A link between host plant adaptation and pesticide resistance in the polyphagous spider mite Tetranychus urticae

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Volume	110
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Pages	E113-E122
Publication	Proceedings of the National Academy of Sciences
Date	01/08/2013
DOI	10.1073/pnas.1213214110
Résumé	Plants produce a wide range of allelochemicals to defend against herbivore attack, and generalist herbivores have evolved mechanisms to avoid, sequester, or detoxify a broad spectrum of natural defense compounds. Successful arthropod pests have also developed resistance to diverse classes of pesticides and this adaptation is of critical importance to agriculture. To test whether mechanisms to overcome plant defenses predispose the development of pesticide resistance, we examined adaptation of the generalist two-spotted spider mite, Tetranychus urticae, to host plant transfer and pesticides. T. urticae is an extreme polyphagous pest with more than 1,100 documented hosts and has an extraordinary ability to develop pesticide resistance. When mites from a pesticide-susceptible strain propagated on bean were adapted to a challenging host (tomato), transcriptional responses increased over time with ∼7.5% of genes differentially expressed after five generations. Whereas many genes with altered expression belonged to known detoxification families (like P450 monooxygenases), new gene families not previously associated with detoxification in other herbivores showed a striking response, including ring-splitting dioxygenase genes acquired by horizontal gene transfer. Strikingly, transcriptional profiles of tomato-adapted mites resembled those of multipesticide-resistant strains, and adaptation to tomato decreased the susceptibility to unrelated pesticide classes. Our findings suggest key roles for both an expanded environmental response gene repertoire and transcriptional regulation in the life history of generalist herbivores. They also support a model whereby selection for the ability to mount a broad response to the diverse defense chemistry of plants predisposes the evolution of pesticide resistance in generalists.

An insight into critical endocycle genes for plant-parasitic nematode feeding sites establishment

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Volume	8
Numéro	6
Pages	e24223
Publication	Plant signaling & behavior
Date	Jun 2013
DOI	10.4161/psb.24223
Résumé	Root-knot and cyst nematodes are biotrophic parasites that invade the root apex of host plants and migrate toward the vascular cylinder where they cause the differentiation of root cells into galls (or root-knots) containing hypertrophied multinucleated giant-feeding cells, or syncytia, respectively. The precise molecular mechanisms that drive the formation of such unique nematode feeding sites are still far-off from being completely understood. The diverse gene expression changes occurring within the host cells suggest that both types of plant-parasitic nematodes modulate a variety of plant processes. Induction and repression of genes belonging to the host cell cycle control machinery have shown to be essential to drive the formation of such specialized nematode feeding cells. We demonstrate that nematodes usurp key components regulating the endocycle in their favor. This is illustrated by the involvement of anaphase-promoting complex (APC) genes (CCS52A and CCS52B), the endocycle repressor DP-E2F-like (E2F/DEL1) gene and the ROOT HAIRLESS 1 PROTEIN (RHL1), which is part of a multiprotein complex of the toposiomerase VI, in the proper formation of nematode feeding sites. Altering the expression of these genes in Arabidopsis plants by down- or overexpressing strategies strongly influences the extent of endoreduplication in both types of nematode feeding site leading to a disturbance of the nematode's life cycle and reproduction.

A PCR-based method for estimating parasitism rates in the olive fly parasitoids Psyttalia concolor and P. lounsburyi (Hymenoptera: Braconidae)

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Volume	67
Numéro	1
Pages	44-50
Publication	Biological Control
Date	October 2013
DOI	10.1016/j.biocontrol.2013.07.001
Résumé	Abstract Several parasitoids of the genus Psyttalia have been repeatedly introduced as biological control agents against the principal pest of olive, the fly Bactrocera oleae. However, few of the parasitoids released have become established and proved effective against B. oleae. It may however still be possible to find effective biological control agents adapted to local environmental conditions among the highly diverse Psyttalia species and populations infesting B. oleae worldwide. For this purpose, we have developed a rapid, sensitive molecular method based on the polymerase chain reaction (PCR) for estimating and comparing the parasitism success of Psyttalia parasitoids through the detection of eggs and larvae within the host. This method was tested and shown to be appropriate for two Psyttalia species (Psyttalia concolor and Psyttalia lounsburyi). The possible detection of DNA was also demonstrated for several populations of these species and for other Psyttalia species, namely Psyttalia humilis and Psyttalia ponerophaga. For P. concolor and P. lounsburyi, a strong correlation was observed between the parasitism rates estimated by PCR, host larva dissection and counts of emerging parasitoids. No significant difference was found between the rates of parasitism estimated by host larva dissection and PCR, whereas the rates of parasitism estimated by PCR were significantly higher than those estimated from emergence, suggesting occurrence of mortality during the parasitoid development. This PCR method is thus highly reliable and provides an objective criterion for estimating the efficacy of biological control agent candidates from diverse taxa and populations of Psyttalia.

A review of mate-finding Allee effects in insects: from individual behavior to population management

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Volume	146
Numéro	1
Pages	79–92
Publication	Entomologia Experimentalis et Applicata
Date	2013
DOI	10.1111/eea.12021
Résumé	Like other animals and plants, insects may find it difficult to survive and reproduce in small populations, to the extent that their long-term persistence may be jeopardized. The Allee effect is a theoretical framework that formalizes this decrease in survival or reproduction in small populations, and the resulting decrease in population growth and persistence. Mating failure in low-density populations is likely to generate an Allee effect and, therefore, has a major effect on the functioning of small populations. Here, I review mate-finding Allee effects in insect species, and their consequences for individual mating success, population dynamics, and population management. I focus, in particular, on the comparison of theoretical expectations with observational data. Several studies have reported some degree of mating failure at low density. However, almost none of the datasets available allow comparison with the predictions of classical mate-searching models. A few studies at the population level have reported the co-occurrence of mating failure at low density and a demographic Allee effect, but no study has yet clearly demonstrated a causal relationship between mating failure and lower rates of population growth. Thus, although the theoretical development of management tactics based on Allee effects is considered promising, the current lack of evidence supporting this strategy limits its potential relevance. I call here for a more rigorous approach to the study of mate-finding Allee effects and propose new approaches for this purpose.

