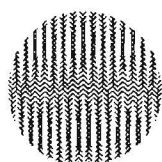# 9TH INTERNATIONAL WORKSHOP ON PLANT DISEASE EPIDEMIOLOGY

FACING CHALLENGES OF THE 21TH CENTURY '

Landerneau, France
April 11-15th, 2005

INRA
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9TH INTERNATIONAL WORKSHOP ON PLANT DISEASE EPIDEMIOLOGY

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Landerneau, France
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INTERNATIONAL SOCIETY OF PLANT PATHOLOGY

Epidemiology Committee
Chair: Laurence V. MADDEN

Local Organizing Committee

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9TH INTERNATIONAL WORKSHOP ON PLANT DISEASE EPIDEMIOLOGY

' FACING CHALLENGES OF THE 21TH CENTURY '

PROGRAMME

BOOK OF ABSTRACTS

Landerneau, France
April 11th-15th, 2005

9th INTERNATIONAL WORKSHOP
ON PLANT DISEASE EPIDEMIOLOGY

PROGRAMME

Sunday 10 April 2005

18:00 - 21:00   Registration – Reception hall - Informal get-together

Monday 11 April 2005

08:00 - 09:00   Registration – Reception hall
09:00 - 09:10   Welcome (Organising Committee)

09:10 - 10:00   **Opening Keynote: 'Botanical epidemiology: some key advances and its continuing role in disease management' (L.V. MADDEN)**

10:00 - 10:30   Coffee break

10:30 - 11:30   SESSION A (chair T. GOTTWALD)
                'Emerging plant diseases and risk analysis'
                Keynote: 'Framework development of plant disease risk assessment and its application in soybean rust study' (X.B. YANG)

11:30 -12:30   Presentation of posters and discussions

14:00 – 15:00   SESSION B (chair D. ANDRIVON)
                'Host plant resistance and population genetics'
                Keynote: 'Landscape ecological genomics and epidemiology: a null models approach' (K. GARRETT)

15:00 -15:30   Coffee break
15:30 -17:30   Presentation of posters and discussions

20:30 – 22:00   EVENING SESSIONS
                (1) - 'Epidemiology of forest / natural systems diseases'
                (M.L. DESPREZ-LOUSTAU)
                (2) - 'New tools and molecular methods in botanical epidemiology'
                (P. VAN DE GRAAF)

Tuesday 12 April 2005

09:00 - 10:00   SESSION C (chair R. SEEM)
                'Spatial and temporal scales in plant disease epidemiology'
                Keynote: 'The practical considerations of scale in plant pathology' (W.W. TURECHEK)

10:00 - 10:30   Coffee break
10:30 -12:30   Presentation of posters and discussions

14:00 – 15:00   SESSION D (chair M.J. JEGER)
                'Theoretical epidemiology: progresses, challenges, and applications'
                Keynote: 'Trends in theoretical plant epidemiology' (H. SCHERM)

15:00 -15:30   Coffee break
15:30 -17:30   Presentation of posters and discussions

20:30 – 22:00   EVENING SESSION
                (3) – 'Botanical epidemiology to deliver: prospects for linking current scientific theories and tools with sustainable disease management'
                (S. SAVARY)

Wednesday 13 April 2005

09:00 - 10:00	SESSION E (chair P.S. TENG)
	'Concepts and thoughts for plant disease epidemiology in the 21th century'
	Keynote: 'Priorities for plant disease epidemiology and developing world food security' (R.W. HERDT)
10:00 - 10:15	Coffee break
10:15 -12:00	**Keynote: 'Challenges in modelling epidemics' (D. MOLLISON)**
	Keynote: 'Plant pathology without systems innovation will become obsolete in the 21th century' (R. RABBINGE and P. TENG)
13:30 – 19:00	Afternoon break. Visit of Quimper (downtown) & HB Henriot faienceries
19:30 – 23:00	Social dinner

Thursday 14 April 2005

09:00 - 10:00	SESSION F (chair A. BERGAMIN FILHO)
	'Crop loss assessment and modelling'
	Keynote: 'Disease assessment concepts and the role of psychophysics in phytopathology' (F. NUTTER)
10:00 - 10:30	Coffee break
10:30 -12:30	Presentation of posters and discussions
14:00 – 15:00	SESSION G (chair C.A. GILLIGAN)
	'Soil health and soil-borne disease management'
	Keynote: 'Relation between soil health, wave-like fluctuations in microbial populations, and soil-borne plant disease management' (A. VAN BRUGGEN)
15:00 -15:30	Coffee break
15:30 -17:30	Presentation of posters and discussions
20:30 – 22:00	EVENING SESSIONS
	(4) – 'Comparative epidemiology, including vector-borne diseases'
	(M.P. CALDWELL)
	(5) – 'Variability, predictability and control of botanical epidemics: from data to models and back'
	(A. KLECZKOWSKI)

Friday 15 April 2005

09:00 - 10:00	SESSION H (chair N. MCROBERTS)
	'Integrated disease management and multiple pathosystem'
	Keynote: ' Patterns and management of crop multiple pathosystems' (S. SAVARY)
10:00 - 10:30	Coffee break
10:30 -11:30	Presentation of posters and discussions
11:30 -12:00	SUMMARY AND CONCLUSION
	Summary and conclusion of the 9th International Workshop on Plant Disease Epidemiology (O. CARISSE)
12:00 -12:30	General discussion

9TH INTERNATIONAL WORKSHOP ON PLANT DISEASE EPIDEMIOLOGY

CONTENTS

SESSION B
'Host plant resistance and population genetics'

SESSION D
'Theoretical epidemiology: progresses, challenges, and applications'

SESSION E
'Concepts and thoughts for plant disease epidemiology in the 21th century'

SESSION F
'Crop loss assessment and modelling'

BOTANICAL EPIDEMIOLOGY: SOME KEY ADVANCES
AND ITS CONTINUING ROLE IN DISEASE MANAGEMENT

<u>L.V. Madden</u>

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Abstract

Epidemiology involves the study of the temporal, spatial, and spatio-temporal dynamics of disease in populations, and the utilization of results of experiments and surveys to describe, understand, compare, and predict epidemics. Such understanding and description of epidemics can lead directly to the development and evaluation of efficient control strategies and tactics. Mathematical and statistical models are key tools of the epidemiologist. Recent advances in statistics, including linear and nonlinear mixed models, are allowing a more appropriate matching of data type and experimental (or survey) design to the statistical model used for analysis, in order to meet the objectives of the investigator. Coupled ordinary and partial differential equations, as well as simpler growth-curve equations, are especially useful deterministic models for representing plant disease development in fields in time and space over single seasons or many years, and their use can lead to appraisal of control strategies through metrics such as the basic reproduction number, a summary parameter that may be calculated for many general epidemic scenarios. Recently, compelling arguments have been made for the use of Bayesian decision theory in developing and evaluating real-time disease prediction rules, based on measured disease or weather conditions and either empirical or mechanistic models for disease or control intervention. Through some simple calculations of predictor accuracy and (prior) probability of an epidemic (or the need for control), the success of any predictor can be quantified in terms of the estimated probability of unknown observations being epidemics when predicted to be epidemics or not epidemics. Overall, despite the many contributions in epidemiology over the past four decades, more effort is still needed to convince those outside of epidemiology to more fully use epidemiological results and insights into the development and evaluation of disease controls.

SESSION A

' EMERGING PLANT DISEASES AND RISK ANALYSIS '

FRAMEWORK DEVELOPMENT OF PLANT DISEASE RISK ASSESSMENT AND ITS APPLICATION IN SOYBEAN RUST STUDY

X.B. Yang

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Abstract

This article reviews the recent developments in plant disease risk assessment. The role of risk assessment as an application area in macrophytopathology and its contribution to the development of macroscale disease study are discussed. This article also discusses the concepts and components of risk assessment for different end points and assessment framework of different potential ranges of a new pathogen: establishment range, suitability range, damage range, and dispersal range. Different end points generate risk information suitable for decision makers at different levels. New insights gained from a few major diseases, especially from the risk assessment due to recent global movement of soybean rust, are presented. The role of pathologists in presenting risk information has extended beyond the professional research domain and has become critical in influencing decision making, evident by soybean rust in both South and North America. The bias components of risk communication are defined and different levels of receivers for risk information are identified based on their interpretation capability of risk information, bias potential, and utilization of risk information. Lack of predictability of dispersal potential contributes to uncertainty of risk assessment for an airborne disease. Potential areas in disease risk assessment are discussed.

SPATIAL ANALYSIS OF BLACK ASPERGILLI IN EUROPE

P. Battilani, C. Barbano, and P. Giorni

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Background and objectives
The worldwide occurrence of ochratoxin A (OTA) contamination in raw and processed agricultural products has been amply documented but, OTA presence in wine was demonstrated for the first time by Zimmerli and Dick in 1996 (3). This is a relevant problem for Europe because it has around 40% of world area planted in vines and 75% of wine production. Fungi responsible for OTA presence in grapes were identified as black aspergilli, *A. carbonarius* in particular (1). It is fundamental to know incidence of these fungi and subsequent OTA content in grapes for their management. Assessment of both fungi and OTA is very important because samples analysis is expensive and time consuming. The objective of this research was to: 1) describe spatial variation of black aspergilli in Europe; 2) identify areas associated to high risk of contamination; 3) appraise yearly variations. The geostatistic approach followed resulted appropriate in previous works (2).

Materials and methods
During the 3-year period 2001-2003 a survey was organised throughout Europe to define incidence of black aspergilli during berries development and OTA content in bunches at harvesting. Portugal, Spain, France, Italy, Greece and Israel were included with a total of 118 vineyards sampled. Fungi were isolated plating berries on DRBC. Their identification took into account 3 groups: uniseriate, *A. niger* aggregate and *A. carbonarius*. HPLC technique was applied to determine OTA.
Semivariances were computed for fungi incidence and OTA content in bunches using GS+ software (1998); best semivariograms equations were chosen based on R^2 values. Ordinary Kriging was run using ArcView (2002) and raster maps were drawn. Cross validation was also applied.

Results and discussion
The survey confirmed the presence of the 3 groups of black aspergilli considered in all countries, uniseriate excluded in Portugal. *A. niger* aggregate represented the highest percentage of black aspergilli isolated in all countries but, attention was mainly paid to *A. carbonarius* because of its relevance in OTA synthesis.
The spatial structure of fungi incidence is well described by semivariograms; as a consequence, maps elaborated can be considered adequate to describe spatial distribution of black aspergilli. Differences were observed between years, probably related to relevant variations in meteorological variables. OTA content was below the detection limit in most cases but, differences between areas were robust.

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Acknowledgement

DISPERSAL PATTERNS OF BACTERIA OF XANTHOMONAS AXONOPODIS PV. CITRI FROM CANKER-INFECTED CITRUS PLANTS

<u>C.H. Bock</u> (1), P.E. Parker (2), A.Z. Cook (2), and T.R. Gottwald (3)

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Background and objectives

Citrus canker (caused by *Xanthomonas axonopodis* pv. citri, *Xac*) is an important disease of citrus in several tropical and sub-tropical citrus growing regions. Canker damaged trees produce less yield and the blemished fruit is unfit for fresh sale, so processing becomes the only option. In several afflicted areas the pathogen is under strict eradication, including in Florida. All trees deemed to have been exposed to inoculum (within 1900 ft of an infected tree) are removed (2). However, little is known about the effect of wind on the biological and physical processes of dispersal and infection of *Xac* (1). The objective of this study was to investigate characteristics of dispersal of *Xac* bacteria downwind from canker infected plants.

Materials and methods

The effect of wind speed and the characteristics of the downwind dispersal plume of bacteria in wind-blown splash were examined. Wind was simulated using a fan, and spray was generated using a grid of overhead sprayer nozzles above canker-infected plants. Panel and funnel samplers were used to collect the rain splash, and rainfall and wind speed were monitored (3). The bacteria counts were related to wind speeds using regression analysis and ANOVA.

Results and discussion

Greater total quantities of bacteria were collected downwind from infected plants at higher wind speeds. In one experiment the number of bacteria collected by panel samplers at 2 m from the inoculum source was 15833 at 5 ms^{-1} wind speed and 36758 at 18 ms^{-1}. The total number of *Xac* bacteria sampled with no wind was 31638, and at 18 ms^{-1} was 138080, illustrating how wind enhances the dispersal of *Xac* in rains splash from the foliage of a citrus canopy. The plume of dispersed canker downwind in this simulated system showed that as wind speed increased the plume of bacteria was dispersed further and greater quantities of bacteria were dispersed at greater heights. Higher wind speeds increased the quantity of *Xac* bacteria dispersed in rain splash away from infected trees. Storm events with high winds are a common occurrence in Florida and could result in enhanced dispersal of *Xac* bacteria from infected plants. We are currently extending the scope of these studies in natural wind/rain events and in a wind tunnel/rain generating facility at the USDA.

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(1) Bock, C.H., Parker, P.E., and Gottwald, T.R. The Effect of Simulated Wind-Driven Rain on Duration and Distance of Dispersal of *Xanthomonas axonopodis* pv *citri* from Canker-Infected Citrus Trees. *Plant Disease* (*In Press*).
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SIMULATIONS OF THE EFFECTS OF A CLIMATIC SCENARIO FOR THE PERIOD 2069-2099 ON THE EVOLUTION OF TWO FOREST PATHOSYSTEMS

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Background and objectives
The effects of climate change on forest ecosystems have recently received increasing attention. Although pathogen-induced diseases are strong forces influencing ecosystem structure and functioning (1), studies devoted to diseases in forest ecosystems are still comparatively scarce. This may likely be explained by the lack of epidemiological models including climate-disease relationships and supporting field data for forest ecosystems. A study was conducted with the aim of modelling the effects of current climate change scenarios on two forest pathosystems, and compare specific epidemiological models with a generic population dynamics model.

Materials and methods
The two pathosystems are *Phytophthora cinnamomi*, the agent of ink disease in oaks, and *Melampsora pinitorqua*, the agent of pine twist rust. *P. cinnamomi* is a generalist parasite with world-wide distribution and a predominant asexual stage. In contrast, *M. pinitorqua* is a pleomorphic (5 different sporogenous stages) and highly specialised parasite, restricted to Europe. Specific models were developed for both pathosystems (PHY and ROU), based on available knowledge of climate effects on epidemiological processes (2, 3). Simulation outputs from these models were compared with those from CLIMEX, a generic bio-geographical model (4). Meteorological data for the periods 1968-1998 and 2070-2099 were extracted from the ARPEGE-Climat model (5), a regionalised Global Circulation Model forced by an effective greenhouse effect corresponding to the provisional IPCC B2 scenario (6).

Results and Discussion
Simulations of the potential geographic range of ink disease in France were made for both time periods. Both PHY and CLIMEX models predicted eastward and northward extension of the disease by the end of the century, with very comparable patterns. ROU and CLIMEX, however, produced dissimilar results for pine twist rust. Potentials and limits of the different simulation methods will be discussed in relation to the differing biological attributes of these pathosystems.

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THE EFFECT OF TEMPERATURE ON THE LIFE CYCLE OF LIMONIUM RUST, CAUSED BY *UROMYCES SAVULESCUI*

The late Nava Eshed and A. Dinoor

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Background and objectives
Limonium is an ornamental crop for export, grown in winter in greenhouses. It suffers from rust, caused by *Uromyces Savulescui*. The quality of the cut flowers is tremendously reduced even by low incidence of disease. Wild Limonium is a perennial plant that harbors rust as well. The objective was to describe the seasonal distribution of the disease in wild and cultivated plants and to find out the mode of over-seasoning.

Materials and methods
Observations were conducted monthly, for 3 years, in several greenhouses and in two sites of wild Limonium. The incidence, severity and stages of the life cycle were recorded. Artificial inoculations were conducted in growth chambers, using urediospores and basidiospores as inoculum. Teliospores are ephemeral, and germinate readily. Infested leaves, carrying teliospores were suspended over young leaves, and the germinated teliospores shed the basidiospores.

Results and discussion
Limonium rust is an autoecious, lepto-cyclic rust, lacking the aecial stage. During 3 years of field observations in two sites of wild perennial Limonium, we have noticed that there are summer and winter types of epidemics. The summer epidemics are caused by the uredial stage, like in many other macrocyclic rusts, while the winter epidemics are caused by the pycnial, telial and basidial stages. The teliospores germinate without dormancy, produce basidiospores, that infect the plants. No aecia or uredia are produced during winter, so that the winter phase is virtually a microcyclic rust.
Artificial inoculations under controlled temperatures have shown that:
a. Upon inoculation with basidiospores, pycnia developed from 5^0C to 20^0C.
b. Upon inoculation with uredospores, uredia developed between 15^0C and 25^0C.
c. Upon inoculation with uredospores, telia developed between 5^0C and 18^0C.

INFORMATION TECHNOLOGIES IN SYSTEM MONITORING OF CEREAL CROPS DISEASES

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Abstract
The information about phytosanitary conditions of cereal crops in the Russian Federation has been collected by the experts of the State Plant Protection Service (SPPS) with the following spatial frame: field – facilities (economy) - area - province (oblast, territory, republic) - economic region - federal district - federation; temporary averaging - 10 days. The protective measures are fixed - degree of development and spread of pathogens, stage of plants, agroecological and meteorological characteristics. The system of collecting and distribution of the data has hierarchical frame because of the organization systems of the SPPS.

The phytosanitary monitoring includes the next problems:
- The organization of supervision for phytosanitary condition of agroecosystems;
- Reception of the objective, regular and operative information on the parameters describing phytosanitary conditions;
- An estimation and the analysis of the received information;
- The description of the current phytosanitary conditions and the forecast of its change for the nearest and remote prospect;
- Delivery of the information for use in systems of decision-making and management of plant protection.

Problems of such complexity cannot be solved without use of modern computer facilities and achievements in the field of information technologies. The basic directions of application of information technologies according to problems of phytosanitary monitoring are:
- Construction of phytosanitary database (DB);
- Construction of geoinformation phytosanitary systems (GIFS);
- Use of the Internet network for reception of the information necessary for phytosanitary examination.

The DB on development and distribution of diseases of ceral crops is based on the information collected by experts of the SPPS. The complete set of forms (tables) of gathering and presentating phytosanitary information for the different levels. Tables of levels - a field - a facilities - area - are primary, the others - derivatives and can be received by settlement way.
In aspect of phytosanitary monitoring GIFS are the modern effective tool of tracking development and distribution of phytopathogenic bio-objects in time and space. Presence of databases and their representation on electronic maps provide visualization of the information, its analysis using modern mathematical methods. The first stage of GIFS creation is an input of phytosanitary, agrometeorological, economic and other data. Forms of the account and methods of generalization are developed. The second stage is the analysis of the initial and formed information and databases with use of quantitative and qualitative models, with the subsequent binding of the received results to electronic maps. The third stage is the creation of interactive thematic maps, schemes, and tables. The geoinformation system for phytosanitary monitoring of cereal crops diseases on basis of GIS "GeoGraph" at a level of the Russian Federation will be developed.

The creation of the specialized website will also help to raise the efficiency of phytosanitary monitoring. On it will be possible to publish the description of concrete diseases, to place the necessary software for the account of plants damage and diagnostics of pathogens, etc. The works on creation of such site (http://www.phytonet.ru) will be done.

CLIMATE-BASED REGIONAL CLASSIFICATION FOR OVERSUMMERING AND OVERWINTERING OF *PUCCINIA STRIIFORMIS* IN CHINA WITH GIS AND GEOSTATISTICS

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(1) Department of Plant Pathology, China Agricultural University, Beijing 100094; (2) National Agriculture Technique Extend Service Centre, Beijing 100026

Abstract

Temperature was a considerable factor to affect the oversummering process of the wheat stripe rust pathogen *Puccinia striiformis*. The high-limit temperature for the pathogen oversummering combined with relevant wheat-growth information was used to classify the wheat-growing regions for the pathogen oversummering in China by using the Geographic Information System (GIS). The study demonstrated that the regions suitable to the pathogen oversummering in China are huge. The pathogen-oversummering regions in Gansu, Sichuan, Yunnan and Shaaxi Provinces are conjunct. The maximum temperature in July and August was between 20 and 23 °C in most parts of eastern Gansu Province with exception in some counties, and the possibility of pathogen oversummering in these regions is low. The most wheat-growing regions in Tibet and Qinghai Provinces are suitable to pathogen oversummering. The regions suitable to pathogen oversummering in Guizhou Province are most likely conjunct with those in Yunnan Province to serve as an integrated area for pathogen oversummering. However, regions in Yunnan Province are geographically complicated, and feature of pathogen oversummering is still under investigation.

Similarly, temperature and host growth are considerable factors to affect the overwintering process of the wheat stripe rust pathogen *Puccinia striiformis*. The multi-year (1960 – 2001) and multi-location weather data were used to determine the probability of the average minimal temperature in December or January greater than –7 °C (P) for each location. The regional classification for the pathogen overwintering in China was conducted with wheat-growth information and GIS technology. The study demonstrated that the P values as 70 – 85% can be used to determine the borderline of the pathogen overwintering to classify the regions. This borderline was primarily consistent to that of previous studies. It can be described as Daxing County (Beijing) – Xushiu (Hebei Province) – Yangquan (Shanxi Province) – Jiexiu (Shanxi Province) - Yanchang (Shaanxi Province) - Qingyang (Gansu Province) - Pinliang-Lixian (Gansu Province)- Songpan (Sichuan Province)- Maerkang (Sichuan Province). The regions in south and east of this borderline are suitable to pathogen overwintering.

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THE MULTIDISCPLINARY RESEARCH NETWORK *EPIEMERGE*
(EPIDEMIOLOGY AND EMERGING RISKS) - 2003-2005 - AIMS AND ACHIEVEMENTS

I. Sache (1), G. Vourc'h (2), and J. Barnouin (2)

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Aims and structure of the *EpiEmerge* network

In the last ten years, France experienced major sanitary crises due to emerging diseases and pests (*e.g.*, BSE, corn rootworm beetle), which emphasized the urgent need of a more efficient organization of epidemiological research, especially at INRA. Accordingly, the multidisciplinary research network *EpiEmerge* was set up, as a means of promoting scientific discussions and joint research projects among research teams belonging to the INRA departments of Animal Health, Plant Health, Biomathematics, Human Nutrition, Forestry, Environmental Sciences and Agronomy, Animal Genetics, and Microbiology. Fifteen research projects involving scientists from at least two of the departments listed above were selected and funded for a three-year period. Three main axes of research were eligible: (1) the detection of emergent diseases; (2) the spread of emergent diseases; and (3) the risk of disease emergence by crossing the "species barrier". The projects deal with animal (10), plant (4) and human (1) diseases.

Achievements of the *EpiEmerge* network

Exchange of questions, information and expertise among the members of the network was performed via an electronic discussion list and targeted meetings scheduled twice a year. There were major advances in the funded research projects, but the most interesting outcome of the network was interdisciplinary discussion. Participants to the network agreed on the following agenda:
- the design of a common terminology for the whole epidemiologists' community;
- the collection, evaluation and publication of data on the emergence of animal and plant diseases in France since the end of the XIXth century;
- the elaboration and validation of common methods for the detection of emerging pathogens without any *a priori* information;
- the design of new methods of multi-scale modelling of introduction, persistance and spread of emerging pests and diseases;
- the urgent need of a better coordination between research scientists, extension services and legal bodies in charge of the epidemiological watch and interception of alien organisms.

What next?

The main outcome of the *EpiEmerge* network was the emergence of common scientific questions and methods shared/needed by epidemiologists working in very different fields. Therefore, the *EpiEmerge* network shall be the cornerstone for larger and more ambitious projects on emerging risks in agriculture and public health. In France, the Mediterranean regions and the ultra-peripherical regions (Guadeloupe and Martinique in the Caribbeans, Réunion in the Indian Ocean) are at high risk of introduction of alien diseases and pests and must deserve specific watch. The expertise of the *EpiEmerge* members will be used in the future to develop international partnerships targeted to the detection and management of emerging diseases.

REGENERATION OF LOCAL SCALE, HIGH-RESOLUTION WEATHER DATA AND THEIR APPLICATION TO PLANT DISEASE FORECASTING

K.R. Kim (1), R.C. Seem (1), J. Zack (2), and R.D. Magarey (3)

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Background
Weather data for disease forecasts are usually derived from automatic weather stations (AWS) that may be dispersed across a region in an irregular pattern. As an alternative, mesoscale weather models are capable of simulating weather conditions such as air temperature and humidity at a resolution as high as 100 m, but the need for intensive numerical calculations has hindered their application to plant disease forecasting. New developments in computer technology have recently enabled large numbers of inexpensive computers to be clustered as a supercomputer, overcoming some of these previous limitations. We have used these models and technology to simulate local scale, high resolution weather and plant disease in a grid pattern.

Methods
The system incorporates a simplified mesoscale boundary layer model, Local-area Agricultural Weather Simulation System (LAWSS), for the regeneration of local conditions such as air temperature and RH. It also integrates special models for estimation of surface wetness duration and disease forecasts, such as the grapevine downy mildew forecast models, DMCast. The system can recreate weather forecasts utilizing the National Center for Atmospheric Research and the National Center for Environmental Prediction (NCAR/NCEP) reanalysis database, which contains over 55 years of archived and corrected global upper air conditions. Maximum horizontal resolution of 150m was achieved by running 5-step nested child grids inside coarse mother grids. All model runs were carried out on a super computer.

Results and Discussion
Over Finger Lakes and Chautauqua Lake regions of New York State (USA), the system simulated several growing seasons for estimating the risk of grape downy mildew with 333m resolution. Outputs were represented as maps or as graphs for specific locations. Highest resolutions can be achieved over North America, but the system is functional for any global location. The system is expected to be a powerful tool for site selection and reanalysis of historical disease epidemics. Computing power is presently a limitation despite the system's current implementation on a super computer.

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ANALYSING A 150-YEAR DISEASE SERIES OBTAINED BY PCR FROM THE BROADBALK EXPERIMENT IN ROTHAMSTED, UK

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Background
In the UK, *Mycosphaerella graminicola* was a minor wheat disease until the early 1980's. Since that time it has increased steadily in importance, while *Phaeosphaeria nodorum* has declined. This change appears to have taken place, to greater or lesser extent, world-wide. A number of theories have been advanced to explain this change; most consider varietal differences in resistance to be critical.

Methods
Since 1844, a series of plots have been planted annually at Rothamsted with winter wheat, and samples of grain and of foliar material dried and saved at harvest. We extracted DNA from this material. We then used species-specific primers and quantitative PCR to quantify how much was present of wheat, *M. graminicola* and *P. nodorum* DNA. Pathogen DNA of both species was readily amplifiable. The DNA abundance of both species in the stored samples closely matched national survey data on foliar symptoms, so the data reflect national trends. It seems reasonable to suppose that DNA of both pathogens would be similarly affected by storage and harvest factors, so the ratio of the two species is more secure than the data from either singly. However, the individual series can be corrected for decay in DNA using the wheat grain decay curve.

