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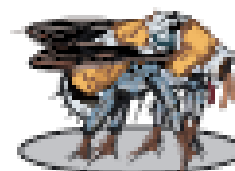
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Integrated management of pest evolution

REPLACEMENT OF THE EUROPEAN WHEAT YELLOW RUST POPULATION

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The wheat yellow rust fungus, *Puccinia striiformis*, represents a crop pathogen with a high potential of aerial spread of spores across large areas and several invasions have been reported in recent years. We studied the origin and level of diversity of isolates of recently spreading yellow rust races in Europe using virulence phenotypic data of 2298 isolates sampled in seven countries between 2000 and 2013. A subset of 342 isolates was additionally investigated by microsatellite markers. At least four race groups of exotic origin (Warrior, Kranich, Triticale-non-aggressive and Triticale aggressive) were identified in the post-2010 populations, where the 'Warrior' race group was present in high frequencies in most of the West European countries and often associated with rust epidemics. Significant genetic divergence was estimated for 'Warrior' and 'Kranich' race groups from the pre-existing European population. It was concluded that they were of non-European origin being genetically related to populations in the near Himalayan region, which represents the pathogen centre of diversity. Although the overall diversity within Europe was higher among post-2011 isolates, compared to isolates sampled from 2000 to 2009, the within race group diversity was still much lower than in the recombinant source populations. The Europe-wide collaboration and compilation of data into a single dataset in a common database proved to be a major advance. It enabled us to identify the current invasion at an early stage, and to assess its implications at field level in many countries. Future collaborative efforts at the European scale should be continued and strengthened for timely early-warning of potential invasions of new variants of important crop pathogens with the capacity to spread very far within a very short period of time.

SPATIAL BLUEPRINTS FOR A MORE DURABLE USE OF RESISTANCE GENES AGAINST PLANT DISEASE

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Resistance to plant pathogens is a cornerstone of integrated pest management. Durable resistance is difficult to achieve because the use of plant resistance selects for pathogen genotypes that break resistance. The effectiveness of resistance genes is therefore often short-lived, and breeders have to continually adapt varieties to challenges by novel genotypes of pathogens. In a modelling study, we explore the effect of resistance gene deployment strategies and pathogen life-cycle components on the useful life of resistance genes. In particular, we try to identify gene deployment strategies that can prolong the useful life of plant resistance.

To develop blueprints for sustainable use of resistance genes, we developed a spatial model on spread of pathogen reproduction and spread on a national level. Blueprints consist of variety choice (gene deployment strategies) and characteristics of spatial deployment, i.e. fraction of resistant fields and degree of clustering of wheat fields. The tested gene deployment strategies include sequential use of varieties with single resistance genes, stacking of resistance genes within one variety, simultaneous planting of multiple varieties with a single resistance gene, and concurrent use that combines the use of a variety with stacked resistance genes and varieties with single resistance genes. We parameterized the model for *Puccinia striiformis* f.sp. *tritici*, the causal agent of yellow rust in wheat. Simulations were run for the whole of France.

The model results indicate that the useful life of a resistance gene is short when a small proportion of the pathogen population belongs to a resistance breaking genotype at the time a resistance is introduced in practice. Furthermore, differences between different gene deployment strategies are small if resistant genotypes are present from the outset. When a resistance breaking pathotype has to emerge by mutation, the useful life of a single-gene resistant variety is shorter than for a double-gene resistant variety (pyramiding of resistance genes). In an environment with a genetic bottleneck between growing seasons, resistance breaking pathogen genotypes for double-resistant varieties emerge each growing season, but are unlikely to survive to the next growing season. It is therefore highly unlikely that they will reach a high enough fraction in the population to render resistance ineffective. Strikingly, when a double resistant variety is deployed together with single resistance varieties with the same resistance genes (concurrent use), resistance breaking pathogen genotypes for double resistant varieties can reach high enough fractions in the population to render the double resistant variety ineffective.

