. Such monthly means are extracted as yearly values and as values referred to the years 1998-2007.

the estimate of potential infection using a generic infection model

2.1. The generic infection model

Plant disease forecasting models, usually referred to as prediction or disease risk models have been developed based on the epidemiological knowledge obtained from controlled environment or field studies. Yang (2003) outlined the use of the terms "risk prediction" and "risk assessment", according to the temporal and spatial scale that uses the risk. "Risk prediction" reflects advances in disease risk communication at the farm level for a single season. "Risk assessment" is an epidemiological study to predict future occurrence of a disease by using non-experimental approaches, often through computer modeling. The study in risk assessment is a macroscale, long-term prediction that encompasses assessment of potential for entry, establishment, epidemic, and/or crop losses in a region or country once an epidemic occurs (Yang, 2006).

Models which simulate the evolution of a plant disease during the season give important information to assess the seriousness of the situation. This activity precedes the choice of an appropriate action to be implemented for reducing the economical damage. Having effective models is a critical issue in modern agriculture, especially in Integrated Protection and Organic Farming, which rest on a set of plant disease management practices with low environmental impact. (Susi, A., et al, 2002)

As for the models concerning leaf wetness, plant disease forecasting models can be classified in two major groups: process based and empirical models. The former models are based on concepts derived from a pathosystem and help to improve the understanding of the structure and behavior of such a biological system (Teng, 1985). Empirical models are typically constructed through the statistical relationships of explanatory variables with experimental data. This data may be from the field on individual (e.g. survival, dispersal, infection, latency, sporulation) or combined epidemic components (e.g. disease progress, final severity). Most models use the response of foliar pathogens to the combined effects of temperature and duration of leaf wetness (Duthie, 1997). These models have commonly been used in disease forecasting systems, with the reliability of model predictions heavily dependent on the quality of the dataset used for model development (Krause et al., 1975).

The evaluation of the potential entry and establishment of a fungal pathogen in a new country, the first thing that has to be explored is if the weather conditions are favorable for the infection process, because all the other phases of the epidemic process depend on the fulfilling of this process. So, for many foliar pathogens, the infection sub-model is one of the most critical components for disease forecasting (Madden et al, 1988).

The most important problem related to the development of such models is that they are created from either laboratory or field observations of resulting disease intensity at multiple combinations of temperature and wetness. However, for many pathogens, especially those from overseas, such data sets may not exist. Instead,

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the data available for many of these less-studied pathogens may be limited to growth studies in culture, simple correlations of disease observations in the field with environmental variables, or inferences made from closely related organisms.

In this framework we have decided to adopt a model for the prediction of potential infection (Magarey et al., 2005) that estimates infection from an organism's cardinal temperatures and surface wetness duration requirement. This generic model can predict infection based only upon estimates of the three cardinal temperatures and a surface wetness duration requirement and so it can be helpful for modeling pathogens for which extensive epidemiological data are unavailable. The model is based upon a temperature response function (Wang, E. L., Engel, T. 1998; Yin, X. et al., 1995) which is scaled to the surface wetness duration requirement.

The infection model used is the one of Magarey et al. (2005) using an implementation which runs with an hourly time step. It needs as weather inputs hourly air temperature and hourly leaf wetness, which are outputs of the component CLIMA and LeafWetness, described in the previous paragraphs. Other needed are some parameters related to the biology of the particular pathogen. They are:

the minimum and maximum values of the wetness duration requirement (because wetness is not always a rate-limiting factor),

the minimum, optimum and maximum values of temperature for the starting of the infection process and

the number of hours allowed for an infection process to be dormant without being terminated (D50).

The complete list of the inputs needed by the model is shown in Tab. 2.

Table 2. Input requirements of the infection model.

Type of the input	Name of the input
WEATHER	HourlyAirTemperature HourlyLeafWetness HourlyRain (for pycnidiospores infection)
MODEL PARAMETERS	MinimumWetnessDurationRequirement MaximumWetnessDurationRequirement MinimumTemperatureForInfection OptimumTemperatureForInfection MaximumTemperatureForInfection D50

The model uses the temperature response function of Yin et al. (Yan, W., Hunt, L. A., 1999), which is a simplified and improved version of the rice clock model (Gao, L. Z. et al., 1992). The function uses the pathogen's cardinal temperatures to estimate the shape parameter and the temperature response:

$$f(t) = \left(\frac{T_{\max} - T}{T_{\max} - T_{opt}}\right)\left(\frac{T - T_{\min}}{T_{opt} - T_{\min}}\right)^{(Topt - T\min)/(T\max - Topt)}$$

if $T_{\min} \le T \le T_{\max}$

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0 *otherwise*

Where:

T = mean temperature (°C) during wetness period,

T_{min} = minimum temperature for infection (°C),

T_{max} = maximum temperature for infection (°C),

T_{opt} = optimum temperature for infection (°C).

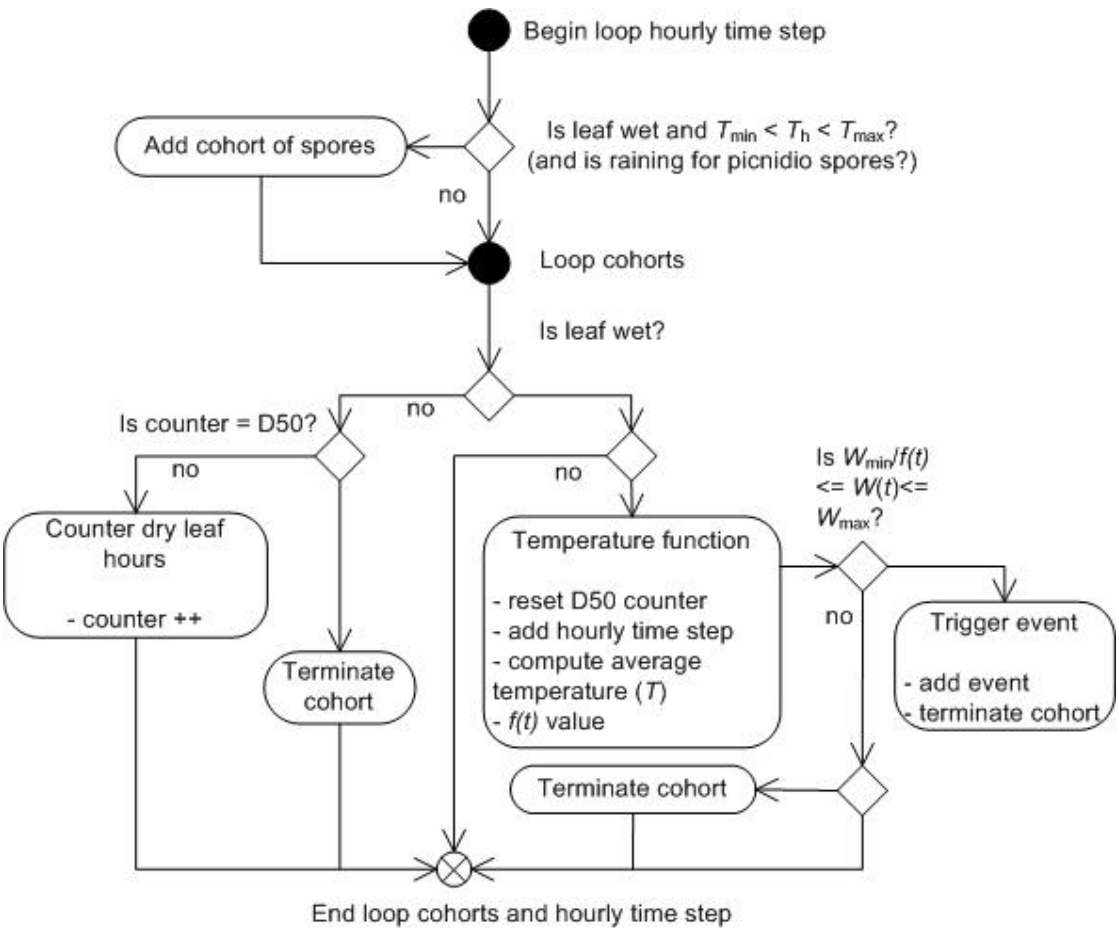

Fig. 2: Flow diagram of Magarey et al. generic model for infection

The advantages of the Yin function compared with other growth functions include the fact that the function has only three parameters (T_{min}, T_{opt}, and T_{max}) and each parameter has a clear biological meaning (Yan, W., Hunt, L. A. 1999).

The implementation of the model is according to the activity diagram of fig. 2.

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RESULTS

The ClimPest model framework

BioMA-ClimPest is a desktop application designed and developed for analyzing, parameterizing and running modeling solutions based on biophysical models against a database which includes spatially explicit units. The application is based on independent components, for both the modeling solutions and the graphical user's interface. The component-based structure allows implementing in BioMA diverse modeling solutions targeted to specific modelling goals. The system allows also for adding new modeling solutions, the target being disease/pest models to be run against a spatially explicit weather database.

The BioMA simulation environment includes integrated tools for Monte Carlo based sensitivity analysis (LUISA – Library User Interface for Sensitivity Analysis), and a solver framework (Optimizer) to assist in parameter calibration. Both LUISA and Optimizer can be used with each modelling solution made available in BioMA, and both can be extended: LUISA for sensitivity analysis engines, and Optimizer for solvers and objective functions, which can be based on either simple or composite indices. It also includes an application to compare either simulation results against reference data, or two simulations, via the component IMMA (Integrated Metrics for Model Analysis).

The modelling solutions currently being implemented in BioMA-ClimPest are:

A generic model for fungal potential infection (Magarey, R. D., Sutton, T. B., Thayer, C. L., 2005. A simple generic infection model for foliar fungal plant pathogens. Phytopathology 95:92-100). The model has parameters for simulating more than 80 diseases; new sets of parameters were obtained from the NAPPFAST project (http://www.nappfast.org/). It also includes the possibility of defining new pathogens by entering a new record of parameters. This modeling solution is already available;

A generic model for airborne diseases development. This modeling solution is being implemented and coupled to a multi-model generic crop simulator

A multi-metric component to compute static indices from weather data. The component was recently extended to include a growing degree day model by EFSA.

A modelling solution for simulating soil temperature, which will be useful for soil-borne pathogens.

BioMA-ClimPest is a dedicated version of the BioMA framework:

The main use cases identified so far are:

run a the potential infection model) on a user selected number of cells (including the use of crop masks), for a user selected number of years

run the simulation of an airborne disease and the impact on a crop, also simulated, as above;

compute weather indices on a user selected number of cells, for a user selected number of years;

browse outputs (map, single cell) both via an installation of BioMA-ClimPest on the local machine, or via a web application;

create difference maps (e.g. for a given variable, the difference from outputs obtained with historical weather and a climate change scenario, or two periods of historical series)

export results (tabular, map files package for map editing)

The BioMA application is part of a framework that allows running a “BioMA compliant” modeling solution. The description of these specifications is beyond the scope of this document. In the definition of the framework the guidelines of the component oriented programming were followed. The framework is written in C# programming language.

BioMA can be extended by third partied adding new modeling solutions or new generic feature through an application plug-in.

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The component based architecture allows the developer to reuse existing components to build new modeling solutions. For example, the weather provider components, made to get a set of weather data from a certain data source, are reusable also to create a new modeling solution.

The configuration of BioMA, managed by XML files, allows the user to specify the modeling solution to run and other configuration details like the connection to the data sources and the loading of application plug-ins.

The general high level use of the application is described in the following list of steps:

Modeling solution selection

Editing/filling out of the configuration tree, which is specific for each modeling solution

Values validation

Run of the simulation

Analysis of the result either using plug-ins (for example the Map Data Visualizer) or exporting the result data

The results of the simulations can be saved in one or more tables of the data source defined in the modeling solution configuration (it can be either remote or local, but in the latter case it limited by space to about 2 Gb of data). The definition of the result table(s) is in charge of the creator of the modeling solution.

It is not mandatory to save the simulation result in a table, but it is a common feature and it is done, for example, for the “potential infection model” modeling solution. The “data layer” architecture level allows BioMA to be interfaced with the most common database management systems (e.g. Oracle, MS SQL Server, MySql, PostgreSQL).

The input weather data currently accessible are:

Portable databases

GridWeather_25_IT.sdf contains Italy real weather data for year 2001,2002,2003

Remote database accessible via the ClimPest deployment, to authorized users (JRC):

- **CGMS real data - all EU27 - years from 1982 to 2010 (air humidity archives completed for 1999-2008)**
- **IPCC SRES A1B climate scenarios, Hadley3 and ECHAM5 realizations, 30 years for each of the reference time horizons 2000, 2020, 2030 reference time horizons. Climate scenario derive from the ENSEMBLES dataset, are downscaled via regional climate models, and are bias corrected**

The workflow to generate climate change data is shown in the diagram of figure 3.

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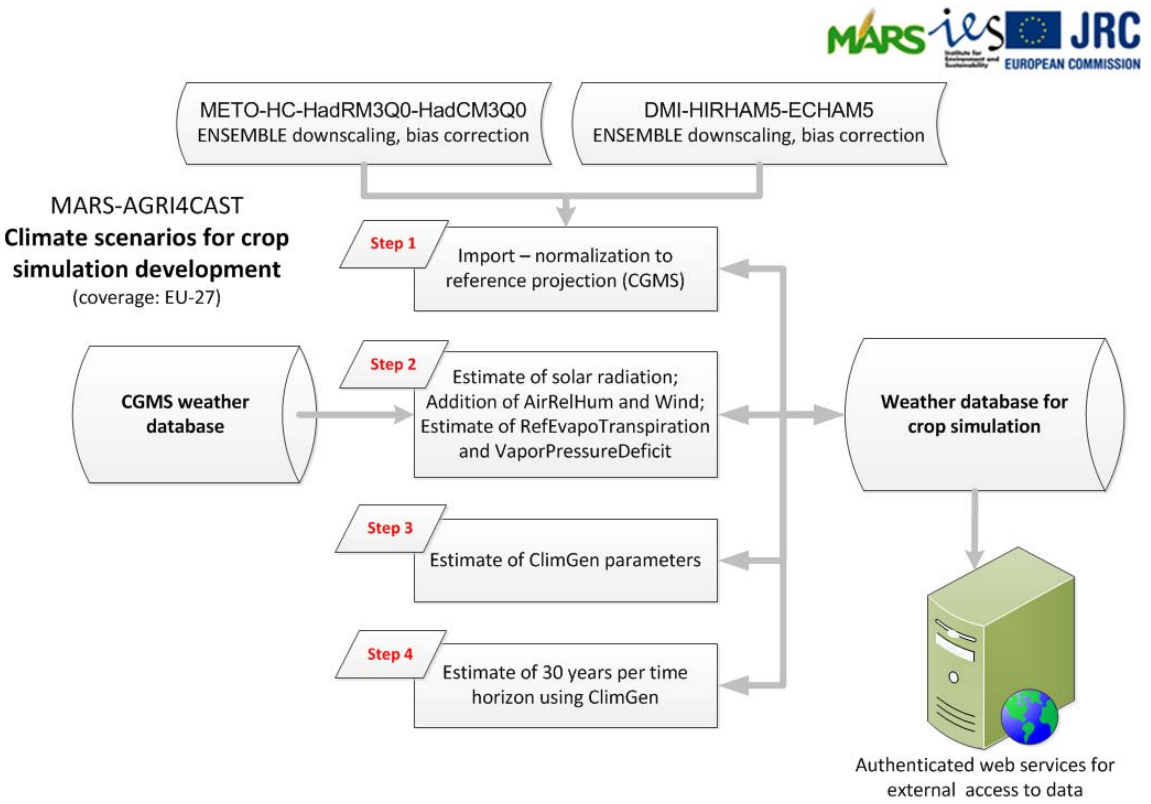

Figure 3. Workflow for the database population from ENSEMBLE data of climate change.

Detailed software specifications are listed in Appendix C.

CONCLUSIONS AND RECOMMENDATIONS

CONCLUSIONS

The model framework BioMA- CLIMPEST proved its usability for the two assessments on the Citrus Black Spot disease and the oak processionary moth. Other modeling solutions, considering also the growth and development of insects, can be implemented, taking advantage of the infrastructure which allows running models on spatially explicit units (represented by cells of 25 x 25 km). In fact, the main goal of this project was to provide a flexible and transparent software platform allowing extensions to address specific problems arisen from EFSA activity in the area of the Plant Heath. Such models could be implemented by JRC or third parties once identified by EFSA.