Results and discussion
P. nodorum predominated over *M. graminicola* from the 1890s to the 1980s. Before and after that time, *M. graminicola* predominated. Conventional time-series analysis shows no internal cycles or patterns and very little autocorrelation structure. Weather factors do not explain the change-over because appropriate long-term trends are not present. There is a weak but clear correlation with the area sown nationally to wheat. Agronomic change, including fungicide and fertiliser factors, occurred only at the end of the 20th century and therefore cannot explain the main pattern. Relationships with variety are weak, but hard to interpret as the data may reflect the national balance of resistance in varieties sown over the whole country. Varietal change was slight during the 19th century, so the change from *M. graminicola* to *P. nodorum* during the latter part of the 19th century – the key feature of the data - seems hard to explain on that basis.
However, national SO_2 emissions correlate very closely with the ratio of the two pathogens. This could, of course, be an accidental correlation with some other causal factor, but is consistent with the widespread increase in *M. graminicola* in many countries as emissions have been controlled. How SO_2 operates (if it is indeed the direct cause) is a matter for speculation and experiment. Allowing for SO_2, there are slight effects of winter temperature and the previous summer's temperature. The *total* of both pathogens is affected very strongly by spring rainfall, very significantly by the previous summer's temperatures, but not at all by SO_2.

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Impact of climate on Oak mildew

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Background and objectives

Oak rnildew, Erisiphe alphitoides, is an exotic pathogen that was first mentioned in Europe at the beginning of the 20th century. In the period following the introduction, the disease has deeply worried the forest managers. After this initial period, the disease has been generally thought to have little impact on oak stand, du to it late development in the growth period. However, the French forest health survey organism, the DSF, mentioned important impact of powdery mildew in oak stands in those last years and showed that it impact in the young stands could be very significant with reduced growth and increased mortality. Moreover, this pathogen is part of the complex of cause involved in the oak decline syndrome and it role in this multifactoriel phenomenon is poorly understood. The aim of work presented here was to use the DSF database to identify the conditions in which the oak mildew may be a significant risk for stand health, and in particular try to identify the regions and the years in which this may occur. A more general aim of the work was to see whether it is possible to derive from this data set maps of forest pathogen impact in France. Indeed, for studies such as the possible impact of global warming, we lack basic information about geographic variability in the impact of forest disease at the country or European level.

Methods

The DSF database is a compilation of spontaneous reports made in the last 15 years by a network of foresters who are trained to diagnose all types of forest health problems i.e. abiotic, entomological or pathological. About 10 000 of health problems on were reported throughout France since 1989with among them about 900 oak mildew problems. The analysis was done using methods that are applied in human epidemiology, i.e. by comparing the distribution in time and space of reports relative to oak mildew with report dealing with problems of oaks others than oak mildew. The underlying assumption is that the number of reports on the same host of others health problem is strongly related to the potential number of the studied problem, given a certain impact level. The relationship between annual number of oak mildew reports in 5 areas of France and selected meteorological parameters was studied using zero-inflated poisson models.

Results and Discussion

The analysis shows that a strong southwest to northeast gradient in disease severity exists in France, with evidence of several years of severe epidemic in southwest France. The study of another set of data on oak mildew collected on the European network, a network of permanent stands located on a regular 16x16km grid throughout France gives very similar results. Years of severe mildew damages on oaks correspond to an early arrival of the disease in the growth season with, potentially, a much stronger impact on tree health. These years of frequent report of damages are characterised by a very mild winter and especially early tree leafing. A study of climatic conditions in the area showed that such mild winters were very seldom in most of 20th century, but became increasingly frequent in the last 15 years. The relationship between winter temperature and the severity and precocity of oak mildew epidemics might by link with either better survival of mycelium in the tree buds or with altered phenology of both host and pathogen leading to greater inoculum presence at the tree leafing.

SESSION B

'HOST PLANT RESISTANCE AND POPULATION GENETICS'

LANDSCAPE ECOLOGICAL GENOMICS AND EPIDEMIOLOGY: A NULL MODELS APPROACH

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Abstract

The huge amount of genomic data now available offers both opportunities and challenges for epidemiologists. Population genomic data can inform epidemiology with new information about genetic sequences and gene expression, but epidemiologists are left with the same types of questions that arose when the collection of environmental data became automated, with data thus available at much finer temporal and spatial scales. How much and what type of genomic information is needed for predicting short-term epidemic features and for understanding host and pathogen evolution? DNA sequencing is now complete for some hosts and several pathogens. Microarrays make it possible to measure gene expression simultaneously for thousands of genes. These tools may contribute to epidemiology by providing information about which resistance genes are present in individuals and populations, what other genes are important in epidemics, the phenotypic status of hosts and pathogens, and the status of the environmental metagenome. Conversely, population biology supplies models of group dynamics that may apply to gene expression within individual organisms. Genomic tools have great potential for improving understanding of resistance gene evolution and the durability of resistance. For example, DNA sequence analysis can be used to evaluate whether an arms race model of co-evolution is supported. Finally, new genomic tools will make it possible to consider the landscape ecology of epidemics in terms of both host genotypic resistance and phenotypic resistance. Host phenotype mixtures can be modeled and evaluated, with epidemiological predictions based on phenotypic characteristics such as physiological age and status in terms of induced systemic resistance or systemic acquired resistance.

GENETIC OF VIRULENCE OF *BLUMERIA GRAMINIS F.SP.TRITICI* IN UKRAINE AND RESISTANCE OF WHEAT TO PATHOGEN

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Background and objectives
Powdery mildew, caused by *Blumeria graminis f.sp.tritici* (*Bgt*) is an important disease of wheat throughout wheat-growing areas of the world. Cultivar resistance is considered the most practical, effective, and economical means of managing powdery mildew. However, the deployment of resistance may be short-lived if variability of the pathogen is great. Resistance genes in the host play an important role in determining powdery mildew virulence gene frequencies (1). The objectives of this study were to characterize the virulence of powdery mildew population in Ukraine and influence of efficiency of resistance genes on its formation.

Materials and methods
Isolates of *Bgt* were collected in 5 regions of Ukraine, that location in different soil-climatic zones. Purification of single-colony isolates, inoculum's production and identification of virulence genes were made according standard method (2). Eight differential cultivars with known resistance genes (Pm1, Pm2, Pm2+mld, Pm3a, Pm3b, Pm4b, Pm5 и Pm8) used in assessment of *Bgt* virulence (1). Nei's standard genetic distance were computed from the virulence gene frequencies from each region by the unweight pair-group method to display relationship (3).

Results and discussion
High genetic identity on the basis of virulence - I_{min}=0,99, I_{max}=0,94 and genetic distance within 0,06 was established between fungi populations from different soil-climatic zones of Ukraine. Analyzed isolates were extracted from 24 different cultivars. At that isolates virulent to genes Pm1, Pm4b, Pm5 and Pm8 occur more then in half of them. In spite of growing different cultivars of wheat through out the Ukraine efficiency of individual Pm-genes is similar: Pm5 and Pm8 are absolutely ineffective, while genes Pm3a, Pm3b and Pm2+mld provide high degree of stability. Facts indicated testify that, evidently, wheat cultivars of Ukrainian selection are genetically homogeneous on the basis of resistance to powdery mildew pathogens. Genetic diversity in *Bgt* population on the territory of Ukraine, evidently, in significant manner sustain due to pathogen migration from neighbor countries, where cultivars of different resistance genes are grown. This assumption confirms that the most genetically outlying is fungi population from Ivano-Frankivsk region, the most closest to European countries. This population also encounters the biggest diversity of pathogen races. Also, zones differ in frequency of isolates popularity ready to overcome each of resistance genes, with differences more considerable with Pm-gene efficiency increase. Thus, variation factors of isolates popularity, virulent to Pm5 and Pm8 were 8,3 and 9,6 % respectively. Variation factors of isolates popularity, virulent to other tolerance genes, were in the range of 44,4 % (to Pm1 gene) to 83,5 % (to Pm3a gene). Moreover, Pm-gene efficiency was showed on the mode of variation factors distribution, possessed definite quantity of virulence genes. Among the isolates virulent to inefficient resistance genes, low-virulent (1-3 virulence genes) were at dominated position. Among the isolates virulent to efficient resistance genes were low-virulent as well as middle- and high-virulent. Regarding Pm1, Pm2 and Pm4b distribution of isolates popularity frequency with different number of virulent genes, was at intermediate mode and in time was close to distribution, typical for virulence to inefficient genes. Thus, virulence of isolates ready for overcoming resistance caused by Pm-gene, turned up to be an indicator of its efficiency.

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DATA ANALYSES OF PLANT PATHOGEN POPULATIONS AND THEIR HOSTS POPULATIONS

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Abstract

The analysis of plant pathogen populations is normally based on experimental data sets which are organized in large tables with two entries (differentials in columns, isolates in rows). Several computer programs for processing this kind of data were developed, e.g. VIRULA (4); HaGiS (2); and KOIND (3), each focusing on only a few aspects of the data. Our collaborative project aims at supporting a more comprehensive, more exhaustive, more effective, and more compatible evaluation and presentation of such data. A new unified package of tools is being developed, that will contains most functions of the mentioned programs but extends them with a number of additional features and some recently developed methods. Our software will include tools for the basic routine steps such as data entry, dichotomization, identification of phenotypes, and characterization of samples by graphical means and by indices. Inference-statistical procedures will provide estimates of various diversity indices and other parameters for sexually and for asexually reproducing populations. These estimates obtained by bootstrap methods (1) will allow further statistical evaluations (e.g. significance tests and confidence intervals). Recommendation concerning minimal sample sizes for reliable estimations in specific experimental situation will be offered. To make results of different researchers more compatible a tool to convert pathotype names from one nomenclature to another (e.g. from binary/octal to binary/hexadecimal) will be implemented.

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INTEGRATED MANAGEMENT OF STRAWBERRY POWDERY MILDEW

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Background and objectives

The fungus *Sphaerotheca macularis* f. sp. *fragariae* is the causal agent of strawberry powdery mildew which occurs on leaves, flowers and fruits. The pathogen can cause severe damages in greenhouse crops as well as in low tunnel crops and in nurseries. Intensive chemical sprays are implemented in order to control the disease, resulting in risk of chemical residues in the harvested fruits and pathogen resistance for fungicides. Initially, microclimatic conditions favoring or limiting disease were not well known and ranges of host susceptibility were not clear. Nevertheless, this knowledge is essential for an efficient control. The objectives of the study were to characterize a biotic factors that may contribute to the development or suppression of the disease and to establish an integrated disease management system.

Experiments were carried out with conidia of the pathogen on detached leaves and with diseased plants in growth chambers and under field conditions. Factors that were considered included temperature, relative humidity (RH) and host resistance.

Results and discussion

We found that optimal conditions for conidia germination are temperatures between 15-25°C and high (75-97%) RH. High irradiation inhibits germination and germ tube elongation. Conidiation of *S. macularis* at 70-85% RH was higher than at 95%. Surprisingly, a percent of the conidia retained ability to germinate up to 5 months. At the optimal conditions of 20°C and above and 75% RH, a disease cycle was completed within 4 days and severity was maximal. Temperatures of 10° and of 30° C, combined with a RH above 95% and high irradiation restricted the disease under controlled conditions. A good correlation was found between the response of conidia germination and disease severity to most of the above-mentioned parameters.

Control agents sprayed in strawberry crop at high frequency are able to reduce disease incidence and severity. The combination of control agents with host resistance was tested under commercial-like conditions. It was found that the most prominent factor that contributes to disease reduction is host resistance/tolerance. Thus durable resistant strawberry cultivars with suitable horticultural characteristics as a major component of disease management combined with control agents at low rate would solve the powdery mildew problem.

STEM CANKER OF OILSEED RAPE: MOLECULAR TOOLS
AND MATHEMATICAL MODELLING TO DEPLOY DURABLE RESISTANCE

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Background and objectives
The *Brassica napus - Leptosphaeria maculans* pathosystem is governed by a gene-for-gene relationship. However, with the narrow genetic basis associated with *B. napus*, resistance genes are rare and resistance under field conditions has been short lived. There is a need for resistance to be carefully managed to increase durability. The main aim of SECURE (StEm Canker of oilseed rape: molecular tools and mathematical modelling to deploy dUrable REsistance) is to deliver a model for deployment of cultivars with resistance to *Leptosphaeria maculans* (phoma stem canker/blackleg) to improve durability of resistance and minimise risk that the resistance will break down.

Materials and methods
The project has four main workpackages. Firstly, a life-cycle model for *L. maculans* has been developed. This is currently being validated using existing data. Secondly, genomic analysis of avirulence and virulence loci of the pathogen and the fitness of virulent/avirulent races of the pathogen is being investigated. Thirdly, the effects of plant genetic background and environmental factors on durability of resistance are being analysed under controlled conditions and at a number of field sites across Europe. Lastly, models are being developed to investigate the effects of different strategies of resistance deployment on durability of resistance so that recommendations can be made for a sustainable strategy. Results are being disseminated to target groups using a website (www.secure.rothamsted.ac.uk), through scientific and popular publications and workshops. The SECURE project is supported by the European Commission under the Fifth Framework Quality of Life Programme (QLK5-CT-2002-01813).

GENETIC DIVERSITY OF *COLLETOTRICHUM GLOEOSPORIOIDES* CAUSING ANTHRACNOSE DISEASE ON YAM (D. *ALATA*) IN GUADELOUPE AND MARTINIQUE

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Background and objectives
Anthracnose disease on water yam (D. *alata*) can lead to 100% yield losses for the most susceptible cultivars. In Guadeloupe, the first anthracnose epidemic on water yam has been officially mentionned in 1966 and is, since then, the major constraint to D. *alata* production. To prevent anthracnose epidemics, resistant cultivars were introduced and fungicides were used. At the end of the 1980s', the main cultivated varieties lost their resistance to anthracnose and fungicides lost their efficiency. Populations of the pathogenic fungus seems to differ from one carribean island to another, because susceptibility of certain cultivars differs from one island to another. In order to understand the erosion of anthracnose resistance in Guadeloupe, we studied population structure of C. *gloeosporioides* at the field and the continental scales.

Materials and methods
The field scale study was carried out in one geographical area in Guadeloupe. We isolated 256 monoconidial strains from infected yam leaves in 6 fields of 3 cultivars; two fields per cultivar. The 3 cultivars studied presented different levels of susceptibility to anthracnose: Pacala (high susceptibility), Kabusah (weak susceptibility) and Tahiti (low susceptibility). A study at a broad spatial scale was carried out on strains isolated in the two islands Guadeloupe and Martinique. Infected Yam leaves were sampled in 5 sites per island, 5 plots per site. Genetic diversity was assessed for neutral molecular AFLP markers and for virulence on the 3 cultivars: Pacala, Kabusah and Tahiti. AFLP data were analysed with the softwares GENEPOP and ARLEQUIN, and pathogenicity tests results were statistically analysed with SAS software.

Results and discussion
At the field scale results showed an important genic and genotypic diversity for AFLP markers, whatever the cultivar or the field of strain origin. High differenciation between each pair of fields suggested weak migration of the pathogen between yam fields during the crop season. The cultivar of origin of strains has a significant effect on the pathotypes distribution. This suggested an adaptation of C. *gloeosporioides* to D. *alata* cultivar. Pathogenicity of the strains from Guadeloupe differs from those of the strains from Martinique. Differences between guadeloupean and martinican D. *alata* production will help to discuss the pathotypes distribution.

CLIMATE-BASED MODELING OF ONTOGENIC RESISTANCE TO FUNGAL DISEASES IN GRAPEVINE

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Abstract

In New York State and areas with similar climates, grape berries acquire ontogenic resistance to powdery mildew (*Uncinula necator*) within 3 weeks after bloom. Experience from areas with Mediterranean climates suggests a more protracted period of susceptibility. Why should host susceptibility vary so with climate and geography? The answer lies in the impact of climate on duration and uniformity of flowering, specifically: the influence of cold temperatures during dormancy results in a protracted and seemingly unpredictable period of berry susceptibility in warmer climates. Under conditions of synchronous flowering in New York, we developed models based upon berry age to describe the development of ontogenic resistance to several major fungal diseases. Through a network of collaborators in the USA, Europe, and Australia, we were able to quantify the climate-based phenological heterogeneity of bloom. Models developed under conditions of synchronous flowering were integrated with climatic data to produce region-specific forecasts of fruit susceptibility. Precise definition of fruit susceptibility markedly improved our ability to direct fungicide applications towards key times that produce maximum suppression of disease. While our research is focused on grapevine, phenological heterogeneity of deciduous fruit crops in warmer climates is a general phenomenon, and our approach could be adapted to other pathosystems.

DIVERSITY FOR VIRULENCE IN *PUCCINIA TRITICINA* POPULATIONS IN FRANCE AND THE ROLE OF HOST SELECTION

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Background and objectives
Adaptation of rusts fungi populations to their wheat hosts cultivars has been widely documented concerning specific host-pathogen interactions. However it has already been suggested that rusts populations are likely to be structured by selective forces other than selection for virulence to host specific resistance genes (Kolmer 1993, Martens 1985). Studying *Puccinia triticina* populations in France, we have looked in a first step to the part of diversity that could be explained by interactions between specific resistance genes and avirulence genes.

Material and methods
Distribution frequency of pathotypes, identified on a differential set with 18 lines, was established in 1999-2002 on the five most widely grown bread wheat cultivars (two susceptible and three resistant) in France. Sample size each year for each cultivar was between 18 and 63, collected from a national trial network on unsprayed plots.

Results and discussion
Population on the susceptible cultivars, Soissons (*Lr14a*) and Isengrain (*Lr14a*), was composed of one dominant pathotype (frequency 50 to 60%), several minor pathotypes (frequency less than 10%), and several rare pathotypes found only once. This structure was confirmed for cv. Soissons on commercial plots, located in three different areas (South, Paris and North areas), with samples of 60 to 200 isolates : virulence as well as AFLP data showed that the same structure was observed at the national scale.

On the cultivars Trémie (*Lr10, Lr13* + Adult Plant Resistance), Apache (*Lr13, Lr37*) and Orvantis (*Lr10, Lr13, Lr37*), some slight sporulation could be observed in the field, and isolates thus collected belonged to 3 to 5 dominant pathotypes (10 to 25%), and to some minor or rare pathotypes. This structure was confirmed for cv. Trémie on commercial plots, for virulence and AFLP markers.

Dominant pathotypes were not the same between the three resistant cultivars, and dominant pathotypes of resistant cultivars were absent or rare on the susceptible cultivars. The population structure was thus strongly influenced by host. Most of the minor and rare pathotypes had the virulence genes required to overcome the host resistance, but still remained at a low frequency. This low frequency of minor and rare pathotypes could not be explained by specific interactions.

Our hypothesis was that differences in aggressiveness between the pathotypes might help to explain the observed structure. We then started to investigate about diversity in aggressiveness as a life trait possibly modeling population structure.

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GENETIC STRUCTURE OF *CRINIPELLIS PERNICIOSA* IN BAHIA, BRAZIL

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Introduction
Witches broom disease of cacao (*Theobroma cacao* L.), caused by *Crinipellis perniciosa* (Stahel) Singer, is the most important disease of cacao in the cacao growing areas of South America and Caribbean Islands. Knowledge of the amount and distribution of its genetic variation within and among populations is an important component to understand the biology of this pathogenic fungus. Pathogenicity assays combined with "Random Amplified Polymorphic DNA" (RAPD) and microssatellites (SSR) markers were used to obtain an initial, broad profile of genetic structure variation of *C. perniciosa* in three agroecological areas from Southeast of Bahia, which vary in ecological, biophysical, climate conditions, land use and cacao planted area. Epidemiological factors could play a major role in substructuring populations. The main goal of this study was to use a hierarchical sampling scheme (tree, plantation, county) to determine whether the population was substructured by the agroecology area from which it was collected.

Materials and methods
Six-hundred isolates of *C. perniciosa* were collected from twelve agroecological areas representing the natural distribution of *C. perniciosa* from cacao plantations in Bahia. However, herein only the data of 52 isolates of three of these areas will be presented, mainly from: Uruçuca, Camacan and Una. These areas are at least 55 km apart each other and are differentiated by climate conditions, land use and soil type. The first locations represents the first foci of the disease, and are considered adequate for cacao production. The last one, Una, is considered marginal for cacao planting. Fungal isolates were collected by hierarchical sampling, from nine naturally infected cacao plantations, in three different agroecological zones during a single growing season. Samples were obtained from diseased pods and vegetative brooms in three trees per site, from resistant and susceptible genotypes. Trees were at least 10 m apart each other and farms; at least 5 km apart. Spatial scales included comparisons within and among trees, within and among fields and within and among agroecological zones.

Data analysis
RAPD assays of each isolate were performed at least two times, with only reproducible, amplified fragments being scored. Data were analyzed using Jaccard's similarity coefficient (Jaccard, 1908), and multi-dimensional scale (MDS) method - SAS® PROC MDS and SAS-graph (SAS,1986). Cluster analysis were based on Ward's minimum variance method (Ward, 1963). The statistics of molecular variants N_{CT} (among regions), N_{ST} (among populations), and N_{SC} (among populations within regions) were evaluated using the software Arlequin version 1.8 (Excoffier et al., 1992, Schneider et al., 2000).

Results
Fungal populations from different zones differed significantly (p=0.1%), out of the total genetic diversity, 78.7% was attributable to differences within populations and only 18.6% to differences between populations. These data is in agreement with the previously reported degree of somatic compatibility groups in the *C. perniciosa* population from different ecological areas, which suggests that the *C. perniciosa* population infecting cacao plantations has a different structure among an agroecological zone and this should be considered when devising control strategies including test of varieties, fungicides and biological control agents.
To our knowledge this is the first evidence of ecotypes in the *Crinipellis–Theobroma cacao* pathosystem. The interpretation of these results is not a clear-cut, and the current study, however, cannot establish which factors are important in shaping the population structure of *C. perniciosa*. A comparison of the genetic composition of isolates from the different agroecological areas would answer some of these questions. In order to answer these questions, a study involving 600 isolates from all the 12 agroecological areas in Southeast Bahia is under way.

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VIRULENCE AND GENETIC DIVERSITY IN *FUSARIUM OXYSPORUM* F. SP. *CICERIS*, THE CAUSAL AGENT OF FUSARIUM WILT IN CHICKPEAS

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Background and objectives
Fusarium wilt of chickpeas (*Cicer arietinum*), caused by the soilborne fungus *Fusarium oxysporum* f.sp. *ciceris* (*Foc*), is one of the most important factors limiting chickpea production worldwide. Use of resistant cultivars is the most practical and cost-efficient management strategy of the disease, but its efficiency can be curtailed by pathogenic variability occurring in the pathogen population. Knowledge of the evolutionary history and potential of the pathogen may help to optimize the use of resistant cultivars for disease management. We examine the virulence and genetic variability existing in populations of *Foc*, and infer a phylogenetic relationship among pathogenic variants occurring in them.

Virulence phenotypes and molecular variability in *F. oxysporum* f. sp. *ciceris*
Two pathotypes, Wilting (W) and Yellowing (Y), were identified within *Foc* based on the distinct syndromes they cause in chickpeas. In addition, eight pathogenic races (races 0, 1B/C, 1A, 2, 3, 4, 5, and 6) can be distinguished based on interactions with a set of differential chickpea cultivars. Races 0 and 1B/C induce the Y syndrome whereas the others cause the W one. The *Foc* races differ also in aggressiveness, as indicated by differences in the amount of inoculum needed to cause severe disease in a chickpea cultivar. Aggressiveness increases significantly from race 0 through races 1B/C, 1A, and 5, in this sequence. Isolates of *Foc* representative of all pathotypes, races, and geographic range were independently assayed using different sets of RAPD primers. UPGMA cluster analyses of RAPD data sets consistently grouped the isolates into two main clusters that correlated with the W and Y pathotypes, respectively; with the Y isolates being divided into two distinct sub-clusters which corresponded to races o and 1B/C.

Genetic variability and inferred phylogeny of *F. oxysporum* f. sp. *ciceris* races
A large set of the above *Foc* isolates was studied by means of DNA fingerprinting using three repetitive DNA sequences from the *Foc* genome. Phenetic UPGMA analysis indicated that the most extreme difference in the amount of fingerprinting similarity occurred between races 0 and 5, which were 64% and 93%, respectively. A cladistic, neighbour-joining analysis of data showed that each of the eight *Foc* races forms a monophyletic lineage. Several lines of evidence indicate that the yellowing race 0 is probably ancestral to wilting races, and that virulence of races to resistant chickpea cultivars has been acquired in a simple stepwise pattern, with few parallel gains or losses.

ASSESING DISSIMILARITY BETWEEN BANDING PROFILES OF HAPLOID AND DIPLOID PATHOGENS WITH MOLECULAR MARKERS

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Abstract

The choice of a suitable index of similarity is an important and decisive point for determining true genetic dissimilarity between individuals, clustering, analyzing diversity within populations and studying relationship between populations, because different dissimilarity indices may yield contrary outcomes. There are no acceptable universal approaches for assessing dissimilarity between individuals with molecular markers (1). Different measures are applicable to dominant and codominant DNA markers depending on ploidy of organisms. We show that the Dice (Nei and Li) coefficient is the suitable measure for haploid organisms with codominant markers and it can be applied directly to {0,1}-vectors representing banding profiles of individuals. None of the common measures, Dice, Jaccard, simple mismatch coefficient (or the squared Euclidean distance), is appropriate for diploids with codominant markers. By transforming multiallelic banding patterns at each locus into the corresponding homozygous or heterozygous states, a new measure of dissimilarity within loci was developed and expanded to assess dissimilarity between multilocus states of two individuals by averaging across all codominant loci tested. There is no rigorous well-founded solution in the case of dominant markers. The simple mismatch coefficient is the most suitable measure of dissimilarity between banding patterns of closely related haploid forms. For distantly related haploid individuals, the Jaccard dissimilarity is recommended. In general, no suitable method for measuring genetic dissimilarity between diploid individuals with dominant markers can be proposed, and rough estimates might be all that is possible. Banding patterns of diploids with dominant markers represent individuals' phenotypes rather than genotypes.

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CHANGES IN *FUSARIUM OXYSPORUM* F. SP. *CICERIS* RACE DIVERSITY AND FUSARIUM WILT INCIDENCE ASSOCIATED WITH CHICKPEA MONOCULTURE

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Background
Fusarium wilt of chickpea, caused by *Fusarium oxysporum* f.sp. *ciceris* (*Foc*), is managed mainly by use of resistant cultivars (1). However, the efficiency of this disease management strategy may be limited by pathogenic diversity existing in *Foc* populations in soil and/or the development of new pathogen strains virulent to available resistant cultivars. We describe the development of a new *Foc* race, race 0 (*Foc*-0) in a field plot artificially infested with *Foc*-5, following continuous use of the plot for disease resistance screening.

Material and methods
In 1992, a field plot without a history of chickpea was selected at Córdoba, Spain to develop a site for *Foc*-5 resistance screening of chickpea germplasm. The field plot was artificially infested with inoculum of a single *Foc*-5 isolate. Since 1993, diverse chickpea germplasm have been evaluated for resistance to *Foc*-5, by assessing the increase in incidence of symptomatic and dead plants during the growing season. In 1997, disease developed in cv. PV1 which is resistant to race 5 but susceptible to *Foc*-0, -1A, -1B/C, and -6; the affected plants showing a yellowing syndrome that is induced only by *Foc*-0 and -1B/C. Some 106 (1998), 101 (2001), and 250 (2002) *F. oxysporum* isolates from stems of different chickpea cultivars were typed for *Foc* belonging and race by means of specific-PCR assay (2), and genetic diversity of *Foc* isolates was determined by RAPD and rep-PCR assay analyses.