Assessment of Potential Sublethal Effects of Various Insecticides on Key Biological Traits of The Tobacco Whitefly, Bemisia tabaci

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Auteur	Yu Zheng
Auteur	Qiyong Weng
Auteur	Antonio Biondi
Auteur	Nicolas Desneux
Auteur	Kongming Wu
Volume	9
Numéro	3
Pages	246-255
Publication	International Journal of Biological Sciences
Date	2013-2-27
DOI	10.7150/ijbs.5762
Résumé	The tobacco whitefly Bemisia tabaci is one of the most devastating pests worldwide. Current management of B. tabaci relies upon the frequent applications of insecticides. In addition to direct mortality by typical acute toxicity (lethal effect), insecticides may also impair various key biological traits of the exposed insects through physiological and behavioral sublethal effects. Identifying and characterizing such effects could be crucial for understanding the global effects of insecticides on the pest and therefore for optimizing its management in the crops. We assessed the effects of sublethal and low-lethal concentrations of four widely used insecticides on the fecundity, honeydew excretion and feeding behavior of B. tabaci adults. The probing activity of the whiteflies feeding on treated cotton seedlings was recorded by an Electrical Penetration Graph (EPG). The results showed that imidacloprid and bifenthrin caused a reduction in phloem feeding even at sublethal concentrations. In addition, the honeydew excretions and fecundity levels of adults feeding on leaf discs treated with these concentrations were significantly lower than the untreated ones. While, sublethal concentrations of chlorpyrifos and carbosulfan did not affect feeding behavior, honeydew excretion and fecundity of the whitefly. We demonstrated an antifeedant effect of the imidacloprid and bifenthrin on B. tabaci, whereas behavioral changes in adults feeding on leaves treated with chlorpyrifos and carbosulfan were more likely caused by the direct effects of the insecticides on the insects' nervous system itself. Our results show that aside from the lethal effect, the sublethal concentration of imidacloprid and bifenthrin impairs the phloem feeding, i.e. the most important feeding trait in a plant protection perspective. Indeed, this antifeedant property would give these insecticides potential to control insect pests indirectly. Therefore, the behavioral effects of sublethal concentrations of imidacloprid and bifenthrin may play an important role in the control of whitefly pests by increasing the toxicity persistence in treated crops.

Biological activities of lignans and neolignans on the aphid Myzus persicae (Sulzer)

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Auteur	Jacques Attoumbré
Auteur	Philippe Giordanengo
Auteur	Sylvie Baltora-Rosset
Volume	7
Numéro	2
Pages	225-233
Publication	Arthropod-Plant Interactions
Date	2013
DOI	10.1007/s11829-012-9236-x

Biology and developmental strategies of the Palaearctic parasitoid Bracon nigricans (Hymenoptera: Braconidae) on the neotropical moth Tuta absoluta (Lepidoptera: Gelechiidae)

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Auteur	Nicolas Desneux
Auteur	Edwige Amiens-Desneux
Auteur	Gaetano Siscaro
Auteur	Lucia Zappalà
Volume	106
Numéro	4
Pages	1638-1647
Publication	Journal of economic entomology
Date	Aug 2013
Résumé	During the years after the invasion of Western Palaearctic tomato crops by the South American tomato leafminer, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae), several indigenous generalist parasitoids have been recorded on this new host. Among these, Bracon nigricans Szépligeti (Hymenoptera: Braconidae) is widely distributed in the Palaearctic region, and has been frequently recovered from South American tomato leafminer. However, most of the available data on this species deal with taxonomic aspects and its recovery in faunistic surveys. The current study documents the biology of B. nigricans on South American tomato leafminer, and provides a scientific basis for its inclusion in South American tomato leafminer management programs in Afro-Eurasia. We studied several B. nigricans life-history traits relevant to juvenile development and reproduction by females. B. nigricans proved to be an idiobiont and a synovigenic ectoparasitoid of mature South American tomato leafminer larvae. Several B. nigricans reproductive traits were influenced by the age of the mothers; on average, the progeny had a slightly male-biased sex ratio (60% males) and a low rate of successful development (37%). Adult females lived 42.8 d and produced an average of 29.8 offspring. These biological parameters yielded an intrinsic rate of increase of 0.052. Females showed behavioral plasticity in host use, as initial host paralysis was followed by host-feeding, oviposition, or host rejection, with a consequent high mortality rate among hosts exposed to parasitism. Although further field studies are needed, these data, obtained in laboratory conditions, suggest that B. nigricans should be considered as a potential biological control agent of in newly invaded areas of the Palaearctic region.

Characterization and choice of Xiphinema nematodes for breeding a stable resistance to fanleaf disease in grapevine

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Auteur	Kunztmann P.
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Auteur	Lemaire O.
Auteur	Ollat N.
Auteur	Demangeat G.
Volume	27
Pages	9-22
Publication	Innovations Agronomiques
Date	2013

Combined phosphate and nitrogen limitation generates a nutrient stress transcriptome favorable for arbuscular mycorrhizal symbiosis in Medicago truncatula

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Auteur	Stéphanie Huguet
Auteur	Daniel Wipf
Auteur	Nicolas Pauly
Auteur	Hoai-Nam Truong
Volume	199
Numéro	1
Pages	188-202
Publication	The New phytologist
Date	Jul 2013
DOI	10.1111/nph.12234
Résumé	Arbuscular mycorrhizal (AM) symbiosis is stimulated by phosphorus (P) limitation and contributes to P and nitrogen (N) acquisition. However, the effects of combined P and N limitation on AM formation are largely unknown. Medicago truncatula plants were cultivated in the presence or absence of Rhizophagus irregularis (formerly Glomus intraradices) in P-limited (LP), N-limited (LN) or combined P- and N-limited (LPN) conditions, and compared with plants grown in sufficient P and N. The highest AM formation was observed in LPN, linked to systemic signaling by the plant nutrient status. Plant free phosphate concentrations were higher in LPN than in LP, as a result of cross-talk between P and N. Transcriptome analyses suggest that LPN induces the activation of NADPH oxidases in roots, concomitant with an altered profile of plant defense genes and a coordinate increase in the expression of genes involved in the methylerythritol phosphate and isoprenoid-derived pathways, including strigolactone synthesis genes. Taken together, these results suggest that low P and N fertilization systemically induces a physiological state of plants favorable for AM symbiosis despite their higher P status. Our findings highlight the importance of the plant nutrient status in controlling plant-fungus interaction.