RECOMMENDATIONS

Technical

Although the ClimPest software can run on a PC disconnected from internet, accessing data from a local database and writing the outputs of analyses on the same machine, clear limits exists given by the amount of data to be processed. Typically, choosing as data persistence option a local machine can be very effective for analysis of regions, but it falls short as hardware (and software in terms of database) resources for running analysis covering Europe. Given the access to input data from JRC resources via internet, it is recommendable to users to set their own data sink as database either on their LAN or in cloud storage. Massive runs may require

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running multiple instance of BioMA-CLIMPEST on a processor server via virtual machines (this is the procedure in use at JRC for large BioMA runs).

Scientific

The potential infection models are very sensitive to air humidity inputs. Whether daily air relative humidity can be estimated, the accuracy of such estimates can be modest; it is then recommended to provide air relative humidity as an input to models. The internal generation, when such inputs are missing, has the variable accuracy discussed above.

Also with respect to simulation outputs, the potential Infection models is very sensitive not only to the minimum and maximum temperature for growth, but also on the relationship between optimal temperature for growth and the two extremes. When a new pathogen is introduced in the database, given that very rarely basic temperature responses can be found in the literature, preliminary tests to verify the plausibility of results should be run before working at a scale that would make anomalies in model responses difficult to identify. This is of course good practices in running simulation work, and we want to stress here the peculiar sensitivity of the model to its parameterization.

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APPENDICES

APPENDIX A - THE CITRUS BLACK SPOT ANALYSIS

- Scientific Opinion of the Panel on Plant Health on a request from the European Commission on *Guignardia citricarpa* Kiely. The EFSA Journal (2008) 925, 1-108.

Citrus Black Spot assessment infection risk: adopting a disease potential infection model.

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- **Citrus Black Spot**

- **Short description** (Based upon CABI, 2002)

Citrus black spot is caused by the fungus *Guignardia citricarpa* Kiely and it is a fruit disease that affects the rind but does not cause decay (Timmer et al., 2000). In citrus, black spot occurs in three stages as described by Kiely (1948): shot hole spot, freckle spot and the virulent spot stage (CABI,

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2002). In the shot hole spot stage, lesions of several millimetres diameter develop on mature fruit. The lesions mature with little expansion, but they become deeper, crater-like, with a light-coloured centre in which the conidiomata develop. The rim of the lesion is dark brown to black and is surrounded by green on an orange background. The freckle spot stage occurs when 50 or more orange to brick-red spots, ca 1 mm diameter, appear on the surface of the fruit in 2-4 days. The spots enlarge to 1-3 mm and turn brown. The virulent spot stage develops on mature fruit during warm weather. The spots expand rapidly, coalescing over large areas on the fruit surface. The lesions become irregular in shape and become active when the fruit reaches a certain stage of maturity. Leaf lesions are rare on most citrus species, but may be found on lemon; they are depressed and range in diameter from 1 to 3 mm. The disease is also evident on leaves, twigs and flowers of citrus species and as latent infections on some other hosts (Weber, 1973; Cook, 1975).

Leaf spots are noted on recently hardened young leaves to older leaves.

Figure 1. Typical symptoms of black spot disease on citrus fruit

- **Lifecycle** (Based upon CABI, 2002)

The citrus black spot life-cycle begins with infected fallen leaves on the orchard floor. Ascospores (sexual spores) are the major source of inoculum, while conidia (asexual spores) are a minor source (McOnie, 1967). The ascomata (microscopic fruiting bodies) develop in 40-180 days after leaf fall, depending on the frequency of wetting. Mature ascospores are forcibly released from the ascoma during rainfall or irrigation and some are carried on the wind currents throughout the canopy (Sutton and Waterston, 1966; Huang and Chang, 1972). Citrus trees can drop leaves all year round in some countries and seasonally in others, and this can affect the availability of inoculum (Huang and Chang, 1972). The most critical period for infection occurs at fruit set and can persist for 4-5 months. As described below, infection requires warm moist conditions. Early symptoms of black spot are not evident for more than 6 months after fruit set. Symptom expression on mature fruit is hastened by rising temperatures, high light intensity, drought stress (Koltze, 1971) and tree vigor (Rodrigues, 1973). Older trees generally develop more black spot than the younger trees.

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- ***Guignardia citricarpa*'s hosts**

The principal hosts of Guignardia citricarpa *are Citrus species:* C. limonia, C. nobilis, C. poonensis, C. tankan*, grapefruits (*C. paradisi*), lemons (*C. limon*), limes (*C. aurantifolia*), mandarins (*C. reticulata*), oranges (*C. sinensis*). Sour oranges (*C. aurantium*) are not susceptible. Non-citrus hosts reported to harbour G. citricarpa include almonds (*Prunus dulcis*), avocados (*Persea americana*), Eucalyptus spp., guavas (*Psidium guajava, P. montanum*), mangoes (*Mangifera indica*), passionfruits (*Passiflora edulis*),* Rubus *spp. and a variety of ornamentals such as Caesalpinia pulcherrima, Callistemon citrinus,* Camellia japonica*,* Dendrobium speciosum*, holly (*Ilex aquifolium*),* Magnolia *sp.,* Smilax *sp. (Kiely, 1948; Kiely, 1949b; McOnie, 1964a). Other recorded hosts are cardamoms (*Elettaria 2 Guignardia citricarpa cardamomum*) (Allen, 1971),* Cola nitida*,* Dioscorea pentaphylla *(Roy, 1965),* Eucalyptus deglupta *(FAO, 1960) and sugarcane (*Saccharum officinarum*) (Hudson, 1962). The non-citrus host list is controversial and doubtful for two main reasons: 1) adequate cross inoculation details are lacking and 2) on* Camellia*,* Dioscorea*,* Ilex*,* Persea*,* Psidium, Mangifera *and* Smilax*, species have been described under the names* Guignardia camelliae *(Cooke) Butler,* G. dioscoreae *A.K. Pande,* G. philoprina *(Berk. & M.A. Curtis) Van der Aa,* G. perseae *Punithalingam,* G. Camellia*,* Dioscorea*,* Ilex, Persea*,* Psidium Mangifera Smilax camelliae*,* G. dioscoreae*,* G. philoprina*,* G. perseae , Guignardia psidii *B.A. Ullasa & R.D. Rawal,* G. mangiferae *A.J. Roy and* G. smilacis *A.J. Roy, respectively.*

- **Economic impact**

Black spot of citrus is a serious disease of citrus cultivars in Australia (Kiely, 1949b; 1969), Guangdong province in China (Fawcett, 1936) and South Africa (McOnie, 1964b). In the Windsor and Hawkesbury River areas of Australia in 1931, all orchards of orange cvs Washington Navel, Joppa and White Siletta were severely affected and losses of 80% were common in individual orchards (Kiely, 1960). Before the adoption of control measures, heavy losses in orange cv. Valencia had been reported in the coastal orchards in New South Wales (Kiely, 1949a; 1949b). In South Africa 90% of fruits from unprotected trees were claimed to be unfit for export (McOnie, 1964b) and losses of more than 80% of unprotected fruits were reported to be common (McOnie, 1964d). In Zimbabwe black spot was known from 1965 but reached epidemic proportions in 1978 (Kotzé, 1981). In South Africa, summer rains on lemon orchards is the most important factor in establishement of an epidemic and so far black spot has not been known to disappear or decline once it has reached the epidemic stage (Kotzé, 1981). It is mainly a fruit disease and the unsightly lesions do not cause post-harvest decay but render the fruits unmarketable. During the period between 1929 and 1939, when epidemics were at their worst in Australia, the wholesale market for oranges in Sydney was depressed due to growers creating a glut for fear of their fruits developing disease.

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G. citricarpa is considered to be the most important pathogen of citrus in China, Australia and South Africa, where the citrus industry is of major importance (McOnie, 1967). Recent statistics on crop losses are unavailable.

- **Phytosanitary risk**

G. citricarpa has recently been added to the A1 quarantine list of EPPO; it is an A1 pest for CPPC and an A2 pest for APPPC and IAPSC. True *G. citricarpa* is absent from the EPPO region. Though of tropical origin, the fungus has established itself and causes serious damage in subtropical climates, e.g. China, Australia, Argentina, and South Africa. It could be expected to establish and cause significant losses if introduced into the Mediterranean citrus-growing areas.

- **Evaluation of risk assessment**

- **Plant disease forecasting models**

Plant disease forecasting models, usually referred to as prediction or disease risk models, have been developed based on the epidemiological knowledge obtained from controlled environment or field studies. Yang (2003) outlined the use of the terms "risk prediction" and "risk assessment", according to the temporal and spatial scale that uses the risk. "Risk prediction" reflects advances in disease risk communication at the farm level for a single season. "Risk assessment" is an epidemiological study to predict future occurrence of a disease by using non-experimental approaches, often through computer modeling. The study in risk assessment is a macroscale, long-term prediction that encompasses assessment of potential for entry, establishment, epidemic, and/or crop losses in a region or country once an epidemic occurs (Yang, 2006).

- **Different approaches used by plant disease forecasting models**

Models which simulate the evolution of a plant disease during the season give important information to assess the seriousness of the situation. This activity precedes the choice of an appropriate action to be implemented for reducing the economical damage. Having effective models is a critical issue in modern agriculture, especially in Integrated Protection and Organic Farming, which rest on a set of plant disease management practices with low environmental impact. (Susi, A., et al, 2002)

As for the models concerning leaf wetness, plant disease forecasting models can be classified in two major groups: process based and empirical models. The former models are based on concepts derived from a pathosystem and help to improve the understanding of the structure and behavior of such a biological system (Teng, 1985). Empirical models are typically constructed through the statistical relationships of explanatory variables with experimental data. This data may be from the

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field on individual (e.g. survival, dispersal, infection, latency, sporulation) or combined epidemic components (e.g. disease progress, final severity). Most models use the response of foliar pathogens to the combined effects of temperature and duration of leaf wetness (Duthie, 1997). These models have commonly been used in disease forecasting systems, with the reliability of model predictions heavily dependent on the quality of the dataset used for model development (Krause *et al.*, 1975).

- **The importance of modeling the infection process**

For the evaluation of the potential entry and establishment of a fungal pathogen in a new country, the first thing that has to be explored is if the weather conditions are favorable for the infection process, because all the other phases of the epidemic process depends on the fulfilling of this process. So, for many foliar pathogens, the infection sub-model is one of the most critical components for disease forecasting (Madden et al, 1988). The most important problem related to the development of such models is that they are created from either laboratory or field observations of resulting disease intensity at multiple combinations of temperature and wetness. However, for many pathogens, especially those from overseas, such data sets may not exist. Instead, the data available for many of these less-studied pathogens may be limited to growth studies in culture, simple correlations of disease observations in the field with environmental variables, or inferences made from closely related organisms. In this framework we have decided to adopt a model for the prediction of potential infection (Magarey et al., 2005) that estimates infection
from an organism's cardinal temperatures and surface wetness duration requirement. This generic model can predict infection based only upon estimates of the three cardinal temperatures and a surface wetness duration requirement and so it can be helpful for modeling pathogens for which extensive epidemiological data are unavailable. The model is based upon a temperature response function (Wang, E. L., Engel, T. 1998; Yin, X. et al., 1995) which is scaled to the surface wetness duration requirement.

- **Description of the model used**

In our implementation the infection model runs with an hourly time step, needing as weather inputs hourly air temperature and hourly leaf wetness. In this study we have decided to use the outputs of the component CLIMA and LeafWetness, described in the previous paper.
The only others necessary inputs are some parameters related to the biology of the particular pathogen. They are: the minimum and maximum values of the wetness duration requirement (because wetness is not always a rate-limiting factor), the minimum, optimum and maximum values of temperature for the starting of the infection process and the number of hours allowed for an infection process to be dormant without being terminated (D50). The complete list of the inputs needed by the model is shown in Tab. 1.

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Table 1. Input requirements of the infection model.

Type of the input	Name of the input
WEATHER INPUTS	HourlyAirTemperature HourlyLeafWetness HourlyRain (for pycnidiospores infection)
PARAMETERS	MinimumWetnessDurationRequirement MaximumWetnessDurationRequirement MinimumTemperatureForInfection OptimumTemperatureForInfection MaximumTemperatureForInfection D50

The parameters of *Guignardia citricarpa* used in our study were selected from various sources (see relevant paragraph), and are shown in Table 2.

Table 2. Parameters of *Guignardia citricarpa*

Parameters of *Guignardia citricarpa*	**Ascospores**	**Pycnidiospores**
MinimumWetnessDurationRequirement	**15**	**12**
MaximumWetnessDurationRequirement	**38**	**35**
MinimumTemperatureForInfection	**15**	**10**
OptimumTemperatureForInfection	**27**	**25**
MaximumTemperatureForInfection	**35**	**35**
D50	**0, 3, 14**	**0, 3, 14**

The model uses the temperature response function of Yin et al. (Yan, W., Hunt, L. A., 1999), which is a simplified and improved version of the rice clock model (Gao, L. Z. et al., 1992). The function uses the pathogen's cardinal temperatures to estimate the shape parameter and the temperature response:

$$f(t) = \left(\frac{T_{\max} - T}{T_{\max} - T_{opt}}\right)\left(\frac{T - T_{\min}}{T_{opt} - T_{\min}}\right)^{(Topt - T\min)/(T\max - Topt)} \qquad \text{if} \qquad T_{\min} \le T \le T_{\max}$$

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0 *otherwise*

where T = mean temperature (°C) during wetness period, T_{min} = minimum temperature for infection (°C), T_{max} = maximum temperature for infection (°C), and T_{opt} = optimum temperature for infection (°C). The advantages of the Yin function compared with other growth functions include the fact that the function has only three parameters (T_{min}, T_{opt}, and T_{max}) and each parameter has a clear biological meaning (Yan, W., Hunt, L. A. 1999). The function gives a smooth curve as opposed to a series of lines with abrupt changes between them. The function combines the advantages of several equations: an exponential response at low temperatures, a positive linear response at intermediate temperatures, a parabola response at optimum temperatures, and a negative response
at high temperatures, as shown in fig.2

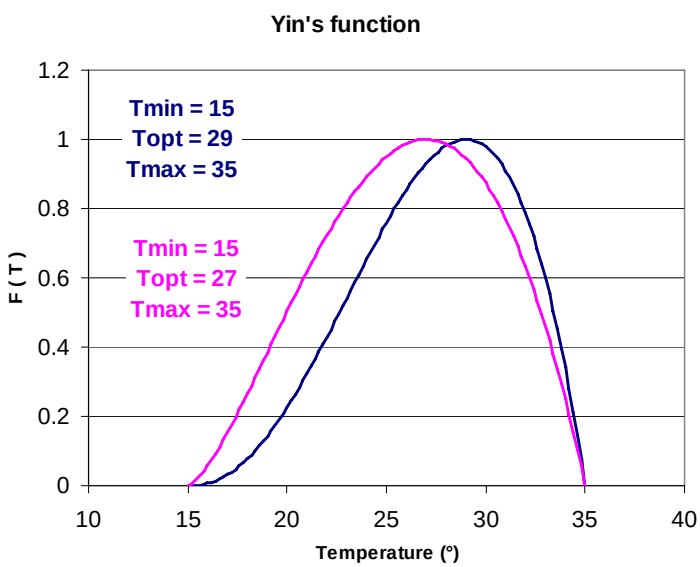

Fig.2 response of the Yin function.