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FUNGICIDE RESISTANCE MANAGEMENT

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The control of fungal plant pathogens has been characterized by repeated cycles of introduction of new fungicides and subsequent loss of efficacy due to the emergence and selection of resistant pathogen strains. Several strategies have been proposed to prevent, or at least delay, resistance problems. Such resistance management strategies should be based on evidence interpreted within a sound experimental and theoretical framework. Industry and regulatory decisions about fungicide resistance management often cannot wait for the accumulation of new evidence, so decisions should be taken by weighing the existing evidence and making judgments about the consequences should decisions prove to be wrong. In discussions on resistance management it is often not explicit what the evidence is, what is opinion and what is speculation. We use a principal from population genetics of clonal organisms to develop a governing principal and use this to review the existing experimental and theoretical evidence on the (i) management of application dose, (ii) managing the number of applications, (iii) use of fungicide mixtures, (iv) use of fungicide alternation, and (v) provision of pathogen refugia, and combinations of these. We review evidence and summarise evidence gaps.

WEED SUPPRESSIVE ROTATIONS: A MODELLING FRAMEWORK FOR SUSTAINABLE WEED CONTROL

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Land scarcity combined with an increasing demand for food, feed and fuel, puts an enormous pressure on agricultural land. Minimizing the negative effect of pests, disease and weeds contributes to increase, or at least maintain, current production levels. A study by Oerke (2006) estimated that, worldwide, actual yield losses due to pest, diseases and weeds are approximately 8% for each of the discerned categories. The potential yield loss of weeds, defined as the yield loss in the absence of control measures, was estimated to be twice as high as the potential yield losses due to pests and pathogens (34% vs. 17%). The large gap between potential and actual estimates of yield loss indicates that current weed control is relatively effective. The concurrent warning is that if we were to lose the ability for controlling weeds, we would face a tremendous problem. Obviously, sustainability of weed management systems is an important pre-requisite for securing future global agricultural production. Diversity is an important element of sustainability, as the continuous reliance on a single control measure will result in the selection of a few difficult-to-control weed species. The fact that herbicide resistant weed populations mostly develop in monoculture or simple rotation systems is a clear consequence of oversimplification.

Crop rotation is an important component of weed management. Each crop, through its sowing time, morphology and growth duration, but also through its associated crop and weed control management, creates the conditions for growth and reproduction of specific weed species, whereas it inflicts serious stresses on others. As a consequence, each crop is commonly associated with its own characteristic weed flora. The alternation of crops creates good opportunities for applying a more diverse set of weed control measures and for that reason crop rotation contributes to the durability of weed management systems. An important question is whether integrated weed management (IWM) strategies applied in a crop rotation context are able to provide a sufficient level of weed control in the short as well as in medium-long term, comparable to that achieved in one-sided herbicide-based management strategies. Are these more diverse systems able to prevent or reverse herbicide resistance, or is the occurrence of herbicide resistance just delayed, and for how long? Finally, does IWM offer potential to reverse the situation on a field heavily infested with a herbicide-resistant weed population?

To answer these questions a modelling framework was developed. Starting point was a model to simulate the dynamics of a weed population in a monoculture cropping system. This model was extended to include the effect of several cultural weed control measures, and to cover the population development of multiple weed species, as well as herbicide and non-herbicide resistant biotypes of the same species. Finally, the monoculture cropping system was replaced by a crop

rotation system. Scenarios were simulated to verify the potential of IWM to replace herbicide based weed management strategies and to avoid selection of herbicide resistant weed communities.

IS THE EFFICACY OF BIOLOGICAL CONTROL AGAINST PLANT DISEASES LIKELY TO BE MORE DURABLE THAN THAT OF CHEMICAL PESTICIDES?

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A meta-analysis of the scientific literature was conducted to assess the potential for plant pathogens and plant pests to become resistant to biocontrol agents. Although many plant bioaggressors are known for their capacity to develop resistance to chemical pesticides or to overcome varietal resistance, only few studies have explored their ability to potentially overcome the effect of biocontrol agents. This presentation will be focused on plant diseases. The case of pests will be discussed in another presentation addressing the resistance of codling moth to *Cydia pomonella* Granulovirus (CpGV).

Reports on the effect of biocontrol agents on plant pathogens often consider only a single strain and one specific stage in the life cycle of the pathogen. However, among the available references analyzed in this review, some studies highlight differences in the sensitivity of various isolates of plant pathogens to biocontrol agents and the capacity of plant pathogens to adapt to biocontrol agents. Is it possible to link specific traits (of the pathogens or of the biocontrol agents) to the loss of effectiveness of biocontrol agents? Data are still too sparse to elaborate a general theory on the use of biocontrol agents in practice. This study highlights the necessity of proper management of these new products to avoid repeating the mistakes made with chemical pesticides.