Results and discussion
Most of *Foc* isolates from 'PV1' belong to *Foc*-0 with less than 2% of them belonging to race 5. Conversely, all *Foc* isolates from race 0-resistant 'JG62' belong to race 5. Fingerprints from RAPD and rep-PCR assays showed that some variation exists within race 0 isolates whereas race 5 isolates are uniform. Fusarium wilt incidence and severity in 'PV1' have increased through the years in the entire plot since the first appearance of the yellowing syndrome in 1997. Because introduction of *Foc*-0 in the plot seems unlikely to have occurred, those results suggest that the yearly use of the infested soil may have favored changes in pathogenicity and/or virulence in *Foc* and/or *F. oxysporum* that inhabited the soil at a low frequency initially.

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AGGRESSIVENESS IN THE FRENCH WHEAT LEAF RUST POPULATIONS

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Background and objectives
Aggressiveness is a quantitative character of the host – pathogen interaction that is under selection in field epidemics (Villareal and lannou 2000), and has consequences on the pathogen adaptation to new cultivars or cropping systems (Chin and Wolfe 1984). In a series of experiments, we evaluated the diversity for aggressiveness in a field population and the adaptation to the host cultivar, and we tested whether aggressiveness differences could account for the frequency distribution of virulent pathotypes on commonly grown cultivars.

Material and methods
Aggressiveness is classically decomposed into spore efficacy and spore production per lesion. In a first experiment, we measured spore efficacy and spore production of 50 isolates sampled at the end of an epidemic in two field plots, each sown with a different cultivar : Soissons (Lr14a) and Tremie (Lr10, Lr13). Aggressiveness of each isolate was tested on four cultivars with different genetic background: Soissons, Trémie, Altria and Isengrain, with the aim to check whether the isolates were better adapted to their host of origin. In another experiment, we measured spore efficacy and spore production of sets of 20 isolates of pathotypes 073100 (highly frequent on cv. Soissons), 014103 (which frequency on Soissons has considerably decreased in the past years), and other pathotypes with a low frequency on Soissons. Our hypothesis was that more frequent pathotypes were in average more aggressive on cv. Soissons.

Results and discussion
In the field population, significant differences in spore efficacy and spore production were found among isolates, including isolates of the same pathotype and AFLP profile. However, we did not find an interaction between isolates and test cultivars. Isolates with a high spore efficacy or spore production were more aggressive on all test cultivars. When comparing isolates from different pathotypes virulent on cv. Soissons, we found again significant differences among isolates for aggressiveness components, but average aggressiveness of the different isolate sets were not different. We were then unable to explain the observed differences in pathotype frequency from the present results. In each experiment, environmental effects (isolate culture, inoculation date, etc.) significantly affected the pathogen aggressiveness.

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CHANGES IN POPULATION STRUCTURE OF THE SOILBORNE FUNGUS *GAEUMANNOMYCES GRAMINIS* VAR. *TRITICI* DURING CONTINUOUS WHEAT CROPPING

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Background and objectives
The severity of soilborne diseases caused by fungi is affected by cultural practices. Among different effects, the population structure of the pathogen could be changed. We tested this hypothesis in continuous wheat cropping by assessing the genetic structure of *Gaeumannomyces graminis* var. *tritici* (*Ggt*) populations, causing take-all (Lebreton *et al.*, 2004).

Materials and methods
A long term wheat monoculture experiment, established since 1994, generated different take-all epidemics with varying the number of wheat crop successions in the 1999-2000 cropping season. Genetic polymorphism in *Ggt* populations was investigated over natural, local epidemics. Four populations of thirty isolates were isolated from necrotic wheat roots in a first, third, fourth, and sixth wheat crop in the same year. Each *Ggt* isolate was characterised with RAPD (Random Amplification Polymorphism DNA) markers and AFLP (Amplified Fragment Length Polymorphism) fingerprinting.

Results and discussions
Seventeen multilocus genotypes based on the combination of RAPD and AFLP markers were identified among all these populations. The 120 isolates were divided into two main groups, G_1 and G_2, according to bootstrap values higher than 86 %, except for an unique isolate from the third wheat crop. Within each group, populations ranged between 93 and 100 % similarity. Both groups included isolates collected from the first, third, fourth or sixth wheat crop. However, G_1 group profiles dominated amongst isolates sampled in the first and the sixth wheat crops, whereas G_2 group profiles largely dominated amongst isolates collected from the third and fourth wheat crops. Aggressiveness of group G_2 (38 %) was significantly greater than that of G_1 (29.5 %). These results suggest that changes in *Ggt* population structure occur during continuous wheat cropping. The distinction of two *Ggt* groups provides a simple basis for further spatio-temporal analysis of *Ggt* population during polyetic take-all decline.
This genotyping method was also used to test the hypothesis of an association between successive fungicide treatment effects and changes in *Ggt* population structure in the same area during the seasons 2001/2002, 2002/2003 and 2003/2004.

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EXPLOITING *T. MONOCOCCUM* DIVERSITY AND TILLING TECHNIQUE TO IDENTIFY NOVEL DISEASE RESISTANCE TO *MYCOSPHAERELLA GRAMINICOLA*

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Background
Leaf blotch remains consistently within the top three diseases of wheat in all North Western European countries (1). Natural plant resistance has been identified in exotic wheat accessions. However, the genetic basis of this resistance is not well understood and remains difficult for plant breeders to exploit. Due to a lack of reliable resistance in commercial cultivars, disease control is attained by treatment with fungicide. With the recent development of disease resistance to the strobilurin fungicide group (2), greater reliance will now be placed on plant resistance.

Triticum monococcum is a diploid wheat with an AA genome. It is considered a rich source of novel genes and variant alleles and is accessible to wheat breeders as a gene / trait source via established sexual crossing procedures. Many novel resistance loci are already known to reside within *T. monococcum* accessions or to reside on the A genome of hexaploid bread wheat.

The high throughput TILLING technique (Targeting Induced Local Lesions IN Genomes), is used to identify, by a PCR based method, gene sequence variants with biological relevance (3). TILLING can be applied to either mutagenised populations or diverse genotype collections.

Overall scientific objectives
(a) To assess the utility of the diploid wheat *T. monococcum* as a novel source of resistance to *M. graminicola*. (b) To explore the diversity in *T. monococcum* of candidate genes, *RAR1*, *SGT1* and *NPR1* proposed as global regulators of broad spectrum disease resistance. (c) To explore correlations between variant gene sequences and the resistance of accessions to multiple fungal and viral pathogens.

Main results and conclusions to date
1: Almost all the tested accessions were immune to natural field isolates of *Mycosphaerella graminicola*. Only four accessions developed small lesions in mid-March 2004 but epidemics failed to result on the upper leaves. However, of fourteen commercial hexaploid accessions planted in the same trial, all exhibited lesions by early-January 2003 with subsequent epidemics developing on the yield forming upper canopy leaves.

2: Five isolates recovered from different *T. monococcum* accessions were able to cause severe disease symptoms on hexaploid bread wheat under glasshouse conditions, with a latent period of approximately 18 days. However, only very limited symptoms were observed on *T. monococcum* accessions that were re-inoculated with their respective field isolates, and then only after an extended latent period of approximately 35 days as leaves were dying.

3: Consistent with reports in the literature, *TmRAR1* and *TmSGT1* appeared to be single-copy genes, but *TmNPR1* has at least two copies. At amino acid level, *TmRAR1*, *TmSGT1*, and *TmNPR1* share high similarities with the corresponding barley, rice and *Arabidopsis* genes.

These preliminary results collectively suggest that *T. monococcum* is an excellent novel source of resistance to *M. graminicola* and possibly other cereal pathogens.

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ANALYSIS OF TUBER BLIGHT RESISTANCE TO *PHYTOPHTHORA INFESTANS*

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Background and objectives
Late blight of potato, caused by *Phytophthora infestans,* continues to be a global threat to potato production. It is one of the most devastating plant diseases and requires more fungicide for disease suppression than any other plant disease. Due to the lack of market-acceptable resistant cultivars, an intensive fungicide schedule is employed to minimize loss. One of the most devastating aspects of late blight is the tuber blight phase. Tubers infected with late blight and accompanied by soft rot can lead to total loss in storage. In the USA, infected tubers are typically the primary source of inoculum and are also involved with the migration of new aggressive isolates of *P. infestans* (Fry et al. 1993). The objective of this research is to identify regions in the potato host genome that may play a role in tuber blight resistance.

Materials and methods
Two populations were used for genetic analysis of tuber blight resistance/susceptibility in both the field and laboratory. One set of analyses were conducted with a diploid backcross population to *Solanum tuberosum* (BCT) using a hybrid progeny obtained from a cross between *S. tuberosum* and *S. berthaultii.* Previous studies in our lab using this population have identified a major R-gene for resistance to foliar blight on chromosome X (R-12). The second population (NY)analyzed was produced with two tetraploid cultivars (NY 121 X NY 115) which differ in maturity and foliar resistance to late blight and were developed in the state of New York.

Results and discussion
In both populations tuber resistance segregated whether the assays were conducted in the field, or laboratory. An isolate compatible with all of the BCT clones revealed a residual effect of the defeated R-12 gene (75 % tuber blight with the R-gene absent vs. 54 % tuber blight with the R-gene present). This result is consistent with a previous demonstration of a residual effect of this defeated R-gene in assays of foliar resistance. In the NY population, analysis of the phenotypic data revealed that the most significant markers associated with tuber blight resistance were located on chromosomes IV and V. In addition, individual clones with more resistance than either parent were observed.

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NEW ACQUISITIONS ON *PLASMOPARA VITICOLA* EPIDEMIOLOGICAL CYCLE

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Background and objectives
Downy mildew, caused by the heterotallic diploid Oomycete *Plasmopara viticola* (Berk.&Curt.) Berl.& de Toni, is one of the most important grape (*Vitis vinifera*) diseases world-wide. The pathogen arrived in Europe in 1878 from North America and in the following years was found in several other countries around Europe. The current conception about the pathogen's epidemiology assumes that the disease starts from a few germinating oospores that cause primary/oosporic infections early in the season. The infective capability of oospores is believed to exhaust rapidly and then, abundant secondary infections produced by a few genotypes are assumed to lead to the explosive increase of the epidemic.
The aim of this study was to quantify the magnitude of the primary and secondary cycle. We will report here the Italian epidemiology in the wider contest of European epidemiology.

Materials and methods
Oospore germination was recorded for five years in an experimental site in Italy (Adige Valley, Trentino Region). For molecular analyses the SSR-genotyping method was used. Distinction between primary and secondary infections is based on the assumption that "isolates" having a different SSR-allele-pattern derive from independent sexually produced oospores, whereas isolates presenting identical SSR-allele-pattern derive from the same oospore (asexual reproduced clones).

Results and discussion
As far as sexual reproduction is concerned, a large number of different genotypes were found in *P. viticola* populations in most regions. This fact reflects the massive occurrence of oosporic infections and, consequently, the high incidence of oospores in the soil. We found that primary infections are numerous and occur throughout the season.
Considering the asexual component of reproduction, a large number of genotypes were identified only once or twice throughout the survey period. Only about 1/4 of the total genotypes sampled gave rise to asexual progeny. One or two genotypes per epidemic had a significant impact on overall disease severity. Exceptionally, secondary infections played a leading role in epidemics where a low number of oosporic infections occurred. The overall finding is that cycles of asexual reproduction play only a moderate role in downy mildew epidemics. The spatial distribution analysis showed that secondary infections were spatially localized in most cases. In one asexual cycle, the clones' dispersal usually did not cover an area wider than a few vines around the site where the oosporic infection was first identified. Our recent findings are in sharp contrast with the existing assumptions about *P. viticola* epidemics, but further analyses will be necessary to complete the ambitious task of accurately quantifying the quantitative role of primary and secondary infections on *P. viticola* epidemics.

DURABILITY OF RESISTANCE AND OPTIMUM DEPLOYMENT STRATEGIES FOR RESISTANT CULTIVARS

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Background and objectives
The introduction of resistant cultivars is a useful method to control diseases. Unfortunately, in most cases, the question is not whether or not the resistance will be broken but rather how long this will take. However, this time is very variable and can be influenced by many factors. Here, we present a model to help better understand (1) which epidemiological and agronomical factors are most relevant to durability of resistance and (2) how those factors affect the breakdown time.

Materials and methods
Based on a generic model (van den Bosch and Gilligan 2003), we developed a model where sowing, crop growth and harvest follow a seasonal pattern and where pathogen survival between seasons is governed by transitional rules. We started with a simple model with two strains (virulent and avirulent) of the pathogen and two cultivars (resistant and susceptible). The spatial deployment of both crops was fixed in time (i.e. static model) and it was assumed that the probability of infection of one crop by a given spore was proportional to the ratio of this crop in the field (i.e. local scale). We then studied the effects of some of the model assumptions on the qualitative model predictions. We also compared several definitions of durability of resistance and studied the effects of parameter values on durability of resistance (Pietravalle and van den Bosch 2004; Pietravalle, van den Bosch, and Evans 2004). In a second stage, we generalized this baseline model to include spatial (on a large (e.g. regional) scale where spore infection was distance-dependant) and temporal (rotation of the resistant and susceptible crops) effects.

Results and discussion
Model outputs indicate that the fitness cost associated with virulence of the pathogen is of major influence on the durability of resistance. We also compare spatial and temporal deployment strategies and discuss both their long-term and short-term benefits. We show that fitness cost not only affects the time it takes for the resistance to be broken but also the way different deployment strategies affect durability of resistance. Finally, we explain how those findings can help when defining optimum deployment strategies in the field.

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DETECTION AND QUANTIFICATION OF *LEPTOSPHAERIA MACULANS* IN THE PETIOLE OF *BRASSICA NAPUS*

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Abstract

Leptosphaeria maculans is the main causal agent of phoma stem canker, the most important disease of oilseed rape (*B. napus*) in the UK and worldwide. Leaves are infected by air-borne ascospores in autumn, causing pale lesions full of pycnidia. The fungus grows from these lesions down the petiole to the stem base where it causes a canker and subsequent yield loss. To determine whether there is a component of resistance in the petiole which would impede or prevent fungal growth different winter oilseed rape cultivars are being compared. Methods for detection and quantification of the fungus in the petiole are being developed and evaluated. These include isolation, end-time PCR diagnostics, maceration and plating and a chitosan assay to assess the presence and abundance of *L. maculans* in different cultivars. Results will be related to the field characteristics of these cultivars. In addition results obtained from quantitative (real-time) PCR and the tracking of GFP (green fluorescent protein) transformed isolates down the petiole from foci of infection on leaves to the stem, will also be presented.

STABILITY OF GRAIN YIELD AND QUALITY OF WHEAT CULTIVAR MIXTURES IN ON-FARM TRIALS

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Abstract

The stability of yield and grain quality of bread wheat cultivar mixtures was compared to that of the control pure stands, over 19 locations and 2 years. One mixture of 4 cultivars was tested. The cultivars were chosen with the proportion of 1 susceptible for 3 resistant for all foliar diseases whenever possible. In addition to resistance to disease and agronomic characteristics such as high grain yield and homogeneity for earliness, we had to include the quality criteria imposed by the miller. The environment of each location was characterized by yield limiting factors of a reference cultivar. These factors were fungal diseases, Nitrogen and water deficit and soil compactions. The locations were classified as a function of yield reduction of the reference cultivar compared to its optimal value under the experimental conditions. The interaction genotype x environment was studied by factorial regression and showed that whatever the potential of the location during the years and the locations was, the cultivar mixtures were among the most stable and the most productive, compared to the 4 pure stands. When the grain yield was limited by water deficit just before anthesis, the cultivar mixtures were more stable than the pure stands and had a higher yield than the best pure stand. These results showed that heterogeneous populations can better exploit the environmental resources and be particularly advantageous under suboptimal conditions. Similarly, baking score stability was assessed in function of cropping seasons. The cultivar mixture was as stable as the lowest quality cultivar and had a baking score on average equal to the highest quality cultivars.

LATE BLIGHT MODELING WITHIN THE NORPHYT PROJECT

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Abstract

Late blight in the Nordic countries (Denmark, Norway, Sweden and Finland), caused by *Phytophthora infestans*, is a different disease compared to what existed before the introduction of the new population in the 1970's. Fungicide application seems to have increased (probably due to more aggressive strains in the new population), oospores are commonly found in potato fields, and the population structure of the newer late blight population reflects regular sexual reproduction. At the same time political action plans demands growers to decrese the use of pesticides.

A joint Nordic project, NorPhyt, was started in 2003 with the aim of characterizing the new population of *P. infestans* in the Nordic countries. The overall goal of the project is to improve decision support systems for managing late blight. As part of this project, both genotypic and phenotypic characterization of these new populations is taking place, though this presentation will not cover the genotypic variation (measured with microsatellites). In addition, simulation models are used for the management of data, but will also be used for improvement of decision rules. A user-oriented final product in the project is a common Nordic framework for Internet based late blight warning system.

Phenotypic variation is being measured by measuring critical parameters such as infection efficiency, latency period, and spore production of *P. infestans* isolates collected from early-season epidemics. Substantial variation in these parameters has been dectected from isolates collected during the early stages of epidemics in 2003.

The Cornell late blight simulator (current version is designated LB2004) has also been used to compare modelled late blight development with observed disease development. Validation of this model (in original or modified form) would enable development of better decision rules for the decision support system.

LOCAL ADAPTATION OF *PHYTOPHTHORA INFESTANS* TO RESISTANT AND SUSCEPTIBLE POTATO CULTIVARS

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Background and objectives
Understanding host selection and its consequences on pathogen population structures is crucial for effective disease management, through the breeding of resistant cultivars and the identification of the best deployment strategies of these cultivars in time and space. Rapid response to selection exerted by R gene resistance, known to be race-specific, has been repeatedly demonstrated in the past, including for potato late blight. Conversely, little is known about selection by quantitative, partial resistance, which is often postulated to be race-non specific. We therefore wanted to assess whether adaptation patterns in *Phytophthora infestans* populations were similar for both types of resistance, and were related to genotypic polymorphism determined with molecular markers.

Material and methods
French isolates of *Phytophthora infestans* were sampled during two consecutive years (2001, 66 isolates; 2002, 73 isolates) on cultivars exhibiting various levels of resistance: Bintje, a susceptible cultivar; Désirée, a cultivar with quantitative resistance; and Naturella, a cultivar with race-specific resistance due to the gene R2. The isolates collected were established as pure axenic cultures, and characterised for mating type, pathogenicity traits – virulence to the international set of differential clones, except R9 (Andrivon, 1994), and aggressiveness to each of the three cultivars sampled (Andrivon et al., 2003)-, and genetic fingerprints through Amplified Fragment Length Polymorphism (AFLP) analysis (Van der Lee, 1997).

Results and discussion
Local populations were clearly structured by the host for virulence: only isolates from Naturella were able to attack this cultivar. They were also structured by the host for aggressiveness: in both years, isolates from the susceptible cultivar (Bintje) were the most aggressive on both Bintje and Désirée. There was no significant differential adaptation (*ie*, differences in the aggressiveness to each cultivar according to the host of origin) for these two genotypes.

Although 60 of the 156 AFLP bands detected were polymorphic, the genotypic diversity was low in the population: the most genetically distant isolates had 89.65% similarity. Seven AFLP groups could be distinguished with an UPGMA analysis of the matrix of genetic distances, one of these groups consisting of the four A2 isolates. These data suggest that the collection consists of a few closely related clonal lineages, and that sexual reproduction played no role in these populations. No correlation was detected between pathogenicity traits and AFLP groups.

Overall, our data indicate that adaptation for pathogenicity takes place in *P. infestans* populations, but that adaptive patterns depend on the type of resistance considered. It is therefore important to design and assess management strategies tailored to these patterns. A modelling approach to this end is currently underway.

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SESSION C

'SPATIAL AND TEMPORAL SCALES IN PLANT DISEASE EPIDEMIOLOGY'

THE PRACTICAL CONSIDERATIONS OF SCALE IN PLANT PATHOLOGY

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Abstract
The concept of scale has only recently gained recognition as central theme in ecology. The rise in significance of scale in ecology can be attributed to the increase in hypothesis driven, experimental ecology over the last quarter century and the realization that experimental results do not sufficiently explain past or predict subsequent observations in nature. Plant pathologists, who rely heavily on hypothesis-driven research, have confronted these same issues for nearly a century. In this talk, I will provide a concise presentation and discussion of the important concepts of scale and how they apply to the discipline of plant pathology.

Key words
quantitative epidemiology, strawberry

SPATIAL DYNAMICS OF CITRUS LEPROSIS VECTOR AND DISEASE IN NON CONTROLLED EPIDEMICS

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Background and objectives
Citrus leprosis is caused by Citrus leprosis virus that is transmitted by mite in the genus *Brevipalpus*. It is a very important disease of citrus in Brazil because directly reduces production and life span of citrus tree. The control of disease has been done essentially by the mite control what represents 15% of total citrus cost. Pruning of affected branches is an additional practice to reduce the virus inoculum. In general, acaricide sprays are applied based on empirical sampling process and threshold levels that indicate mite occurrence within 1-30% of samples (1). Even that, the sampling and spray decision are taken without any information about mite or affected trees distribution. The aim of this work was to characterize the spatial distribution patterns of mite infested trees as well as of leprosis affected trees in groves without mite control to design new strategies of mite and disease sampling and control.

Materials and methods
All trees from two blocks of late sweet orange varieties, planting in 1996, one parallel and other perpendicular to wind direction, were periodically assessed for leprosis mite and symptoms incidence from January 2002 to September 2004. Mite incidence was assessed in five internal fruits and five external twigs and disease incidence was assessed by observation of symptoms on fruits, twigs and leaves. Maps of mite infested trees and diseased trees were analyzed using ordinary runs, binomial dispersion index, the binary Taylor's law (2), isopath areas, and foci dynamics and structure analysis (3).

Results and discussion
A general and significant pattern of aggregation of mite infested and leprosis symptomatic trees were detected in all levels of spatial hierarchy examined, indicating that *Brevipalpus* mite and, mainly, viruliferous mites were preferentially disseminated among the nearest trees. The degree of aggregation was a function of infested and infected tree incidences. The aggregation was observed in low incidence of infested (>2%) and infected trees (>1%). However, at the same incidence, the degree of aggregation of symptomatic trees was always higher than the one of mite infested trees. It could be an artifact due to the difficult of mite sampling, or the presence of non-viruliferous mites continually been introduced and disseminated into the blocks, or because there was a natural variation of mite population during the year seasons. A tendency of higher incidence of leprosis mite and diseased trees being at grove edges was observed by isopath areas analysis. A relationship between mite foci localization and leprosis symptom foci was observed with a lag period close to 60 days. It was also demonstrated the influence of wind direction and canopy proximity on leprosis vector and consequent virus spreading. The mite foci were mostly isodiametric, while leprosis foci grew preferentially in the row direction but both were very compact.

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EPIDEMIC DEVELOPMENT OF YELLOW RUST IN A GROWING WHEAT CROP ANALYSED BY A DISCRETE TIME GROWTH MODEL

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Background and objectives
Epidemics caused by polycyclic plant diseases are often observed under conditions not meeting the assumptions of classical growth models. Under field conditions, changes in weather and host canopy size may significantly influence the temporal development of disease. The application of discrete time growth models[1], which relate disease severity at one time-point (y_{t+1}) to disease severity at a preceding time-point (y_t), may be useful in the characterization and estimation of epidemic parameters within sub-intervals of the epidemic. The objectives of this study were to develop discrete time epidemic models and apply these on the model system wheat yellow rust (*Puccinia striiformis* f.sp. *tritici*).

Materials and methods
Epidemics were created by inoculations in the centres of field plots measuring 8 by 8 metres. Disease assessments were done in 40 subplots in varying distance from the initial spore sources of each plot. By this, synchronized epidemics were established in subplots characterized by identical crop development stage but with different loads of initial inoculum due to varying distances from the source. Observations were done in year 2001 at May 22 (GS 32), June 7 (GS 50), June 20 (GS 61), and July 4 (GS 75), corresponding to four yellow rust generations. During the first and the last period, the growth model assumption of a constant leaf resource was not met due to flag leaf emergence and/or leaf senescence. An approximate correction for canopy changes was made by estimating disease severities on leaf layers present throughout a period. Yellow rust epidemic development between subsequent observation dates was analysed by a discrete time logistic growth model extended with effects of spore influx: $y_{t+1}(y_t) = \lambda_t{}^*(y_t+m_t) / (1+(\lambda_t-1)^*(y_t+m_t)/K^*_t)$; where y_t is the disease severity at time t, λ_t is the finite epidemic rate, m_t is the disease effect of spore influx, and K^*_t (which is equal to the maximum disease severity if $m_t = 0$).

Results and discussion
The discrete time growth models were well suited for estimation of period specific epidemic parameters. The advantages of such period specific estimates are that they relate to defined sub-intervals of the epidemic characterized by well defined crop age and canopy changes, and by less variable climatic conditions. A novel feature is that maximum disease severities (or K^*_t) can be determined for sub-intervals of the epidemic.

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DEVELOPMENT OF *PHAKOPSORA PACHYRHIZI* AT DIFFERENT TEMPERATURES, RELATIVE HUMIDITIES AND LEAF WETNESS DURATION

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Abstract

In order to successfully control a plant pathogen, its epidemiology must be well understood. To investigate the interaction between temperature, leaf wetness duration and relative humidity (RH) infection studies of rust (*Phakopsora pachyrhizi* Syd.) on soybean plants (*Glycine max* (L.) Merr.) were carried out under controlled environmental conditions. Development of *P. pachyrhizi* on the susceptible cultivar (LS 5995) was quantified at seven temperatures (15, 19, 21, 24, 26, 28 and 30°C) and five leaf wetness durations (6, 9, 12, 14 and 16h) at 85 and 95%RH. Following the temperature, RH and leaf wetness treatments, plants were removed from the dew chamber and placed in a growth chamber (21-22°C, 80%RH, 14h photoperiod and a PAR of 260µmol/m^{2}sec^{-1}). Number of pustules per lesion and lesion size on the abaxial and adaxial leaf surfaces were calculated at 21 days post-inoculation. Infection did not occur on plants incubated at 15°C and 30°C at 85% or 95%RH regardless of leaf wetness duration. Number of pustules per lesion as well as lesion size increased with increasing leaf wetness duration at 85 and 95%RH. At 85%RH, lesion size on both the leaf surfaces increased after 12h leaf wetness at 21°C. However, at 95%RH, lesion size only increased after 14h leaf wetness at 24°C. The number of pustules per lesion produced at 85 and 95%RH was highest at 24°C and showed a gradual increase with increasing leaf wetness duration. Results are being used to develop a model to predict the onset and development of soybean rust. The model will also indicate which soybean growing areas are likely to be infected by *P. pachyrhizi*.

SPATIOTEMPORAL ANALYSIS OF ONION LEAF BLIGHT EPIDEMICS

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Background and objectives

Onion leaf blight (*Botrytis squamosa* Walker) is endemic in eastern Canada, New York, and Michigan. Destructive epidemics can develop during warm and moist summers, causing reduction in bulb size and thus economic losses. The disease is initiated and spread by airborne conidia. Combining inoculum quantification with conventional disease assessment has been shown to improve disease management (1). However, the reliability of inoculum quantification may vary with the spatial distribution of airborne inoculum. The objectives of this work were (1) to characterise the spatiotemporal structures of airborne conidia concentration (ACC) and of lesion density (LD), and (2) to establish spatiotemporal relationships between ACC and LD.