The effect of leaf wetness is taken into account in the following equation:

$$W(t) = \frac{W_{min}}{f(t)} \qquad \text{if} \quad \frac{W_{min}}{f(t)} \le W_{max}$$

$$W_{max} \, otherwise$$

Where W_{min} = minimum value of leaf wetness duration for the infection (h), $f(t)$ = temperature response function, W_{max} = optimum value of the leaf wetness duration requirement (h). In our implementation we

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have also considered the the number of hours allowed for an infection process to be dormant without being terminated (D50), as described in the Fig. 3

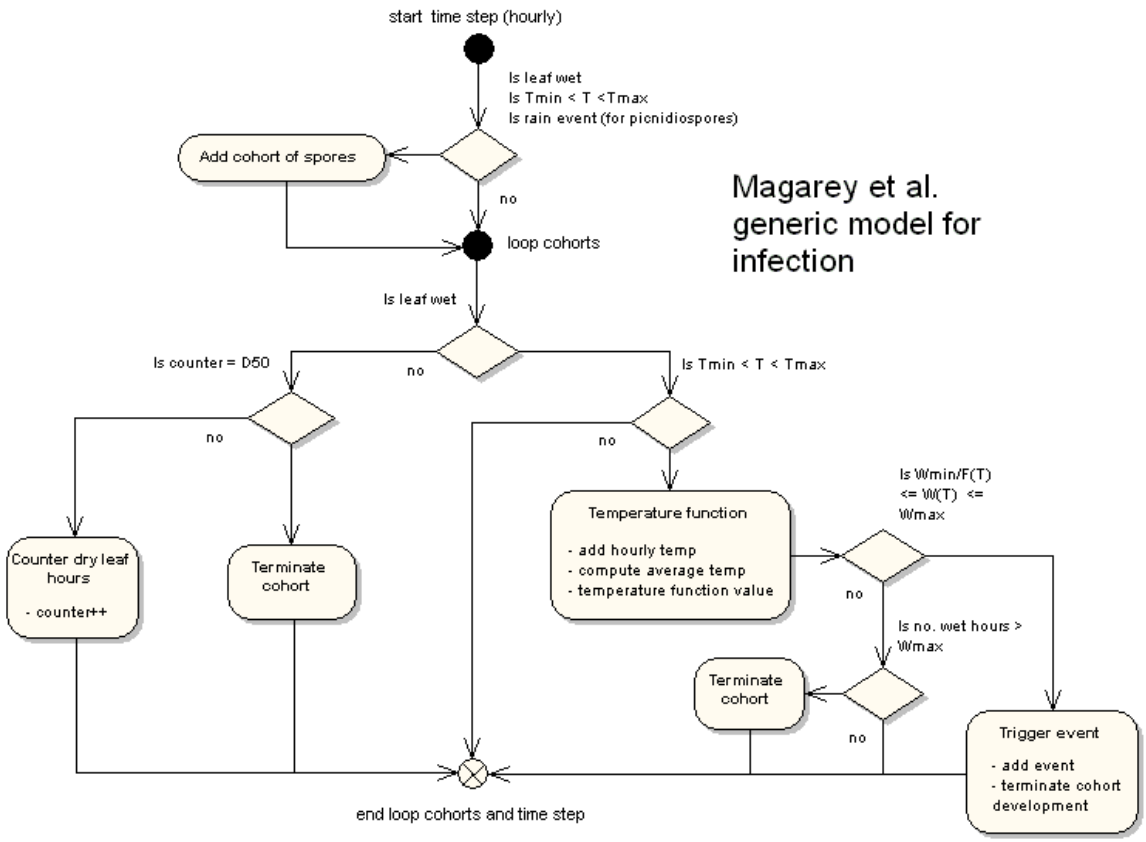

Figure 3. Flow diagram of Magarey et al. generic model for infection.

The model was implemented within a software component which includes other modeling approaches, using the same architecture of the LeafWetness component and described by Donatelli and Rizzoli, 2007). The software component will be made available to public at the beginning of 2009.

- **Model tests with weather data from infected areas**

Preliminary tests of the infection model with the parameters of *Guignardia citricarpa* have been done for two years at two sites of Australia, where the citrus black spots' disease is well established. The sites, and the references where the infection is mentioned are:

- Maryborough, Queensland (Paul et al., 2005)
- Gayndah, Queensland (Miles et al., 2004; Paul et al., 2005).

We extracted daily data in order to provide the same type of input we get from the EU weather grid:

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- daily air temperature maximum and minimum
- rain
- global solar radiation
- wind
- relative humidity maximum and minimum (missing)

So, a complete model run included the following steps:
- estimate of daily relative humidity maximum and minimum,
- estimate of all hourly values,
- estimated of leaf wetness (SWEB) (as described in the relevant section)
- run the Magarey infection model

The result from the Australian sites are larger number of infections completed at each hour / year) than the samples run in Europe. This preliminary test was performed using the the parameterization reported in table 2.

- **Model runs**

The model was run for the 418 cells of the citrus growing areas of the European Union, with 6 sets of parameters both for ascospores infection and pycnidiospores infection.
Besides the values of table 2, two values levels were tested for the parameter optimum temperature for the infection, because the response of the model resulted very sensitive to this parameter in the preliminary tests (see also fig. 2).

- **Run results**

Results presented are preliminary because: 1) the parameter calibration for generation of hourly weather data was run on a limited number of grid cells, and 2) the tests of all the steps of the workflow to move from daily data to the estimates of infection were not completed.
The model output contains “simulation events”, that is the infection events which could complete in a number of wet leaf hours greater than the minimum and smaller than the maximum allowed. Results are presented as total number of potential infections by ascospores over the time period 1998-2007, and as standard deviation across years.
The first two maps in the following pages are simulations run the value for D50 = 14, that is, allowing for at most 14 hours of continuous dry leaves for an infection cycle to complete (the specific cohort of spores is terminated when dry hours reach the value of D50) . The second two maps are runs with D50 = 0 that is, no interruption of leaf wetness allowed.

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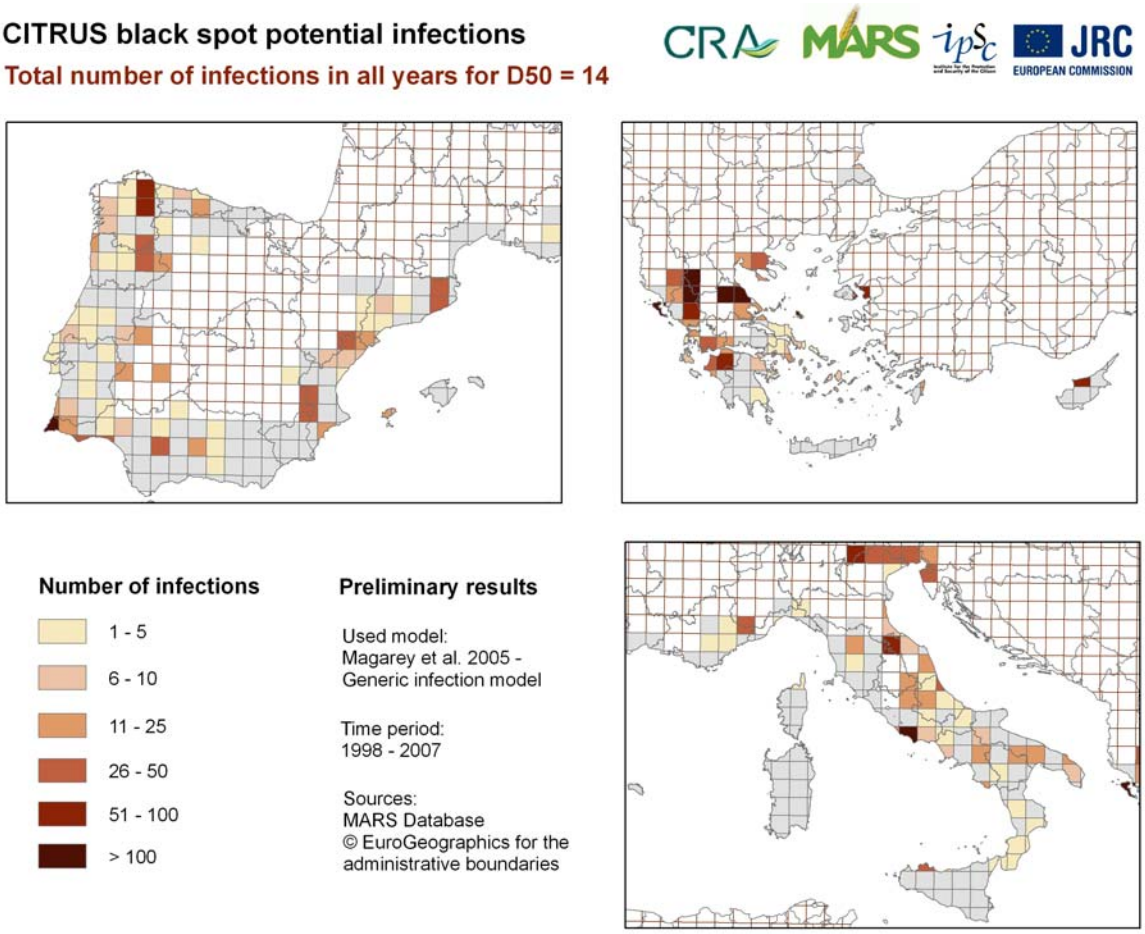

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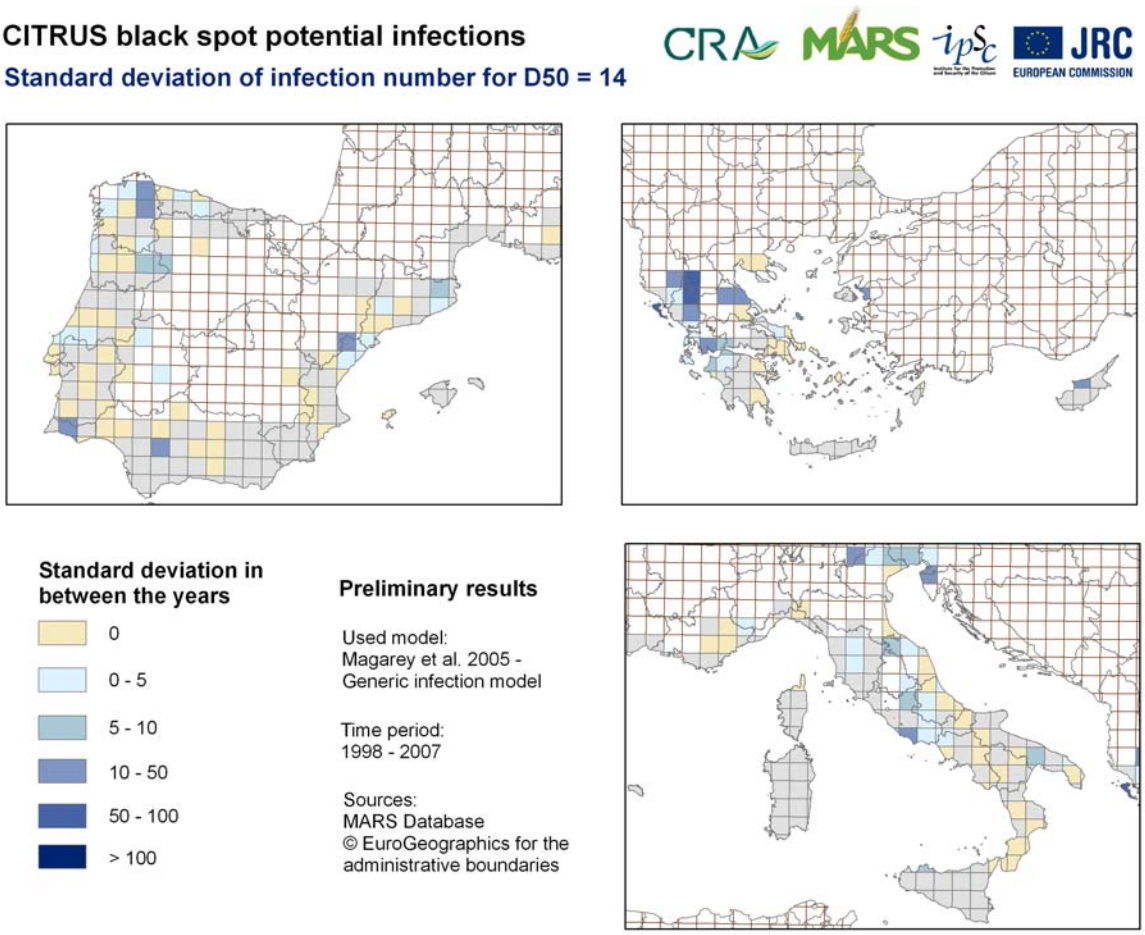

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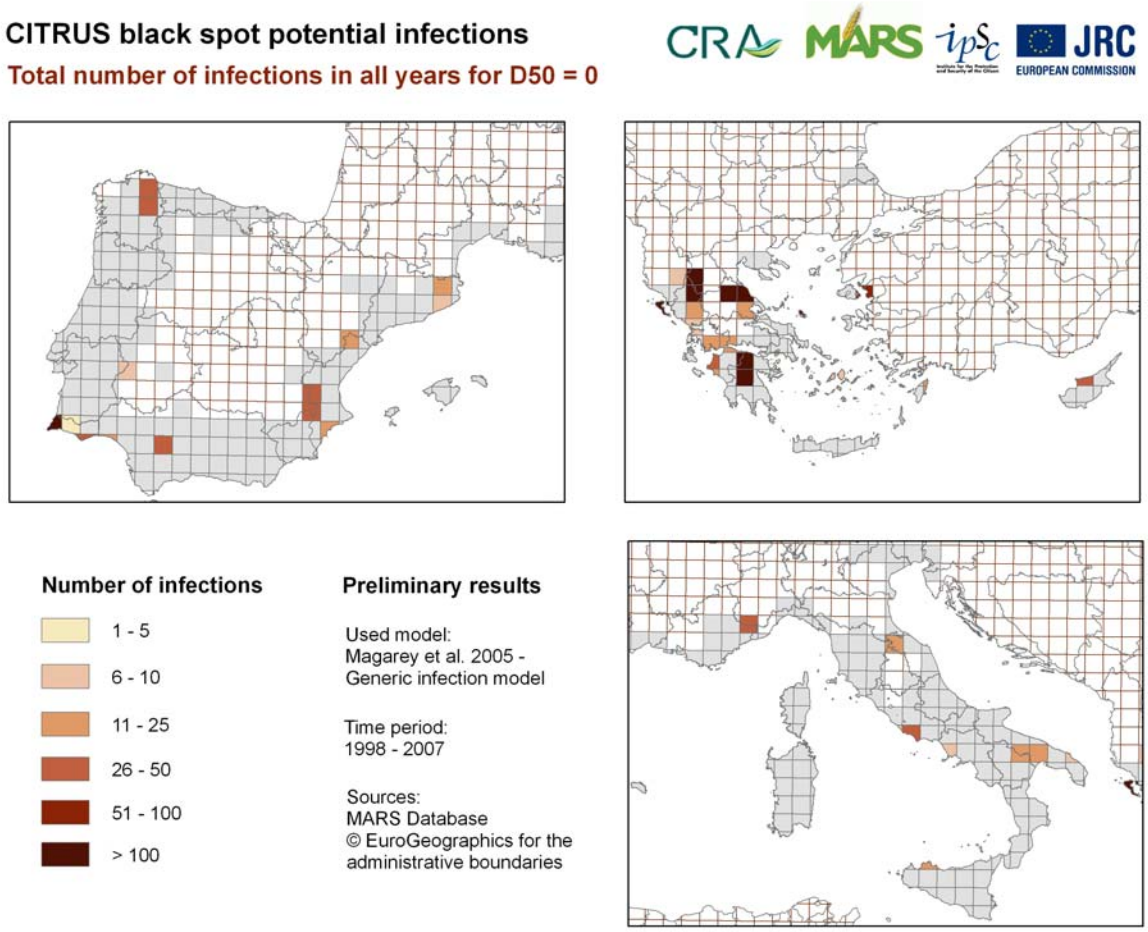