Significant research efforts are still needed to acquire sufficient knowledge on the mode of action of biocontrol agents to optimize their use, to anticipate the potential failure of biological control and finally to integrate durability concerns in the screening procedure of new biocontrol agents and the careful management of their use once they become commercially available.

IS THE EFFICACY OF BIOLOGICAL CONTROL AGAINST INSECT PESTS LIKELY TO BE MORE DURABLE THAN THAT OF CHEMICAL PESTICIDES? LESSONS LEARNED USING CPGV TO PROTECT APPLES FROM CODLING MOTH

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A meta-analysis of the scientific literature was conducted to assess the potential for insect pests to become resistant to biocontrol agents. Although many plant bioagressors are known for their capacity to develop resistance to chemical pesticides or to overcome varietal resistance, only few studies have explored their ability to potentially overcome the effect of biocontrol agents. This presentation will be focused on the resistance of codling moth to *Cydia pomonella granulovirus* (Mexican isolate) (CpGV-M). The case of resistance to plant diseases will be discussed in another presentation.

The codling moth is the major pest of apple orchards, showing resistances to most chemical insecticides. The use of CpGV-M represented a primary choice for organic producers and a useful alternative in IPM.

Generalization of use of the almost pure genotype CpGV-M against codling moth resulted in an increasing failure of apple protection in various orchards in Europe, due to selection of a CpGV-M resistant insect genotype. Previous work allowed the identification of virus isolates active against these CpGV-M resistant populations, by screening virus natural populations and by selection of existing isolates. However, the question of an "arms race" remained. To evaluate the risk of development of new resistances it is important to understand how, in the natural environment, equilibrium is reached between virus and host populations, and how populations containing mixed genotypes behave.

Various aspects have been addressed both by partners of the PURE project or by other research teams, particularly, the cost for a larva to become resistant; the cost for a virus to overcome this resistance; the possibility of new kinds of resistance, and the importance of retaining genetic variability on the virus population.

We can now draw a more global picture allowing us to better protect our orchards reducing the risk of new outbreaks.

A FRENCH NETWORK FOR THE MONITORING OF CROP PESTS IN A CONTEXT OF IPM IMPLEMENTATION

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The crop health bulletins (BSV) have been implemented since 2009, to succeed the agricultural warnings. They answer the axis 5 of the National Project Ecophyto 2018 which aims to „ Strengthen the monitoring networks of pests and the non target effect of the use of pesticides „.

The protocols were harmonized for the most part of the arable crops. They describe the methods of observations and the variables to be used by all contributors.

The observers are technicians of cooperatives, trading companies, farmers' associations, and institutes, as well as farmers themselves. Advise centers rely on the bulletins to draft their recommendations for the farmers at the field scale.

Every week, the observers record the observations carried out in the fields they are in charge of. With the Internet portal Vigicultures® tool, they can have a look on all observations presented in maps, graphs or templates. Vigicultures® is an Internet portal to provide data from observation networks to the crop health bulletins (BSV). Launched in 2008 the network has today some 30,000 plots, and more than 2 million observations. The data are then validated and linked with forecast models. The bulletin is prepared by each crop facilitator, endorsed by referent groups, and published on the web site of the Regional Chambers of agriculture, as the web-based platform www.yvoir.fr of Arvalis-Institut du végétal.

Beyond this weekly information to help the decision-making, it is important to progress in the protocols for field observations and the available monitoring tools. Annual crop-health reports allow a preventive multi-year management against some pests, in particular by preventive measures. The observations also help the technical institutes (ARVALIS Institut du végétal, Cetiom, ITB) to establish regional and national assessments.

The database gathers enough information to proceed with the analyze of annual data to allow a year-by-year comparison. The poster will present interannual evaluations of cereal and beet diseases, as well as the weevil of the terminal bud of the rape seed.