Conserved DNA Motifs, Including the CENP-B Box-like, Are Possible Promoters of Satellite DNA Array Rearrangements in Nematodes

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Auteur	Pierre Abad
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Volume	8
Numéro	6
Pages	e67328
Publication	PLoS ONE
Date	June 27, 2013
DOI	10.1371/journal.pone.0067328
Résumé	Tandemly arrayed non-coding sequences or satellite DNAs (satDNAs) are rapidly evolving segments of eukaryotic genomes, including the centromere, and may raise a genetic barrier that leads to speciation. However, determinants and mechanisms of satDNA sequence dynamics are only partially understood. Sequence analyses of a library of five satDNAs common to the root-knot nematodes Meloidogyne chitwoodi and M. fallax together with a satDNA, which is specific for M. chitwoodi only revealed low sequence identity (32–64%) among them. However, despite sequence differences, two conserved motifs were recovered. One of them turned out to be highly similar to the CENP-B box of human alpha satDNA, identical in 10–12 out of 17 nucleotides. In addition, organization of nematode satDNAs was comparable to that found in alpha satDNA of human and primates, characterized by monomers concurrently arranged in simple and higher-order repeat (HOR) arrays. In contrast to alpha satDNA, phylogenetic clustering of nematode satDNA monomers extracted either from simple or from HOR array indicated frequent shuffling between these two organizational forms. Comparison of homogeneous simple arrays and complex HORs composed of different satDNAs, enabled, for the first time, the identification of conserved motifs as obligatory components of monomer junctions. This observation highlights the role of short motifs in rearrangements, even among highly divergent sequences. Two mechanisms are proposed to be involved in this process, i.e., putative transposition-related cut-and-paste insertions and/or illegitimate recombination. Possibility for involvement of the nematode CENP-B box-like sequence in the transposition-related mechanism and together with previously established similarity of the human CENP-B protein and pogo-like transposases implicate a novel role of the CENP-B box and related sequence motifs in addition to the known function in centromere protein binding.

Development, validation and use of a dynamic model for simulate the climate conditions in a large scale greenhouse equipped with insect-proof nets

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Volume	98
Pages	54-61
Publication	Computers and Electronics in Agriculture
Date	October 2013
DOI	10.1016/j.compag.2013.07.008
Résumé	Abstract Easily simulating inside climate conditions in the large insect screened Canary type greenhouses used intensively along the Moroccan coast is particularly important in enhancing this production system. We have therefore developed a global greenhouse climate model based on combined sensible and latent heat balances in which the ventilation flux has been simulated combining buoyancy forces and wind effect. In the region of Agadir in South Morocco, a big commercial greenhouse, farming tomatoes and equipped with insect-proof nets provided the measurements which validated this model. The precise estimation of sensible and latent heat fluxes exchanged among the different components of the greenhouse balanced the energy and the mass in the system so that inside air temperature and water vapour content were deduced accurately. A study on the effects of various types of insect-proof nets was carried out later to analyse the impact on the climate of varying the net mesh size in the greenhouse. It was shown that with an unchanged open vent surface, the use of an anti-Thrips net was incompatible most of time with a satisfactory climate for plant growth in the coastal areas of southern Morocco.

Diversity and Evolution of Root-Knot Nematodes, Genus Meloidogyne: New Insights from the Genomic Era

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Auteur	Laetitia Perfus-Barbeoch
Auteur	Pierre Abad
Volume	51
Numéro	1
Publication	Annual Review of Phytopathology
Date	2013
DOI	10.1146/annurev-phyto-082712-102300
Résumé	Root-knot nematodes (RKNs) (Meloidogyne spp.) are obligate endoparasites of major worldwide economic importance. They exhibit a wide continuum of variation in their reproductive strategies, ranging from amphimixis to obligatory mitotic parthenogenesis. Molecular phylogenetic studies have highlighted divergence between mitotic and meiotic parthenogenetic RKN species and probable interspecific hybridization as critical steps in their speciation and diversification process. The recent completion of the genomes of two RKNs, Meloidogyne hapla and Meloidogyne incognita, which exhibit striking differences in their mode of reproduction (with and without sex, respectively), their geographic distribution, and their host range, has opened the way for deciphering the evolutionary significance of (a)sexual reproduction in these parasites. Accumulating evidence suggests that whole genome duplication (in M. incognita) and horizontal gene transfers (HGTs) represent major forces that have shaped the genome of current RKN species and may account for the extreme adaptive capacities and parasitic success of these nematodes. Expected final online publication date for the Annual Review of Phytopathology Volume 51 is August 4, 2013. Please see http://www.annualreviews.org/catalog/pubdates.aspx for revised estimates.

Do Biopesticides Affect the Demographic Traits of a Parasitoid Wasp and Its Biocontrol Services through Sublethal Effects?

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Volume	8
Numéro	9
Pages	e76548
Publication	PLoS ONE
Date	September 30, 2013
DOI	10.1371/journal.pone.0076548
Résumé	Pesticide risk assessments are usually based on short-term acute toxicity tests, while longer-term population dynamic related traits, critical to the success of biological control and Integrated Pest Management (IPM) programs, are often overlooked. This is increasingly important with respect to new biopesticides that frequently cause no short-term acute effects, but that can induce multiple physiological and behavioral sublethal effects, leading to a decrease in population growth and ecosystem services. In this study we assessed the lethal and sublethal effects of six biopesticides [abamectin, azadirachtin, Bacillus thuringiensis, borax plus citrus oil (Prev-Am®), emamectin benzoate, and spinosad], used in tomato crops to control the invasive pest Tuta absoluta (Lepidoptera: Gelechiidae), on adults and pupae of the parasitoid Bracon nigricans (Hymenoptera: Braconidae). Data on female survival and production of female offspring were used to calculate population growth indexes as a measure of population recovery after pesticide exposure. Spinosad caused 100% and 80% mortality in exposed adults (even 10 d after the treatment) and pupae, respectively. Although most of the biopesticides had low levels of acute toxicity, multiple sublethal effects were observed. The biocontrol activity of both females that survived 1-h and 10-d old residues, and females that emerged from topically treated pupae was significantly affected by the application of the neurotoxic insecticides emamectin benzoate and abamectin. Furthermore, very low B. nigricans demographic growth indices were estimated for these two insecticides, indicating potential local extinction of the wasp populations. Among the tested products, Bt proved to be the safest for B. nigricans adults and pupae. Our findings emphasize that acute toxicity assessment alone cannot fully predict the actual impact of pesticides on non-target parasitoids. Thus, sublethal effects related to the species specific life-history variables must be carefully considered in order to assess pesticide risks and to incorporate new pesticides, including biopesticides, into IPM programmes.

Does prescribed burning affect leaf secondary metabolites in pine stands?