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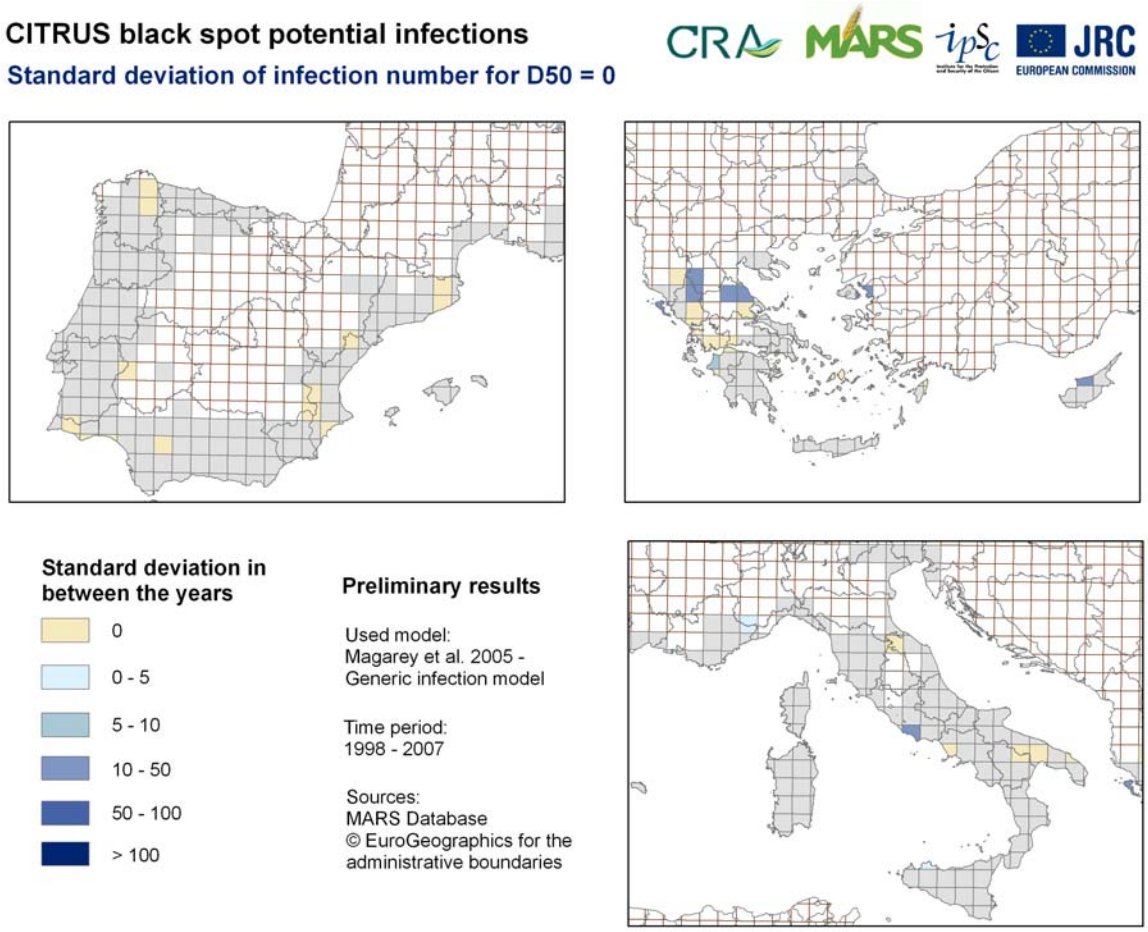

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- **Conclusions**

The analysis run shows that infection from ascospores can propagate (the simulation of infection start from pycnidiospores is being run), even if not at all location, and even if with magnitudes smaller than in the Australian sites tested so far with the same model.

The most critical value of parameter D50 still shows possibility for infection, being the most conservative estimate to reject the null hypothesis.

The sensitivity analysis run both with respect to hourly data generation and with model simulation show results that might decrease the magnitude of the infection estimated, allowing however for some risk in some areas.

The results currently presented do not include the potential risk of initial infection via pycnidiospores.

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APPENDIX B - THE OAK PROCESSIONARY MOTH ANALYSIS

Used in:

- Scientific Opinion of the Panel on Plant Heath on a request from the European Commission on the Plant health risk of *Thaumetopoea processionea* L., the oak processionary moth, for the EU territory. The EFSA Journal (2009) 491, 1-64

Growing Degree Days maps

Project ClimPest – Support to the EFSA Plant Health Panel

M. Donatelli, B. Baruth, L. Seguini, P. A. Bianchi
JRC IPSC AGRI4CAST

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- **Growing degree day accumulation in Europe**

The OPM, oak processionary moth (Thaumetopoea procesionea L.) is apparently newly established in the London area. JRC was requested by EFSA to evaluate climatic suitability of northern Europe to OPM establishment. Presence of OPM was recorded in the Netherlands in 2005 and following years, and in the London area, UK in 2006 and 2007. The phenology of OPM is mostly temperature driven, and it is supposed to be similar to the one of Gypsy moth; however, data are very scarce both as recorded presence and as pattern of response to temperature.
Objective of this work was to explore climate suitability for OPM based on the EU weather grid run at JRC.

- **Methodology**

Weather data from the JRC AGRI4CAST 25 km grid were used to build maps of Growing Degree Days (GDD) according to the formula:

GDD = (Tmax + Tmin) / 2 – Tbase;

If GDD < 0 then GDD = 0

Where:

Tmax = Daily maximum air temperature
Tmin = Daily minimum air temperature
Tbase = base temperature (values used: 8 and 10 C)

The starting date for accumulating GDD was April 1st, and the last day August 31st.

Years considered were from 1980 to 2008. Calculations were done for every year, but results were averaged for:
1980-89, 1990-99, 2000-2008. Years from 2005 to 2008 were also kept separated.

Data are presented as maps. Maps are cumulated values and “difference maps”, where values shown are *ValueOfPeriod – Value1980-89*.

- **Data Availability**

Processed data and GIS project were made available to EFSA via a FTP link. Restrictions to the dissemination of data are detailed in the memo of April 20, 2009.

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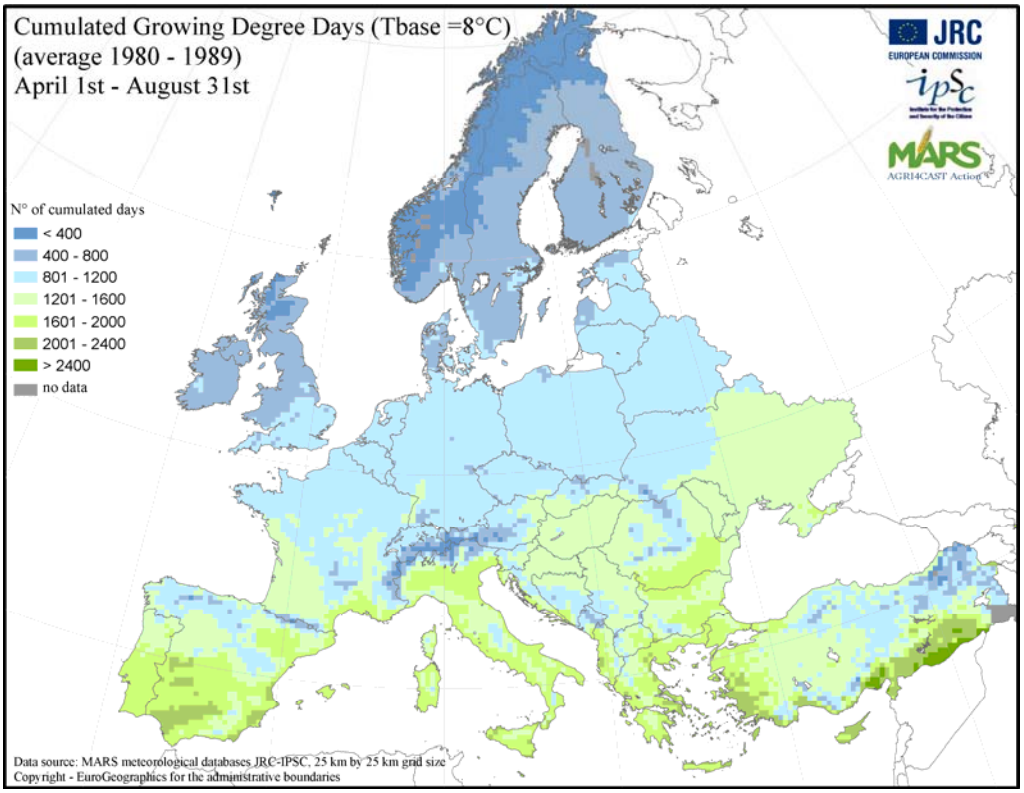
- **Base temperature 8 C maps**

- **Cumulated values**



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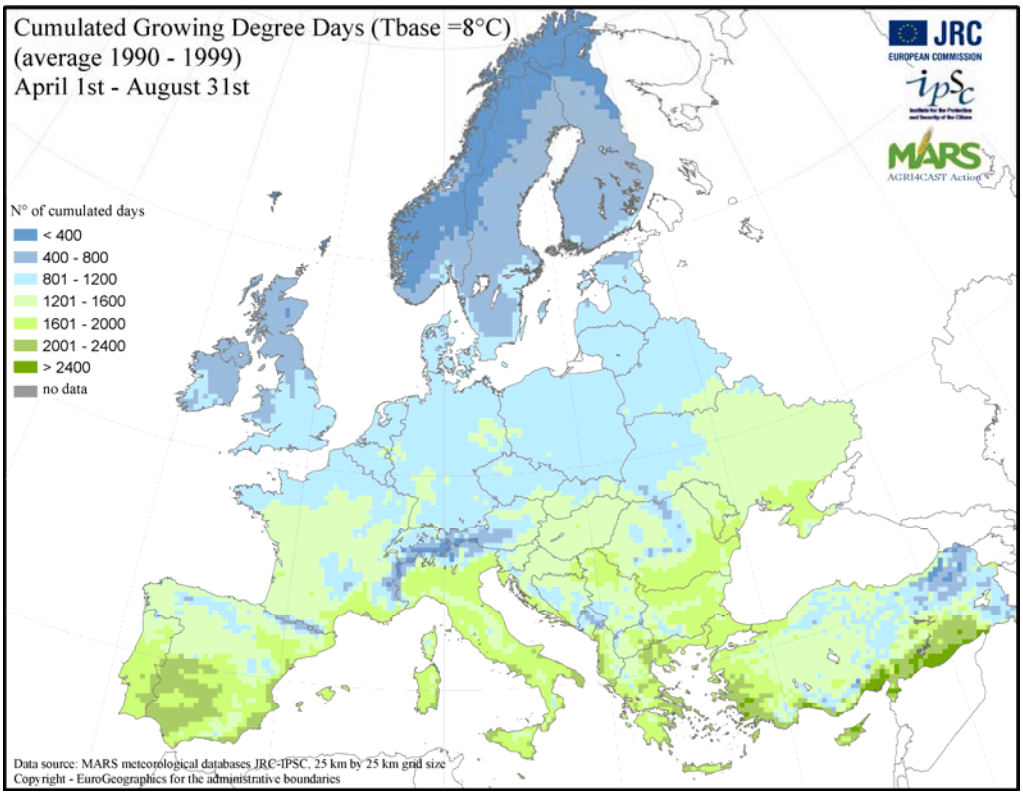

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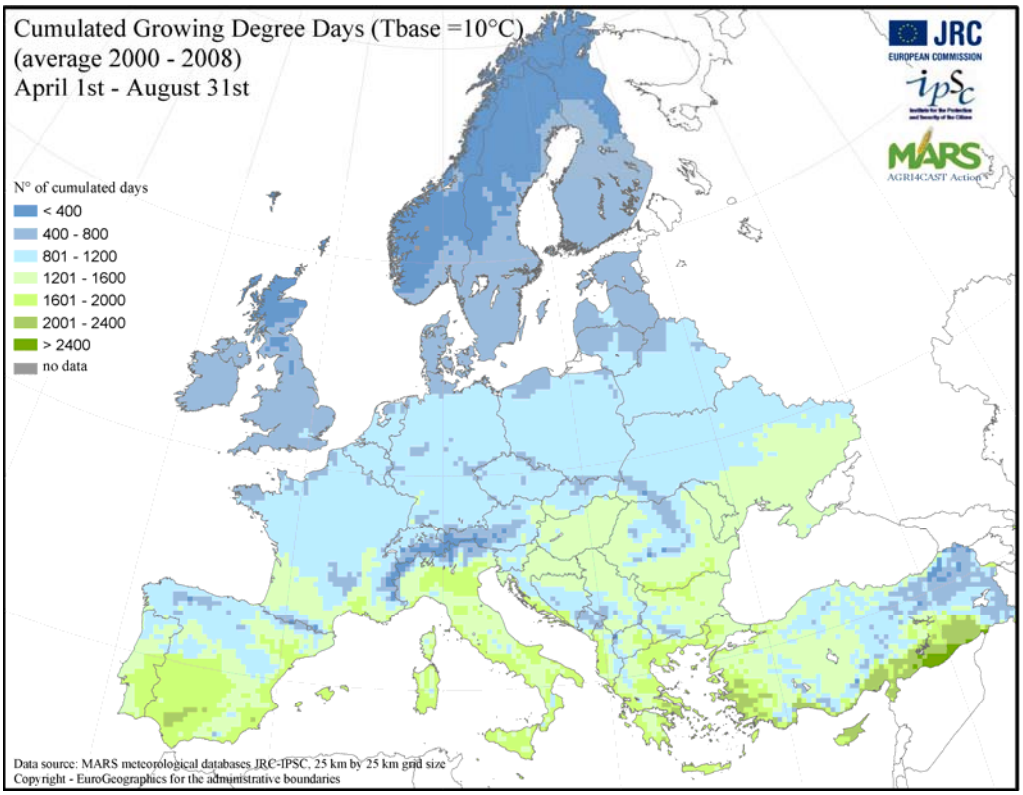

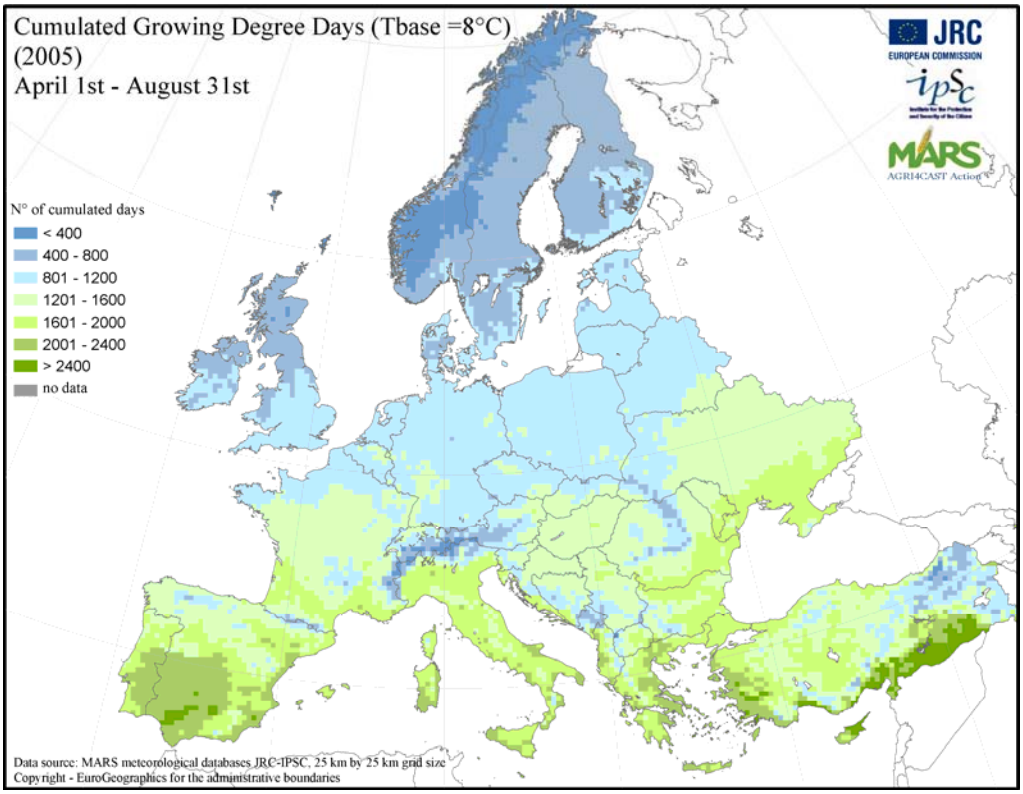

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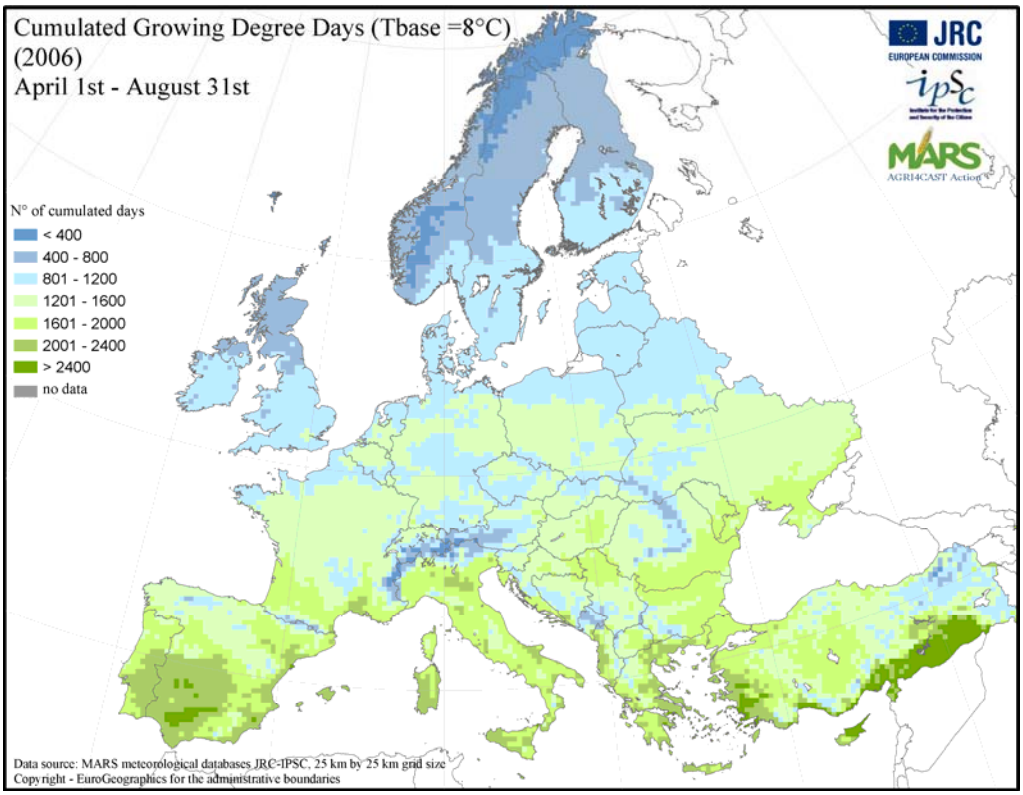