Materials and methods

An experimental plot, 60m X 80m, was sown on May 7, 2003 with onion (cv Tribute) at a rate of 30 seeds per meter with row spacing of 0.36 meter. The plot was split into 48 quadrats of 10 X 10 m. Airborne conidia concentration was measured using rotating-arm samplers placed at the center of each quadrat at the canopy level. The samplers were operated, once a week from June 12 to August 21, for 2 hours from 10:00 to 12:00. On each spore sampling day, lesion density was also estimated as the number of lesions per leaf on 5 plants per quadrat. Variance-to-mean relationships, spatiotemporal autocorrelations and spatial analysis by distance indices were used to characterise the spatiotemporal structure of epidemic and to establish the spatiotemporal relationships between ACC and LD.

Results and discussion

Trends in Lloyd index over sampling dates were similar for both variables with presence of under dispersion at the beginning of the epidemic followed by a slight over dispersion. For both ACC and LD, positive trends in partial autocorrelation were observed mainly for spatial lag of 1. For ACC, no partial autocorrelation was observed on June 12 and June 20, but from June 26 to July 23 a positive and significant partial autocorrelation was observed (spatial lag of 1). For the remaining part of the epidemic, there was no positive autocorrelation. The overall trend was similar for LD with positive significant autocorrelations at spatial lag of 1. No significant partial autocorrelations were observed at the beginning of the epidemic (June 12 to July 3) followed by positive autocorrelations for the rest of the epidemic. For both variables and most sampling dates the index of aggregation measured by SADIE was above 1, indicating some level of aggregation. However, based on X^2 tests, spatial aggregation was detected only on June 26 for ACC and on July 17, August 1, 7 and 17, 2002 for LD. Spatial correlation between ACC and LD was detected only during the period of rapid disease progression Consequently, ACC was not aggregated in the early stage of epidemics; thus, an adequate monitoring of disease inoculum for management might be achieved using few samplers per field only.

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USE OF SPACE-TIME POINT PROCESS MODELLING TO DETERMINE SPATIAL AND TEMPORAL DEPENDENCE OF PAPAYA PHYTOPLASMAS IN AUSTRALIA

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Background and objectives
Phytoplasma diseases of papaya have had a negative economic impact on the Australian papaya industry. In the Northern Territory, the most prevalent phytoplasma associated with papaya is yellow crinkle. This disease is caused by two predominant strains: sweet potato little leaf (SPLL-V4) and tomato big bud (TBB). Analytical methods are often applied in plant pathology to examine only the temporal or spatial changes alone, without consideration of the effects of space and time acting in unison. Following an approach developed by Diggle et al. (1995), we suggest a better understanding of the patterns could be achieved by examining spatial-temporal changes simultaneously. Our objectives were to determine if phytoplasma-positive papaya had an impact on neighboring healthy papaya.

Materials and methods
Data collection and field description have been previously published (Padovan and Gibb 2001). A single papaya plantation was planted in January 1996 and then beginning in May 1996, each plant was assessed monthly (n $\approx$ 3,500) for symptoms typical of papaya yellow crinkle. These assessments continued for 36 months (April 1999). Samples from symptomatic papaya plants were tested for phytoplasma by PCR and strains identified by RFLP analysis. The spatio-temporal point patterns were analyzed using an extension of Diggle et al. (1995) space-time cluster analysis in R (R 1.9.0, www.r-project.org). We tested the hypothesis of complete spatio-temporal randomness for both SPLL-V4 and TBB.

Results and discussion
Based on spatial analysis, it was suggested that SPLL-V4 infected papaya were aggregated (i.e., clustered) upwards of 30 m (10-15 plants along or across rows), whereas TBB-infected papaya were found to be randomly dispersed. However, when you combine temporal information for TBB-infected papaya, we observed small-scale aggregation of infected plants (< 10 m spatially and < 5 months temporally). This suggests that combining temporal information to study point processes is necessary and important, as it provides more information to quantify disease risk to neighboring plants.

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PREDICTING THE RISK OF INFECTION IN A CITRUS TRISTEZA VIRUS EPIDEMIC AND TESTING FOR THE INTENSITY OF VIRUS COMPETITION WITH SURVIVAL ANALYSIS

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Background and objectives

Citrus Tristeza Virus (CTV) can cause several diseases of citrus and has been responsible for the death of over 50 million citrus trees in numerous citrus growing countries worldwide. The spatial and temporal changes in incidence of CTV during epidemics have been described for two virus/insect pathosystems: the CTV/*Toxoptera citricida* and CTV/*Aphis gossypii* pathosystems (2). The present study focuses on the CTV/*T. citricida* pathosystem. Aggregation of infected trees occurs due to local movement of viruliferous aphids. In addition, long distance spread of CTV has been document for both pathosystems. Two questions are addressed here, 1)"What threat do trees with prior CTV-infections present to healthy trees in the vicinity and how does this threat vary over distance?", and 2)"If two isolates of CTV are present in a planting, do they interact in any way within the population or do they spread independently irrespective of prior infection by an opposing isolate?"

Materials and methods

Survival analysis has been used recently to investigate the occurrence and timing of plant disease events (1,3) and here was used to examine the probability of survival (remaining in a non-infected state) of CTV-free trees located at various distances from CTV-infected trees through time. A risk index was calculated via a modified Cox proportional hazards model to estimate the probability of survival through time of CTV-free trees when located at various distances to trees that became CTV-infected in prior years. The risk of becoming infected was related to 'local areas of influence' (i.e., proximity of previously infected trees), as previously reported. CTV Isolates (T30 and T36, mild and decline-inducing isolates, respectively) were differentiated serologically.

Results and discussion

The contribution of short distance transmissions and the influence they have on the overall spatial pattern of CTV that develops through time was examined using the Cox model. A substantial proportion of newly infected trees within a planting could be accounted for as trees determined to be infected 6 months previously within a 'local area of influence' of 8, 16, 24 or 32 m radii, and that 'survival' in a disease-free condition decreased significantly through time as the number of prior infected trees within these areas increased. Secondly, it was found that isolates of CTV that previously were thought to co-migrate independently, actually did have a subtle but measurable affect on subsequent infection by the opposing isolate as measured by the 'hazard ratio' estimated by the Cox model. Although this effect varied among the citrus plantings studied, the occurrence of prior infection by the opposing CTV isolate appeared to decrease the probability of infection by the other isolate by 10-20%, an affect that had previously gone unnoticed in field populations.

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SPATIAL AND TEMPORAL ANALYSIS OF ONION BACTERIAL BLIGHT IN SEED PRODUCTION FIELDS

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Background and objectives
Bacterial blight of onion (BBO), a biennial plant species, is an emerging disease now present in many onion-producing areas. The causal agent, *Xanthomonas axonopodis* pv. *allii* (*Xaa*), is seedborne (2). Although the importance of seedborne *Xaa* as an initial inoculum source associated with the early stages of epidemics has been reported (3), no study concerning the epidemiology of BBO in seed production fields was conducted. In addition, the process of contamination of onion seeds in diseased fields is not understood and has never been measured. Our objectives were to (i) describe the temporal and spatial dynamics of the disease in experimental onion seed production plots, and (ii) evaluate contamination rates of seeds from these plots.

Materials and methods
Epidemic progress in experimental plots of 121 x 60 onion plants contaminated onion bulbs (random inoculation was performed on 0.27% of the plants) was monitored. This experiment was done in duplicate over two consecutive cropping seasons. Disease incidence (percentage of infected plants per plot) was monitored each two weeks. Temporal analyses were performed by nonlinear regression analysis. Logit, Gompertz, complementary log-log and Probit link function models were tested. Akaike Information Criterion was used to choose the most appropriate model. The beta-binomial parameter (tetha) and the binary form of Taylor's power law were used to assess disease aggregation in quadrats consisting of 2x4, 4x8 and 6x12 plants. Spatial patterns were also examined using semivariance analysis. Bacterial analyses of seeds were performed after harvests using both a semi-selective medium (2) and a *Xaa*-specific nested-PCR (1).

Results and discussion
Disease progress curves differed highly between the two years (incidence ranged from 0.05 to 0.6) probably because of climatic differences between the two studied seasons: winter season and late-summer season. Gompertz and probit link function model were the most appropriate models for describing the temporal increase of incidence. Aggregation of the disease incidence was detectable in all plots tested except for one plot at one date. When aggregation was detected, it tended to be a function of disease incidence at the three quadrat sizes tested, as shown by the binary form of Taylor's power law. The exponential model was a good descriptor of the semivariograms. Spatial dependencies were different between the two years, and ranged from 1.63 m in winter to 3.99 m in late-summer. Seed contamination was associated with high disease incidence (≥ 0.44).

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SPATIAL-TEMPORAL DYNAMICS OF CITRUS VARIEGATED CHLOROSIS IN SÃO PAULO STATE, BRAZIL

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Background and objectives
Citrus variegated chlorosis (CVC) is one of the most important citrus diseases in Brazil. It is caused by *Xylella fastidiosa*, a xylem-limited bacterium transmitted by sharpshooter leafhoppers (cicadellids). CVC is widespread in most brazilian citrus areas but incidence and severity can be quite different. In São Paulo state there's an incidence gradient between regions and some hypothesis were created to explain it. This study aimed to point out differences and similarities between Northwest, Center and South regions of São Paulo concerning CVC progress and spread, and also describe and find relationships between seasonal patterns of vectors, host growth, pathogen and disease.

Materials and methods
Three areas ('Pera' sweet orange grafted on Rangpur lime), one in each region, were evaluated for two years by visual assessments performed two times a month. For each evaluation all plants were inspected, assigned as diseased or healthy and cumulative maps were produced. Nine models were fit to each CVC progress curve, and three were fit to segments of original curves. Also, first and second derivatives were estimated for each curve. The following spatial analysis were performed: ordinary runs, isopath areas, Taylor law, dispersion index and foci structure and dynamics analysis. In order to establish differences in seasonal pattern of pathogen, vectors, host and disease, 20 symptomatic plants in each orchard were monthly evaluated. The following variables were measured: number of new flushes (nf), percentage of symptomatic branches (psb), percentage of infected assymptomatic branches (piab), percentage of infected branches (pib), estimation of bacteria concentration (ebc), lower and higher temperatures, rain fall and number of sharpshooters in yellow traps. The correlations among variables were tested by Distributed *Lag* Analysis, and the comparison between regions and seasons was performed by Kruskal-Wallis, Friedman ANOVA and Nemenyi test ($p < 0,005$).

Results and discussion
Temporal. Good fitting was obtained for segments of original curves. First and second derivatives showed many peaks over time. Most of those peaks occurred at spring and summer months. Our hypothesis is that derivative peaks are related to flush emission peaks, considering that new sprouts are the preferred feed site of *Xylella fastidiosa* vectors. *Spatial.* Ordinary runs indicated a trend to randomness. Isopath areas analysis showed few compact foci and a trend to uniform incidence in all areas. The other analysis showed few if any differences between regions and results that could classify CVC pattern as slightly aggregated. *Seasonal patterns.* The CVC related variables (psb, piab, pib and ebc) showed seasonal patterns but no statistical differences were detected among seasons. The Northeast orchard showed the highest number of new flushes and percentage of symptomatic branches. The South orchard had the higher percentage of assymptomatic infected branches. There were no statistical differences among regions concerning *Xylella* concentration.

SPATIAL PATTERNS OF MANGO MALFORMATION
IN IRRIGATED AREAS OF THE BRAZILIAN SEMI-ARID

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Background and objectives
There are over 18.000 ha of irrigated mango in the São Francisco River Valley, and 90% of the fruit produced in this semi-arid region is exported to the european and american markets. With the expansion of the mango areas in the last decade, the intensity of malformation has been increasing, and there are many unresolved questions on the dynamics of the disease in the region, such as the role of the mango bud mite (*Aceria mangiferae*) or mechanical transmission in the dissemination of the disease. This study aimed to characterize the spatial patterns of mango malformation in commercial orchards, of the brazilian semi-arid.

Materials and methods
Seventeen plots – Haden, Kent or Tommy Atkins cultivars, ranging from 6 to 21 years old and from 64 to 720 plants- were evaluated when blossoming. Each tree was visually evaluated and the percentage of symptomatic inflorescences was recorded, as well as tree position in a XY map. Ordinary runs test was performed for within-row and across-row directions and, additionally, spatial correlation was performed using LCOR2 software. After quadratization - 2x2 and 3x3 plants (Quadratizer Excel Macro), binomial dispersion index (Vobs/Vbin) was calculated for each plot as well as binary power law for the entire data set. Original XY maps were also employed to produce isopath maps using Statistica software.

Results and discussion
Plot average percentages of affected inflorescences ranged from 0.45% to 57.9%, median of 2.88%. Ordinary runs test pointed at a significant departure from randomness for 55.6% and 31.2% of the plots, within and across rows, respectively. The aggregation within the row may indicate mechanical transmission of the disease and/or of the mite vector. Spatial correlation reinforced runs results but, in general, the strength of aggregation could not be considered high. Also, only half of the plots presented a core cluster size with more than 1 significant lag, but significant spatial correlation was not limited to the core cluster. Nevertheless, the spatial correlation revealed an edge effect only for three plots. For 2x2 quadrat size, the dispersion index ranged from 0.82 to 1.97, median of 1.39; 9 out of 16 dispersion indices were significantly greater than 1. For 3x3 quadrat size, the indices ranged from 1.27 to 2.50, median of 1.92; 9 out of 11 indices were significantly greater than 1. The parameter b of binary power law was not significantly different from 1, and parameter A was not significantly different from 0 (t test) for both quadrat sizes. Isopath mapping showed that although conspicuous isolated foci could be seen, at least 12 of 16 plots had important high incidence sub-regions associated to the orchard borders, what may imply a role for a wind-borne inoculum introducing the disease to an area. Results did not pointed out clear, kindred patterns for all plots, which probably reflects the plot differences of age, cultivars and cultural practices. Some of them presented Z statistic (runs test) as low as −5.35, while others had an indication of regularity (Z= 1.88). The same variation was observed for binary dispersion indices and lack of aggregation brought up by binary power law analysis is a proof of this fact. The last but not the least, this variation and isopath mapping findings need to be carefully examined, based on multi-year assessments and a broader range of orchard´s history.

SPATIAL PATTERN AND TEMPORAL DYNAMICS OF BEET TUMOR (*PHYSODERMA LEPROIDES*) IN FALL SOWN SUGARBEET CROPS IN SOUTHERN SPAIN

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Background and objectives
Beet tumor of sugarbeet, caused by the fungus *Physoderma leproides,* is becoming of increasing importance in fall sown sugarbeet crops in southern Spain. In those crops, plants growth during late winter and early spring in soil with high humidity that favour fungal infection and disease development (Ruppel, 1995). The objective of this study was to examine the spatial pattern and temporal dynamics of Beet tumor in fall sown sugarbeet crops in southern Spain.

Materials and methods
Beet tumor incidence was monitored in eight plots located in the Sevilla province during 2002/03 (5 plots) and 2003/04 (3 plots) crop seasons. Disease incidence was assessed by visual disease inspection of every plant in each plot (4,000 plants per plot) at 2 to 4 wks intervals from January to July in each season. Point pattern and correlation-type approaches were undertaken using binary data directly or after parsing them in contiguous quadrats of 10, 40, 80 and 160 plants.

Results and discussion
Ordinary runs analysis generally indicated a departure from randomness of diseased plants status adjacent plants within rows. The binomial index of dispersion and the interclass correlation for various quadrat sizes suggested aggregation of symptomatic plants for all plots within the quadrat sizes tested. Also, estimates parameters of the binary form of Taylor's power law provided an overall measure of aggregation of symptomatic plants for all quadrat sizes tested. Aggregation in each plot appeared to be related with disease incidence. Spatial analysis by distance indices (SADIE [Perry et al., 1999], Rothamsted Research Institute, Harpenden, Herts, UK) showed a non-random arrangement of quadrats with infected plants. Spatial pattern at the plot scale were often characterized by the occurrence of several clusters of infected plants. Increasing clustering over time was generally evidenced by stronger values of clustering index over time and by increasing patch cluster size. Strong significant spatial associations were detected between all spatially aggregated time periods and the successive time period in each season. This study provides a better understanding of Beet tumor patterns in affected plots which may help for increase efficiency in disease control.

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EFFECTS OF LIGHT INTENSITY AND QUALITY ON SPORULATION
OF LETTUCE DOWNY MILDEW (*BREMIA LACTUCAE*)

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Abstract

Although light quality, light intensity, and environmental factors are incorporated in many present models for lettuce downy mildew, exactly how they interact to reduce sporulation by *Bremia lactucae* is poorly understood. At Nordic latitudes, day length, light intensity and quality differ substantially from most other lettuce producing regions and are therefore of great interest in evaluating these models. We inoculated 7-day-old lettuce seedlings with a suspension of 3×10^5 spores per ml and incubated them until the 6th night, whereupon cotyledons were detached, placed upside down on wet filter paper and incubated at 20°C and 100% RH at different light qualities and intensities for 10 hours, including daylight-balanced and dark controls. Sporangia were harvested and enumerated the following morning. Violet light provided through a wide bandpass filter (400-500 nm) suppressed sporulation to nearly the same extent as the daylight control, while red (650-750 nm) and yellow light (550-650 nm) caused nearly no suppression. However, light provided through narrow bandpass filters in the violet range (400-500 in 50 nm steps) did not suppress sporulation, indicating a threshold quantum of light within the violet range is required for suppression. We have also found that the suppressive effect of light is moderated by temperature, and that the magnitude of the suppressive effect of light increases with increasing temperature.

TEMPORAL PROGRESS OF SEPTORIA LEAF SPOT ON BLUEBERRY

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Background and objectives

Septoria leaf spot, caused by *Septoria albopunctata*, decreases flower bud set and return yield of blueberry by reducing photosynthesis (2) and inciting premature defoliation (3) in the summer and fall. The objectives of this study were to characterize seasonal progress of the disease in relation to host phenology and inoculum availability and determine the effect of selected host attributes on disease development. We were particularly interested in establishing whether leaves are infected season-long or only during the short period of leaf expansion, as has been suggested previously (1).

Materials and methods

The study was carried out in 2002-2003 in a planting of 'Premier' rabbiteye blueberry (*Vaccinium ashei*). Each year at leaf bud break in early spring, 50 shoots were selected for season-long monitoring. For each individual leaf on these shoots, time of emergence and time of full expansion (date when the leaf attained 95% of its final length) were recorded and leaves assessed regularly for disease severity. Dissemination of pycnidiospores was monitored with funnel samplers. For each leaf, cumulative spore numbers were summarized for three temporal windows: 1) a 2-week period centered on the date of full leaf expansion; 2) a 2-week period beginning at the date of full expansion; and 3) the entire season from full leaf expansion to the last disease assessment in early November. Potted trap plants with leaves in different phenological stages were exposed to natural inoculum in the field to provide complementary data on infection windows.

Results and discussion

Disease progress followed a sigmodal pattern typical of polycyclic epidemics. Based on the logistic model, the highest absolute rate of increase and final disease severity was observed on leaves that emerged early in the season, on lower (i.e., older) leaves on a shoot, and on leaves in the lower canopy. Inoculum was present throughout the season with numbers being highest between mid-July and early August. A positive correlation ($r = 0.36$, $P = 0.0229$ and $r = 0.44$, $P < 0.0001$ in the 2 years) was observed between final disease severity and cumulative spore numbers in the entire-season window, compared with weak and/or non-significant correlations for the 2-week windows around the time of leaf expansion. Disease incidence on trap plants was high (> 72%) regardless of the leaf stage at the time of exposure. Taken together, the results show that infection by *S. albopunctata* can occur throughout the season on leaves of any age.

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MODELLING DISEASE GRADIENTS IN PYRETHRUM DUE TO *PHOMA LIGULICOLA* USING TOBIT AND NONPARAMETRIC REGRESSION

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Background and objectives
Pyrethrum is an economically important export crop for Tasmania, Australia. Since 2000, pyrethrum production has been significantly impacted by ray blight disease, caused by *Phoma ligulicola* (Pethybridge and Hay 2001). Little quantitative information, however, is known concerning the epidemiology of this disease. This disease manifests itself as: leaf defoliation, stem lesions, and ray blight (of the flowers). We hypothesize that a minimum level (threshold) of leaf defoliation is present before stem lesions will be observed and then subsequently ray blight. We also hypothesize a shallow disease gradient for splash-dispersed conidia in first harvest crops. Therefore, our objectives were to (i) determine minimum disease thresholds for visually assessed diseased intensities and (ii) quantify disease gradients within pyrethrum fields.

Materials and methods
At each of three locations in Tasmania, three disease gradients were assessed with respect to distance from an untreated strip of pyrethrum. Disease assessments (incidence, severity) were made from the source and continued along a line transect every 0.5 m to 9.5 m. At each interval, 10 stems were obtained, from which the severity of defoliation, stem severity and the incidence of ray blight on the flowers were obtained. This was accomplished using a left-censored Tobit regression model. Disease gradients were quantified using non-parametric regression as normality assumptions were not satisfied.

Results and discussion
Based on Tobit regression, the minimum leaf defoliation before stem lesions (stem severity) were observed ranged between 25 to 30% at the three locations. The same range was also observed from examining the minimum leaf defoliation and before the occurrence of ray blight.
Disease gradients, as measured using nonparametric regression, were observed to range from 2.5 to 5.0 m (leaf defoliation), 3.0 to 6.0 m (stem severity), and 3.0 to 7.0 m (ray blight).
The results from these analyses provides useful new information regarding epidemiological factors important to ray blight epidemics in Tasmania.

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IMPORTANCE OF PLANT PHENOLOGY TO TEMPORAL SCALE IN EPIDEMICS OF RYEGRASS STEM RUST

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Background and objectives
In the *Puccinia*/grass pathosystem, host phenology strongly affects temporal development of epidemics, due to unique growth and morphology characteristics of grasses. After infection of seedlings in the autumn, persistence of the fungus through the winter depends on the temporal interplay between pathogen life cycles (latent period, pustule duration) and grass phenology (leaf initiation, duration and senescence). The tempo of pathogen cycles, as well as that of leaf presentation, is driven largely by weather conditions. The result may be local persistence or extinction of the stem rust epidemic. Another period when temporal epidemic characteristics are strongly determined by interaction of pathogen biology with host phenology occurs during stem and inflorescence extension. In this phenomenon, within-plant increase of disease is very prominent due to the unique growth habit of grasses, and the pace of disease increase is directly linked to the timing of stem extension. The research goal was to develop a quantitative model for epidemics of stem rust in perennial ryegrass, accounting for temporal aspects of host phenology.

Materials and methods
Individual plants of perennial ryegrass in field plantings were monitored from emergence (autumn) through spring. Measurements of leaf size and duration were taken repeatedly on the same plants, and detailed plant phenology was analyzed with respect to the continuously-measured weather conditions at the sites. Similarly, duration of individual stem rust pustules was monitored. Our previously-developed models for infection and latent period (driven by temperature, leaf wetness and precipitation) were combined with the quantitative descriptions of leaf presentation and pustule persistence. The resultant model of pathogen population persistence was evaluated with observations from additional experiments in which pathogen population changes were observed on individual, inoculated plants in the field over winter. Measurements were taken on individual reproductive tillers of perennial ryegrass in the field, to produce equations describing extension rate of the various internodes and the inflorescence. Experiments in the greenhouse quantified rates of within-plant disease increase on stems following inoculation of leaf sheaths at single sites.

Results and discussion
Overwinter survival of the pathogen, and pathogen population available to initiate the springtime epidemic, could be effectively modeled based on growth rates, duration and senescence of sequential host leaves interacting with pathogen infection efficiency, latent period and pustule duration. Cycles of pathogen appearance (pustules) and absence (present as latent infections only) observed in field experiments were simulated with the model. The manner in which winter weather conditions can affect epidemic survival through effects on interacting host phenology and pathogen biology was demonstrated. Equations for stem extension were used to model the rapid increase in stem rust that occurs during and after tiller extension.

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IMPACT OF PARTIAL RESISTANCE IN MANGO TO *XANTHOMONAS* SP. PV. *MANGIFERAEINDICAE* ON THE TEMPORAL AND SPATIAL DEVELOPMENT OF BACTERIAL BLACK SPOT DISEASE

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Background and objectives

Mango Bacterial Black Spot (MBBS) is a potentially destructive disease in many tropical and subtropical areas of Asia, Eastern Africa and Oceania (2). Control is attempted through IPM techniques mainly consisting of prophylactic measures and copper sprays. A limited number of mango cultivars with desirable agronomic traits are partially resistant to *Xanthomonas* sp. pv. *mangiferaeindicae* (*Xm*), the causal agent of MBBS. No quantitative epidemiology data is available on this pathosystem. Our objectives were to (i) describe the temporal and spatial development of MBBS in an area conducive to epidemics and (ii) evaluate the impact of partial resistance on disease development.

Materials and methods

Experimental design consisted of one plot (approx. 250 trees) of cultivar Haden (highly susceptible) and one of cv. Heidi (partially resistant) (1), and was monitored for 2.5 years after establishment. A first set of plots was established in Oct. 1998 in Saint Pierre (Réunion Island) CIRAD experimental station and a second set was established in December 2001. Disease incidence and severity were determined. Temporal analyses were performed by nonlinear regression analysis. Logistic, Gompertz and probit link function models were used. Akaike information criterion was used to retain the most appropriate model. We compared the experiments through the model parameters using likelihood ratio test. Spatial autocorrelation analyses were performed to explore spatial data structure (3).

Results and discussion

All trees remained disease-free until the occurrence of a tropical storm. Disease incidence exceeded 0.95 in all plots. Gompertz was the most appropriate model for describing the temporal increase of incidence. Rates of disease increase (r_G) were not statistically different on the susceptible and partially resistant cvs. However, disease severity on the susceptible cv. was up to 100 times higher. Furthermore, lab experiments indicated that *Xm* population sizes in one month-old lesions on the partially resistant cv. were approx. 100 times less than on the susceptible cv.

No aggregation was detected early in the epidemics. Aggregated patterns were detected after 5-7 months and 17-20 months on the susceptible and partially resistant cv., respectively. In contrast with the susceptible cv., the size of core clusters for the plots established with the partially resistant cv. did not increase over time. No directionality of spatial patterns was observed on the susceptible cv.

Analyses based on *Xm in planta* growth and spatial MBBS patterns could be helpful for evaluating partial resistance to *Xm* in promising material from breeding programs.

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INFLUENCE OF PEA CANOPY ARCHITECTURE ON THE DISPERSAL OF PYCNIOSPORES OF MYCOSPHAERELLA PINODES

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Background and objectives
Ascochyta blight caused by *Mycosphaerella pinodes* (*Mp*) is one of the most damaging diseases of field pea world-wide. In a recent study, six spring pea cultivars, all equally susceptible to Ascochyta blight, but differing in architectural features (stem height, branching ability, standing ability) displayed differences in the profile of disease on leaves (Le May *et al.*, 2004). Those differences could be explained by either a direct effect of canopy architecture on spore dispersal or an indirect effect on spore germination and symptom development by influencing the microclimatic environment. The aim of this study was to investigate the rain-splash dispersal of *Mp* pycniospores in canopies varying in plant density and plant development stage.

Materials and methods
Experiments were conducted in controlled conditions. Two plant densities (49 and 81 plants/ m^2) and three plant development stages (6, 8 and 10 nodes) were tested. The experimental design involved a crop canopy of $1m^2$ consisting of plants in pots (7x7 or 9x9 pots per m^2). A suspension of pycniospores (10^6 spores/ml) was placed at the centre of each crop canopy. A rainfall simulator was fixed at 3.5m height above the plants and activated for 4min56s to simulate a 2mm rainfall. Plants were then incubated in a climatic chamber at 20°C during 5 days and the number of flecks was counted on stipules of each node.