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Auteur	C Fernandez
Volume	39
Numéro	3
Pages	398-412
Publication	Journal of chemical ecology
Date	Mar 2013
DOI	10.1007/s10886-013-0256-5
Résumé	Prescribed burning (PB) is gaining popularity as a low-cost forest protection measure that efficiently reduces fuel build-up, but its effects on tree health and growth are poorly understood. Here, we evaluated the impact of PB on plant defenses in Mediterranean pine forests (Pinus halepensis and P. nigra ssp. laricio). These chemical defenses were estimated based on needle secondary metabolites (terpenes and phenolics including flavonoids) and discussed in terms of chlorophyll fluorescence and soil nutrients. Three treatments were applied: absence of burning (control plots); single burns (plots burned once); and repeated burns (plots burned twice). For single burns, we also explored changes over time. In P. laricio, PB tended to trigger only minor modifications consisting exclusively of short-lived increases (observed within 3 months after PB) in flavonoid index, possibly due to the leaf temperature increase during PB. In P. halepensis, PB had detrimental effects on physiological performance, consisting of (i) significant decreases in actual PSII efficiency (ΦPSII) in light-adapted conditions after repeated PB, and (ii) short-lived decreases in variable-to-maximum fluorescence ratio (Fv/Fm) after single PB, indicating that PB actually stressed P. halepensis trees. Repeated PB also promoted terpene-like metabolite production, which increased 2 to 3-fold compared to control trees. Correlations between terpene metabolites and soil chemistry were found. These results suggest that PB impacts needle secondary metabolism both directly (via a temperature impact) and indirectly (via soil nutrients), and that these impacts vary according to species/site location, frequency and time elapsed since last fire. Our findings are discussed with regard to the use of PB as a forest management technique and its consequences on plant investment in chemical defenses.

Drosophila suzukii, vers une lutte biologique contre ce ravageur des fruits rouges.

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Auteur	Poyet M
Auteur	Ris N
Auteur	Gibert P
Volume	660
Pages	34-38
Publication	Phytoma, la défense des végétaux
Date	2013

Ectopic expression of Kip-related proteins restrains root-knot nematode-feeding site expansion

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Auteur	Pierre Abad
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Publication	The New phytologist
Date	Apr 10, 2013
DOI	10.1111/nph.12255
Résumé	The development of nematode feeding sites induced by root-knot nematodes involves the synchronized activation of cell cycle processes such as acytokinetic mitoses and DNA amplification. A number of key cell cycle genes are reported to be critical for nematode feeding site development. However, it remains unknown whether plant cyclin-dependent kinase (CDK) inhibitors such as the Arabidopsis interactor/inhibitor of CDK (ICK)/Kip-related protein (KRP) family are involved in nematode feeding site development. This study demonstrates the involvement of Arabidopsis ICK2/KRP2 and ICK1/KRP1 in the control of mitosis to endoreduplication in galls induced by the root-knot nematode Meloidogyne incognita. Using ICK/KRP promoter-GUS fusions and mRNA in situ hybridizations, we showed that ICK2/KRP2, ICK3/KRP5 and ICK4/KRP6 are expressed in galls after nematode infection. Loss-of-function mutants have minor effects on gall development and nematode reproduction. Conversely, overexpression of both ICK1/KRP1 and ICK2/KRP2 impaired mitosis in giant cells and blocked neighboring cell proliferation, resulting in a drastic reduction of gall size. Studying the dynamics of protein expression demonstrated that protein levels of ICK2/KRP2 are tightly regulated during giant cell development and reliant on the presence of the nematode. This work demonstrates that impeding cell cycle progression by means of ICK1/KRP1 and ICK2/KRP2 overexpression severely restricts gall development, leading to a marked limitation of root-knot nematode development and reduced numbers of offspring.

Effects of azadirachtin on Tetranychus urticae (Acari: Tetranychidae) and its compatibility with predatory mites (Acari: Phytoseiidae) on strawberry

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Auteur	Dori Edson Nava
Volume	69
Numéro	1
Pages	75-80
Publication	Pest management science
Date	Jan 2013
DOI	10.1002/ps.3364
Résumé	BACKGROUND: The spider mite, Tetranychus urticae, is the major strawberry pest in Brazil. The main strategies for its control comprise synthetic acaricides and predatory mites. The recent register of a commercial formula of azadirachtin (Azamax(®) 12 g L(-1)) can be viable for control of T. urticae. In this work, the effects of azadirachtin on T. urticae and its compatibility with predatory mites Neoseiulus californicus and Phytoseiulus macropilis in the strawberry crop were evaluated. RESULTS: Azadirachtin was efficient against T. urticae, with a mortality rate similar to that of abamectin. In addition, the azadirachtin showed lower biological persistence (7 days) than abamectin (21 days). Azadirachtin did not cause significant mortality of adult predatory mites (N. californicus and P. macropilis), but it did reduce fecundity by 50%. However, egg viability of the azadirachtin treatments was similar to that of the control (>80% viability). The use of azadirachtin and predatory mites is a valuable tool for controlling T. urticae in strawberry crop. CONCLUSIONS: Azadirachtin provided effective control of T. urticae and is compatible with the predatory mites N. californicus and P. macropilis. It is an excellent tool to be incorporated into integrated pest management for strawberry crop in Brazil.

Enhanced levels of plant cell cycle inhibitors hamper root-knot nematode-induced feeding site development

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Volume	8
Numéro	12
Pages	e26409
Publication	Plant Signaling & Behavior
Date	Dec 2013
DOI	10.4161/psb.26409
Résumé	Root-knot nematodes (RKN) are highly specialized, obligatory plant parasites. These animals reprogram root cells to form large, multinucleate, and metabolically active feeding cells (giant cells) that provide a continuous nutrient supply during 3-6 weeks of the nematode's life. The establishment and maintenance of physiologically fully functional giant cells are necessary for the survival of these nematodes. As such, giant cells may be useful targets for applying strategies to reduce damage caused by these nematodes, aiming the reduction of their reproduction. We have recently reported the involvement of cell cycle inhibitors of Arabidopsis, named Kip-Related Proteins (KRPs), on nematode feeding site ontogeny. Our results have demonstrated that this family of cell cycle inhibitors can be envisaged to efficiently disrupt giant cell development, based on previous reports which showed that alterations in KRP concentration levels can induce cell cycle transitions. Herein, we demonstrated that by overexpressing KRP genes, giant cells development is severely compromised as well as nematode reproduction. Thus, control of root-knot nematodes by modulating cell cycle-directed pathways through the enhancement of KRP protein levels may serve as an attractive strategy to limit damage caused by these plant parasites.