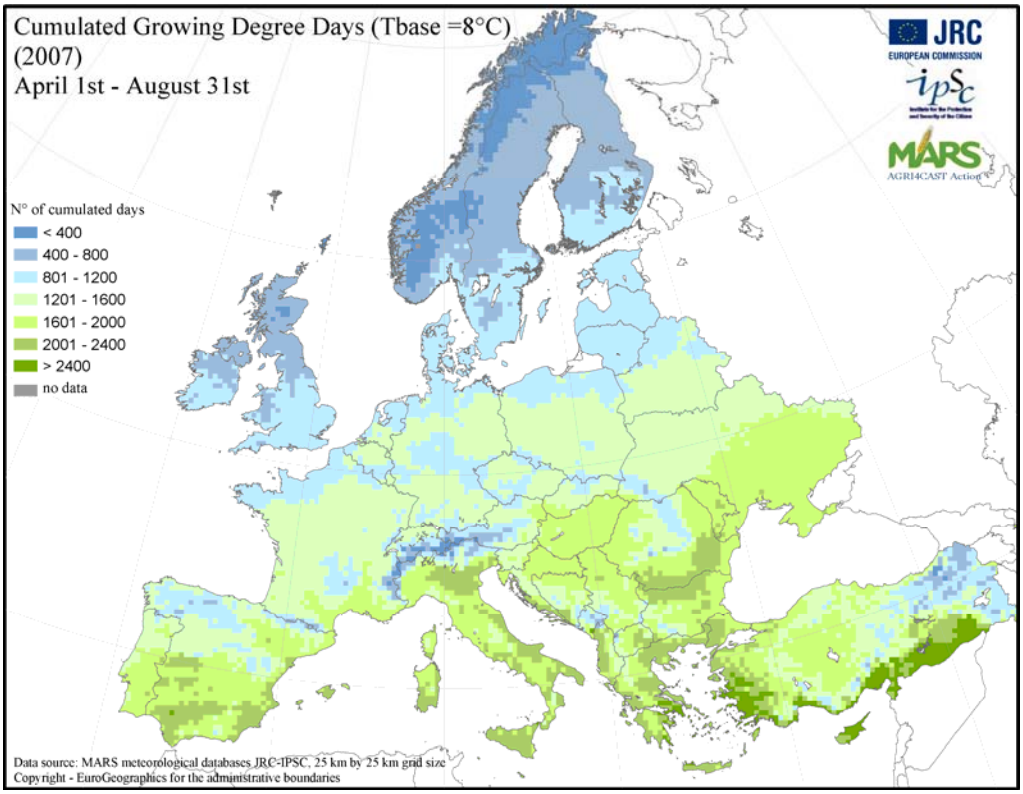

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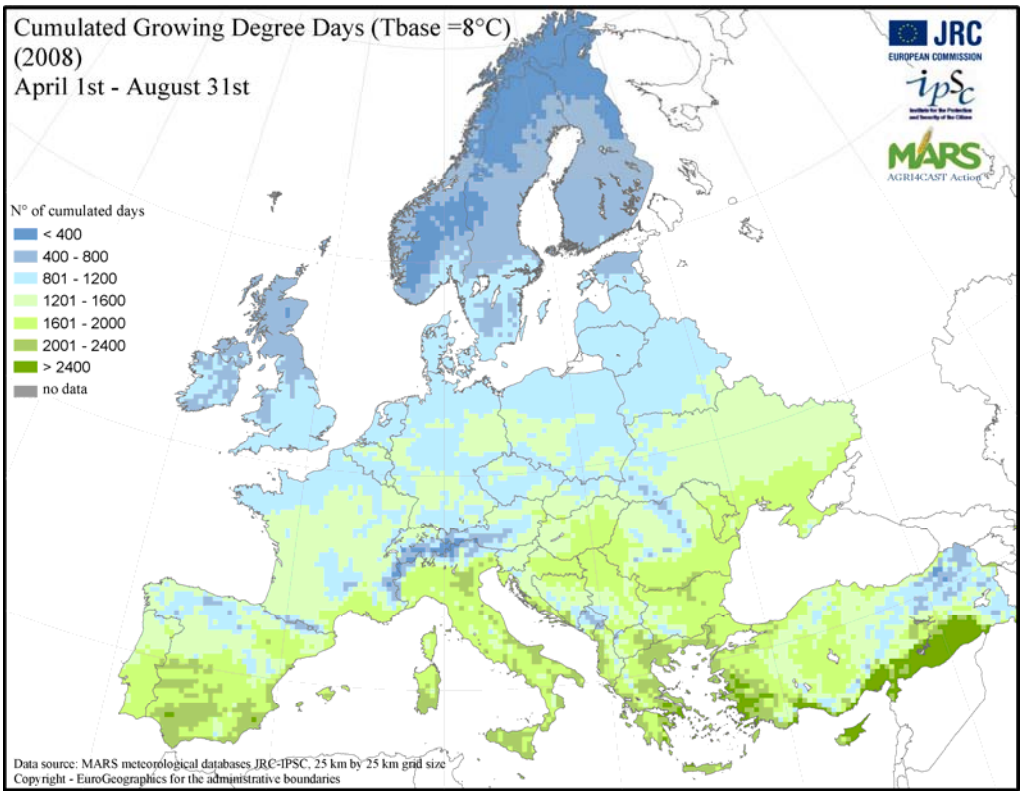

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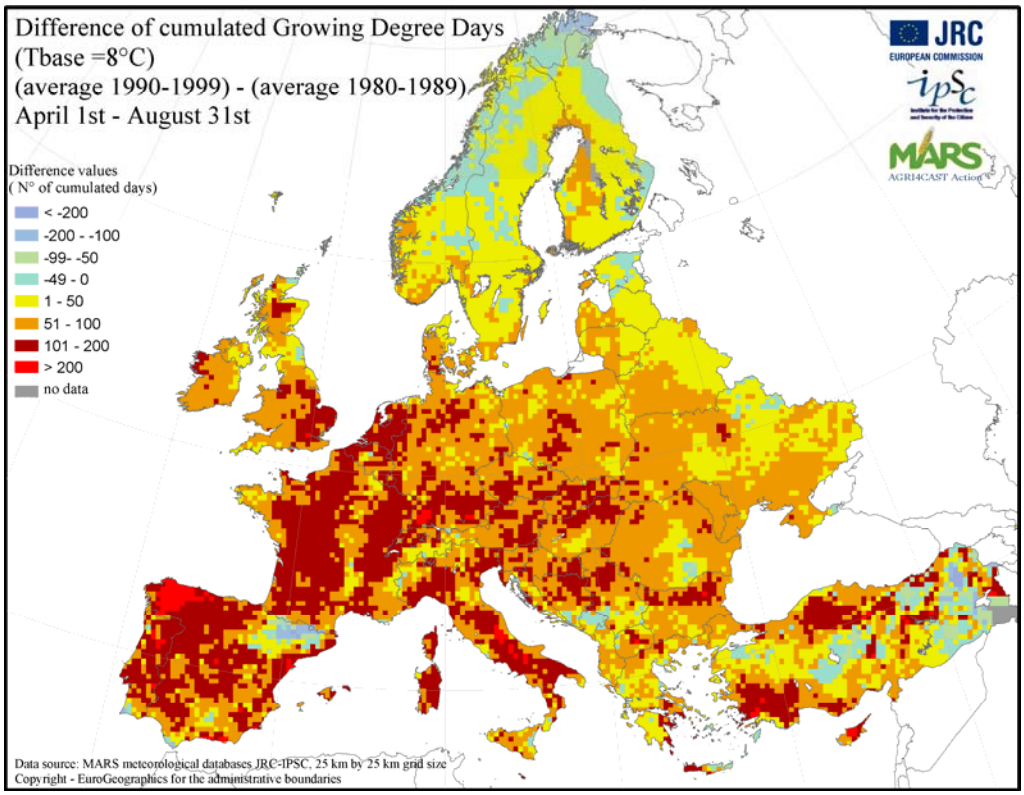
- **Difference maps**



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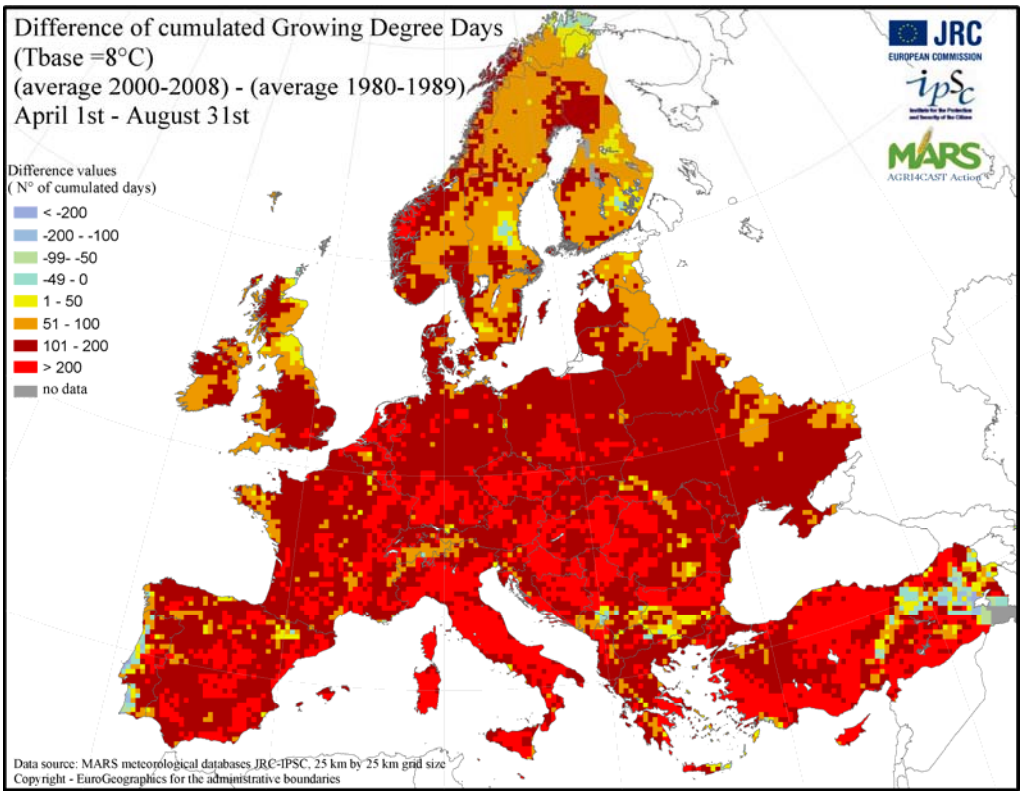

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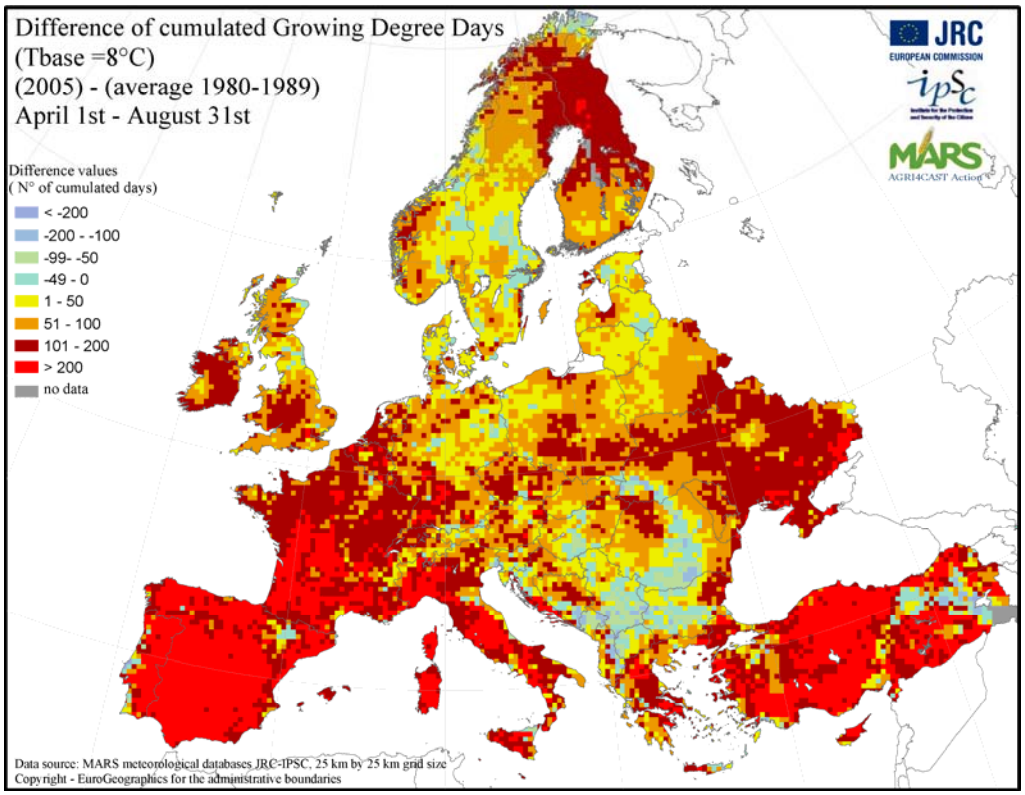

