Modelling the effect of the grapevine growth and susceptibility on the dynamics of a powdery mildew epidemic

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mildew-related locus. The use of MAS disclosed the existence of seedlings with pyramided five resistance loci within this population.

MATRIX METALLOPROTEINASES ARE INVOLVED IN PLANT RESISTANCE TO *BOTRYTIS CINEREA*.

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Botrytis cinerea causes massive losses to grapevine, strawberry and tomato production. A thorough understanding of the plant defences against *Botrytis* may provide new approaches for disease prevention, thereby securing food quality under changing global conditions. The genome of *Arabidopsis thaliana* contains five matrix metalloproteinases (*At1-MMP* to *At5-MMP*) and their gene expression profiles after *B. cinerea* inoculation were investigated. Using RT-PCR analysis, we found expression of both *At2-MMP* and *At3-MMP* upregulated in *Arabidopsis* leaves after *B. cinerea* infection. Because *At2-MMP* showed the strongest pathogen-responsiveness, we tested the *Arabidopsis at2-mmp* mutant for disease resistance. We found that *at2-mmp* was more susceptible to *B. cinerea* than wild-type plants. Consistently, ectopic over-expression of *At2-MMP* in *Arabidopsis* increased resistance to *B. cinerea* compared to control transformants. We addressed the question whether resistance to *B. cinerea* depended on the salicylate (SA) or jasmonates (JA)/ethylene (ET) defence pathway. *B. cinerea* induced an expression of *At2-MMP* in the signaling-defective mutants including *NahG, jar1.1, ein2-1, npr1-1* comparable to wild-type plants. These data suggest that *B. cinerea*-induced expression of *At2-MMP* might be independent of SA, JA and ET signaling. *At2-MMP* has typical characteristics of other plant and animal MMPs, i.e. the recombinant protein exhibited myelin basic protein proteolytic activity, and was inhibited by the zinc-chelator EDTA in a dose-dependent manner. Considering the conservation and wide distribution of matrix metalloproteinases in the plant kindom, we speculate a general role of MMPs as modulators of plant defences.

RAIN-INDUCED GRAPE BERRY SPLITTING: A PROBLEM OF SURFACE WATER TRANSPORT?

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Cracking of grape berries is thought to result from increased volume and turgor that strains the berry skin beyond its limit of extensibility. Water transport may occur through the vascular system of the vine or through the surface of the berry. We focused on transport through the surface of detached cvs Chardonnay, Müller-Thurgau, and Riesling berries. Sealing the receptacle including the pedicel/fruit juncture with silicon rubber decreased water uptake by about 80%, but transpiration by only 20%. Thus, water uptake in the receptacle region was rapid and must have occurred by viscous flow, but transpiration through the surface was slow and occurred by diffusion. The water potential of cv. Riesling berries decreased throughout development from -0.52 (±0.18) MPa at 20 DAFB to -1.56 (±0.04) MPa at maturity. In the same time period, the permeability of the skin decreased, averaging 4.1 (± 1.2) and 1.6 (±0.0) nm/s in osmotic water uptake and transpiration, respectively. Comparison of our data with those on transport through the vascular system of table grape cv Italia [Lang and Thorpe (1989), downscaled by a factor of 4 because of difference in mass] revealed that on a rainy day, the increase in mass caused by water uptake through the surface may account for up to 38.5% of the increase in berry volume, but transpiration may reduce the mass gain by up to 61.7%.

Lang A., Thorpe M.R., 1989. Xylem, phloem and transpiration flows in a grape: application of a technique for measuring the volume of attached fruits to high resolution using Archimedes' principle. *Journal of Experimental Botany* **40**: 1069-1078.

SECONDARY METABOLITE PRODUCTION IN ESCA-ASSOCIATED FUNGI AND IMPACT OF FUNGICIDES ON THE BIOSYNTHESIS RATE.

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Esca is a destructive disease of grapevine caused by several endophytic fungi, mainly *Phaeoacremonium chlamydospora*, *Phaeomoniella aleophilum* and *Fomitipora mediterranea*. It has been suggested that phytotoxins are secreted by the fungi inducing disease development in the leaves and bunches. Several toxins produced by Esca-associated fungi have been reported. To characterize phytotoxic metabolites produced by the different pathogenic fungi, they were grown individually and in co-culture in submerged cultures. Several metabolites were identified by bioactivity-guided isolation and HPLC-MS as well as by NMR-analysis. The isolation and identification of the compounds were based on phytotoxic, cytotoxic and antimicrobial activities. Several fungal secondary metabolites were identified which have not been reported for Esca-associated fungi. Amongst the bioactive metabolites identified there were siderophores, e.g. triacetylfusigen as well as linoleic acid, methylemodin, phaeofuran and methoxycoumarin. The production rates of the bioactive secondary metabolites were analysed under stress conditions, such as heat stress, salt stress or stress induced by sublethal concentrations of F500, a fungicide of the strobilurin class. It was found that the application of the fungicide at sublethal concentrations under salt stress conditions resulted in a significantly lower production rate of phytotoxic compounds.