Results and discussion
Pycniospores were dispersed vertically up to 24,8cm and horizontally up to 64,4cm from the inoculum source under a 2mm simulated rain. Splash dispersal patterns were fitted with an exponential model. The slope of the gradient was steeper in the loose canopy (49 plants/m^2) than in dense canopy (81 plants/m^2). The development stage had also an effect on spore dispersal : the most developed plants seemed to play a role of physical barrier.

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TESTING THE ASSOCIATION OF DISEASE PATTERNS
BETWEEN TWO DATES IN REGULAR PLANTINGS

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Background and objectives
Identifying the biological processes involved in disease spread is fundamental to understand the epidemiology of a disease. The analysis of spatiotemporal patterns provides an opportunity to address questions that are related to these processes. A basic objective is often to assess if there is a secondary transmission at the orchard scale and thus if the spatial pattern of diseased plants at one date is associated with the pattern of previously diseased plants. The lack of knowledge on the underlying phenomena often calls for the use of nonparametric tests to answer this question, but at present such a test is not available for spatiotemporal maps of binary data (healthy or diseased plants) in regularly spaced plantings, although this kind of data is frequent.

Materials and methods
Here we propose a Monte Carlo test of the hypothesis that the location of newly diseased plants (cases 2) is independent of the location of previously diseased plants (cases 1), conditional on the observed pattern at each date. This spatio-temporal test is based on Lotwick and Silverman's test (1), modified following Chadœuf *et al.* (2) to cope with the censoring arising on a lattice when plants are missing or cannot recover between the two dates. Under the null hypothesis of independence between the two patterns, the distribution of toroidal distances between cases 1 and cases 2 should be the same for observed and expected patterns. Expected patterns are simulated by shifting on a torus the whole pattern of cases 2 by a random number of plants along and across rows. For each simulation, we discard the censored points (superposition of cases 1 and cases 2 at the same location) from observed and simulated data. Then we compute the difference between the number of simulated and observed case 1 / case 2 pairs closer than a given distance. If there is a positive association between disease patterns at the two dates, we expect more pairs at small distances in observed than in expected patterns. As an illustration, we analyze the dependence between patterns of trees showing *Plum pox virus* symptoms at two dates.

Results and discussion
The chosen example shows the potential of this test to provide crucial clues about the processes of disease spread between two dates in regularly spaced plantings. In this generic test, the censoring can result in a slight lack of statistical power. Thus when one of the two patterns shows no significant structure, other tests with more statistical power have been developed. We consider our test as a first step in a broader approach integrating other hypotheses tests, other methods to analyze spatial and temporal patterns, as well as modeling and biological investigations.

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INTEGRATION OF SPORE TRAPPING WITH MOLECULAR TECHNIQUES TO ENHANCE EPIDEMIOLOGICAL STUDIES

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Abstract

Traditionally, spores have been collected on sticky surfaces (e.g. trap surfaces of Hirst-type or rotating-arm samplers) and viewed by microscope to study the timing and dispersal of propagules of many plant pathogens. Problems can arise in identification to the species level and, particularly for small or hyaline spores, underestimation of numbers due to masking by other spores. Visual counting is not only time consuming, it also does not provide additional genotypic information such as virulence group, race or presence of fungicide resistance, that is now possible using appropriate molecular diagnostic methods. Recent studies have demonstrated that molecular diagnostic techniques can be integrated with samples taken from traditional spore traps such as the Hirst-type spore sampler (Calderon et al., 2002) and from novel formats such as the Burkard miniature cyclone sampler (Williams et al., 2001).

The potential power of these new techniques is illustrated by a recent study (Fraaije et al., submitted) in which daily numbers of M. graminicola ascospores, trapped using traditional Burkard spore samplers, were not only quantified but also the proportion with alleles conferring resistance to strobilurin (QoI) fungicides was determined. Each daily spore trap tape section was divided longitudinally to give a sub-section for microscopy and a sub-section for the real-time PCR assay. The advantage of this technique over using molecular diagnostics on samples collected directly in Eppendorf tubes (e.g. using the Burkard Automatic Multi-Vial Cyclone Sampler) is that the section available for microscopy can be used to confirm that the DNA detected was from ascospores and not conidia that may become airborne in certain weather conditions.

A similar technique has been used to investigate the pathogen Rhynchosporium secalis, which causes leaf blotch or scald of barley. A sexual stage for this fungus has not been described but is suspected due to its genetically diverse population. Rarely, small amounts of R. secalis DNA has been detected on tapes of a spore trap, which was located in a barley field. Further work is in progress to confirm whether these positives represent the presence ascospores or airborne conidia.

A new design of passive spore trap, which relies on spores being deposited or impacted onto its surfaces can also be integrated with molecular diagnostic techniques. This approach is currently in use to identify the main inoculum source, among different farm habitats, of Claviceps purpurea, the cause of ergot of cereals.

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MODELLING PLANT DISEASE EPIDEMICS IN A SPATIAL HIERARCHY

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Background and objectives

Development of plant disease epidemics over space and time has been addressed for a few decades, with major advances from empirical (measurement of spore and disease gradients), modelling (explicitly spatialised or mean-field models), and statistical approaches (analysis of frequency distribution, correlation coefficients).

The objective of our work was first to assess the effects of host structure and propagule auto- and allo-deposition patterns on the spatio-temporal development of epidemics with a simulation model. The model was then expanded to assess the effects of (1) variation of deposition patterns over time, and (2) association with non-host genotypes, on epidemics.

Materials and methods

The simulation model (PANDA) addresses epidemics at three nested scales: site, leaf, and plant. The main hypotheses of the model are as follows:

- Propagules dispersed from a lesion can be deposited on a different plant – allo-plant deposition, on a different leaf within the same plant – allo-leaf deposition, or on the same leaf – auto-deposition.

- At the site scale, three types of vacant sites are defined: vacant sites located on healthy plants (VHP), vacant sites located on healthy leaves within diseased plants (VHL), and vacant sites located on diseased leaves (VDL).

- VHP sites can be infected through allo-plant deposition only; VHL sites can be infected through allo-plant and allo-leaf deposition; and VDL sites can be infected through the three types of propagule deposition.

- The increase in number of diseased plants is related to the decrease in number of VHP sites, and the increase in number of diseased leaves is related to the decrease in number of VHP and VHL sites.

Results and discussion

Simulation results indicate that the increase in auto-deposition reduces epidemic speed at the three scales. Host structure with small leaves is associated with epidemics slower than host structure with larger leaves when auto-deposition is high, but epidemics occurring in the two host structures are similar when auto-deposition is low. These results thus indicate that there is an interaction between host structure and deposition patterns on epidemics [1].

Epidemics were simulated with deposition patterns corresponding to dispersal by rainfall (high auto-deposition, [2]) and by wind (medium auto-deposition, [3]). Simulations indicated that epidemics at leaf and plant scales were faster for deposition patterns corresponding to wind dispersal. Differences were small at the site scale.

The system's response to presence of non host concurs with previous studies: epidemics on susceptible hosts are more reduced by the presence of non-hosts when allo-plant-deposition is the highest.

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SESSION D

'THEORETICAL EPIDEMIOLOGY: PROGRESSES, CHALLENGES, AND APPLICATIONS'

TRENDS IN THEORETICAL PLANT EPIDEMIOLOGY

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Abstract
We examine trends and advances in three specific areas of theoretical plant epidemiology, viz. models of temporal and spatial dynamics of disease, the synergism of epidemiology and population genetics, and progress in statistical epidemiology. Recent analytical modeling of disease dynamics has focused on SIR (susceptible-infected-removed) models modified to include spatial structure, stochasticity, and multiple management-related parameters. Such models are now applied routinely to derive threshold criteria for pathogen invasion or persistence based on pathogen demographics (e.g. Allee effect or fitness of fungicide-resistant strains) and/or host spatial structure (e.g. host density or patch size and arrangement). Traditionally focused on the field-level, the scale of analytical models has broadened to range from individual plants to landscapes and continents; epidemiological models for interactions at the cellular level, e.g. during the process of virus infection, are still rare, however. There is considerable interest in the concept of scaling, i.e. to what degree and how data and models from one scale can be transferred to another (smaller or larger) scale. Despite assertions to the contrary, the linkages between epidemiology and population genetics are alive and well as exemplified by recent efforts to integrate epidemiological parameters into population genetics models (and vice versa) and by numerous integrated studies with applied focus (e.g. to quantify sources and types of primary and secondary inoculum). Statistical plant epidemiology continues to rely heavily on the medical and ecological fields for inspiration and conceptual advances, as illustrated by the recent surge in papers utilizing ROC (receiver operating characteristic), Bayesian, or survival analysis. Among these, Bayesian analysis should proof especially fruitful given the reliance on uncertain and subjective information for practical disease management. Nonetheless, apart from merely adopting statistical tools from other disciplines, plant epidemiologists need to be more proactive in exploring potential applications of their concepts and procedures in rapidly expanding disciplines such as statistical genetics or bioinformatics. Although providing the scientific basis for disease management will always be the raison d'être for plant epidemiology, a broader perspective will help the discipline to remain relevant as more efforts and resources continue to be devoted to both genomic and ecosystem-level science.

Key words
decision analysis, mathematical model, population genetics, spatial structure, statistical epidemiology, stochasticity

A DETERMINISTIC MODEL FOR THE UNDERSTANDING AND MANAGEMENT OF POWDERY MILDEW IN VINEYARDS

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Background and objectives
The powdery mildew-viticulture pathosystem is characterised by (i) a polycyclic pathogen capable of explosive multiplication, (ii) a host population with a highly structured spatial arrangement between plants, a complex architecture within plants and by rapid changes in host susceptibility to disease with time, (iii) a management regime that includes high levels of human interference. Within the framework of integrated pest management strategies for improving powdery mildew control would depend on our understanding of the dynamical interactions between the pathogen, host and the environment that lead to invasive spread of disease. We describe here the early results of a mechanistic simulation model coupling the dynamics of powdery mildew and that of grapevine. The model would be used to (i) grade and quantify the most important factors which modulate the interactions (earliness of the attack, quantity of primary inoculum, aggressiveness, ontogenic resistance of the organs, vine vigour, canopy structure...), (ii) to simulate a spatio-temporal dynamic starting from various climatic conditions, production system and pathogen initiation, (iii) to identify the miss of knowledge, (iv) to assess the importance of variables very difficult to measure or to experiment (infection period, isolate aggressiveness), (v) to test some strategies to control invasive spread.

Methods
The model simulates the 3D development of vine from a single vinestock to a whole plot during a single season coupled with the simulation of inoculum and disease dynamics. Functions, parameterised from literature or experimental data, are used to describe growth of the host (apparition and size of the organs) and growth of the pathogen (infection, latency, lesion development, sporulation, dispersion). The model input variables are climatic (temperature, wind speed and direction) or related to the pathogen (location and onset of primary infection) and dictate the growth of the crop, the spread and dispersion of the pathogen. Input parameters are characterising the crop system (number of buds, training system) and conditions of growth. Two mechanisms of dispersion are considered: i) dispersion at short distance (inside the vinestock and its close neighbours) performed by rays and taken into account the interception by leaves, and ii) the redistribution of escaped spores at long distance according to a density curve. The output of the model describe i) change in the number, location and age of healthy and infected host organs over time, ii) change in the density of spores over time.

Results
Early simulations were examined for consistency with field data to demonstrate two important features of the model. (i) Estimation of hidden, yet important, epidemiological component like the duration of infectious period, (ii) Estimation of criteria for invasive spread of disease like the date of contamination.

WHEN THE MEAN IS MEANINGLESS: THE ROLE OF EPISODIC AND/OR AGGREGATED BEHAVIOR IN EPIDEMIOLOGY.

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Background
The determination of the parameters needed for the calibration of epidemiological models most often depend on averaged data. This averaging process may be over space, over time, over tissue type or age, or any combination of these and other factors. When, as is often the case, the epidemiological response to such an averaged variable is inherently nonlinear, the practice of choosing model parameters based on bulked data becomes highly questionable. This fact has been discussed for wind dependent spore release (Aylor 1990), yield loss due to spatially aggregated plant damage (Ferrandino 1989) and host age dependent disease susceptibility (Merril and Finley 1981). In fact, the literature abounds with many specific cases where inhomogeneous behavior at some length or time scale of behavior must be included. This problem becomes more complicated when models of within-field disease spread are combined with plant growth and between-field spore transport to yield predictive models of continental scale pandemics.

Objective
To elucidate some of the interesting ramifications of episodic and/or inhomogenous behavior using simple mathematical models.

Method
A simple boxcar model of infection (Healthy→Asymptomatic Infected→Symptomatic→Reproductive →Non-reproductive→Removed Tissue) was combined with a plant growth/yield model. This allowed for the phenological variation of host tissue susceptibilty to disease. The spore transport function was assumed to be given by the radially symmetrical Half-Cauchy distribution. The model was applied to field data of the potato/late blight, tomato/septoria leaf spot and the birch/neo-nectria patho-systems. The role of intermittent weather and variation in the age/susceptibility of host tissue was examined.

Results
For the heavily defoliating diseases (late blight and septoria leaf spot) the course of the epidemic was highly sensitive to intermittent favorable (wet) conditions due to loss of inoculum during dry spells. For the birch/nectria system, since disease susceptibility is strongly dependent on tree age, tree density and the initial age distribution of the stand totally determined the asymptotic levels of canker.

Conclusions
Epidemiological models based on average response to average conditions can never adequately describe real epidemics.

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EPIDEMIOLOGY, METAPOPULATIONS AND INVASIVE SPECIES: A COMMON MODELLING FRAMEWORK?

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Background and objectives
Community ecology aims at understanding the structure and dynamics of communities from the interactions between species. An aspect of epidemiology aims at understanding the spatio-temporal dynamics of diseases from the local host/parasite interactions. Metapopulation theory aims at understanding the sustainability of a fragmented population, where the fragments are connected by dispersal. Modelling the dynamics of invasive species becomes an increasing concern in monitoring semi-natural ecosystems. All these theories have a common conceptualization framework: some processes are inferred at the level of interactions between individuals or species, and the outcome is modelled from these processes at the community or landscape level. Is it possible to formalize these similar theories with a common modelling framework, leading to generic properties, relevant in each field?

Materials and methods
Following a general trend in recent literature (Newman, 2003), we propose to use a graph (a simple mathematical object with nodes and edges) to describe the geometry of the interactions, and, some processes (like the contact process) to model the interactions. The model at the scale of the node is very simple, and stochastic (transmission or non transmission between nodes connected by an edge of, say, the propagule, the disease, the invasive species). This establishes a connection between epidemiological models and metapopulation dynamics, which can very easily be extended towards modelling invasive species (Dobson, 2003; Franc, 2004).

Results and discussion
Using some approximations classical for particles interactions in statistical physics, it is possible to compute some global states at the level of the whole network, as the fraction of infected or invaded or living nodes. Beyond these calculations, some classical models can be read like this: the Levins model in metapopulation is a mean field model of a contact process, and is very similar to a SIS model in epidemiology. Some less trivial results can be transferred from theory to theory, like the existence of a lower threshold for the infectivity rate for the whole network to be susceptible at equilibrium to invasion or infection. A general goal and recent research trend of these models is to identify which are the geometrical properties of the graph (random, regular, self-similar, etc. ...) which facilitate or impede the transmission of the states.

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A COMPARATIVE ANALYSIS OF TWO-PARAMETRIC MODELS TO DESCRIBE PLANT DISEASE EPIDEMICS

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Background and objectives
In plant disease epidemiology, simple mathematical models, like the logistic and the Gompertz function, are often used to describe disease progress curves. These models, usually given as a differential equation with one rate parameter, are non-flexible models with a fixed disease level at the point of inflection. More flexibility in analysing disease progress curves can be achieved when differential equations with a second parameter, a shape parameter, are applied like the Richards function. The objective of this study was to compare two-parametric models proposed in epidemiology and in other disciplines.

Materials and methods
In the analysis, eleven two-parametric models were compared based on seven criteria: existence of an analytical solution, relation to one-parametric models, point of inflection, behaviour at the beginning of an epidemic, asymptotic behaviour, weighted mean absolute (WMAR) and relative (WMRR) rate. In addition, all models were fitted to two experimental datasets using ModelMaker4, which allows fitting the differential equations to the data even if no analytical solution exists.

Results and discussion
From the comparative analysis it can be concluded that the most flexible and biologically relevant models were those of Richards (2), Waggoner & Rich (3) and of Fleming (1), the latter being formally identical to two other models proposed. All models could be successfully fitted to the experimental data sets resulting in similar coefficients of determinations. For most models, formulae could be gained to express some characteristics of the progress curve (like the disease level at the point of inflection, the time needed to reach this point, WMAR and WMRR) as functions of the rate and the shape parameter. Based on these formulae it is possible to calculate the values of the rate and shape parameter of a certain model if the values are known for another model.

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INOCULUM MONITORING: AN AID TO DISEASE RISK ASSESSMENT?

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Background

Assessing disease risk plays an important role in modern crop disease management. Disease epidemics occur when the crop is susceptible, the environmental conditions are conducive to infection and inoculum is present. Monitoring the presence of inoculum can therefore provide additional information of potential value for decision-making. However, because monitoring inoculum is difficult it has rarely been use in disease management systems. The development of new methods of disease diagnosis and inoculum detection should make inoculum monitoring a practical proposition. However, under what circumstances would inoculum monitoring be likely to be successful?

Approach

There have been relatively few studies of the relationship between disease and inoculum in the field. Therefore simple mechanistic disease epidemic models were used to try and identify when inoculum monitoring could be worthwhile. Both monocyclic and polycyclic epidemics were modelled. The models accounted for the effects of both latency and multiple infections.

Results

Monocyclic disease. Cumulative inoculum concentration during the infection period may mimic the disease development curve delayed by about a latent period, giving an "early warning" of disease. The maximum disease reached could be predicted from the cumulative or average inoculum concentration for the infection period.

Polycyclic disease. If there is little "imported" inoculum and environmental or crop factors are not limiting, daily inoculum concentrations may give a good indication of disease status. But, if inoculum is intermittent, daily concentrations may be misleading. However, cumulative inoculum concentrations may mimic disease progress even when inoculum is intermittent. Further, for crops with a succession of susceptible tissue (e.g. new leaves), the area under the disease progress curve (AUDPC) follows the cumulative inoculum curve delayed by about a latent period. Thus inoculum monitoring may be an effective substitute for disease monitoring.

Discussion and conclusions

Can inoculum monitoring be an aid to disease risk assessment? For monocyclic diseases epidemic modelling and examples taken from the literature suggest that inoculum monitoring, in combination with the measurement of environmental factors, could give early warning of potential epidemic development. This situation is perhaps more complex for polycyclic diseases. Where clear disease thresholds have been identified, it may be possible to use inoculum monitoring to trigger disease control measures. As the AUDPC, appears to follow cumulative inoculum concentrations, inoculum monitoring may be a useful alternative to direct disease assessment. Further work is needed to define the relationship between disease and inoculum in the field and to devise sampling strategies to make the best use of the new methods of inoculum measurement that are becoming available.

QUANTITATIVE RELATIONSHIPS BETWEEN DIFFERENT DISEASE INTENSITY MEASUREMENTS IN PLANTS

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Background and objectives
Disease intensity in crops is usually assessed using one of three forms of measurement: (1) **incidence** (I), for which individual plants or plant parts are classified as diseased or healthy, and totals or proportions determined; (2) **severity** (S), for which the percentage or proportion of tissue diseased is recorded, or (3) **density** (m), for which the number of lesions per plant or plant part is counted. Relationships between incidence and severity (I-S), incidence and density (I-m), and between incidence made at adjacent pairs of scales in a spatial hierarchy (I-I) are of practical and theoretical interest. Practical applications of such relationships can be found in the development of sampling plans and variety evaluation. Theoretical interest arises because relationships between the incidence of diseased plants and measurements made at a finer scale reflect the dispersal processes of the pathogen responsible for disease and link models of spatial and temporal processes in epidemics. In the case of I-m and I-I relationships, there is a distributional basis on which to develop empirical models. The Poisson and negative binomial distributions provide the starting point in the case of I-m relationships, while the binomial and beta-binomial are appropriate for I-I relationships. In both cases, empirical variance-mean relationships can also be used to model data in which heterogeneity varies as a function of the mean. The complimentary log-log transform [$CLL(\bullet) = \ln(-\ln(1-\bullet))$] has been found to be useful in the development of empirical I-S, I-m and I-I relationships (McRoberts et al., 2003; Hughes et al., 2004) but a suitable distributional model for severity is lacking, limiting the development of I-S relationships and their full exploitation in practice and in the development of epidemiological theoretical studies. The aims of this research are to identify suitable distributional models for severity data and to develop appropriate protocols for their analysis.

Results and discussion
Initial inspections of data sets for a number of foliar pathosystems have shown that severity data are often skewed at low to moderate mean severity. Changes in the distribution of severity during disease progress are reflected in the variance-mean relationship and in parameter values of distributions fitted to sets of data. The suitability of the beta (type 1) distribution and Johnson's S_B distribution as candidates for the development of a distributional model of I-S relationships is discussed form theoretical and practical perspectives.

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COMPARATIVE EPIDEMIOLOGY OF FLOWER INFECTION BY FUNGI

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Abstract

Studies of diseases affecting flowers can be considered part of the wider field of plant reproductive biology. Diverse fungal pathogens are able to infect flowers at various stages of development causing some of the most economically important plant diseases. Although numerous studies have been undertaken on isolated aspects of individual fungal-flower pathosystems, few attempts have been made to synthesize the accumulated information to determine whether there exists a unifying theory on diseases affecting plant reproduction. The objective of this study is to collate, analyze, and compare published reports dealing with various aspects of flower infection by fungi to determine whether useful generalizations can be made. Fungal-flower infections may be distinguished based on 1) the mode of spore dispersal and disease transmission within host populations (ranging from direct flower-to-flower infection via various vectors to infections transmitted through the soil); 2) the point of entry of the pathogen into the flower, ranging from fungi capable of indiscriminate infection of any floral tissues to those specialized to enter the ovary via the stigma-style pathway); 3) the degree of specialization in host-pathogen interaction, from necrotic to biotrophic or localized to systemic infections; 4) the diversity of symptoms and signs (e.g., blossom blight, hypertrophy, or sclerotium formation); and 5) the ecological and evolutionary impacts on both host and pathogen (e.g., changes in host/pathogen abundance and distribution, host mimicry by the pathogen [2], or stylar shut-down by the host to block infection). Posterior analysis procedures (1) will be used to test the validity of such a priori classifications and determine the host and pathogen characteristics that account for the support of the resulting groups. Potential explanatory variables for classification of floral pathosystems include pathogen reproduction (e.g., sexual vs. asexual, number of cycles per year and their synchrony with host phenology), pathogen life history (e.g., K- vs. r-selected), length of the latent period, and number of hosts and vectors. Host-related variables of interest include annual vs. perennial growth habit, mating system (e.g., self- vs. cross-pollinated), and flower anatomy (e.g., wet vs. dry stigma, single vs. compound style, number and length of styles). The results will be discussed in the context of host-pathogen coevolution and in relation to concepts from sexually transmitted diseases in animals and humans.

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DYNAMICS OF CONTACT STRUCTURE AND DISEASE TRANSMISSION IN MIXED SPECIES POPULATIONS: AN ANALYSIS OF DAMPING-OFF EPIDEMICS

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Background and objectives

The suppressive effects of mixed species populations on invasion have been demonstrated in numerous mathematical and empirical studies. Whereas mathematical studies are ordinarily based on generic epidemiological concepts, the analysis of empirical studies is mostly aimed at various measures of efficacy of a mixture. Often such empirical measures do not explain the underlying mechanisms driving an epidemic. In this paper we combine both approaches. We derive simple regression relationships from generic epidemiological models, and apply those to epidemics in mixed plant populations. The analysis is an extension of a method previously tested for homogeneous plant populations. Here we demonstrate its application to experimental data from replicated damping-off epidemics in mixed plant populations. In particular we ask:
1. How do the contacts between neighbouring susceptible and infected plants within and between species change over time as one species is infected preferentially?
2. How do the *inter-* and *intra*-specific transmission rates change over time?
3. How do differences in infectivity and susceptibility affect the transmission rates?

Materials and methods

We produce spatio-temporal maps of damping-off epidemics caused by *Rhizoctonia solani* in replicated microcosms of >400 randomly mixed radish and mustard seedlings to obtain daily counts of the number of infected plants for each species, and the change in the number of neighbouring pairs of plants with one infected and one susceptible for each of the four host combinations. We use these daily counts to obtain simple estimates of the *inter-* and *intra*-specific transmission rates, defined within a compartmental *S-I* model with transmission between neighbouring plants only (1,2). This provides estimates of the intrinsic dynamics in the transmission rates and we relate these to dynamical changes in relative infectivity and susceptibility of each host species.

Results and discussion

We show that as an epidemic progresses through mixed populations, it changes the contact structure so that the resistant plant is challenged progressively more frequently, thereby slowing the epidemic. We show that it is possible to estimate the transmission rates for each of the four *S-I* pair combinations. All transmission rates rose initially with time and then declined, with overall lower rates for the more resistant species. However, the *inter*-species transmission rates were unexpectedly high. We explain this by the relative infectivity and susceptibility of each host species, with mustard and radish differing mainly in susceptibility, whereas the infectivity was surprisingly similar for the resistant and susceptible species.

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DISEASE-WEATHER RELATIONS:
ELASTICITY ANALYSIS OF EPIDEMIC PROGRESS PARAMETERS

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Background and objectives
The dynamics of epidemics are steered, to a large extent, by weather variables. Modelling has been used for various diseases and under various disguises in the past to study the effect of weather variables on epidemic progress (Papastamati et al. 2002). Here we present a method for elasticity analysis that helps to unravel the effect of weather variables on epidemic progress.

Materials and methods
Starting from the Kermack-McKendrick model an expression is derived for disease progress as dependent on characteristics of the disease life-history (latent period, infectious period, spore infectivity) (Segarra, Jeger, and van den Bosch 2001). Using knowledge on the dependence of each disease on weather factors, the expressions outlined above can be parameterised as functions of weather variables. A method will be developed for the sensitivity and elasticity of the disease growth rate on weather variables. Deriving these measures from a generic mechanistic model leads to a generally applicable tool for elasticity analysis of plant disease progress.

Results and discussion
We show that the elasticity of the potential epidemic growth rate to weather variables can be expressed as a sum of the effects of the weather variables on the various life-history characteristics. This finding makes it possible to determine which life-history parameters are most important for the development of epidemics under different environmental conditions. We apply the method to the effect of temperature on the development of the rust fungus *Puccinia lagenophorae* on *Senecio vulgaris* (Kolnaar and van den Bosch 2001).

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HETEROGENEITY, SCALE AND FUNGICIDE RESISTANCE

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Background and objectives
We introduce two models to investigate the influence of spray heterogeneity on the dynamics of fungicide resistant pathogen populations. The first model concerns processes at the scale of an individual field and focuses on the influence of heterogeneity in spray application on the invasion and persistence of resistant strains. As the invasion of resistant strains within a single field does not guarantee successful invasion over many fields, the second model concerns the regional scale invasion and persistence of resistant strains.

Model and methods of analysis
The field scale model is comprised of three components: the host dynamics, the pathogen dynamics and the spore dynamics. We consider resistant and sensitive pathogen strains which compete for a limited supply of susceptible host tissue, some of which is treated by the fungicide and some is untreated. This leads to a system of six linked differential equations.

The second model considers a large regional setting comprised of a number of sprayed and unsprayed fields and comprises a system of four linked differential equations.