Environment Exploration and Colonization Behavior of the Pea Aphid Associated with the Expression of the foraging Gene

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Auteur	Laury Arthaud
Auteur	Marcel Amichot
Auteur	Alain Robichon
Volume	8
Numéro	5
Pages	e65104
Publication	PLoS ONE
Date	May 29, 2013
DOI	10.1371/journal.pone.0065104
Résumé	Aphids respond to specific environmental cues by producing alternative morphs, a phenomenon called polyphenism, but also by modulating their individual behavior even within the same morph. This complex plasticity allows a rapid adaptation of individuals to fluctuating environmental conditions, but the underlying genetic and molecular mechanisms remain largely unknown. The foraging gene is known to be associated with behavior in various species and has been shown to mediate the behavioral shift induced by environmental changes in some insects. In this study, we investigated the function of this gene in the clonal forms of the pea aphid Acyrthosiphon pisum by identifying and cloning cDNA variants, as well as analyzing their expression levels in developmental morphs and behavioral variants. Our results indicate that the expression of foraging changes at key steps of the aphid development. This gene is also highly expressed in sedentary wingless adult morphs reared under crowded conditions, probably just before they start walking and foraging. The cGMP-dependent protein kinase (PKG) enzyme activity measured in the behavioral variants correlates with the level of foraging expression. Altogether, our results suggest that foraging could act to promote the shift from a sedentary to an exploratory behavior, being thus involved in the behavioral plasticity of the pea aphid.

Environment: Overhaul pesticide testing on bees

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Auteur	Mickaël Henry
Auteur	Nicolas Desneux
Volume	497
Numéro	7448
Pages	188-188
Publication	Nature
Date	May 9, 2013
DOI	10.1038/497188a

Estimation of the dispersal of a major pest of maize by cline analysis of a temporary contact zone between two invasive outbreaks

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Auteur	Thibaut Morel-Journel
Auteur	Thomas Guillemaud
Pages	n/a-n/a
Publication	Molecular Ecology
Date	September 1, 2013
DOI	10.1111/mec.12489

Evidence for specific genotype-dependent immune priming in the lophotrochozoan Biomphalaria glabrata snail

Auteur	Julien Portela
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Auteur	Jérôme Boissier
Auteur	Christine Coustau
Auteur	Guillaume Mitta
Auteur	André Théron
Auteur	Benjamin Gourbal
Volume	5
Numéro	3
Pages	261-276
Publication	Journal of innate immunity
Date	2013
DOI	10.1159/000345909
Résumé	Historically, the prevailing view in the field of invertebrate immunity was that invertebrates that do not possess acquired adaptive immunity rely on innate mechanisms with low specificity and no memory. Several recent studies have shaken this paradigm and suggested that the immune defenses of invertebrates are more complex and specific than previously thought. Mounting evidence has shown that at least some invertebrates (mainly Ecdysozoa) show high levels of specificity in their immune responses to different pathogens, and that subsequent reexposure may result in enhanced protection (recently called 'immune priming'). Here, we investigated immune priming in the Lophotrochozoan snail species Biomphalaria glabrata, following infection by the trematode pathogen Schistosoma mansoni. We confirmed that snails were protected against a secondary homologous infection whatever the host strain. We then investigated how immune priming occurs and the level of specificity of B. glabrata immune priming. In this report we confirmed that immune priming exists and we identified a genotype-dependent immune priming in the fresh-water snail B. glabrata.

Evolution of a physiological trade-off in a parasitoid wasp: how best to manage lipid reserves in a warming environment

Auteur	Damien Denis
Auteur	Joan van Baaren
Auteur	Jean-Sébastien Pierre
Auteur	Eric Wajnberg
Volume	148
Numéro	1
Pages	27–38
Publication	Entomologia Experimentalis et Applicata
Date	2013
DOI	10.1111/eea.12075
Résumé	Ectothermic animals, especially insects, are probably the ones most affected, for better or worse, by variable thermic environment, for example in the case of global warming, as their metabolic rate is controlled by the ambient temperature. Parasitoid insects, at the third trophic level, are widely distributed worldwide, and they influence the population dynamics of their highly diverse insect hosts. An important feature of parasitoid wasps is their supposedly limited or non-existent capacity to synthesize lipids during adulthood. As lipid level can be expected to determine whether they engage in maintenance or reproduction, parasitoid wasps are useful biological models for investigating how evolutionary trade-offs in energy allocation to maintenance or reproduction are likely to alter in response to global climate change. To address this, we developed a state-dependent stochastic dynamic programming model, which we parameterized using empirically derived data. The model shed light on the adaptive response of parasitoids with regard to three traits: activity rate, initial egg load, and egg production over the adult female's life span. We show that in a warmer climate, parasitoids devote smaller amounts of lipids to their reproductive effort and favour maintenance over reproduction. However, the bias towards maintenance is reduced when the parasitoids are able to adapt their activity rate to the features of their environment. This model could be tailored to a wide range of organisms with limited energy intake during their adult life.

Expression Dynamics of the Medicago truncatula Transcriptome during the Symbiotic Interaction with Sinorhizobium meliloti: Which Role for Nitric Oxide?

Auteur	Alexandre Boscari
Auteur	Jennifer del Giudice
Auteur	Alberto Ferrarini
Auteur	Luca Venturini
Auteur	Anne-Lise Zaffini
Auteur	Massimo Delledonne
Auteur	Alain Puppo
Volume	161
Numéro	1
Pages	425-439
Publication	Plant physiology
Date	Jan 2013
DOI	10.1104/pp.112.208538
Résumé	Medicago truncatula is one of the most studied model plants. Nevertheless, the genome of this legume remains incompletely determined. We used RNA-Seq to characterize the transcriptome during the early organogenesis of the nodule and during its functioning. We detected 37,333 expressed transcription units; to our knowledge, 1,670 had never been described before and were functionally annotated. We identified 7,595 new transcribed regions, mostly corresponding to 5' and 3' untranslated region extensions and new exons associated with 5,264 previously annotated genes. We also inferred 23,165 putative transcript isoforms from 6,587 genes and measured the abundance of transcripts for each isoform, which suggests an important role for alternative splicing in the generation of proteome diversity in M. truncatula. Finally, we carried out a differential expression analysis, which provided a comprehensive view of transcriptional reprogramming during nodulation. In particular, depletion of nitric oxide in roots inoculated with Sinorhizobium meliloti greatly increased our understanding of the role of this reactive species in the optimal establishment of the symbiotic interaction, revealing differential patterns of expression for 2,030 genes and pointing to the inhibition of the expression of defense genes.