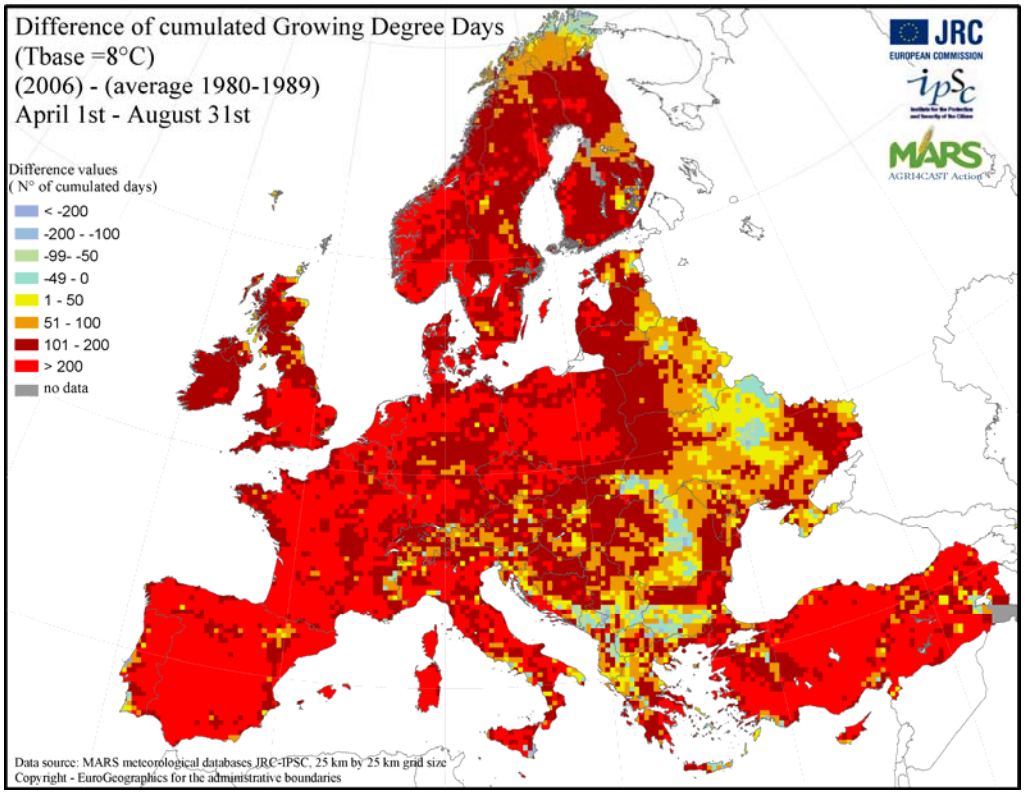

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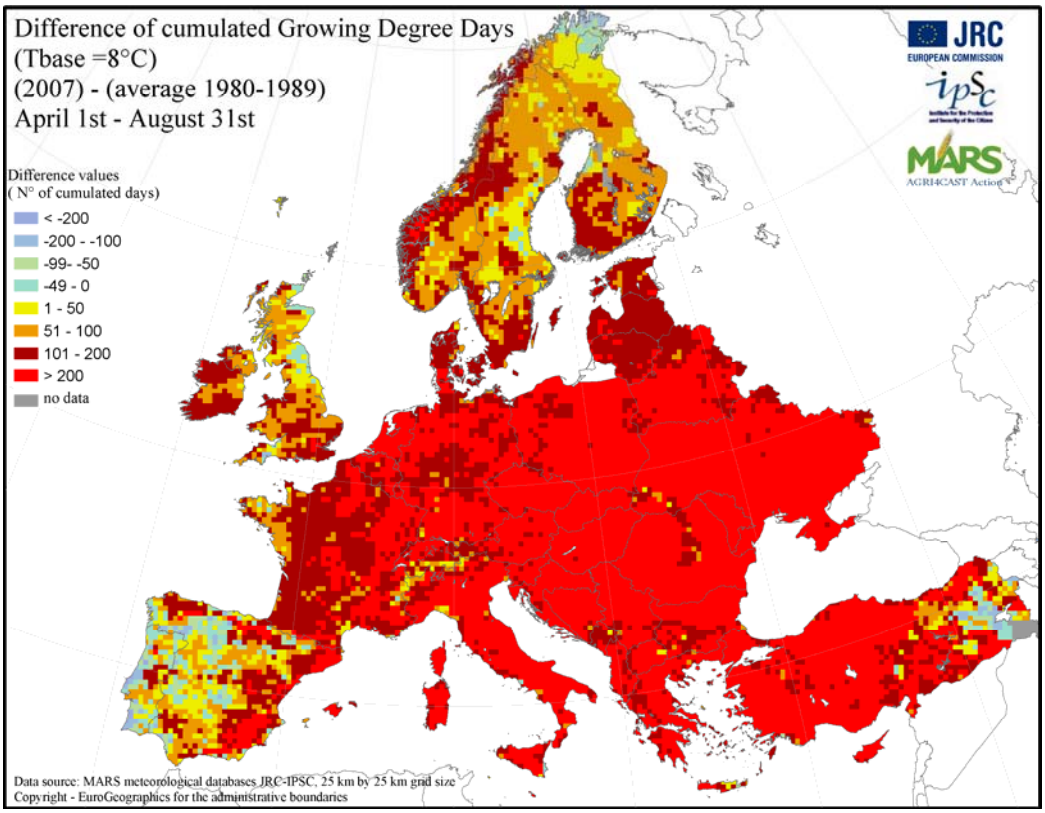

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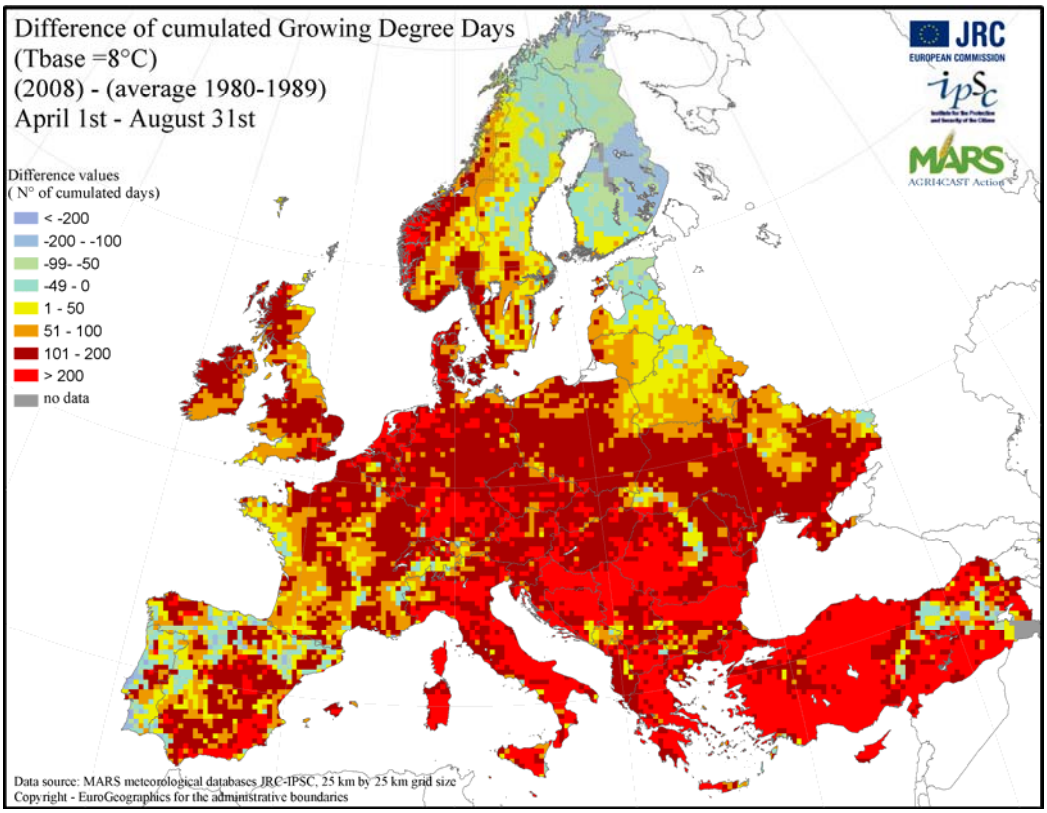

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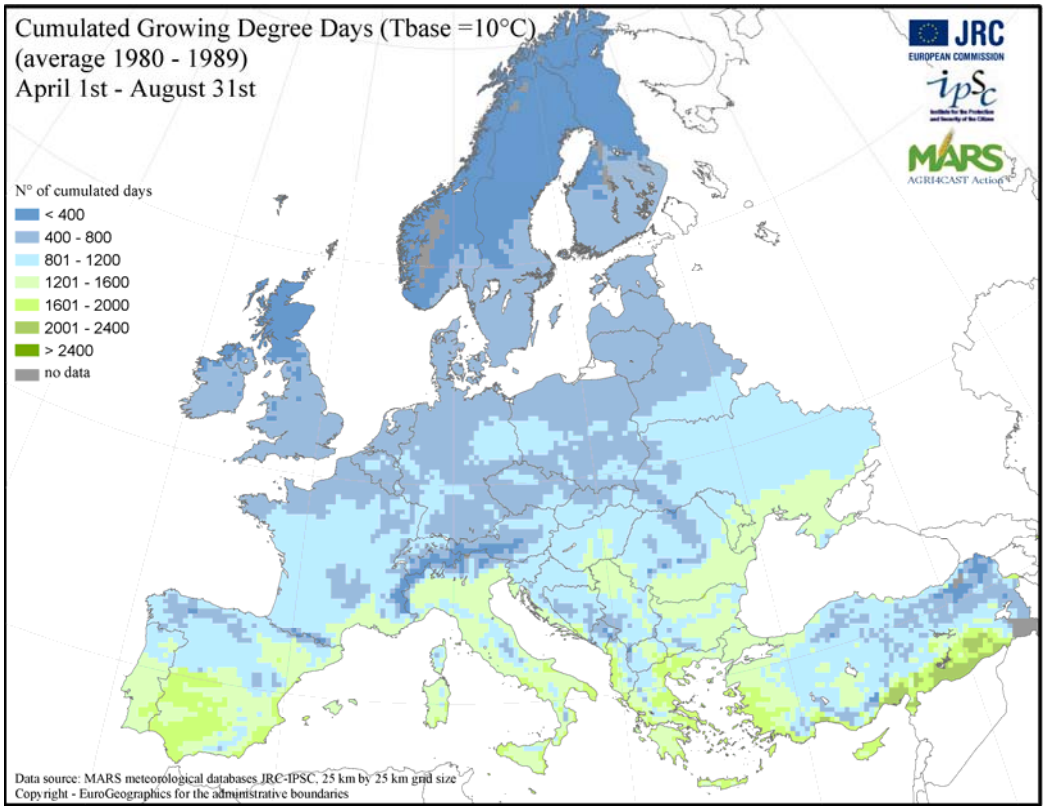
- **Base temperature 10 C maps**

- **Cumulated values**



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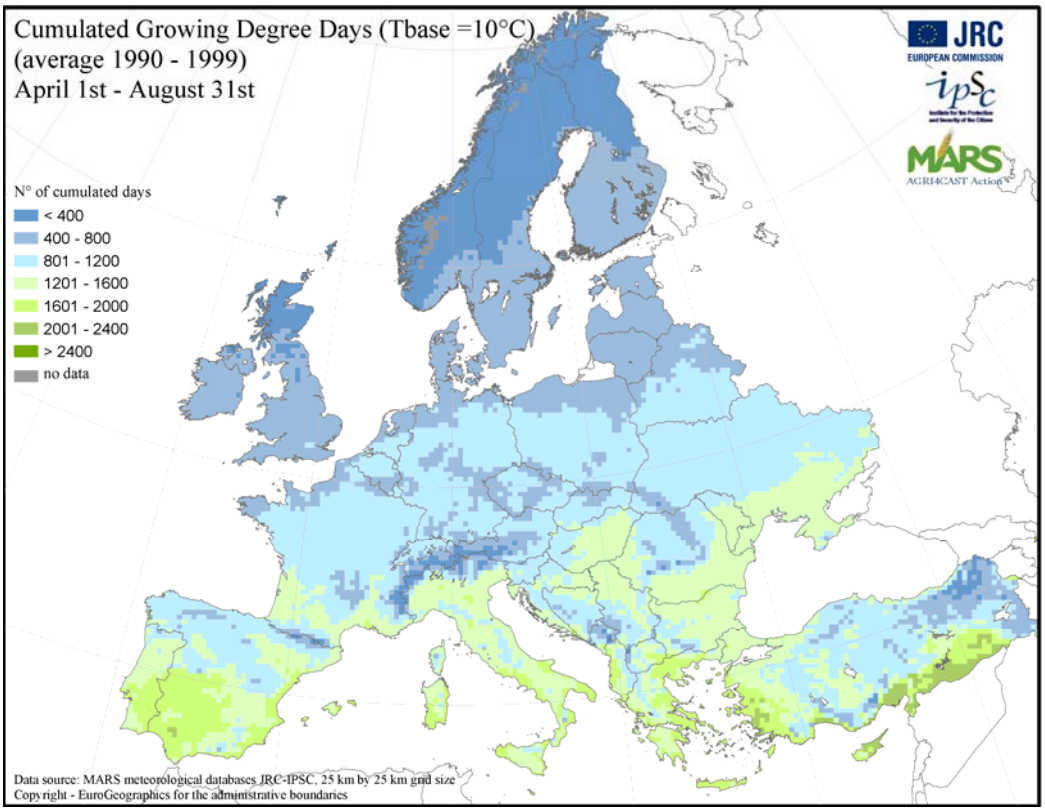

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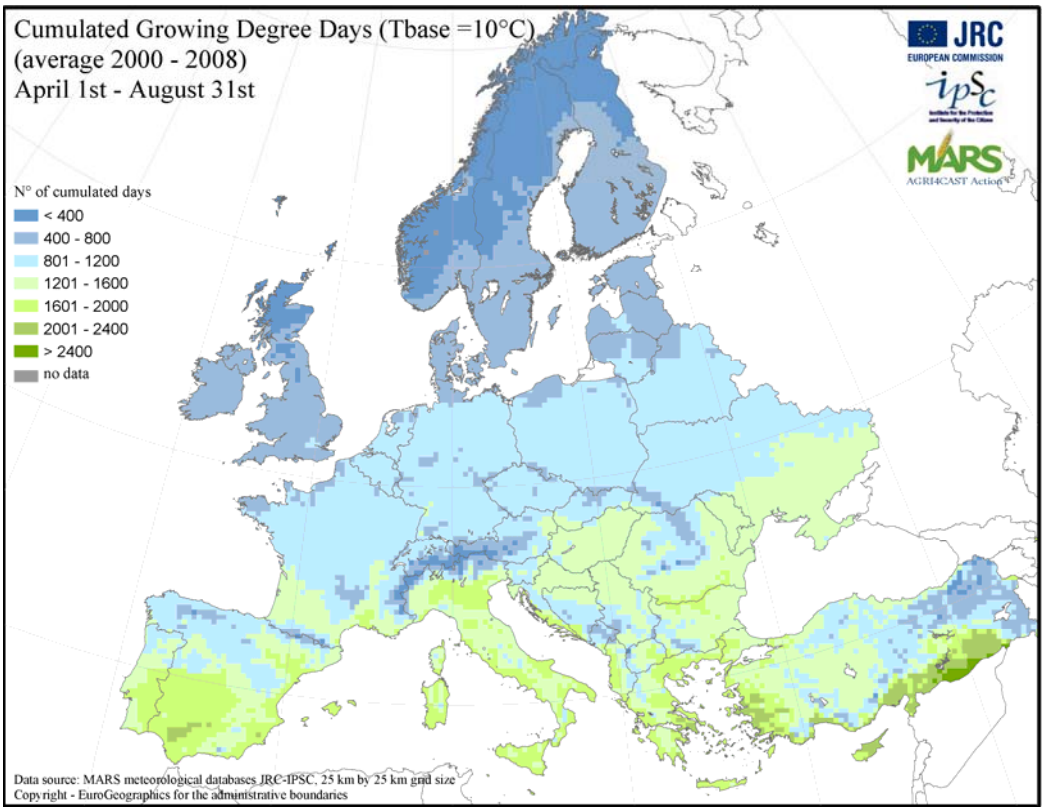