In both models a combination of linear stability analysis and model simulations are used to determine criteria for the invasion and persistence of resistant and sensitive strains.

Results and discussion
The models show that there are three possible competitive outcomes following the introduction of a fungicide to a host-pathosystem: non-invasion of resistant strains, invasion and exclusion of sensitive strains, or coexistence. Each of these three outcomes have been found in empirical studies (1, 2) but have not been predicted by previous models.

In the field scale model, although coexistence is facilitated by spray heterogeneity, the actual competitive outcome (invasion, exclusion or coexistence) depends critically on the effectiveness of the fungicide and the fitness cost to resistance. In the regional scale model we find clear differences in the factors that influence each competitive outcome to those at the field scale, highlighting the importance of acknowledging scale and long range spore migration events in studies of fungicide resistance.

The practical implications of the results for resistance management and risk analyses are discussed.

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PAIR AND BETHE APPROXIMATIONS FOR THE CONTACT PROCESS ON A GRAPH

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Background and objectives

Our objective is to progress in the accuracy of modelling methods for the spread of diseases in plant/pathogens interactions, where the spatial structure of hosts can be relevant. A classically used model is the time continuous Contact Process, where the rules for each host evolution are stochastic and the model takes into account the spatial correlations between hosts states. It cannot be solved analytically and among the approximations available the mean field solution is the more naive: it assumes that the hosts are well mixed. The Contact Process under the mean field approximation has been largely studied due to its simplicity. However, in plant/pathogens systems, the well mixed assumption is not valid and the mean field approximation can become really poor. Our objective here is to develop a better approximation while taking into account the actual network of contacts between hosts. Therefore, we describe the contact network with graphs, and aim at understanding the graph characteristics which can influence the system at equilibrium (Keeling, 1999 ; Newman, 2003).

Materials and methods

Approximations finer than the mean field are available. We investigate here the pair approximation which arose long ago from the study of systems of particles in physics (Filipe, 2001). The pair approximation is more realistic since it preserves spatial structure of first neighbors. In the context of the Contact Process, it has been developed for a regular grid (a lattice) and has been shown to improve the mean field approximation. We propose to extend pair approximation to the case of a graph (non constant number of neighbors, explicit spatial contact structure).

Results and discussion

We derive the analytic expression on the equilibrium corresponding to the pair approximation. Then, we identify, through simulations, the types of graphs where the (simpler) mean field approximation is good enough and the ones where this simple method reaches its limits and can be improved by pair approximation.

We discuss also the difference between the pair approximation one one hand, as classically implemented in ecological and epidemiological literature for lattices, and the Bethe approximation, the Kikuchi approximation and the cluster variation method on the other hand, implemented in statistical physics and image restoration.

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MODELING MAXIMUM DISEASE ON A GROWING HOST:
AN EXAMPLE OF POWDERY MILDEW OF BARLEY

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Background and objectives
In plant disease epidemiology the maximum disease level reachable is commonly set to 100%. In this case the analysis of disease progress can be performed easily e.g. by the logistic model, estimating the growth rate r and the amount of initial disease y_0. This simplification is not reasonable if the maximum disease is considerable lower than 100%, which may be the case for many leaf spot and rust diseases, or if disease is measured as "severity" and not as "incidence". Another problem may arise towards the end of an epidemic, when the amount of disease decreases very often, most likely because of tissue loss by the host. Generally varying host tissue over the course of the epidemic will affect disease progress. In order to describe this interrelationship we studied powdery mildew disease severity data of barley (*Blumeria graminis* f.sp *hordei*) considering host and disease development simultaneously.

Materials and methods
Field experiments were conducted with barley plots of approximately 160m^2 located in an oat or wheat field, plots were either treated by fungicide or remained untreated. Samples of 20 barley plants were collected from each plot every week to assess disease severity. For each leaf from a plant's main tiller the whole leaf area was measured. Disease severity was determined as percentage of whole leaf area that was infected. Additionally the percentage of the green leaf area was estimated. From this the corresponding absolute values of green and infected leaf area was obtained.

The experimental data were fitted by a system of linked differential equations, where the disease was described by a logistic function whos asymptote was itself at each time point a function of the available host tissue, i. e. by the green leaf area. The latter being modeled by the difference of two logistic growth functions, one representing the increase, the other the loss of host tissue.

Results and discussion
The green leaf area was well described by the model, whereas the fit of the disease development was poor. Especially the pronounced decline towards the end of the epidemic was not reflected by the model. One possible explanation for the failure of the model might be due to quite low values of disease severity. This means that the host tissue is not a limiting factor and prevents the decline of the infected area in the model. To reach a better fit an additional parameter for a virtual lesion extension was included. The extended model resulted in a good fit of disease development. However the biological meaning of the additional parameter remains unclear, most likely it represents a set of several physiological and environmental effects.

MODELLING HOST-PATHOGEN-HYPERPARASITE INTERACTIONS: CAN A HYPOVIRUS STOP THE SPREAD OF CHESTNUT BLIGHT DISEASE?

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Background and objectives

The dynamics of chestnut blight disease caused by *Cryphonectria parasitica* is an important ecological example of host-pathogen-hyperparasite interactions. The *Cryphonectria HypoVirus* 1 (CHV1) is responsible for attenuation of the pathogen virulence of *C. parasitica*: the trees containing a CHV1 infected fungal strain (hypovirulent strain) can wall off the infection and thus survive. For example, in Europe high levels of CHV1 have resulted in a lower mortality of trees than in North America where in the absence of pronounced hypovirulence the blight epidemic has caused widespread mortality of chestnuts. In China, the country of origin of *C. parasitica*, coexistence among chestnut trees, fungus and hypovirus is observed.

We apply mathematical modeling to explore different scenarios of spread of the chestnut blight in the presence of a hypovirus in different environmental conditions.

Methods

First we analyze a 'minimal' model (derived from the classical SIR model in epidemiology) of four compartments: susceptible trees, trees infected by a virus free fungus, trees infected by a hypovirulent and dead trees. Further we study more realistic cases taking into account the coexistence of different fungal vegetative compatibility types and the possibility of multiple infections of trees. We describe the host-pathogen-hyperparasite interactions in terms of nonlinear ordinary differential equations by applying both analytical methods (theory of bifurcations) and numerical simulations. The existence of different regimes was found and the diagrams in parameter space corresponding to different regimes were built.

Results

We show that for a wide range of model parameters the introduction of hypovirus can stop the spread of disease and thus maintain the population of susceptible trees at a relatively high level. However, for a small number of initially infected trees the introduction of the hypovirus does not lead to its establishment in the forest ecosystem even for a large rate of virus transmission. For all models we studied the influence of the initial population sizes on the system dynamics by analyzing the critical values of the population sizes leading to the attenuation of the disease spread.

MODELLING EPIDEMIOLOGICAL SITUATION OF CEREAL CROPS RUST IN RUSSIA

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Abstract

In Russia the most widespread and destructive diseases of cereal crops in the basic agricultural regions are the following rust diseases: leaf rusts of wheat (*Puccinia triticina*) and rye (*Puccinia dispersa*), a stem rust of wheat (Puccinia graminis tritici) and rye (*Puccinia graminis secalis*), a stripe rust of wheat (*Puccinia striiformis*). Annually cereal crop losses from rust is 10.0-15.0 %; in epidemic years crop losses can reach 30.0-50.0 %.

Laws of originating and development epidemics cereal crop rust in time and space are investigated.

Epidemics cycles rust infection include 6 basic, consistently proceeding time stages: 1) accumulation of the contagious beginning in the locuses of a lesion; 2) issue of spores in air from the struck sowings; 3) transmission of pustules by air streams; 4) subsidence of the contagious beginning on sowing; 5) realization of a "primary" infection contamination of plants; 6) development of diseases on infested sowings.

Spatial diffusion of epidemic reminds locomotion of a wave on the character. With each new wave all is absorbed new and new territory. The direction of a wave and its extent depend on a direction of transmission of air masses and developing aerologic and agroecology conditions. It is experimentally shown, that the number of such waves can make for a growing season from 4 to 8, extent of each wave from 80,0 to 450,0 km, speed of their diffusion from 20,0 to 35,0 km / day, general extent of the territory covered epidemic - 800-2400 km.

Systems of mathematical models and applied computer programs for calculation of spatial diffusion epidemic on Russia territory are developed.

HOMOEOSTASIS IN A PERENNIAL SEA-SIDE PATHOSYSTEM: SEA LAVENDER, RUST AND MILDEW

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The pathosystem

Sea lavender (SL - *Limonium vulgare*) grows along European coasts. In the Netherlands it occurs on the salt marshes of the barrier islands separating North Sea from Wadden Sea. In August the isle of Terschelling charms tourists with hectares of purple bloom. Perennial SL is a pioneer on low mud flats, which become high flats by silt accretion. Populations are genetically diverse, but each individual (genet) consists of up to 1000 genetically identical rosettes (ramets). Individuals, up to 30 years old, measure up to 4 m Ø.

SL-rust (*Uromyces limonii*) is macrocyclic, autoecious and heterothallic. It overwinters as telia. Stormy winter floods disperse detached telia. Spring rains induce formation of basidiospores. Pycnia appear in spring followed by aecia. Some five generations of uredinia occur but the majority of uredinial infections leads to telia. Uredinial overwintering was never found. SL-mildew (*Erysiphe limonii*), more serious than rust, appears late in spring in small within-genet foci. Spreading rapidly in summer it forms abundant cleistothecia in autumn. Circumstantial evidence points to overwintering of mildew as mycelium in small winter leaves. Mildew overwinters less frequently than rust.

At spring tide the whole pathosystem may be flooded so that it disappears from sight, flowers and all. SL and its pathogens are salt resistant. SL excretes salt by foliar glands. Its seed is dispersed by the sea. For germination seeds need fresh water. Urediniospores are dispersed primarily by sea water, also by rain splash and wind. They germinate in fresh water having survived suspension in salt water. Mildew conidia are dispersed by wind. They can stand brackish water for a few hours. The pathosystem shows zonation from the lower sea side to the higher land side. After some 20 to 40 years soil level is 10 to 25 cm higher and SL is outcompeted, mainly by *Festuca rubra*. Rust and mildew are most frequent in a belt where SL vegetation is at its densest, with rust tending to the lower and wetter side and mildew to the higher and drier side. In the *Festuca*-dominated vegetation mildew disappears faster than rust. Large differences among SL genets in resistance to rust and mildew are seen in reaction types, final severities and rates of rusting or mildewing. Differences were reproduced in the greenhouse, but field-grown plants are more resistant than greenhouse-grown plants. A differential interaction between SL genotypes and rust genotypes was demonstrated.

Conclusion

Homoeostasis is promoted by the genetic diversity of SL and of its rust, possibly also by their differential interaction, by horizontal resistance, by slow rusting and mildewing, and by zonation of the pathosystem. Rust and mildew kill an unknown fraction of their hosts whereas fresh recruitment of SL occurs at the lower side of the salt marsh. Years before killing rust and mildew may prevent reproduction of SL and hence recruitment of susceptible offspring. Apparently, the long-term homoeostasis mechanism is highly complex.

AN INVESTIGATION ON THE MANAGEMENT OF RACE SPECIFIC AERIAL FUNGAL PATHOGENS USING CULTIVAR MIXTURES BOTH WITHIN AND BETWEEN SEASONS

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Abstract

In all previous research studies, researchers focused on the mixture efficacy in reducing disease in relation to various factors for one season only. For experiments spanning several seasons, there was no systematic effort in altering the mixture spatial structure to achieve eve greater disease control. The purpose of the present research was to determine the potential in increasing the efficacy of mixtures in reducing race specific pathogens by altering mixture spatial structures between seasons, using an individual-based spatially-explicit stochastic simulation model. Simulation results indicated that disease development could be significantly reduced by altering mixture spatial configurations between seasons.

SESSION E

'CONCEPTS AND THOUGHTS FOR PLANT DISEASE EPIDEMIOLOGY IN THE 21TH CENTURY'

PRIORITIES FOR PLANT DISEASE EPIDEMIOLOGY
AND DEVELOPING WORLD FOOD SECURITY

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Abstract
This paper begins with a broad review of food security in the developing world; I argue that technological change has made a key contribution to improving food security wherever it has been achieved. Potential development assistance by epidemiologists from outside the developing world will have to be funded through development assistance; a perspective on development assistance and the role of assistance to agriculture in particular provides a useful background to the role of plant epidemiology. Development assistance directed toward agricultural research is demonstrably effective and research is where plant epidemiologists can likely contribute the most to developing country food security. Optimizing the contributions of epidemiology entails five steps: (1) identifying developing country food security challenges, (2) defining where and how development assistance, specifically in Plant Epidemiology, can address the problems or meet the needs, (3) selecting a problem or problems that can be addressed using the resources available, (4) implementing work on those problems, and (5) sticking with the work long enough to make a difference. Part II of the paper outlines a theoretical approach to setting plant epidemiology research priorities for the developing world and uses a simple model to illustrate how the model might be applied.

SMALL WORLDS AND GIANT EPIDEMICS

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Abstract
Key problems for models of disease spread relate to threshold, velocity of spread, final size and control. All of these depend crucially on the network structure of individual interactions.
Networks of interest range from the local extreme case, where typically the population is evenly distributed as on a lattice, with interactions only between nearest neighbours; and the homogeneously mixing (or `mean-field') extreme, where all interact equally with all. Intermediate cases of practical interest include `small-world' and meta-population models.
I shall discuss the various structures of such models, their similarities and differences, and some approximations to them. The main aim is to identify what features of contact structure need to be captured when formulating a model for any specific problem of disease spread.

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PLANT PATHOLOGY WITHOUT SYSTEMS INNOVATION WILL BECOME OBSOLETE IN THE 21TH CENTURY

P. Rabbinge and P. Teng

Abstract
The development of plant pathology as a science dominated by reductionistic approaches was quite successful in the 20th century and contributed considerably to an improved crop protection. However, new insights and better understanding of plant-pathogen interactions, multitrophic relations and spatio-temporal phenomena have much to offer for a further improvement. That requires systems approaches and systems innovation where various spatio-temporal scales are included and the possibilities of interventions at various integration levels are maximally used. That will lead to a dramatic change in pesticide use in crop production systems and farming systems and contribute considerably to sustainable development. Plant pathology that does not use these new possibilities and allies is not contributing at full to societal goals and will ultimately become obsolete.

SESSION F

'CROP LOSS ASSESSMENT AND MODELLING'

DISEASE ASSESSMENT CONCEPTS
AND THE ROLE OF PSYCHOPHYSICS IN PHYTOPATHOLOGY

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"How can plant pathologists apply advanced statistical procedures or develop quantitative predictve models based upon disease assessment data of unknown accuracy and precision"
(David R. Mackenzie)

Abstract
New concepts in phytopathometry continue to emerge. These include the concepts of pathogen vs. disease intensity and the concept of pathogen severity, defined as a quantitative measurement of the amount of a pathogen per sampling unit, whereas the concept of disease severity is the amount of disease on a sampling unit. The accuracy and precision of visual disease severity assessments can be improved by quantitatively measuring and comparing the accuracy and precision of raters and/or assessment methods using linear regression. The accuracy and precision of visual disease severity assessments can also be improved by using computer-based disease assessment training programs, and by developing and using diagrammatic keys (standard area diagrams). Finally, the accuracy and precision of disease severity assessment data could be improved if there was a better understanding of how the laws of psychophysics actually relate to the theory and practice of phytopathometry. In this regard, we utilized a classical method developed in the field of psychophysics (the method of camparison stimuli) to test Horsfall and Barratt's claim that raters cannot accurately discriminate disease severity levels between 25 and 50 % because, according to the Weber-Fechner Law, visual acuity is proportional to the logarithm of the intensity of the stimulus. We show for two pathosystems, grapevine downy mildew and the wheat leaf rust, that raters can accurately discriminate disease severity levels between 25 and 50 %, and that although Weber's Law appears to hold true, Fechner's Law does not. Furthermore, based upon our results, the relationship between actual disease severity (X) and estimated disease severity (Y) is linear, not logarithmic as proposed by Horsfall and Barratt.

Key words
Accuracy, Fechner's Law, Precision, Stevens' Power Law, Weber's Law

QUANTIFICATION OF POSTHARVEST DECAY OF PEACHES
IN DIFFERENT PHASES OF FRUIT PROCESSING

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Background

Postharvest decay is the major factor limiting the extension of shelf life of peaches in Brazil. The most frequent pathogens detected on peaches at the São Paulo wholesale market in 2002 and 2003 were: *Monilinia fructicola, Rhizopus stolonifer, Geotrichum* sp., and *Cladosporium* sp. (Martins et al., 2003). In this market, the incidence of decay in peaches ranged from 4.3 % to 15.2 % of diseased fruits based on the assessment date. The incidence of decay was related to mechanical injuries in the fruits. Infection by these pathogens probably occurred between harvest and transport to the market. As most of brown rot symptoms appeared far from shoulders on the peaches, latent infection was not considered significant. Our objective was to identify the phase of postharvest processing where the infections occur and to quantify more precisely the loss to disease. From this information, we propose to develop effective control measures.

Methods

The incidence of decay in peaches was estimated six times, from September to November 2003, in four postharvest stages: after harvest; in the entrance of packinghouse; after classifying machine; before loading peaches in the truck. An 'ideal harvest' was performed by a technician to establish the minimal damage possible in the fruit. One hundred fruits per stage and per date were assessed for disease incidence and mechanical injuries. Fruits were incubated in a humid chamber for 24 hours and assessed immediately after the removal of the chamber and again 7 days later. The instrumented sphere (Techmark, Inc., Lansing, MI, USA, 70mm) was used to measure impact intensities at the different postharvest phases. Impacts were measured as maximum acceleration (MA) in G (Gravity=9.81 m/s^2) and velocity change (VC) in m/s.

Results and discussion

The average incidence of diseases in stages 'ideal harvest', 'after harvest', 'packinghouse entrance', 'after classifying machine' and 'before loading in the truck' were 16.5%, 33.6%, 36.7%, 44.7% and 43.5% and the average incidence of mechanical injuries in the same stages were 7.8%, 22.5%, 27.5%, 38.7%, and 33.7%. Disease incidence was positively correlated to mechanical injuries (R^2=0.97). The critical stages of postharvest processing of peaches were the harvest and the fruit selection in the packing house. The increase of disease incidence was 17.1% at harvest and 8% more at fruit selection. The impact to which fruit were submitted in these stages was high (up to 90 G). Harvest training and improvements in the processing line should reduce the incidence of decay of peaches.

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CROP GROWTH AND YIELD LOSSES DUE TO LATE WHEAT LEAF DISEASES: TOWARDS A SIMPLIFICATION

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Background

Four main difficulties are often encountered when predicting crop losses due to leaf diseases: 1) leaves are often bulked even though diseases are not homogeneously distributed, 2) interactions between diseases are usually neglected, 3) effects on Radiation Interception Efficiency (RIE) and Radiation Use Efficiency (RUE) are not fully separated and 4) losses are often simulated relative to control plots (Johnson, 1987; Bastiaans, 1991; Robert, 2003). Based on previous results of Robert (2003), we hypothesized that, in the case of late wheat leaf blotch and rust, the two diseases do not interact on damages and do not have any effect on RUE of green leaf parts. We further evaluated if growth and yield losses mainly depend on RIE accounting for the vertical location of diseases through green leaf area measurements.

Materials and methods

Growth variability of wheat crops affected by late leaf rust and blotch epidemics (occuring after earring) were studied over seven experimental years (from 1995 to 2001) in Grignon (France). We investigated a wide range of green leaf area evolutions during the post-anthesis period in relation to both climatic years, nitrogen and density treatments as well as natural aerial epidemics of leaf rust and blotch on winter wheat (mainly c.v. Soissons). Disease records, total and green leaf area per leaf layer, crop growth and yield were measured throughout the grain filling period.

Results

A large range of absorbed PAR was created by the previous experimental treatments, varying from 33 MJ m^{-2} to 350MJ m^{-2} during the grain filling period. When using bulk plant green leaf area to calculate absorbed PAR, only 67% of growth variability was explained by absorbed PAR, further resulting in significant differences in RUE between healthy and diseased crops. When the different contributions of leaf layers to photosynthesis according to their vertical location were evaluated, the variations of PAR absorption by green leaf parts accounted for 84% of total growth variability observed in both diseased and control plots, without any effect on radiation use efficiency (2.3 g/MJ for both diseased and healthy crops). Yield was then related to post-anthesis growth in a single linear relationship ($r^2 = 0.91$; df=23) showing out a slope of 0.9 not significantly different from one (p=0.11; df=24).

Discussion

Taking into consideration previous work (Johnson, 1987; Bastiaans, 1991), this study clearly points out the importance of taking into account for the repartition of diseases and senescence between leaf layers to accurately relate absorbed PAR to growth. It results in no significant differences of RUE between diseased and healthy crops. This is in agreement with previous results at the leaf scale that showed leaf photosynthesis was not altered when sporulating, yellow halo and necrotic areas were considered as not functional (Robert, 2003). We further discuss morpho-physiological traits tolerant genotypes may developp to reduce crop losses.

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DECISION SUPPORT SYSTEMS FOR MANAGEMENT OF FOLIAR BLIGHT ON LENTIL AND FIELD PEA IN WESTERN CANADA

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Background and objectives
In western Canada, yield and quality losses caused by *Colletotrichum truncatum* and *Ascochyta lentis* in lentil (*Lens culinaris*) can be as high as 75%; in field pea (*Pisum sativum*), losses of up to 50% are caused by *Mycosphaerella pinodes*. Several foliar fungicides are efficacious against these pathogens, but application is expensive and is not required every season. Growers need information on the conditions under which fungicide application will be cost-effective. The objectives of this study were to develop fungicide decision support systems (DSS) for consistent, economic management of foliar blights of lentil and field pea, and make the systems available to producers.

Materials and methods
Most of the tests were conducted in commercial fields, arranged in a four-replicate RCBD. Each plot was 2.4 x 6 m. Treatments were chlorothalonil (Bravo 500, Syngenta, at 1.0 kg a.i. ha^{-1}) or azoxystrobin (Quadris, Syngenta, at 125 g a.i.) applied at early, mid, or early + mid flowering and a non-sprayed control. Fungicides were applied using a CO_2 sprayer with TeeJet 8003 nozzles at 275 kPa in 200 L ha^{-1}. Disease ratings (Horsfall-Barratt scale, 0-11) were made prior to each application, and again about 3 wk after the final application. Seed yields were taken. Results from previous trials and empirical observations were used to design the DSS for lentil and pea. They were based on inspection of the crop starting at the 10-12 node stage and an estimate of the risk of loss associated with: i) disease severity; ii) number of days with rain in the 14 days prior to inspection; iii) likelihood of rain in the next 5-day period, based on weather forecasts; and iv) plant stand density. Risk points were assigned to levels of each factor. A total risk value between 0 and 75 (85 for pea) was calculated as the sum of individual risk values, and at a threshold of 50, a fungicide application was indicated.

Results and discussion
Data from 22 site-years was used to evaluate the DSS for lentil. It provided correct recommendations in 35 of 40 assessment intervals, with the majority of the recommendations being not to spray. The DSS was recommended to growers through factsheets and a website that also included descriptions of disease symptoms and disease management options. A DSS for mycosphaerella blight of field pea was also assessed. Over 23 site-years, fungicide application was rarely economical due to the late onset of disease, variable yield potential, and low crop prices. Also, several cultivars exhibited what we interpreted to be disease tolerance - application of fungicide reduced blight severity but did not improve yield. We concluded that the DSS for field pea was not effective. However, the study showed that disease tolerance may represent a useful approach for pea breeding programs.

THEORETICAL ANALYSIS OF WHEAT CROP LOSS DUE TO SEPTORIA TRITICI: THE CONTRIBUTION OF DIFFERENT DAMAGE TYPES TO THE TOTAL BIOMASS LOSS

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Background and objectives
Understanding how disease reduces crop yield is necessary to facilitate crop design, variety selection and fungicide application schemes. The first step in mechanistically modelling foliar-disease induced biomass loss is quantification of damage at the leaf level. Previous experimental work allowed us to quantify leaf net photosynthesis loss, dark respiration increase and induced apical necrosis caused by *Septoria Tritici* blotch (STB). Here, in order to analyse the relative importance of these different types of leaf damage, we develop a family of models that model biomass loss but contain different damage mechanisms. By comparing model predictions, several questions are addressed: Which of these three damage mechanisms are significant effects in the total biomass loss induced by the disease? Could we assess only STB lesion area or total necrotic area (including induced apical necrosis), or is it necessary to distinguish between them for accurate biomass estimation? This exploration will allow us to have a better understanding of damage mechanisms and to develop more robust models of crop damage.

Materials and methods
We constructed 7 models that simulate biomass loss due to STB which either include or ignore induced apical necrosis, photosynthesis loss in the symptomless parts and dark respiration increase. They also either take total necrotic area or lesion area and apical necrosis separately as input. Experimentally derived parameters were taken from previous work (Robert et al. 2005). A quadratic fit links STB severity with induced apical necrosis, and another with increased dark respiration. Finally Bastiaans' model (1991) was used to describe the link between disease severity and photosynthesis loss. Epidemic progress data, assessed on the flag leaf of wheat *cv. Soissons* (Robert et al. 2004) were used as model input. We estimated biomass accumulated during disease progress.

Results and discussion
We show that STB-induced apical necrosis has a large effect, accounting for >20% of total estimated biomass loss. This provides motivation for further investigation of the mechanisms behind this phenomenon. We also show that STB-induced dark respiration accounts for <2% of total estimated biomass loss. This suggests that it is not important when considering variety selection or predictive simulation modelling. It was found that for STB, assessment of total necrotic area produced a good approximation of the more detailed reference model (difference in modelled biomass loss ≈ 6%).

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COMPREHENSIVE REPORT ON CAUSAL FACTORS INVOLVED IN RUBBER TREE (*HEVEA BRASILIENSIS*) BARK NECROSIS SYNDROME: A NON-PATHOGENIC DISEASE DUE TO ACCUMULATION OF STRESSES?

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Background and objectives

Bark Necrosis (BN), described and first studied in Côte d'Ivoire in the 1980s (1), now affects most modern rubber plantations worldwide, with a wide range of severity across sites. Initial BN symptoms (necrosis of the inner phloem) start at the collar zone, then spread upward to the tapping cut. BN induces irreversible cessation of latex production, then intense cracking of the bark. BN spreading to neighbouring trees suggested the existence of a causal pathogen, possibly transmitted by the tapping knife. Meanwhile, various previous and recent etiological investigations on various potential pathogens failed or led to non-conclusive results (2).

Results and discussion

* Conversely, environmental factors were shown to be associated with BN outbreak. Epidemiological surveys conducted in African and Asian young plantations revealed a non-random location of the earliest diseased trees. These risk areas are mainly characterized by the proximity of a swamp, road, windrow, bulldozer track, forest stump or slope break, etc. In BN outbreak areas, no significant correlation was found with chemical soil parameters. Meanwhile, physical soil analyses (e.g. penetrometry in metric squaring grids) revealed higher soil compaction around BN trees. Roots mapping indicated also a poorer rhizogenesis. These epicentres of compacted soil were related to (i) areas where bulldozers had been widely used in forest clearing and land cleaning before planting (for a better root diseases control) and to (ii) natural soil compaction. While the pathogenic hypothesis was invalidated (2), BN "spread" can be explained by soil physical constraints and a "dome" effect: the closest tree to one soil compaction epicentre being affected first, its neighbour next, and so on, until the border of the centre. Thus, planted blocks might be considered as a mosaic of compaction centres where progressive effects of physical soil constraints result as a sham of disease extension.