Extending the concept of keystone species to communities and ecosystems

Auteur	Nicolas Mouquet
Auteur	Dominique Gravel
Auteur	François Massol
Auteur	Vincent Calcagno
Éditeur	Bernd Blasius
Volume	16
Numéro	1
Pages	1-8
Publication	Ecology Letters
Date	01/2013
DOI	10.1111/ele.12014

Extensive inter- and intraspecific venom variation in closely related parasites targeting the same host: The case of Leptopilina parasitoids of Drosophila

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Auteur	Emeline Deleury
Auteur	Caroline Anselme
Auteur	Dominique Cazes
Auteur	Julie Poulain
Auteur	Carole Azema-Dossat
Auteur	Maya Belghazi
Auteur	Jean-Luc Gatti
Auteur	Marylène Poirié
Publication	Insect Biochemistry and Molecular Biology
Date	2013
DOI	10.1016/j.ibmb.2013.03.010
Résumé	Abstract The arms race between immune suppressive parasites that produce virulence factors and hosts that evolve resistance to these factors is suggested to be a key driver for the diversification of both partners. However, little is known regarding the diversity of virulence factors in closely related parasites or the mechanisms underlying the variation of virulence. One of the best-described model to address this issue is the interaction between Leptopilina parasitic wasps and their Drosophila hosts, in which variation of virulence is well documented. Thanks to a combined transcriptomic and proteomic approach, we have identified the main secreted proteins in the venom of Leptopilina heterotoma (Gotheron strain, 66 proteins) and of two well-characterized strains of Leptopilina boulardi, ISm and ISy (65 and 49 proteins, respectively). Results revealed significant quantitative differences in venom components between the L. boulardi strains, in agreement with their different virulence properties. Strikingly, the two related Leptopilina species did not share any abundant venom protein. The main identified proteins in L. boulardi were RhoGAPs and serpins while an aspartylglucosaminidase was found abundant in L. heterotoma. The extensive quantitative variation observed between these species may be related with their use of different virulence strategies and/or to differences in their host range (specialist versus generalist). Altogether, our data suggests that parasitoid venom can quickly evolve, mainly through rapid changes in regulation of gene expression. It also evidences venom evolutionary processes largely described in other venomous animals i.e. the convergent recruitment of venom proteins between phylogenetically unrelated organisms, and the role of duplications in the emergence of multigenic families of virulence factors.

Fatty Acid-and Retinol-Binding Protein, Mj-FAR-1 Induces Tomato Host Susceptibility to Root-Knot Nematodes

Auteur	Ionit Iberkleid
Auteur	Paulo Vieira
Auteur	Janice de Almeida Engler
Auteur	Kalia Firester
Auteur	Yitzhak Spiegel
Auteur	Sigal Brown Horowitz
Volume	8
Numéro	5
Pages	e64586
Publication	PLoS ONE
Date	May 22, 2013
DOI	10.1371/journal.pone.0064586
Résumé	Plant-parasitic nematodes produce at least one structurally unique class of small helix-rich retinol- and fatty-acid-binding proteins that have no counterparts in their plant hosts. Herein we describe a protein of the plant-parasitic root-knot nematode Meloidogyne javanica, which is a member of the nematode-specific fatty-acid- and retinol-binding (Mj-FAR-1) family of proteins. The mj-far-1 mRNA was detected through M. javanica pre-parasitic J2s, migratory and sedentary parasitic stages by quantitative reverse transcriptase polymerase chain reaction (qRT-PCR). Immunolocalization assays demonstrate that the FAR protein of Meloidogyne is secreted during sedentary stages, as evidenced by the accumulation of FAR at the nematode cuticle surface and along the adjacent host root tissues. Tomato roots constitutively expressing mj-far-1 demonstrated an increased susceptibility to root-knot nematodes infection as observed by accelerated gall induction and expansion, accompanied by a higher percentage of nematodes developing into mature females compared to control roots. RNA interference assays that expressed double-stranded RNA complementary to mj-far-1 in transgenic tomato lines specifically reduced nematode infection levels. Histological analysis of nematode-infested roots indicated that in roots overexpressing mj-far-1, galls contained larger feeding cells and might support a faster nematode development and maturation. Roots overexpressing mj-far-1 suppressed jasmonic acid responsive genes such as the proteinase inhibitor (Pin2) and γ-thionin, illustrating the possible role of Mj-FAR-1 in manipulating the lipid based signaling in planta. This data, suggests that Meloidogyne FAR might have a strategic function during the interaction of the nematode with its plant host. Our study present the first demonstration of an in planta functional characterization and localization of FAR proteins secreted by plant-parasitic nematodes. It provides evidence that Mj-FAR-1 facilitates infection most likely via the manipulation of host lipid-based defenses, as critical components for a successful parasitism by plant-parasitic nematodes.

First detection of Tomato black ring virus (TBRV) in a French vineyard.

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Volume	47
Numéro	3
Pages	191-194
Publication	Journal International des Sciences de la Vigne et du Vin
Date	2013
Résumé	Aim: Grapevine plants from the Bordeaux wine region (France) showing symptoms of fanleaf degeneration, but negative for the two main fanleaf viruses were screened by ELISA for other nepoviruses that could explain the symptoms. Methods and results: ELISA tests were performed over a 3-year period (2009-2011) on leaves and woody canes. A total of 665 grapevine plants grafted with Merlot, Cabernet franc and Cabernet-Sauvignon, were found free from Grapevine fanleaf virus (GFLV) and Arabis mosaic virus (ArMV) but infected with Tomato black ring virus (TBRV). The Longidorid nematode species Longidorus attenuatus, known as the TBRV vector in grapevine, was detected from soil samples collected in the infected area. Conclusion: Both the virus and its vector might have originated from a vegetable garden established prior to vine planting, considering that the TBRV-infected area with the most fanleaf degeneration symptoms co-localizes with this previous garden. Significance and impact of the study: This is the first record of TBRV infection in a grapevine plot in France.