ATTRACTION AND OVIPOSITION OF PEA WEEVIL (*BRUCHUS PISORUM* L.) ON HOST AND NON-HOST PLANTS

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Pea weevil (*Bruchus pisorum* L.) is a major pest of field pea (*Pisum sativum* L.) worldwide causing a considerable amount losses in yield and quality of the crop. The objectives of this study were to assess attraction of female and male weevils to flower of host genotypes using a Y-tube olfactometer. Furthermore, we determined oviposition preference of the weevil among host and non-host plants in no-choice and dual-choice conditions. Results of behavioral study showed that female weevils were significantly attracted to host plant floral volatile. Moreover, female insects were equally attracted to volatiles of susceptible and moderately resistant host genotypes regardless of their feeding status. Oviposition bioassay results indicate that both under no-choice and dual-choice tests, female weevils significantly prefer to oviposit on *Adet*, (which is a susceptible genotype) compared with two moderately resistant genotypes and non-host plants. The weevils laid significantly less number of eggs on non-host plants as compared to host genotypes. Morphological traits of the pod and seed might be partly attributed to preference of the weevil among test plants for oviposition. The present study demonstrate that floral volatiles play a role in attraction of the weevil, and female weevils showed a clear preference for oviposition to susceptible host genotype compared with moderately resistant one and non-host plants.

SEARCH FOR THE MARKERS ALLOWING FOR DIFFERENTIATION BETWEEN AGRICULTURALLY IMPORTANT THRIPS SPECIES

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Thrips are common plant pests of crops that feed by puncturing the epidermal layer of host tissue and by sucking out the cell contents, causing in this way large damages in the plant quantity and quality. The most harmful species are *Thrips tabaci* Lindeman, *Frankliniella occidentalis* Pergande, and *T. palmi* Karny. The last one is under quarantine regulations in European Union (EPPO/CABI 1997). For non-specialists, larval stages of these agriculturally important pests are morphologically indistinguishable, *e.g.* in the case of *T. palmi* and *F. occidentalis* as well as other frequently occurring thrips.

Taxonomic identification of thrips species is an important element in the integrated and biological plant protection. To ensure proper diagnostics, molecular biology techniques are employed, on the basis of which several protocols for thrips detection have been developed. However, the emergence of new sequences in the GenBank database as well as recent reports revealed the existence of variants of the same genetic marker within one species. Thus, it seems that there is a risk that some of protocols might not amplify all of these variants or might give cross-reactions with non-target species.

In this study, we have focused on the characterization of genetic markers typically used for the differentiation of the most harmful thrips. We analyzed their usefulness in their diagnostics by comparison of DNA sequences obtained in this study for several *Thrips* and *Frankliniella* species as well as data available in GenBank. The analyzes were done on *mtCOI/mtCOII* genes, rDNA fragments, and sequence-characterized amplified region (SCAR) marker obtained in RAPD analysis. In this way we were able to indicate sequences which can be used for genetic differentiation of these harmful pests.

FIRST APPROACH PREDICTING ASCOSPORIC INFECTIONS OF GRAPEVINE POWDERY MILDEW IN THE DOURO WINE REGION USING A MECHANISTIC MODEL

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The grapevine powdery mildew caused by *Erysiphe necator*, is the main disease of the Douro Wine Region (DWR), having in this region an endemic behaviour. This region have around 45000 ha of vineyards, divided in three sub-regions clearly distinct from the climatic point of view. The fungus overwinters mainly in the form of clamosthelia since the flag shoots (caused by the parasitized buds) are rarely observed. The beginning of his capture always occurs before budbreak (BBCH stage 05) and usually end by the ripening phase (BBCH stage 69–71). Disease management strategy is usually based on fungicide applications, according the phenology, performed from pre-flowering (stage BBCH 53) to bunch closure (BBCH stage 79). The existence of weather stations in the region allowed to collect the data necessary as input for running the model for ascospore infections developed by the University of Piacenza (Italy) and provided by Horta srl (www.horta-srl.com). This model simulates the ascospores maturation curve, the infection periods, the progress of latency and the possible symptoms onset. In 2014 a collaboration was started in order to test the applicability of this model in DWR with the aim of reducing the number of treatments in the control of the disease throughout the vegetative cycle, minimizing their impact on the environment and maximizing their efficacy and, finally, reducing input costs for growers.