* Earliest BN symptoms were preferentially observed near the grafted bud at the rootstock/scion (rs/s) junction. Numerous comparative ecophysiological measurements of leaf water potential using a PMS sap pressure chamber indicated higher water stress in BN trees. These results and preliminary dye transfer studies at the rs/s junction suggested a non-optimal vascular relation between the root system and the trunk of BN trees.

* Attempts to identify bn molecular markers in the phloem highlighted overexpression of a linamarase (cyanogenic b-glucosidase). Further results suggested that, probably due to cell decompartmentation near the rs/s junction, occurrence of an imbalance between cyanogenic and cn-detoxifying activities in the phloem could lead to a local release of highly diffusive cyanide, then to the poisoning and necrosis of the neighboring tissues (3).

In conclusion, compaction-associated reduced water availability of the soil, poor root capacity to meet the water demand during drier dry seasons, disturbed sap flows between root system and trunk, and recurrent local water drainage after tapping, are now suspected to jointly act as the main causal stresses that induce the BN process at the rs/s zone, before spreading upward to the tapping cut. The present multidisciplinary approach gives a new comprehensive scenario for the outbreak of this multifactorial physiological disease.

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WHEAT LEAF PHOTOSYNTHESIS LOSS DUE TO LEAF RUST

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Background and objectives
Environmental and economic concerns increase the demand for more accurate fungicide application schemes. Decision systems based on predicted yield loss rather than epidemic thresholds must be developed to meet this demand. Quantification of the effects of pathogens and inclusion of these effects in crop simulation models are necessary to understand the response of yield to disease. In the case of foliar pathogens, a consistent relation between leaf disease severity and leaf photosynthesis is a prerequisite of any robust crop loss model. In the literature however, there is a large variability in the relation between photosynthesis loss and leaf rust severity. The purpose of our work is to understand why such variation occurs and to propose a robust relationship. We test 3 hypotheses to explain this variability: it may result from variations in i) the fungus' age ii) the disease assessment method (rust develops different symptoms); or iii) the leaf's physiological state.

Material and methods
In adult wheat flag leaves (Cv. Soissons) infected by *Puccinia triticina* we quantified at regular intervals during one sporulation cycle 1) symptoms development, and 2) leaf photosynthesis loss. Plants were grown under three different fertilisation treatments. The development of the different types of symptoms induced by the pathogen (chlorotic, sporulating, and necrosed tissues) was evaluated using image analysis. Net photosynthesis was assessed with a portable photosynthesis system. We used Bastiaans' (1991) model: $Y = (1 - x)\beta$ to characterize the relation between relative leaf photosynthesis (Y) and disease severity (x).

Results and discussion
The relation between photosynthetic rate of infected leaves and the proportion of sporulating area varied greatly as lesions develop (β=2-11). When considering the proportion of both sporulating and necrotic area, this relation varied much less (β=1.4-2). Finally, when considering the total diseased area, this relation was almost constant (β=0.8-1). Leaf nitrogen levels did not change the effect of the disease on host photosynthesis. The large variation in the quantification of leaf rust effect on the host, as found in the literature, could thus be accounted for by considering the different symptom types. We also show that leaf rust has no global effect on the photosynthesis in the symptomless parts of the leaves which suggests that for estimating damage with crop growth models the key variable is the total visible diseased area. By contrast epidemics kinetics are based on pathogen multiplication rate. Thus sporulating area is a key variable in epidemic models, allowing the estimation of spore production (Robert *et al.* 2004). This illustrates the importance of choosing an appropriate measure of disease severity dependent on the context.

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DYNAMIC MODELLING OF MYCOTOXIN PRODUCING *FUSARIA* ON WHEAT

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Background and objectives

Fusarium head blight (FHB) is a serious disease of wheat caused by several fungal species. A dynamic simulation model for the risk of FHB on wheat has been elaborated based on the Systems Analysis (3). This model calculates a daily infection risk based on sporulation, spore dispersal and infection of host tissue by the four main species causing the disease *(F. graminearum, F. culmorum, F. avenaceum,* and *Microdochium nivale)*. Spore yield and dispersal are calculated as functions of temperature, rainfall, and relative humidity, while the main factors affecting the infection rate are temperature, wetness duration and the host growth stage.

F. culmorum and *F. graminearum* produces several mycotoxins, including deoxynivalenol (DON) and zearalenone (ZEN). Because of the impact of these mycotoxins on animals and humans, contamination of wheat kernels assumes a great and increasing relevance. Therefore, the infection model was enlarged by including a sub-model for mycotoxin accumulation.

Materials and methods

A relational diagram for the "mycotoxin sub-model" was drawn based on the available knowledge, and specific experiments were carried out to determine mathematical relationships between mycotoxin accumulation and the influencing variables, particularly: host growth stage, free water inside host tissue, and air temperature. Experiments were performed over a 2-year period; using mycotoxin producing strains of *F. culmorum* and *F. graminearum* were artificially inoculated either on wheat ears in field or in environment controlled conditions. Mathematical equations resulting from these experiments were organized in a coherent sub-model and this "mycotoxin sub-model" was linked to the "infection model". Model outputs were then validated against field data not used for model building.

Results and discussion

The most important factors affecting DON in ripe kernels were included into the model. They were: i) the growth stage of wheat at the infection establishment; ii) the rate of kernel invasion by fungal mycelium between infection and the kernel hard stage, which depends on air temperature and relative humidity; iii) the rate of mycotoxin production by the invading mycelium, which also depends on temperature. The FHB epidemics simulated by the model were accurate and robust.

This work demonstrates that the Systems Analysis is an useful tool for developing mechanistic dynamic models for mycotoxin producing fungi; this approach can improve simulations of the epidemics caused by these fungi compared to an empirical approach based on the regression analysis of field collected data (1,2).

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SESSION G

'SOIL HEALTH AND SOIL-BORNE DISEASE MANAGEMENT'

RELATION BETWEEN SOIL HEALTH, WAVE-LIKE FLUCTUATIONS IN MICROBIAL POPULATIONS, AND SOIL-BORNE PLANT DISEASE MANAGEMENT

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Abstract
A healthy soil is often defined as a stable soil system with high levels of biological diversity and activity, internal nutrient cycling, and resilience to disturbance. This implies that microbial fluctuations after a disturbance would dampen more quickly in a healthy than in a chronically damaged and biologically impoverished soil. Soil could be disturbed by various processes, for example addition of a nutrient source, tillage, or drying-rewetting. As a result of any disturbance, the numbers of heterotrophic bacteria and of individual species start to oscillate, both in time and space. The oscillations appear as moving waves along the path of a moving nutrient source such as a root tip. The phase and period for different trophic groups and species of bacteria may be shifted indicating that succession occurs. DGGE, Biolog and FAME analysis of subsequent populations in oscillation have confirmed that there is a cyclic succession in microbial communities. Microbial diversity oscillates in opposite direction from oscillations in microbial populations. In a healthy soil, the amplitudes of these oscillations will be small, but the background levels of microbial diversity and activity are high, so that soil-borne diseases will face more competitors and antagonists. However, soil-borne pathogens and antagonists alike will fluctuate in time and space as a result of growing plant roots and other disturbances, and the periods and phases of the oscillations may vary. As a consequence, biological control by members of a single trophic group or species may never be complete, as pathogens will encounter varying populations of the biocontrol agent on the root surface. A mixture of different trophic groups may provide more complete biological control because peaks of different trophic groups occur at subsequent locations along a root. Alternatively, regular addition of soil organic matter may increase background levels of microbial activity, increase nutrient cycling, lower the concentrations of easily available nutrient sources, increase microbial diversity, and enhance natural disease suppression.

Key words
biological control, disease management, harmonic fluctuations, resilience, soil-borne pathogens, soil health

SEEDLINGS ARGAN PRODUCTION IN NURSERY:
PRE-EMERGENCY AND POST-EMERGENCY DAMPING-OFF.

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Abstract

The damping-off is one of the principal causes of the low production rate of seedlings starting from the seeds of argan. In front of the lfack of information on the extent of the losses caused by this disease as well as the pathogenic agents blamed, we are carried out a test of production of seedlings starting from the seeds collected under canopy of 15 different mother-tree genotype. The percentage of seeds germination oscillates between 68,3 % and 91,7 % and the total percentage of contaminated seeds vary between 12,5 % and 33,3 % according to genotypes. *Fusarium* is the most frequent fungus (44,1%), followed by *Aspergillus* (39,1%) then *Penicillium* (15,1%) and in weak frequency by Mucor (1,6%). The percentage of contamination by these genera of fungi is very variable according to the genotype. The percentage of seedlings destroyed at the one month age varies between 0 % and 20 %. Nevertheless, this percentage increases with the duration passed after plantation, reached 65% five months following raising. Three pathogenic agents responsible for this damage are highlighted: the most frequent genus is *Fusarium* (69,4%), followed by *Aspergillus* (22,3%) and in weak frequency by *Penicillium* (8,3%). The reaction of the genotypes to these three pathogenic is very variable, some are more sensitive, others are more resistant.

Key words

Argania spinosa, *Aspergillus,* damping-off, *Fusarium,* genotype, *Penicillium.*

EPIDEMIOLOGICAL ANALYSIS FOR CHEMICAL CONTROL OF TAKE-ALL ON SEMINAL AND ADVENTITIOUS ROOTS OF WHEAT

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Background and objectives

Recent development of novel chemicals for control of take-all on winter wheat offers the opportunity for better management of the disease. Optimisation of disease control depends on identification of the epidemiological processes affected, and complementation of chemical control with existing cultural strategies to reduce disease. In this paper we fit an epidemiological model (model 1) (Bailey and Gilligan 1999) to changes in the numbers of diseased and susceptible roots over time to examine the effect of a chemical seed treatment, silthiofam, on the disease dynamics of take-all. Data were utilized from extensively sampled field trials. Specifically we asked, did silthiofam affect primary infection from soil inoculum and/or secondary infection from diseased roots? Seminal and adventitious roots play different roles in resource capture of the wheat plant (Sallans 1942) and may contribute differently to epidemic development. We extended the model (model 2) and fitted to change in the numbers of diseased and susceptible seminal and adventitious roots in order to distinguish between, and examine differences, in the disease dynamics and infectivity of the two types of root.

Results

Disease dynamics were consistent with consecutive phases of primary and secondary infection. Silthiofam reduced the number of diseased roots, an effect that was most evident during the secondary infection phase of the epidemic. Fitting model (1) detected a significant reduction of 28.8% in the rate of primary infection but no effect of chemical treatment on parameters for root growth nor on the rate of secondary infection. Fitting model (2) detected a 69.2% reduction in the rate of primary infection on seminal roots but no effect of silthiofam on secondary infection for either diseased seminal or adventitious roots.

Discussion

Historically most work on analysis of methods for the control of soil-borne disease have been empirical, often with only a single observation of disease at harvest. Such methods fail to identify epidemiological mechanisms that determine the efficiency of control. By taking extensive observations over the course of the growing season and fitting these to simple epidemiological models that distinguish primary from secondary infection on both seminal and adventitious roots, we have been able to identify these mechanisms for silthiofam. Consistent with previous reports (Schoeny and Lucas 1999), this epidemiological analysis showed that the mechanism responsible for these differences was associated with the control of primary infection. Moreover, silthiofam did not affect either the seminal or adventitious roots as a source of inoculum for secondary infection.

Conclusion

We conclude that control of disease afforded by the seed treatment was restricted to reduced infection of the seminal roots by particulate soil inoculum and that, once infected, it did not affect the ability of these roots nor of the adventitious roots to pass-on the disease. The differences detected during the later stages of epidemics were the consequence of these initial effects on primary infection, subsequently amplified by secondary infection.

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EFFECT OF SOWING DATES ON NATURAL EPIDEMIC OF TAKE-ALL AFTER THIRD WHAT CROP IN SOUTHERN IRAN

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Background and objectives
Take -all disease of wheat caused by *Gaeumannomyces graminis* var. *tritici* has recently been reported in Fars province of Iran (1). The most damage of take-all occurs in the third and fourth successive wheat crop in this area (unpublished results).The principle objectives of this study were to identify differences in the shape of disease progress curves that could be attributed to the various sowing dates treatments.

Materials and methods
The experiment was conducted in a naturally infested field which has been sown successively to wheat crop for three years. Five sowing dates including 20th october, 5th November, 20th November, 5th December, and 20th December were applied in a completely randomized block design with 20 plots each measuring 10 x 3 m giving four replicates plot for each five sowing dates. Take-all disease was assessed at growth stages 15, 23, 37, 45, 57, 69, and 75 according to Zadoks scales. Through the cropping season, four samples of 25 cm x 2 rows was taken randomly from each plot. Root system were washed free from soil and take-all was visually assessed on ten randomly selected plants per sample.Disease incidence was measured as the proportion of plants with black stelar discoloration on nodal roots.Disease severity was measured by the proportion of disease (take-all lesion) on roots. Take-all index was also assessed on nodal root system by scoring according to five class scale of 0-4 corresponding to no symptom and more than 60% of roots blackened.

Results and discussion
Take-all developed earley prior to tillering in various field plots showing high inoculum density build up in soil from previous three successive wheat crop. Disease incidence was high (87%) at the first sowing date treatment and reaching 100% at the flowering and milky stage.Significant difference was found between the first (20th October) and the last sowing (20th December) treatments in disease incidence at the tillering stage. No difference was found between second, third and the fourth sowing dates in disease incidence at the tillering stages. A similar trend on the effect of various sowing dates on disease severity of take-all was observed. The proportion of the diseased roots was 29% at GS15 and the reaching 80% at GS 75 (Milky stage).Signicant difference was found between the first and the last sowing date treatment in disease severity at GS15, GS23, GS37, GS45, GS57, GS69, and GS75. No signifcant differences were found between the first, second, third and fourth sowing dates. The average rainfall during the growing season was 354 mm which was about the average and nearly most of it (>70%) occurred in a week in November. The results of this study showed that late sown crops generally reduced disease severity by nearly 50% and support previuos workers (2). The result also indicated that later sown crop do not produced better yield due to short growing season.

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DEVELOPING A MODEL TO EVALUATE DISEASE RISK OF *RHIZOCTONIA SOLANI* IN FIELD VEGETABLES

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Introduction and background
Conventional approaches to study effectiveness of disease control rely on empirical experiments, often with few replicates and a single observation of disease over time. However, the absence of epidemiological understanding makes it difficult to see how to optimise or enhance control or to assess the risk of failure.

Materials and methods
We have been using an epidemiological theory (1) to develop a model to evaluate disease risk of Rhizoctonia solani in field vegetables. The model identifies main components of a damping-off outbreak, including pre-emergence, primary and secondary infections, and death and recovery of plants (2). Parameters in the model were identified for a series of highly replicated and closely monitored field data on damping-off of radish, spanning 2 years, 4 crops and 3 densities of inoculum plus a control.

Results and discussion
Infection rates followed a rise-and-fall pattern following inoculation (3), whereas recovery was predominantly related to older plants, and death to younger plants. The estimates allowed us to construct a generic (worst-case scenario) model. The model was subsequently used to study a risk of a large outbreak of damping-off disease in the field and to identify factors enhancing or controlling the spread. Three types of outbreaks (limited, large 'invisible' and large 'visible' outbreak) were identified, depending on the levels of infecting throughout the crop and recovery. The size of the epidemic and cryptic infestation depends crucially on the balance between pathogen dynamics (infectivity, saprotrophic potential, primary and secondary infection) and host dynamics (susceptibility, recovery and death). We show that even though plants might recover, there is potential for hidden infestation of a plant and of soil, leading to a potential for carry-over of inoculum to the next crop. Finally, we use a stochastic framework to analyse variability among patches and crops, to assess risk of an outbreak and to optimise predictability.

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SUMMER-FALLOW MANAGEMENT TO REDUCE TAKE-ALL DISEASE (*GAEUMANNOMYCES GRAMINIS* VAR. *TRITICI*) ON WINTER WHEAT

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Background and objective
Crop rotation is the oldest and certainly the most efficient cultural practice in reducing take-all disease on wheat. In France, rotations at low take-all risk face two challenges : low economic interest of some break crops and large predominance of wheat and barley in the market demand and thus in the cropping systems. Facing these constraints, farmers' choice has become limited. Even though we know very well the effects of crops sown prior to the wheat in a rotation, we do not know much about the opportunities that some crops offer to the farmer when they are introduced during the summer period between harvest of wheat and planting of a subsequent winter wheat crop. While policy on soil conservation and reduction of nitrate leaching encourages farmers to avoid bare soil between two commercial crops, it is important to have a better knowledge of the effect of intermediate cropping on the following wheat crop health, depending on the plant grown as intermediate cropping.

Material and methods
The effects on take-all of winter wheat of five summer-crops plus a bare soil situation, in interaction with tillage (till *vs* no-till) and wheat seed treatment (silthiofam *vs* none) were investigated in a five site-year experiment. Summer-crops were oat, rape, mustard, rye-grass and wheat volunteers.

Results and discussion
The epidemics of take-all varied among years and sites from low to severe. The effect of summer-crops was more important in the till situation. Take-all incidence and severity were significantly higher in the wheat volunteers plots, while maintaining bare soil provided the lowest level of disease, although not acceptable for environmental reasons. Rape did not show any significant effect on take-all incidence in our experiment. The best candidates appeared to be oat, mustard and rye-grass. These summer-crops decreased disease incidence and severity only when associated to conventional tillage. Summer-crops did not alter take-all decline as does a break crop after a wheat monoculture.

Conclusion
Thus, summer-crops have a potential to reduce take-all in a following winter wheat crop. The summer-crop effects cannot be explained only by the non-host status of the plants that were grown. The way the summer-crop canopy residues are managed before wheat sowing seems to be very important. More investigation is needed to understand the effects of intermediate cropping on take-all fungus survival, on microbial changes and/or through allelopathic effects and their consequences on take-all disease cycles.

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INTEGRATED SOIL-BORNE DISEASE MANAGEMENT IN PROTECTED VEGETABLE CROPS IN SOUTH-EAST FRANCE

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Backgrounds
Vegetable crops cultivated under plastic tunnels represent favorable conditions for the development of soil-born pathogens : intensive crop sequences (2 to 4 crops per year) with a limited number of species (lettuce, tomato, cucumber, zucchini...), hot temperature and high humidity levels, which has led to increasing use of chemical desinfection for several years. For environmental reasons and increasing demand for healthy food, systematic chemical treatments are now avoided and growers have to combine non chemical alternatives (diversified crop sequences, solarization, organic amendments...), which individually are far less effective than chemical soil desinfection.

Objectives
The project aims at modeling the effects of combined cultivation techniques and crop sequences on a complex of diseases. The major soil-borne diseases observed on lettuce protected crops in South-east France will be considered: bottom rot diseases (rhizoctonia, sclerotinia), root-knot nematods, virus (big-vein).

Methods and first results
To reach this goal, scientific knowledge is far from sufficient: pathologists rarely studied several diseases altogether; neither did they study the cropping systems as a whole. Agronomic experimentations, usually consisting in factorial designs, rarely evaluate more than 2 or 3 cultural factors at the same time. And yet, there are plenty of partial information [1]. On the other hand, growers' knowledge has seldom been listed and assessed. Therefore, our aim is to combine scientific and empirical knowledge, in order to produce new agronomical knowledge [2]. The major steps of the project have been identified. A first inventory of the knowledge available and the analysis of its consistency and contradictions is under way. Information collection from several sources is under way: scientific bibliography, surveys of growers and technical advisors, diagnosis of diseases on several farm plots and experimental trials. The second step will consist in choosing the adequate modeling method, in the field of Qualitative Modelling [3] and implementing the model. After validation, the model will then be used to evaluate several cropping systems and compare them as regards their ability to limit soil-borne diseases and their efficiency as regards yield and quality.

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CAN INCOMPLETE SPATIAL COVERAGE OF CONTROL MEASURES PREVENT INVASION OF FUNGAL PARASITES?

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Background
Whilst protection of each host in a plant population prevents invasion, such a complete spatial coverage is often not achieved. In particular in soils, where the root system needs to be protected from invasion, the delivery of a control agent to every susceptible root is seldom possible. Even at the field-scale it may be desirable to reduce the area over which a control measure is applied, for example to slow the rise of fungicide resistance or if economic costs are high. This raises the question *what fraction of susceptible hosts needs to be protected to prevent an epidemic*?

Materials and methods
In this paper we evaluate empirical evidence and theoretical arguments for the existence of spatial thresholds to control invasion of the soil-borne fungus *Rhizoctonia solani* in heterogeneous populations of substrates. The work is centred on the hypothesis that the invasion of soil-borne fungi in populations of substrates is analogous to the spread of infection through discrete host populations or fields with susceptible crops (1). For such spatial systems, *percolation theory* predicts that if a critical fraction of susceptible hosts is protected, invasion stops. To test this hypothesis, we use artificial but replicable microcosms in which the spread of *R. solani* is quantified through a population of agar sites on a lattice. A random fraction of sites is removed as an analogue of locally successful but spatially incomplete control.

Results and discussion
Analysis of fungal growth in the microcosms revealed the following epidemiologically important features (2):
1. removal of a *critical fraction* (60%) of susceptible sites is sufficient to *prevent invasion* into a population that otherwise would have been invaded;
2. removal of susceptible sites introduces a *shield* preventing a large proportion of the population from being invaded;
3. with an increasing number of protected sites, the remaining sites are less well-connected forming a tortuous network with bottlenecks resulting in a reduced rate of invasion, but with *occasional outbursts* of fungal spread.
We conclude that there is a threshold for spatial coverage of a control measure above which invasion is prevented. We conjecture that this holds for a broad class of organisms spreading through heterogeneous environments within crops. This means that not all plants have to be protected by a biocontrol agent in order to prevent invasion of a pathogen. The extent at which a control strategy is applied spatially can therefore be a critical component of disease management.

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EFFECT OF CROPPING FACTORS ON SECONDARY INFECTION IN A CARROT CAVITY SPOT EPIDEMIC

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Background and objectives

Cavity spot of carrot (csc), one of the most important soil-borne disease on this crop in the world, is characterised by the appearance of small sunken lesions on the taproot due to a *Pythium* pathogenic complex, in part composed of *P. violae* and *P. sulcatum*. Soil inoculum of several soil-borne diseases is the source of primary infection. New diseased plants serve as the inoculum source and support secondary infections, i.e. autoinfection on the same root and alloinfection by the spread from root to root. Objectives are to develop epidemiological studies based on mechanistic hypotheses (occurrence of secondary infections) and to test effects of cropping factors according to the csc epidemic stage.

Materials and methods

We developed an infestation method to demonstrate and generate cycles of secondary infection of csc in controlled conditions, and establish the polycyclic nature of a csc epidemic. In this purpose an original methodology consisting of artificial inoculation of a thickened carrot root (the donor plant) before transplantation in a microcosm is described. This reproducible method could generate methodological advances to delay inoculation and distinguish effect of different cropping factors or treatments on primary and secondary infections: soil moisture (irrigation), seed density, and fungicide treatment.

Results and discussion

We first demonstrated that csc lesions on carrot residues are potentially infectious for healthy roots, using fragment of lesions due to *P. violae* as soil inoculum, and secondly proved the ability of csc to spread from root to root by alloinfection, using an alive transplanted root after artificial inoculation.

We tested in micro-fields the effect of soil moisture on an entire epidemic (primary and secondary infections) using a sprinkler irrigation system: in moderately and intensively irrigated soils disease levels were significantly higher than in non-irrigated soils.

We showed an effect of the distance between the source of inoculum (the donor plant) and the target healthy roots (the receptor plants) on secondary infection. We also established an effect of the seed density: a lower density is responsible of a smaller total diseased area on the target roots. This study produced other information about the propagation of *P. violae*: the maximal distance for successful secondary infection is at least 90 mm and the latency period is between one and two weeks.

Finally a fungicide (mefenoxam) which is currently used before seed emergence by growers was able to reduce the secondary infections when sprayed during the cropping season, thus slowing the progression of the disease in time and space.

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EPIDEMIOLOGY AND RISK ANALYSIS OF POTATO BROWN ROT IN SCOTLAND

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Background and objectives
The quarantine bacterium *Ralstonia solanacearum* biovar 2 race 3, the cause of potato brown rot, was previously found in parts of the Tay river system in Scotland (1). In recent years the pathogen has been eradicated after removal of its wild host, *Solanum dulcamara*, from the affected waterways. Any surface water contaminated with *R. solanacearum* used for irrigation could form a major threat to the health of potato crops, and thus to the Scottish seed potato industry. For this reason, SASA, in co-operation with CSL and SCRI, is currently analysing the risk of brown rot to Scottish seed potato crops in a three-year SEERAD funded project.

Materials and methods
The location of possible sources of future contamination of Scottish rivers with *R. solanacearum*, in particular waste from imported potatoes in sewage and potato processing effluent, have been identified. Information has been gathered on the distribution of potato crops grown near waterways and of *S. dulcamara* along riverbanks. This information will be used to assess the risk of contamination of waterways and survival of the bacterium. Additional data are being collected on the effect of environmental factors, varietal resistance and inoculum level on the infection of potato crops. These will be used to predict the chance of contamination of Scottish seed with *R. solanacearum* in different potato growing areas.

Results and discussion
Six river systems in seed growing areas have been identified as 'high risk' on the basis of the presence of several possible contamination sources (Rivers Lossie, Deveron, Tay, Whiteadder, Tweed & Lunan Water). Some of these rivers are regularly used for irrigation of seed crops. *S. dulcamara* is not widespread in Scotland and has been found in parts of only two out of six river systems surveyed (River Tay & Lunan Water). It appears to be most common in slow flowing rivers. All ten most commonly grown seed potato varieties in Scotland have been found to be susceptible to brown rot in greenhouse trials. Further information is being gathered for integration into a risk analysis model.

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NEW APPROACHES TO ASSESSING AND MANAGING SOIL HEALTH IN RELATION TO CROP HEALTH AND PRODUCTIVITY

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Background and objectives

Our basic understanding of the diversity and ecological function of soil organisms has expanded greatly in recent years, and new methods for determining soil community composition and activity are being developed. The emerging concept of soil health attempts to integrate new information about soil biological processes with our knowledge of soil physical and chemical processes affecting crop health, crop productivity, and environmental impacts of farming. Our regional "Soil Health Team" is an interdisciplinary group of faculty with expertise in plant pathology, soil ecology, crop production, Extension educators, and commercial farmers. One goal is to develop cost-effective approaches to quantify soil biological status in relation to soil and pest management.

Research approach

Promising new indicators of soil health include: the pathogenic: saprophytic nematode ratio; a bean root disease assay for soil disease suppressive capacity; potential nitrogen mineralization rate; decomposition rate; soil glomalin levels (reflecting historical mycorrhizal fungi activity); and wet aggregate stability.
Indicators will be evaluated based on reliability and cost of measurement, and potential impact on crop and soil management decisions. Indicators/methods that emerge as the most cost-efficient and interpretable will eventually be included in "decision tree" software to help users determine the minimum data set of biological, physical, and chemical tests best suited to their needs.

Results and discussion

Data from several on-going replicated long-term soil management studies and from several on-farm trials are being pooled and statistically analyzed (range, means, frequency distributions, correlations, linear regression, principle components analysis) to develop an interpretive framework (e.g., range of acceptable vs. unacceptable values) for these new indicators. We are also evaluating several cover crops and cropping systems for their impact on soil disease-, insect- and weed-suppressive activity.