Notes :

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First Insights into the Genetic Diversity of the Pinewood Nematode in Its Native Area Using New Polymorphic Microsatellite Loci

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Auteur	Paulo Vieira
Auteur	Jonathan D. Eisenback
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Auteur	Thomas Guillemaud
Auteur	Philippe Castagnone-Sereno
Volume	8
Numéro	3
Pages	e59165
Publication	PLoS ONE
Date	March 15, 2013
DOI	10.1371/journal.pone.0059165
Résumé	The pinewood nematode, Bursaphelenchus xylophilus, native to North America, is the causative agent of pine wilt disease and among the most important invasive forest pests in the East-Asian countries, such as Japan and China. Since 1999, it has been found in Europe in the Iberian Peninsula, where it also causes significant damage. In a previous study, 94 pairs of microsatellite primers have been identified in silico in the pinewood nematode genome. In the present study, specific PCR amplifications and polymorphism tests to validate these loci were performed and 17 microsatellite loci that were suitable for routine analysis of B. xylophilus genetic diversity were selected. The polymorphism of these markers was evaluated on nematodes from four field origins and one laboratory collection strain, all originate from the native area. The number of alleles and the expected heterozygosity varied between 2 and 11 and between 0.039 and 0.777, respectively. First insights into the population genetic structure of B. xylophilus were obtained using clustering and multivariate methods on the genotypes obtained from the field samples. The results showed that the pinewood nematode genetic diversity is spatially structured at the scale of the pine tree and probably at larger scales. The role of dispersal by the insect vector versus human activities in shaping this structure is discussed.

Gènes et résistance des plantes aux insectes

Auteur	Dogimont, C.
Auteur	Sauge-Collet, M.-H.
Auteur	Saguez, J.
Auteur	Giordanengo, P.
Édition	Paris (FRA) : Editions Quae, Paris (FRA) : IRD Editions 2013.
Pages	427-439
Date	2013
Titre du livre	Interactions insectes-plantes

Genome of the red alga Porphyridium purpureum

Auteur	Debashish Bhattacharya
Auteur	Dana C. Price
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Auteur	Shannon Morath
Auteur	Frédérique Hilliou
Auteur	Andrea Egizi
Auteur	Marie-Mathilde Perrineau
Auteur	Hwan Su Yoon
Volume	4
Publication	Nature Communications
Date	June 17, 2013
DOI	10.1038/ncomms2931

Genomic evidence for ameiotic evolution in the bdelloid rotifer Adineta vaga

Auteur	Jean-François Flot
Auteur	Boris Hespeels
Auteur	Xiang Li
Auteur	Benjamin Noel
Auteur	Irina Arkhipova
Auteur	Etienne G. J. Danchin
Auteur	Andreas Hejnol
Auteur	Bernard Henrissat
Volume	500
Numéro	7463
Pages	453-457
Publication	Nature
Date	August 22, 2013
DOI	10.1038/nature12326
Résumé	Loss of sexual reproduction is considered an evolutionary dead end for metazoans, but bdelloid rotifers challenge this view as they appear to have persisted asexually for millions of years. Neither male sex organs nor meiosis have ever been observed in these microscopic animals: oocytes are formed through mitotic divisions, with no reduction of chromosome number and no indication of chromosome pairing. However, current evidence does not exclude that they may engage in sex on rare, cryptic occasions. Here we report the genome of a bdelloid rotifer, Adineta vaga (Davis, 1873), and show that its structure is incompatible with conventional meiosis. At gene scale, the genome of A. vaga is tetraploid and comprises both anciently duplicated segments and less divergent allelic regions. However, in contrast to sexual species, the allelic regions are rearranged and sometimes even found on the same chromosome. Such structure does not allow meiotic pairing; instead, we find abundant evidence of gene conversion, which may limit the accumulation of deleterious mutations in the absence of meiosis. Gene families involved in resistance to oxidation, carbohydrate metabolism and defence against transposons are significantly expanded, which may explain why transposable elements cover only 3% of the assembled sequence. Furthermore, 8% of the genes are likely to be of non-metazoan origin and were probably acquired horizontally. This apparent convergence between bdelloids and prokaryotes sheds new light on the evolutionary significance of sex.

Glutathione and plant response to biotic environment

Auteur	Pierre Frendo
Auteur	Fabien Baldacci-Cresp
Auteur	Sofiane M Benyamina
Auteur	Alain Puppo
Publication	Free radical biology & medicine
Date	Aug 1, 2013
DOI	10.1016/j.freeradbiomed.2013.07.035
Résumé	Glutathione (GSH) is a major antioxidant molecule in plants. It is involved in regulating plant development and responses to the abiotic and biotic environment. In recent years, numerous reports have clarified the molecular processes involving GSH in plant-microbe interactions. In this review, we summarize recent studies, highlighting the roles of GSH in interactions between plants and microbes, whether pathogenic or beneficial to plants.

Heterogeneity of selection and the evolution of resistance

Auteur	REX Consortium : D. Bourguet, F. Delmotte, Pierre Franck, Thomas Guillemaud, Xavier Reboud, Corinne Vacher and Anne-Sophie Walker.
Volume	28
Numéro	2
Pages	110-118
Publication	Trends in ecology & evolution
Date	Feb 2013
DOI	10.1016/j.tree.2012.09.001
Résumé	The evolution of resistance to pesticides and drugs by pests and pathogens is a textbook example of adaptation to environmental changes and a major issue in both public health and agronomy. Surprisingly, there is little consensus on how to combine selection pressures (i.e., molecules used in the treatment of pests or pathogens) over space and time to delay or prevent this evolutionary process. By reviewing theoretical models and experimental studies, we show that higher levels of heterogeneity of selection are associated with longer-term sustainability of pest or pathogen control. The combination of molecules usually outcompetes other resistance management strategies, such as Responsive alternation, Periodic application, or Mosaic, because it ensures 'multiple intragenerational killing'. A strategic deployment over space and/or time of several combinations can ensure 'multiple intergenerational killing', further delaying the evolution of resistance.

High-resolution mapping of the RMia gene for resistance to root-knot nematodes in peach