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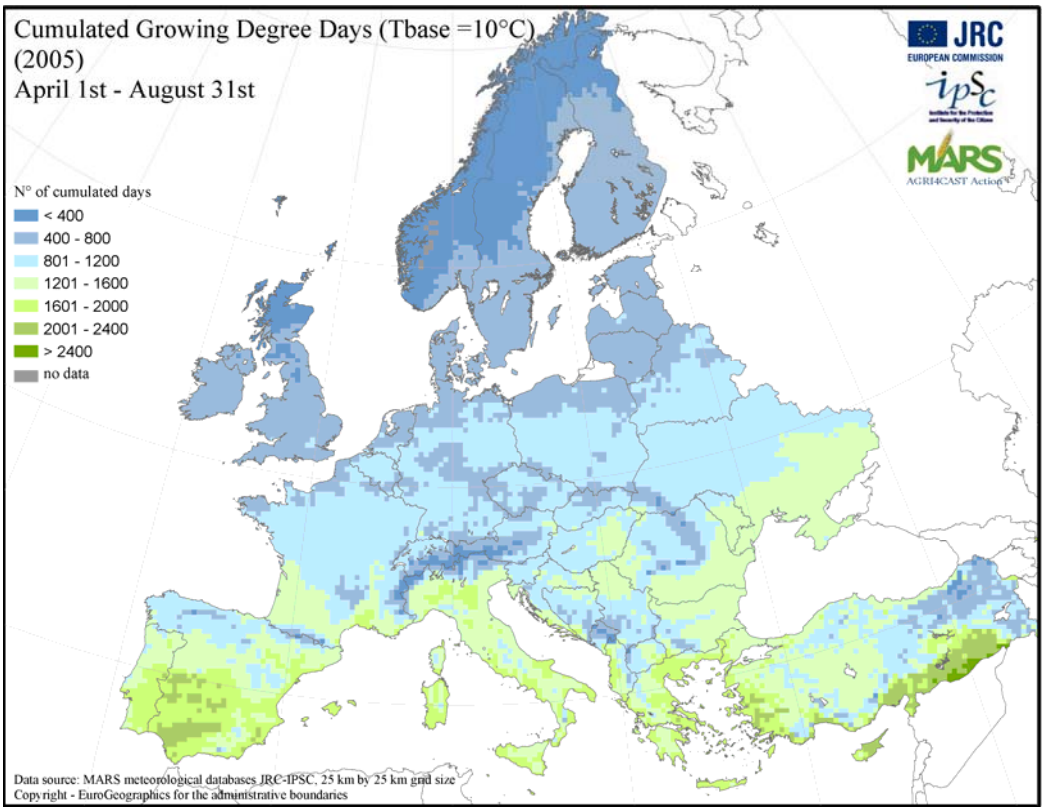

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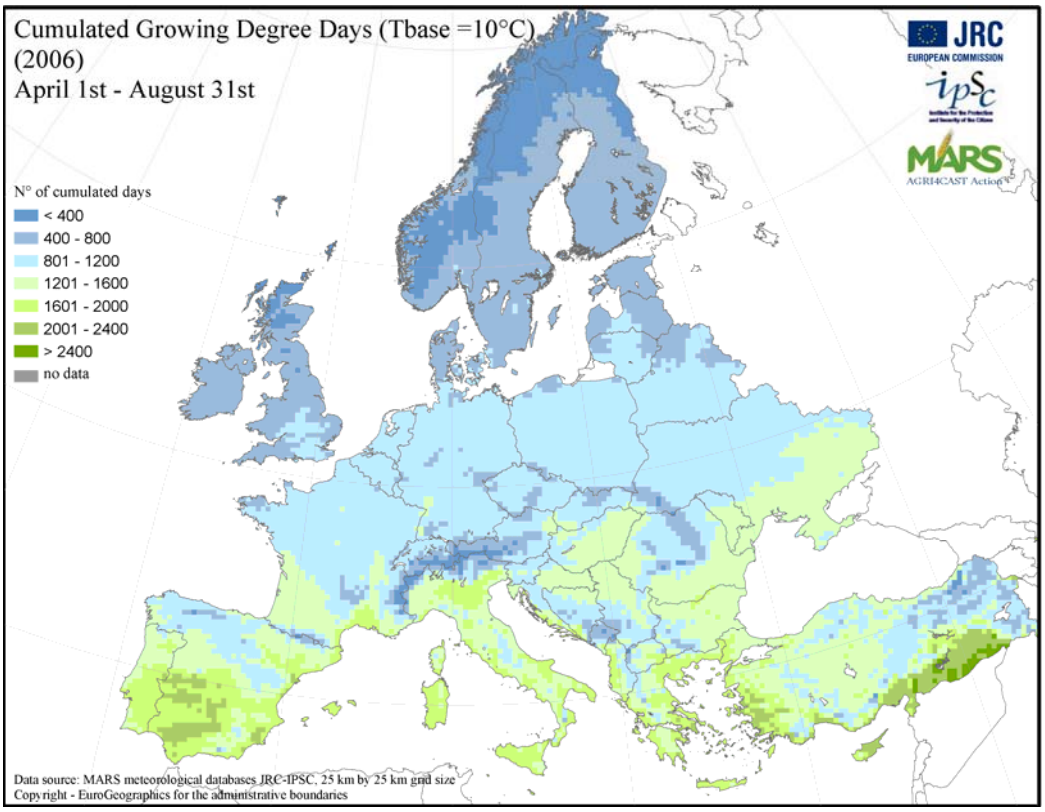

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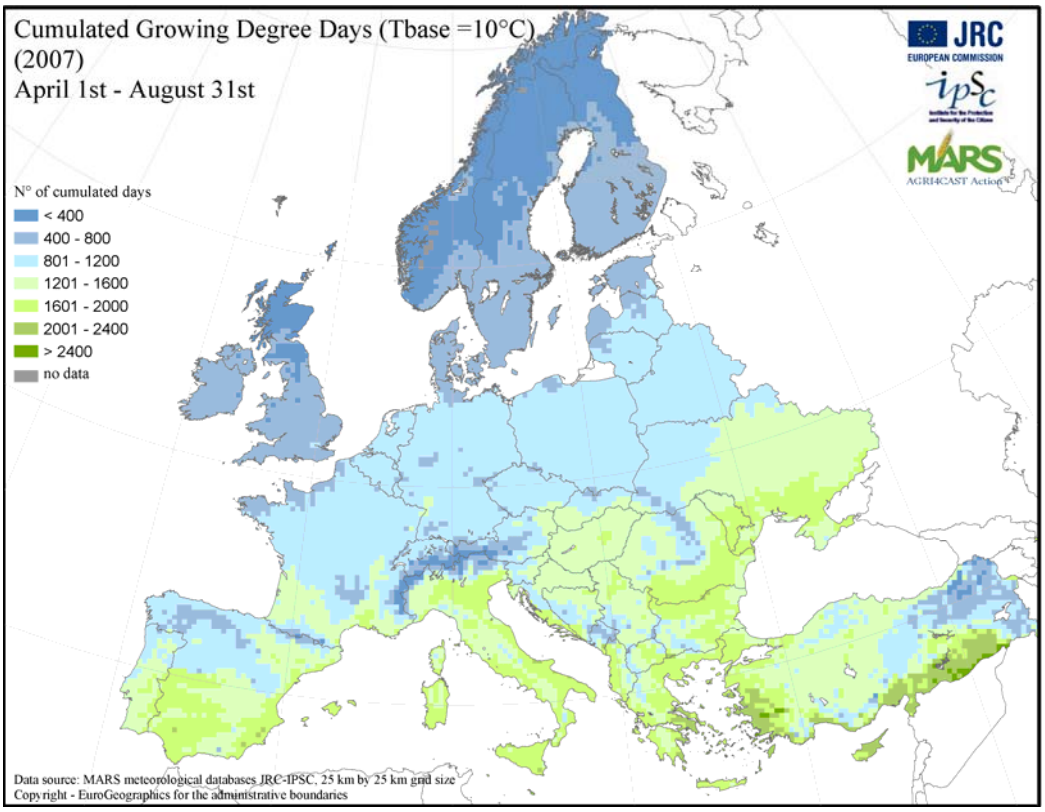

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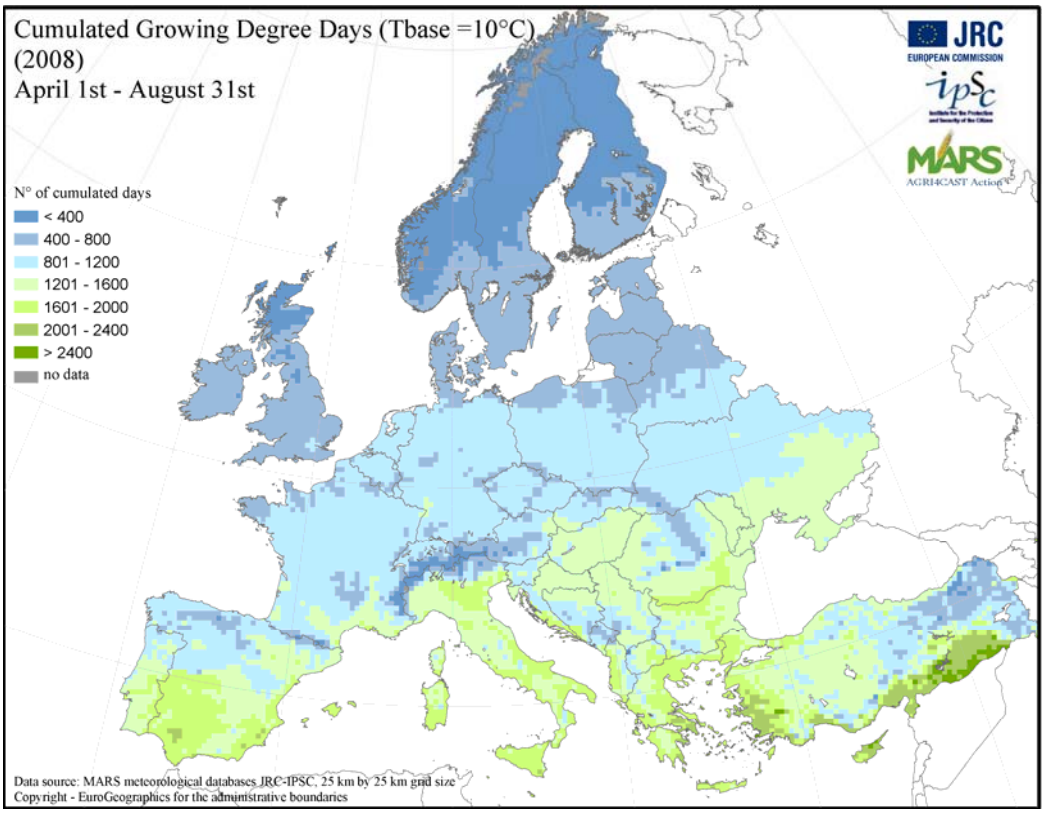

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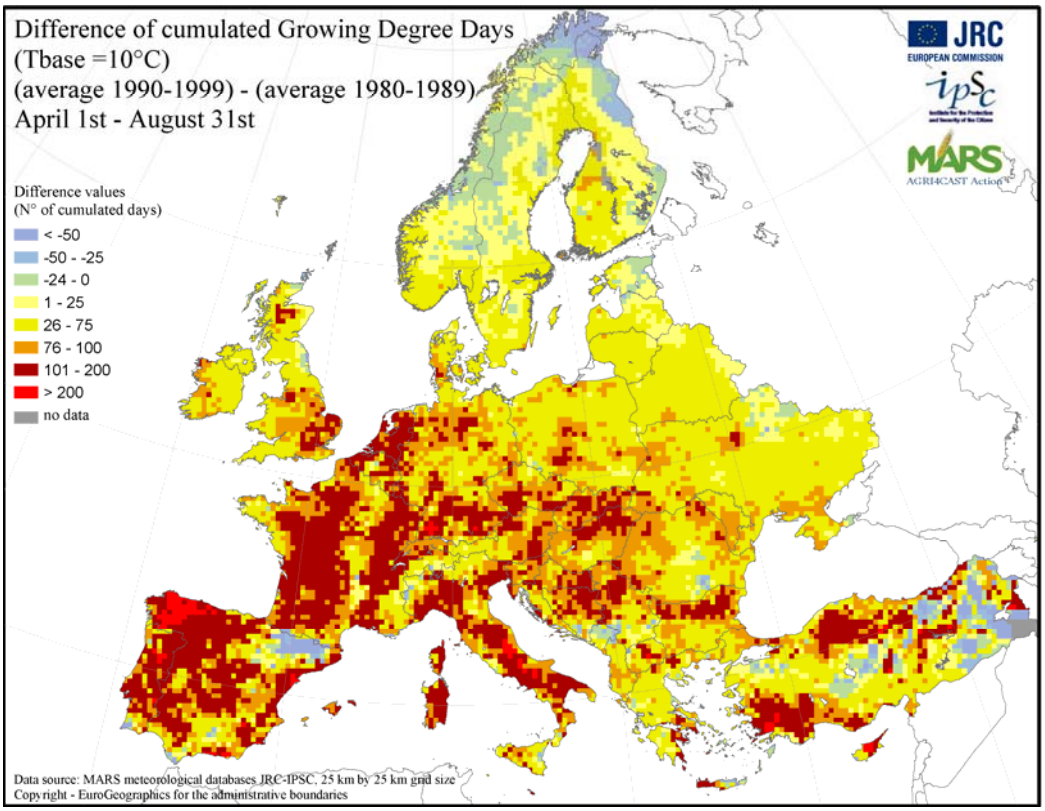
- **Difference maps**



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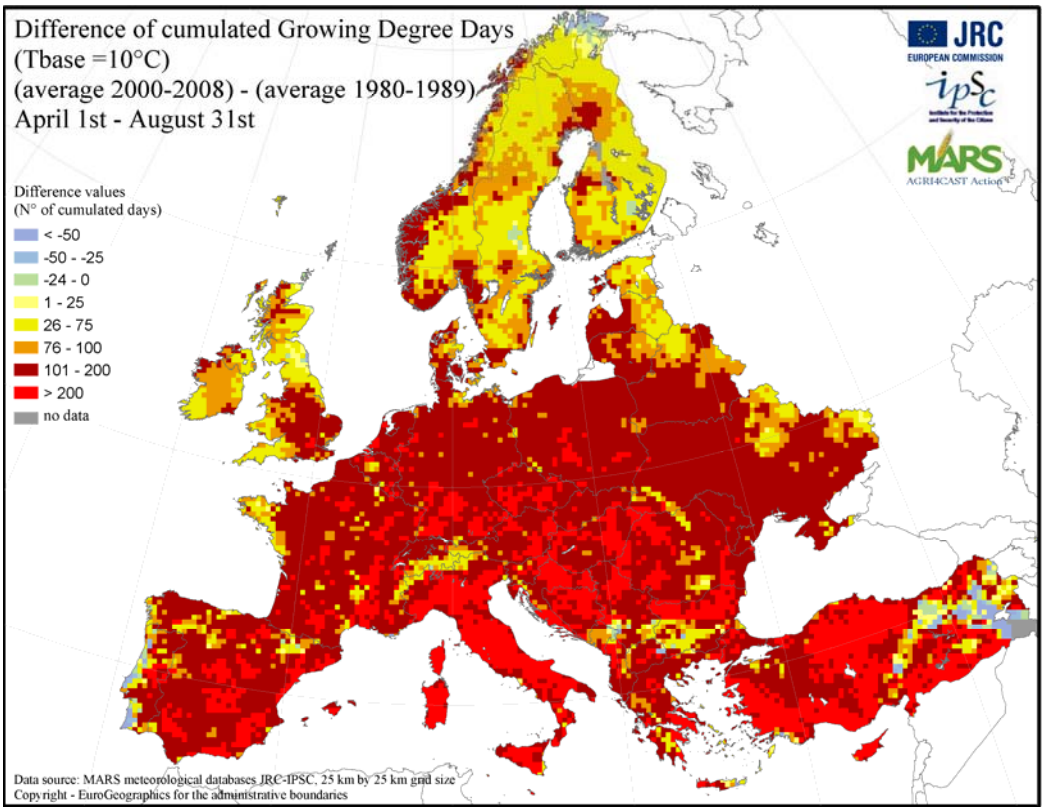