MODELLING THE EFFECT OF PLANT GROWTH AND SUSCEPTIBILITY ON THE DEVELOPMENT OF A PLANT DISEASE EPIDEMIC: POWDERY MILDEW OF GRAPEVINE.

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Vitis vinifera is highly susceptible to many pathogens. According to a survey by the European Commission, in 2007, growers in Europe used 70,000 tons of fungicides for grape protection. In term of investment, downy mildew (33%) and powdery mildew (22%) are the main concern, preceding grey mould (9%) and insects (16%), and are responsible for 533M€ expenditure in Europe (data from Bayer CropScience 2005-2008). It is therefore urgent for the grapevine pathosystem to move towards an integrated production of grapes giving priority to production systems that are economically viable with respect to the environment. Understanding the factors that trigger the development of an epidemic is essential if we are to create and implement effective strategies for disease management. Modelling is a key approach allowing to handle various scenarios for pathogen, host, and/or crop management. We have to differentiate empirical models from mechanistic ones. Empirical models tend to summarize the general relationships among the host, the pathogen and the environment and can be used to infer the underlying biology of a system without directly identifying causality (De Wolf and Isard, 2007). For example, they look for the relationships between climatic variables and the appearance of disease symptoms. These kinds of models usually trigger one stage of the disease cycle (e.g.. primary infection, dormancy, etc.). Most of the time, for the grapevine pathosystem, these models are weather-driven with no or little input variables linked to the disease (e.g. source of primary inoculums). They can be developed to predict the risk of disease appearance for one region but need to be calibrated to be useful for another region. They often lack in predicting a level of risk. Mechanistic models provide a convenient means to combine a number of sub-models representing unique parts of the disease cycle to discover causal relationships between the components of the system. These models are used to explore the relationship in the pathosystem for a wide range of scenarios to find the most favourable or unfavourable conditions for disease development or to identify part of the disease cycle that needs further experiments. These types of models are however usually not appropriate for disease risk prediction. The grape-powdery mildew pathosystem is characterised by a polycyclic pathogen capable of explosive multiplication, a host population with a high degree of spatial structure at the field level and with a complex architecture at the individual plant level, exhibiting rapid changes over time. Different kinds of models have been developed, either empirical models, to predict the primary inoculum risk based on more or less complex rules and data (Kast, 1997; Gubler *et al.*, 1999; Gadoury *et al.*, 1990) or mechanistic models to describe the secondary infections or the epidemics' development (Chellemi and Marois, 1992; Sall, 1980). A brief review of these models can be found in Legler *et al.* (2010). However, none of these models are yet able to predict the time and amount of primary inoculum and the protection against the disease is very often systematic. Because of the tight relationship between powdery mildew and its host (Doster and Schnathorst, 1985; Gadoury *et al.*, 2003) and of the spatial localization of primary inoculum on the vine stock, we hypothesized that the dynamic changes in crop structure and susceptibility should be considered as key factors for explaining variability in the severity of epidemic behaviour. Interactions between diseases and vine growth were investigated in several studies (Evans *et al.*, 2006; Gadoury *et al.*, 2001; Zahavi *et al.*, 2001) and we could show that the high heterogeneity in disease progression makes the spatial disease prediction very difficult (Calonnec *et al.*, 2009). Then, we devised a simulation model to better understand the vine/powdery mildew interactions and to explore how the host development and management can modify disease spread. The model is an epidemiological simulation coupling vine growth with the dispersal and disease dynamics of *Erysiphe necator* at the vine stock scale (Calonnec *et al.*, 2008). It is mechanistic, with sub-models either coming from the literature or from empirical data. The model allowed simulating the spatio-temporal dynamics of host growth and epidemic development beginning from a range of climatic conditions, production systems and initial conditions for the density and location of the pathogen. Particularly, the model takes into account shoot topping, which has for effect, to enhance the development of secondary shoots and the emergence of new susceptible leaves during the epidemic process. Input variables are environmental (temperature, wind speed and direction) or related to the pathogen (location and onset of primary infection). Input parameters characterise the crop system (number of buds, distance between buds, shoot topping, vigour), and conditions of growth for the vine and the pathogen. Output describes, at each time step, number, age and pattern of the healthy and infected organs, infected and infectious leaf area and aerial density of spores released. A focus will be done on the bases of the model and the sensitivity of the epidemic to variation of parameters of pathogen, plant growth or crop management as well as the relationship between host and disease variables at key periods in the epidemic process for different conditions of vine vigour.

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ELABORATION AND VALIDATION OF A DOWNY MILDEW FORECAST MODEL REGARDING SOIL-BORNE INFECTIONS.

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