SESSION H

'INTEGRATED DISEASE MANAGEMENT AND MULTIPLE PATHOSYSTEM'

PATTERNS AND MANAGEMENT OF CROP MULTIPLE PATHOSYSTEMS

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Abstract

The study of multiple pathosystems has played a central role in the development of botanical epidemiology, leading to a number of approaches and concepts. Multiple pathosystems are facts, which are experienced by many non-cultivated, or cultivated, plant communities. Multiple pathosystems have elements and shapes, both in space and time. A wide array of methods has been used to describe and analyse them. Linked differential equations can for instance be used, as in the case of the dynamics of a multiple pathosystem in groundnut. The shapes and composition of multiple pathosystems vary in space and time because of their inherent structure of relationships, and also in response to management. Examples of variation in multiple pathosystems are given, of groundnut in Côte d'Ivoire, of wheat in Brittany, and of upland rice in northern Laos. Variation in the yield reducing effects of multiple pathosystems is discussed, including interactions among disease elements, relationships with attainable performances, and linkages with production situations. Progress has been achieved in understanding the links between injury profiles, production situations, and attainable performances. Questions about the functioning and consequences of multiple pathosystems are central to defining the scientific bases for, the design of, and the implementing of IPM. The complexity of multiple pathosystems however remains a deterrent, not a challenge, to many plant pathologists. Progress achieved in designing production systems for hardy wheat in France however is very promising, because of the multidisciplinary science it involves, and because of the promise to deliver it carries. The concepts of epidemiological guilds and of guilds of harmful agents are offered as perspectives to address and manage syndromes of production and syndromes of disease.

Key words

agro-ecosystem, multiple epidemics, epidemiological guilds, guilds of harmful agents, syndrome of production, syndrome of disease, IPM

INTEGRATED CROP MANAGEMENT REQUIRES TO BETTER TAKE INTO ACCOUNT CROPPING SYSTEMS IN EPIDEMIOLOGICAL MODELS

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Background and objectives

The objective of Integrated Crop Management (ICM) is to achieve agronomic, economic and environmental goals simultaneously. Plant disease models should play a key role in the construction of integrated cropping systems that contain the development of various pests, especially pathogens. However, today, epidemiological models do not sufficiently integrate the effects of cropping systems (as defined by Sebillotte, 1995) to help in defining ICM strategies. The presented paper is an argument for better integration of the effects of cropping systems on disease development in epidemiological models.

Discussion

Each element of a cropping system can affect the health status of the crop. For instance, in regard to diseases, cropping systems affect the quantity of the primary inoculum and its localisation, the development and spread of epidemics, the coordination of the life cycle of cultivated plants and that of their parasites, and disrupt ecological equilibria (Meynard et al., 2003). In order to limit pest development, it is therefore natural to try to adapt crop management (besides chemical, genetic, biological and physical controls) and crop successions. It is the basic principle of cultural control, one of the oldest types of control in crop protection.

Whereas great progress in crop and epidemiological modelling has been achieved during the last few decades, it did not allow for significant applications of ICM in major crops. There are two main reasons. Firstly, crop models that can be used to propose innovative crop management strategies do not take into account the biologic component of cultivated fields. Secondly, the effects of cropping systems are not sufficiently taken into account in models that represent pest development and yield loss due to these pests. In regard to the application of ICM, epidemiological studies should now focalise on the analysis of the relationships between cropping systems and the development of pathogen populations. Remarkable methodological progress has been made in the instrumentation to monitor crops, environment and pathogens. In addition, molecular biology now permits to characterise the genetic structure of pathogenic populations. Hence, experiments, experimental networks, and diagnoses in commercial fields can now successfully be conducted to analyse the effects of cropping systems on pathogen populations and their effects on yield components and yield quality. Those studies should not be aimed at establishing direct relationships between cultural practices and disease symptoms. Instead, they should analyse the interactions between cropping system, crop development, environment and diseases through state variables of the agro-system. This requires observing additional intermediate variables in epidemiological studies, for a wide range of production situations.

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A TOOL FOR EVALUATING THE ACCURACY OF FORECASTING MODELS FOR POTATO LATE BLIGHT

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Background and objectives
Many weather-based disease forecasting models have been proposed to assist with fungicide management for potato late blight (*Phytophthora infestans*) (2). It is unclear from the literature how useful these models are for their intended purpose and whether they can be successfully transported between cropping regions. This study sought to develop a simple spreadsheet-based tool that could be used with disease data from fungicide field trials and weather data to determine which forecasting models could best explain late blight development in New Zealand.

Methods
The method assumes that less disease develops in crops where the timing of fungicide applications maximizes foliar protection in relation to the timing of weather conditions suitable for infection. Daily evaluation was made of two indexes: 1) potential infection (PI_i), using weather-based forecasting model output, and 2) the degree of fungicide protection (FP_i), using rules describing the way fungicide effectiveness decreases with leaf canopy growth after the day of fungicide application. PI and FP each varied between 0.0 and 1.0. Net infection was calculated as $NI_i = PI_i \times FP_i$. $NI_i = PI_i$ if there was no fungicide protection ($FP_i = 1.0$). For the whole season an overall risk index was calculated as $RI = \Sigma NI_i / \Sigma PI_i$. $RI = 1.0$ if no fungicides were applied and would be 0.0 if a fungicide were applied every day. Consideration of the "reach back" activity of systemic fungicides and fungicide application rate were included in calculating FP.

The degree to which RI explained late blight severity was tested in three replicated-plot field trials carried out in three seasons from 1999-2001. Each trial had four fungicide treatments: unsprayed control, propineb and propineb+iprovalicarb at two rates. Disease data were kindly made available by Bayer CropScience. Blight severity was assessed four times in each trial and area under the disease progress curve relative to that in the unsprayed control ($AUDPC_r$) was calculated for each fungicide treatment. Weather data were monitored within 2 km of the trial sites.

Results and discussion
$AUDPC_r$ was used as the Y-variate in regression analysis, with RI as the X-variate, calculated using various late blight prediction models. Whereas the Fry (1) model explained 0% of the variation in $AUDPC_r$ ($P=0.826$), the Wallin (3) model explained 60% ($P=0.009$). Hypothetical random timing of the infection periods identified by the Wallin model gave a mean $R^2 = 1.6\%$ for five iterations ($P=0.894-0.244$). This suggested the significant regression for the Wallin model did not arise by chance.

This analysis tool needs to be further tested on field data, but appears to be useful for identifying disease forecasting criteria suitable for a specific climatic region or cropping system. It could also be used for developing new forecasting criteria and should be applicable to a wide range of crops in which polycyclic foliar pathogens are controlled with repeated fungicide applications.

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MONOCYCLIC COMPONENTS OF THE ASIATIC CITRUS CANKER IN PRESENCE OF *PHYLLOCNISTIS CITRELLA*

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Backgroud and objectives

The Asiatic Citrus Canker (ACC), caused by *Xanthomonas axonopodis* pv. *citri* (*Xac*) is one of the most serious problems of citrus in São Paulo State, Brazil. After the introduction of the Citrus Leafminer (CLM), *Phyllocnistis citrella*, the behavior of ACC changed drastically, becoming more severe. To understand the interaction of *Xac* and CLM on Tahiti Lime, it were carried out three experiments under controlled conditions: (A) influence of the way of *Xac* penetration (stomata, mechanical wound and CLM injury at different stages: egg, 1st instar, 3rd instar and pupa) and of inoculum concentration (10^1, 10^2, 10^4 and 10^6 CFU/mL); (B) effect of age of mechanical wound, of CLM injury and of unwounded leaf in the progress of the ACC; (C) influence of temperature and period of leaf wetness in the development of ACC.

Results and discussion

In experiment A, the minimum inoculum concentration to express symptoms by penetration of *Xac* through stomata was 10^4 CFU/mL, 10^2 CFU /mL by mechanical wound and CLM injury of egg stage and 1st instar; and 10^1 CFU /mL by injury of 3rd instar and pupa stage. The injury of 3rd instar and pupa stage have generated higher severity in relation to other ways of penetration on all concentrations. The severities in leaves with mechanical wound and with injury of egg stage and 1st instar have not differed from the unwounded leaves. In experiment B, mechanical wound between 0 and 6 days, CLM injury between 0 and 32 days after eggs laying of *P. citrella* (0-32 days) and unwounded leaves between 5 and 35 days have shown susceptibility to *Xac*. The severity decreased linearly with increasing age of the wound and age of unwounded leaves. In relation to age of injury, the severity varied in function of generalized Beta model. The maximum severity was 10 times bigger in wounded leaves than in unwounded leaves. In experiment C, the optimum conditions for disease development were 25-35°C under minimum wetness duration of 4 hours. The Beta-monomolecular function provided a good description of severity variation in relation to the temperature and duration of leaf wetness. The estimated minimum and maximum temperatures were 14.9 and 42°C. The estimated maximum severity was determined under wetness of 24 hours and 31.7°C. In general, the LMC injury (up to 3rd instar stage) increased *Xac* infection and allowed *Xac* infection for longer periods (up to 32 days).

EFFECT OF NITROGEN MANAGEMENT IN IRRIGATED RICE ON SHEATH BLIGHT

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Background

Rice sheath blight (caused by *Rhizoctonia solani* Kühn) has two phases: soilborne phase, in which the pathogen causes lesions on the base of sheath, and leafborne phase in which the disease spreads to the leaves. Various studies show that high nitrogen (N) supply favours the disease. Thus, a better understanding of the effect of N management approaches, which are being developed to increase fertiliser N-use efficiency and yield in irrigated rice, would help define an integrated approach for N and sheath blight management.

Materials and methods

Experiments were conducted at the International Rice Research Institute, Philippines during the 2004 dry (DS) and rainy seasons (RS). Treatments, consisting of four urea-N management and four varieties (IR72, PSBRC52, PSBRc72H, and IR752717H), were arranged in split-plot design with N management as main plot and variety as subplot. Treatments were replicated four times. In DS, N management treatments were no N, 75 kg ha^{-1} [20 kg ha^{-1} each as basal, at maximum tillering (MT) and at panicle initiation (PI), and 15 kg ha^{-1} at heading (H) to flowering (F) stages], site-specific N management (SSNM), and 215 kg ha^{-1} (60 kg ha^{-1} as basal, 40 kg ha^{-1} at MT, 75 kg ha^{-1} at PI, and 40 kg ha^{-1} at H to F). For SSNM, N fertiliser was applied in several splits based on chlorophyll meter readings to match the actual requirements of the crop. The total N rate for all varieties in SSNM plots was 145 kg ha^{-1} (30 to 50 kg N ha^{-1} at MT and PI, and 15 kg ha^{-1} at H to F). In RS, N treatments were no N, 45 kg ha^{-1} (three equal splits as basal, at MT, and at PI), SSNM, and 130 kg ha^{-1} (40 kg ha^{-1} each as basal, at MT and 50 kg ha^{-1} at PI). In SSNM, total N rate differed among varieties and ranged from 90 to 130 kg ha^{-1} (25 kg ha^{-1} at early tillering, 20 to 45 kg ha^{-1} at MT and PI, and 15 kg ha^{-1} at H to F). Sheath blight was inoculated by placing rice grain/rice hull mixture on the base of plants at 40 to 45 days after transplanting. Sheath blight severity on the leaves (SL) and on the stem (SS) in plants was assessed two weeks after flowering stage.

Results and discussion

In DS, SS of all varieties did not significantly differ between fertilised plots. N management significantly affected SL, but the effect differed among varieties. SL of IR72 and IR752717H was significantly lower in SSNM than in 215 kg ha^{-1}. However, SL of PSBRc52 and PSBRc72H did not significantly differ between SSNM and 215 kg ha^{-1}. In RS, N management did not significantly affect SS of all varieties. It also did not significantly affect SL except that of IR752717H. SL of IR752717H was significantly lower in 45 kg ha^{-1} and SSNM than in 130 kg ha^{-1}. In both seasons, SL increased linearly with the total N rate in a cropping season (r = 0.66 to 0.78 in DS, r= 0.57 to 0.77 in RS). In contrast, there was no linear correlation between SS and total N rate. These results suggest that the current approach for site-specific N management can effectively manage sheath blight in the dry season. However, more studies are necessary to understand how this approach can better manage sheath blight in the rainy season. These results also suggest that N management more strongly affects the leafborne phase than the soilborne phase of sheath blight epidemics as shown in previous studies. The mechanisms behind the effect of these N management treatments on sheath blight epidemics are currently being analysed.

INTEGRATED MANAGEMENT OF SWEET PEPPER POWDERY MILDEW (*LEVEILLULA TAURICA*)

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Background and objectives

Powdery mildew (*Leveillula taurica*) severely affects sweet pepper during the whole year. Yellowish spots appear on the upper side of the leaves and the powdery mildew pathogen appears underneath or sometimes on the upper side of the leaves. Infected leaves shed and yield quantity and quality are decreased. The objectives of the study were to identify conditions for disease suppression and to combine climate control with environmentally friendly agents.

The effect of temperature and relative humidity were studied under commercial greenhouse conditions. The interaction of *L. taurica* and the biological control agents *Trichoderma harzianum* T39 (TRICHODEX) and *Ampelomyces quisqualis* (AQ10), mixed or unmixed with the mineral oils JMS Stylet Oil and AddQ, respectively, were studied. The effect of the control agents on *L. taurica* important life cycle stages (viability of conidia, conidia germination, leaf colonization by hyphae and disease severity on leaves) were studied under ·controlled conditions and in greenhouse. In field experiments the aforementioned and more treatments were examined in different micro-climate conditions.

Results and discussion

Optimal conditions for germination of conidia of pepper *Leveillula* powdery mildew were found to be 20°C and high RH whereas the growth of hyphae in the leaf and conidiation where optimal at 15-25°C and 15-20°C, respectively. In commercial greenhouses the conditions for restraining epidemics were day temperatures above 25°C.

The biological control agents were more effective in disease control at 15°C and 25°C as compared with 20°C. The mineral oils and TRICHODEX reduced conidia germination. Disease control under commercial greenhouse conditions by the different agents and by a treatment of alternation of the control agents was more efficient under warm temperature conditions (above 25°C during the day achieved by curtain closure, and 19° C at night) than at lower temperatures (20°C during the day and 13°C at night time). Therefore it was suggested to combine the sprays with raised day temperature.

An integration of alternation of 'friendly' control agents (helio-sulfur, TRICHODEX, Neemgard and AQ10) with warm greenhouse climate resulted in effective epidemic restraining, similar to the standard alternation and mix of chemical agents. The former treatment in colder greenhouses was inferior to the chemical treatment. It can be concluded that a combination of increased temperature in the greenhouse with alternative sprays of the 'friendly' agents, effectively controls pepper powdery mildew.

PEST ASSESSMENT IN WHEAT, RICE AND MAIZE CROPS IN GARHWAL HIMALAYAS IN INDIA

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Abstract

Wheat, rice, and maize are the major crops of Garhwal Himalayas. Impact of pests (diseases, insects and weeds) constitute major limiting factor in realizing full yield potential of these crops in the region. Garhwal Himalayas have a diverse ecosystem, which harbour a range of farming situations that ultimately support a spectrum of disease and pest scenario causing varying degree of losses. Developing a rational pest monitoring before management is contemplated will be of enormous value in sustaining the productivity of different crops for the region. Therefore, surveys were carried out to map out epidemic areas of major diseases and pests in the targeted areas through determination of distribution and severity of pest problems and farmers' perceptions of the pests in order to establish pest zones that favour certain pests. Monitoring was carried out at three crop stages in six farming situations (irrigated low hills, rainfed low hills, irrigated mid hills, rainfed mid hills, irrigated high hills rainfed and rainfed high hills) with three fields from each village representing a farming situation in any one location. A total of 57, 29 and 66 villages were surveyed for pest assessment in rice, maize, and wheat, respectively following four routes covering an approximate distance of 2600 kms. For each field samples were taken at 10 points (or 3 quadrates) along a diagonal transect and the type of pest profile was recorded. Initially we began characterizing combination of pests that may be perceived as a threat to the successful cultivation of the three crops in any farming situation. The generalized results are: i). in rice, brown spot was the major disease problem in all farming situations. Though blast was also common to all the situations it was more severe under rainfed than irrigated conditions. Kharif grasshopper followed by rice leaf folder were the most common pests recorded in all the farming situations with varying impacts. Infestation of various weeds was more in rainfed than irrigated conditions under all the farming situations. ii). In maize turicum blight was of serious concern at mid and high altitides, while maydis blight was predominant in low hills. Impact of pink borer was predominant in four farming situations while Cyprus rotundus and oxalis latifolia were the most frequent and dense weeds in most farming situations. iii). In wheat, powdery mildew was the most widespread, predominant and severe disease at the three crop stages under irrigated conditions. In the rainfed system incidence of hill bunt was higher. There was no significant prevalence and damage to wheat as a result of insects in any of the farming situation. However, weeds posed a problem in the irrigated conditions in lower and mid hills with Poa annua being the most predominant weed. The study led to the formulation of time profile for different pests in the three crops and identification of putative hot spots in different farming situations for guiding effective deployment of pest management strategies.

NITROGEN RATE INFLUENCES DEVELOPMENT OF ALTERNARIA AND CERCOSPORA BLIGHT OF CARROT

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Background and objectives

Carrot leaf blights, caused by *Alternaria dauci* (Kuhn) Groves & Skolko and *Cercospora carotae* (Pass.) Solheim are destructive foliar diseases of carrots in Canada. An important addition to fungicide use is optimal crop nutrition. Alternaria leaf blight can be reduced by application of nitrogen (N), (Vintal *et al.*, and Warncke). There are no reports on the effect of N on Cercospora leaf blight alone, or on the management of N fertilizer on foliage health at harvest. The objectives of this research were 1) to determine the effect of N application rate on Alternaria and Cercospora leaf blight on two carrot cultivars grown on both mineral and organic soil, and 2) examine the overall effect of N application rate on carrot yield and foliage health at harvest.

Materials and methods

'Idaho' and 'Fontana' carrots were grown on both mineral and organic soil near Bradford, Ontario (44 ° 5' N, 79 ° 35' W) over 3 years. Nitrogen was applied as ammonium nitrate at 0, 50, 100, 150, and 200% of Ontario recommended rates (organic soil: 60 kg/ha N preplant; mineral soil: 75 kg/ha N preplant/ 35 kg/ha sidedress. Damage from *Alternaria* and *Cercospora* was rated on a scale of 0 to 10 and area under the disease progress curve (AUDPC) was calculated. The number of lesions per leaf and number of live leaves per plant was recorded.

Results and discussion

Carrot cv. 'Idaho' had consistently less leaf blight than 'Fontana' but showed similar responses to N application rate. In most cases, high N reduced the AUDPC, for both *Alternaria* and *Cercospora* on both soil types. Lesions per leaf decreased with increasing rate of N, and the number of live leaves per plant increased with increasing N. There were no differences in yield as a result of varying N rates or disease severity.

These results are consistent with reports that N application can reduce the severity of Alternaria blight on carrots, and show that the response is similar for Cercospora blight. This is the first study to assess the effects of N rate on both pathogens. Nitrogen application at rates above those needed for optimum yield reduced the rate of disease development. Nitrogen fertilization should be an important consideration in integrated disease management of carrots.

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SIMULTANEOUS EPIDEMIC DEVELOPMENT OF SCALD AND NET BLOTCH ON SINGLE LEAF LAYERS OF A SPRING BARLEY CROP

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Background and objectives

Two pathogens growing on the same leaf compete for the same resources, i.e. space and plant nutrients. This may lead to density dependent disease development. The pathogens may also influence each other directly such that the influence of one on the other is more complex than a simple function of the area of the other pathogen. Different interaction types are, for example, competition, mutualism and exploitation. The importance of such interactions for epidemics of simultaneously occurring pathogens has received little attention. The objective of this study is to investigate the simultaneous epidemic development of *Rhynchosporium secalis* (causing scald) and *Drechslera teres* (causing net blotch) on spring barley under field conditions.

Materials and methods

The field trial was performed with artificial inoculation of *R. secalis* and *D. teres* on three spring barley varieties differing in their susceptibility towards the pathogens. The pathogens were inoculated in three combinations: only one was inoculated, they were inoculated together, the second pathogen was inoculated 26 days after the first. A non-inoculated treatment was included. The trial had three replications. Nine plants were harvested from each plot five times during the season. Leaves were dried and disease severity and senescence observed. Only leaves with $< 50\%$ senescence were included in the analysis.

Whole-plant disease severity over time was calculated as average of disease severity on leaves weighted by leaf area. Disease development per leaf layer was evaluated by fitting an exponential model to severity data over time for each leaf layer per variety, treatment and replicate. Association between scald and net blotch severity on individual leaves was analysed using Kendall's tau.

Results and discussion

Net blotch developed on all leaf layers and reached whole-plant disease severities up to 15%. Scald did not develop on upper leaf layers and whole-plant severity was less than 2%. Disease severity curves at whole-plant level showed no effect of inoculating the other pathogen. The analysis of the growth rate of each disease per leaf layer showed a significant effect of variety and leaf layer within variety but no effect of treatment. However, we observed significant negative associations between the diseases on individual leaves for several combinations of leaf layer and variety. These results show that the individual leaf approach can provide new information and underline the importance of considering interactions between pathogens in the field.

Acknowledgement

BASIS OF A NEW DECISION TOOL BASED ON BAYESIAN MODELLING IMPROVING BARLEY YELLOW DWARF DISEASE MANAGEMENT

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Background and objectives
Barley Yellow Dwarf (BYD) disease is one of the most severe viral diseases in autumn sown cereals. In western Europe, crop losses are mainly due to the PAV species of BYD-Viruses transmitted by the aphid *Rhopalosiphum padi*, the most abundant species in autumn. Since BYD viruses are transmitted by aphids, one method to control the disease relies on the use of insecticide sprays such as the Decis® marketed by Bayer CropScience. Due to the sporadic nature of epidemics, treatments are not required every year and everywhere. Consequently, a considerable reduction in the number of sprays could be derived if they were applied only when necessary. Accordingly, the objective of this thesis is to design a decision making tool helping farmers to decide if whether or not a Decis® spray is needed in their fields.

Results and discussion
The statistical analysis of a large dataset on the effect of Decis® spray on the BYDV vectors shows that a simple model based on the autumnal population dynamics of *R. padi* can accurately predict yield losses caused by BYDV and therefore the need for insecticide treatment (1). To be of practical use, this model has been completed by a predictive model of population dynamics of *R. padi* in autumn. Based on temperature driven simulations of the aphids populations dynamics, this model uses the Bayesian theory to explicitly manage the uncertainty on its parameters (2). This 2 models form the basis of the decision making tool assessing the probability that a spray is needed. The whole model sensitivity is very good (0.97) and its specificity, although defective (0.44), allows to avoid one unnecessary spray out of two. When compared with a systematic spraying strategy, the model use strategy allows to reduce the cost of BYD disease and control of an equivalent of 46 kg.ha^{-1}.

To improve the accuracy of this decision tool, the proportion of viruliferous migrant aphids was studied during 4 years in 4 French small grain production areas. Analyses have shown that the proportion depends on 2 independent factors: the region and the year. Spatial variations were correlated with land use at the regional scale, annual variations being correlated with the climate of the year (3). Implementations of these results into the decision tool are discussed.

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PREDICTING POTATO LATE BLIGHT EPIDEMICS IN PUKEKOHE, NEW ZEALAND

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Background and objectives
Late blight of potato, caused by the Oomycete fungus *Phytohpthora infestans* (Mont.) de Bary, commonly occurs in the humid potato-growing regions of New Zealand. The disease is particularly prevalent in the Pukekohe district throughout most of the potato-growing season (September to January). Frequent fungicide applications are usually required to control the disease in this district. In some growing seasons it may be possible to reduce the total amount of fungicide applied by better targeting the timing of fungicide applications. The objective of this research project was to compare late blight severity in plots left untreated or treated with fungicides applied either calendar-based or according to different forecasting models.

Materials and methods
A field trial was planted on 8 October 2003 in Pukekohe using cultivar Ilam Hardy. The design was an augmented randomised block design with five replicates and two extra plots in the fifth replicate. The six fungicide treatments consisted of untreated control, calendar applications of fungicide mancozeb (every 7 days), a mixture of mancozeb and dimethomorph (Acrobat MZ) applied every 10-14 d, Acrobat MZ applied using the model NegFry first spray timed when accumulated risk valued exceeded 130, Acrobat MZ applied using the model NegFry, first acrobat applied when accumulated risk valued exceeded 160 and Acrobat MZ applied according to the recommendation of PlantPlus (Dacom Automatisering B.V. Netherlands). Disease severity assessment using a key (James, 1971) was carried out at weekly intervals scoring 10 plants per plot a total of six times. Final assessment, including a whole plot score, was carried out on 6 January 2004. AUDPC was calculated for each plot from the mean of the scores made on each plot at each date using the standard formulae. An average plot score was calculated as the mean of the minimum and maximum plot scores. The AUDPC and plot scores were first analysed with a mixed-model analysis using REML, and, as no differences were found, ANOVA was carried out on square-root transformed AUDPC values.

Results and discussion
There was significantly more disease on untreated control plots than fungicide-treated plots. The transformed AUDPC of untreated control plots was 27.9, and the AUDPCs of the other treatments were 3.6 (mancozeb), 4.0 (NegFry 130), 5.2 (NegFry 160), 5.2 (calendar acrobat), and 3.9 (PlantPlus). The $LSD_{0.05}$ was 2.1. There were no differences between fungicide treatments, all treatments suppressed late blight epidemics. The plot score (% disease severity) for untreated plots was 80.5 and scores for treated plots varied from 4.4 to 1.0. The disease was first noted on 29 November 2003, somewhat later than is usual for this area, therefore the final disease levels were lower than expected. Field trial to be completed by February 2005 is underway to determine relationships between late blight severity and the number and timing of fungicide applications in relation to recorded periods of high infection risk, using retrospective analysis with various late blight risk models and the Fungicide Protection Index.

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STRATEGIC PLAN FOR EPIDEMIOLOGICAL RESEARCH AT INRA

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Abstract
INRA, the Institut National de la Recherche Agronomique, is in charge of agricultural research in France. Its research agenda encompasses agricultural production, environmental management, and management of natural resources. Recently (October 4-6, 2004), botanical epidemiologists from different departments of INRA* have met and discussed the current status of their research.

A series of nine themes have been identified:
1- Polyetic processes, linked epidemics, and characterisation of primary inoculum;
2- Canopy architecture and dynamics of epidemics;
3- Large scale epidemiology: from neighbouring fields to landscapes, and regions;
4- Spatio-temporal modelling in botanical epidemiology;
5- Population structures and dynamics at varying scales;
6- Linking population genetics and population dynamics;
7- Field characterisation, risk assessment and analysis;
8- Databases: from data collection, to management, to data mobilisation;
9- Multiple-disease systems: epidemiology and crop loss

These themes and their linkages will briefly be outlined.
Some of these themes are mobilising a fairly large number of scientists (e.g., 1, 2, 3, 6) whereas others are severely understaffed (e.g., 5, 7, 8, 9). Most of these themes represent areas where research is currently taking place. Some of these themes may overlap; some themes may be too large; and others may be too far apart to enable efficient links.
More importantly, new themes that could provide grounds for novel research in botanical epidemiology may need to be created. A discussion of how to best re-arrange and link these themes will be initiated.

* SPE, plant health and environment; EFPA, environment, forests, meadows and freshwater systems, and; MIA, applied mathematics and biometrics

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