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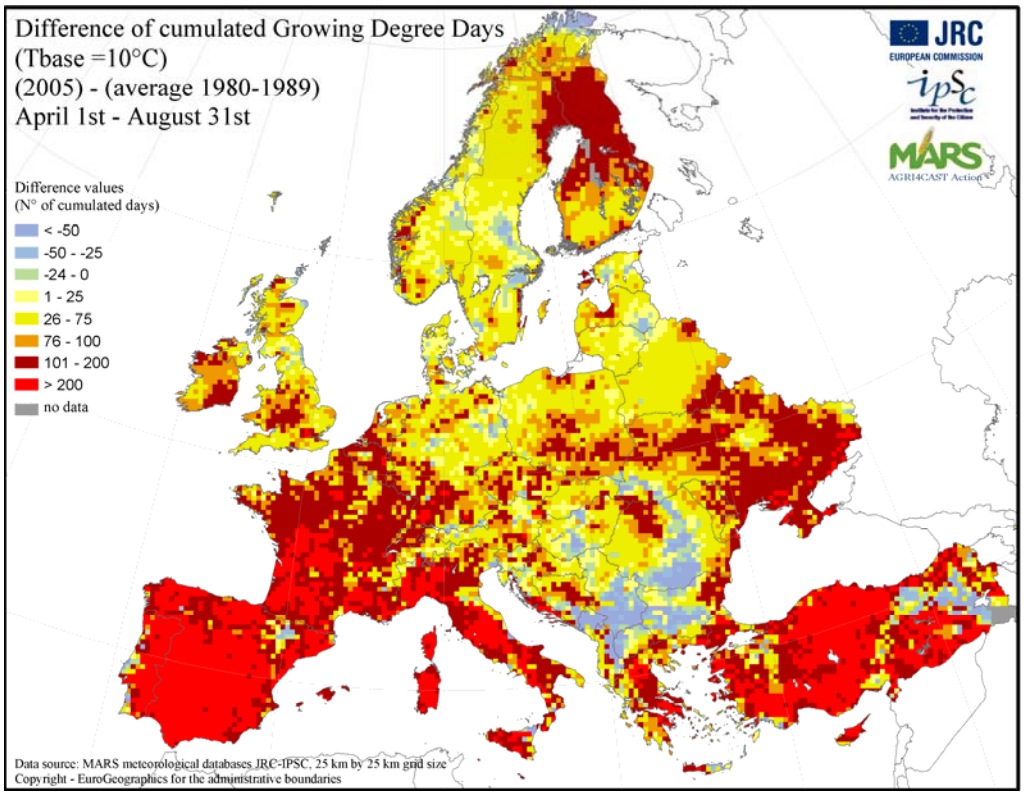

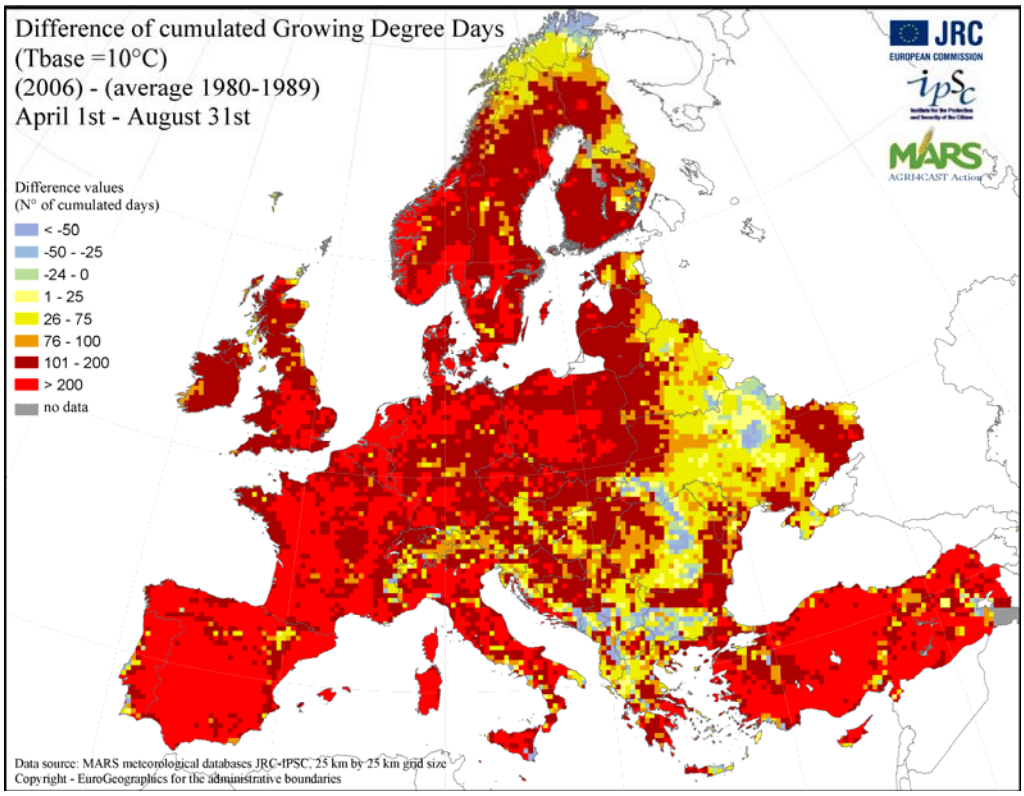

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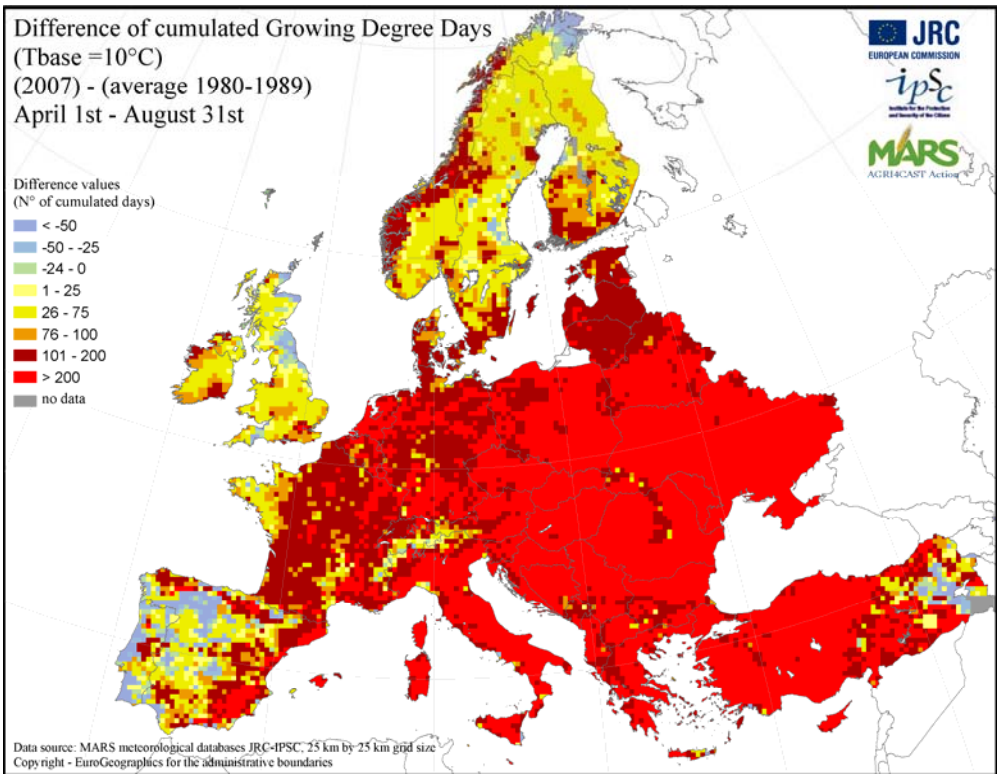

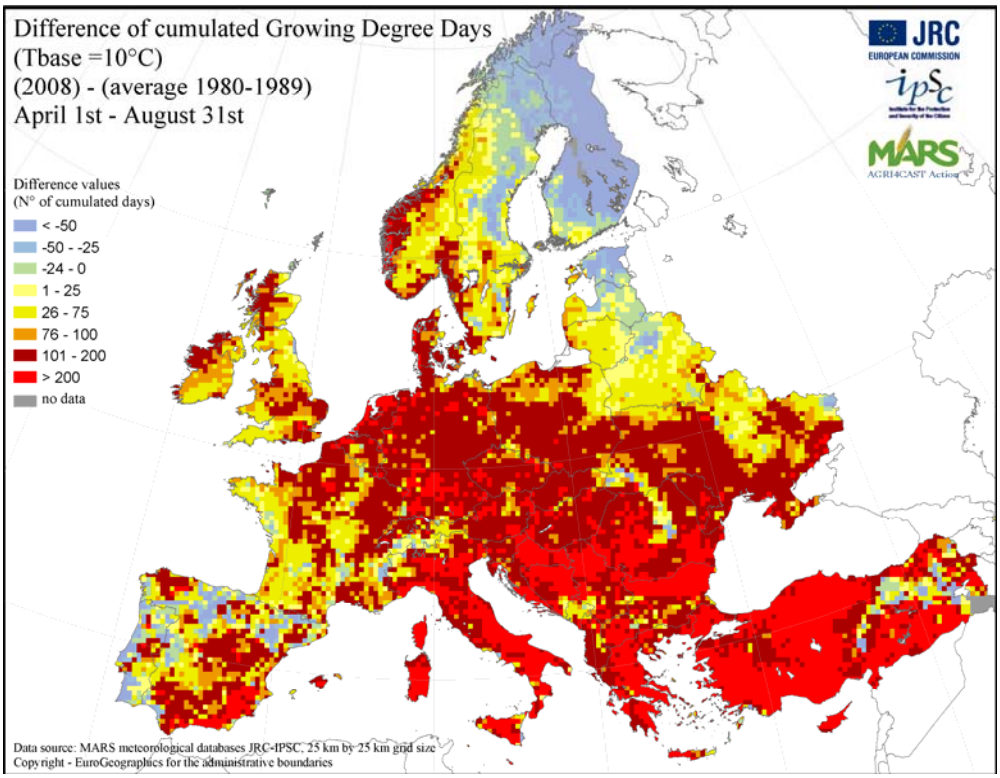

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- **Modelling OPM phenology**

The estimate of site suitability for OPM establishment via a generic heat availability calculation at a site via GDD can be improved by modelling OPM phenology. The one generation per year phenology model of the Oak Processionary Moth (OPM) can be represented via the phases and events of figure 1. The separation in phases allows applying either a different model or a different parameterization of the same model for each phase, as commonly used in the literature. Several authors have reported that a “macro-model”, that is, a composite model in which elementary model units simulate a specific phase of development, is the best predictors of the development cycle of arthropods. A non-linear response to temperature, rather than GDD, is implemented, as known for other models of arthropods. The diagram of figure 1 is a deterministic representation of development, but the model allows for a stochastic representation of development.

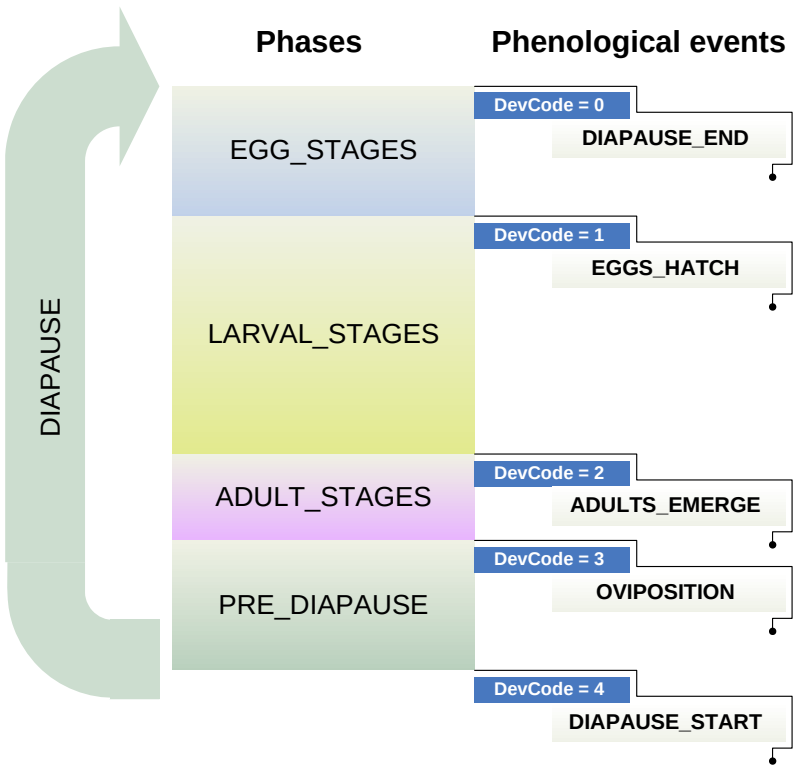

Fig. 1 Phases and phonological events of a phenology model for Thaumetopoea processionaria L. Pupation and the

The main purpose of a phenological model to be used in decision support systems is centred on the correct prediction of the beginning of instars hatch. A site specific calibration of parameters may allows fixing the time for the end of the diapause phase, and a temperature driven model allows estimating the beginning of instars hatch. However, when the purpose of modelling is exploring the expansion of OPM to new habitats with different temperature regimes, two major sources of uncertainty are added. First, the estimate of the completion of the pre-diapause phase is needed to ensure winter survival. Second, the date of the end of the diapause cannot be set based on expert knowledge which is not available in the new habitats, and needs to be modelled to estimate the actual start of the development model (beginning with the egg stages parameterization).

The data available to calibrate such a model, and the limited knowledge of OPM responses to temperature, would make highly speculative the use of the model framework of fig. 1 to estimate potential OPM establishment in new areas. For this reason, the work with the above framework was

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stopped for this specific opinion, and a simpler phenology model based on GDD is recommended for the stages EGG_STAGES and LARVAL_STAGES only.

- **Discussion**

GDD can be used as an indicator of heat available at a given site. Maps of cumulated GDD allow making a visual comparison of similarities between sites. If the development of the organism of interest is mostly driven by temperature (like in the oak processionary moth), the value of GDD at a site in which the insect is established sets a reference of thermal requirements for that insect (in terms of heat during the phenological phases after the diapause). If another site shows a similar accumulation of GDD, this suggest that the thermal regime at that site is likely adequate for the biological cycle of the insect. In other words, the insect could establish at that site. Cumulated GDD during growth do not provide information about survival to winter temperatures.
Differences in Tbase are effective if, at a given site, there are temperatures which fall between 8 and 10. To the extent the interest is into northern latitudes as possible sites where the insect could establish, 10 C is more conservative.

- **Conclusions**

Difference maps show an increase of GDD available comparing the years 2000-08 to 1980-89. Even coolest years (see 2005) are warmer than the average of the 80'.
Colonies of OPM were reported in the Netherlands. The value of accumulated GDD calculated for the Netherlands matches the value of areas in northern Germany, and in southern Denmark and UK. From the point of view of heat requirements during active growth stages, OPM could establish in those areas.

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APPENDIX C- CLIMPEST DETAILED SOFTWARE SPECIFICATIONS

- ClimPest is a stand-alone software application based on the .NET framework 3.5

- It is a desktop application, which provides a GUI based on a Windows Form.

- It is part of a framework of applications designed to run, analyze and calibrate a generic modelling solution. A modelling solution is defined as a .NET class that implements the “IModelCaller” interface defined in the “JRC.IPSC.MARS.Core.dll” software library.

- The modelling solutions are deployable in the BioMA application as DLLs (software libraries). The deploy operation does not require neither a change in the application code nor the rebuild of the application.

- BioMA code does not refer to a particular modelling solution. It interacts with the deployed modeling solutions through the “IModelCaller” interface. The “IModelCaller” interface provides the methods to

    - Configure the run of a simulation of the modelling solution

    - Set the parameters of the model

    - Verify the correctness of the configuration and initialize the model (e.g. reset the internal status of the model)

    - Execute the simulation

    - Retrieve the result of the simulation

- BioMA allows a third part developer to build a plugin: an external code that extends the functionality of the application. The plugins are deployable in BioMA as DLLs. The deploy operation does not require neither a change in the application code nor the rebuild of the application.

- BioMA ClimPest is released with 3 plugins deployed: “Result visualizer”, “Map and graph Visualizer” and “Result DB Cleaner”.

- BioMA must interact with databases to load data or to store the simulation results. To communicate with databases BioMA uses a specific layer called “DataLayer framework”: it is a set of C# libraries that allow to manage the access to database records abstracting the physical implementation of tables and hiding the real database structure (e.g. table and column names). It allows communicating to a generic database without knowing which specific database it is (e.g. Oracle or SQLServer). Domain classes and database tables are related each other via XML mapping files. These files can be automatically generated from database tables or from domain classes. The framework is composed of two distinct libraries:

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o JRC.IPSC.MARS.DB: contains the core of the framework: objects and interfaces that allow the programmer to manage the mapping of the tables and the most common operations on records (insert a new record, delete or modify an existing record, select a set of records).

o JRC.IPSC.MARS.DatabaseUtility: contains a set of tools that allow the programmer to automatically create tables in a pre-existent database, from a strongly-typed DataSet or from domain classes. Moreover they allow the programmer to automatically generate the XML mapping files.

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