Auteur	Henri Duval
Auteur	Mathilde Hoerter
Auteur	Joël Polidori
Auteur	Carole Confolent
Auteur	Martin Masse
Auteur	André Moretti
Auteur	Cyril Van Ghelder
Auteur	Daniel Esmenjaud
Pages	1-10
Publication	Tree Genetics & Genomes
Date	2013
DOI	10.1007/s11295-013-0683-z
Résumé	The RMia gene, which confers resistance (R) to the root-knot nematodes (RKN) Meloidogyne incognita and Meloidogyne arenaria, has been shown to segregate in the peach rootstocks Nemared, Shalil, and Juseitou on LG2 of the Prunus map. Here, we report the high-resolution mapping of RMia in Nemared, using the peach genome sequence and 790 individuals from two segregating peach populations, the F2 cross Montclar x Nemared and the four-way cross [(Pamirskij × Rubira) × (Montclar × Nemared)], in which Montclar, Pamirskij, and Rubira are susceptible (S) to RKN. Among the simple sequence repeat (SSR) markers designed for an initial flanking region of more than 1 Mb, five SSR markers specific for Nemared were characterized. The genotyping and phenotyping of recombinant individuals in this interval narrowed the gene's location to a 300 kb physical distance between the SSR markers AMPP117 and AMPP116. In this interval, SNP polymorphisms were recovered from 1-kb-sequenced DNA fragments that were selected at 20 kb intervals. Two SNP markers (A20SNP and SNP_APP91) were shown to flank the gene in a final 92-kb region, containing four candidate genes from the TIR–NBS–LRR family. Finally, we studied the polymorphism of three closely linked markers, SNP_APP92, SNP_APP91, and AMPP117, on 28 R or S accessions from diverse Prunus species or hybrids. These markers discriminated between most R and S accessions, suggesting that at least the R sources of Nemared, Nemaguard, and Shalil share a common resistant ancestor.

Host-induced gene silencing of cytochrome P450 lanosterol C14α-demethylase-encoding genes confers strong resistance to Fusarium species

Auteur	Aline Koch
Auteur	Neelendra Kumar
Auteur	Lennart Weber
Auteur	Harald Keller
Auteur	Jafargholi Imani
Auteur	Karl-Heinz Kogel
Volume	110
Numéro	48
Pages	19324-19329
Publication	Proceedings of the National Academy of Sciences of the United States of America
Date	Nov 26, 2013
DOI	10.1073/pnas.1306373110
Résumé	Head blight, which is caused by mycotoxin-producing fungi of the genus Fusarium, is an economically important crop disease. We assessed the potential of host-induced gene silencing targeting the fungal cytochrome P450 lanosterol C-14α-demethylase (CYP51) genes, which are essential for ergosterol biosynthesis, to restrict fungal infection. In axenic cultures of Fusarium graminearum, in vitro feeding of CYP3RNA, a 791-nt double-stranded (ds)RNA complementary to CYP51A, CYP51B, and CYP51C, resulted in growth inhibition [half-maximum growth inhibition (IC50) = 1.2 nM] as well as altered fungal morphology, similar to that observed after treatment with the azole fungicide tebuconazole, for which the CYP51 enzyme is a target. Expression of the same dsRNA in Arabidopsis and barley rendered susceptible plants highly resistant to fungal infection. Microscopic analysis revealed that mycelium formation on CYP3RNA-expressing leaves was restricted to the inoculation sites, and that inoculated barley caryopses were virtually free of fungal hyphae. This inhibition of fungal growth correlated with in planta production of siRNAs corresponding to the targeted CYP51 sequences, as well as highly efficient silencing of the fungal CYP51 genes. The high efficiency of fungal inhibition suggests that host-induced gene-silencing targeting of the CYP51 genes is an alternative to chemical treatments for the control of devastating fungal diseases.

Host-Parasitoid Dynamics and the Success of Biological Control When Parasitoids Are Prone to Allee Effects

Auteur	Anaïs Bompard
Auteur	Isabelle Amat
Auteur	Xavier Fauvergue
Auteur	Thierry Spataro
Volume	8
Numéro	10
Pages	e76768
Publication	PLoS ONE
Date	October 7, 2013
DOI	10.1371/journal.pone.0076768
Résumé	In sexual organisms, low population density can result in mating failures and subsequently yields a low population growth rate and high chance of extinction. For species that are in tight interaction, as in host-parasitoid systems, population dynamics are primarily constrained by demographic interdependences, so that mating failures may have much more intricate consequences. Our main objective is to study the demographic consequences of parasitoid mating failures at low density and its consequences on the success of biological control. For this, we developed a deterministic host-parasitoid model with a mate-finding Allee effect, allowing to tackle interactions between the Allee effect and key determinants of host-parasitoid demography such as the distribution of parasitoid attacks and host competition. Our study shows that parasitoid mating failures at low density result in an extinction threshold and increase the domain of parasitoid deterministic extinction. When proned to mate finding difficulties, parasitoids with cyclic dynamics or low searching efficiency go extinct; parasitoids with high searching efficiency may either persist or go extinct, depending on host intraspecific competition. We show that parasitoids suitable as biocontrol agents for their ability to reduce host populations are particularly likely to suffer from mate-finding Allee effects. This study highlights novel perspectives for understanding of the dynamics observed in natural host-parasitoid systems and improving the success of parasitoid introductions.

Hydrogen Peroxide and Nitric Oxide: Key Regulators of the Legume Rhizobium and Mycorrhizal Symbioses

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Auteur	Nicolas Pauly
Auteur	Alexandre Boscari
Auteur	Karine Mandon
Auteur	Renaud Brouquisse
Pages	130228062639007
Publication	Antioxidants & Redox Signaling
Date	2013-02-28
DOI	10.1089/ars.2012.5136

Hydrogen peroxide-regulated genes in the Medicago truncatula-Sinorhizobium meliloti symbiosis

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Auteur	Pierre Frendo
Auteur	Alain Puppo
Auteur	Nicolas Pauly
Volume	198
Numéro	1
Pages	179-189
Publication	The New phytologist
Date	Apr 2013
DOI	10.1111/nph.12120
Résumé	Reactive oxygen species (ROS), particularly hydrogen peroxide (H(2)O(2)), play an important role in signalling in various cellular processes. The involvement of H(2)O(2) in the Medicago truncatula-Sinorhizobium meliloti symbiotic interaction raises questions about its effect on gene expression. A transcriptome analysis was performed on inoculated roots of M. truncatula in which ROS production was inhibited with diphenylene iodonium (DPI). In total, 301 genes potentially regulated by ROS content were identified 2 d after inoculation. These genes included MtSpk1, which encodes a putative protein kinase and is induced by exogenous H(2)O(2) treatment. MtSpk1 gene expression was also induced by nodulation factor treatment. MtSpk1 transcription was observed in infected root hair cells, nodule primordia and the infection zone of mature nodules. Analysis with a fluorescent protein probe specific for H(2)O(2) showed that MtSpk1 expression and H(2)O(2) were similarly distributed in the nodule infection zone. Finally, the establishment of symbiosis was impaired by MtSpk1 downregulation with an artificial micro-RNA. Several genes regulated by H(2)O(2) during the establishment of rhizobial symbiosis were identified. The involvement of MtSpk1 in the establishment of the symbiosis is proposed.

Hyposoter didymator uses a combination of passive and active strategies to escape from the Spodoptera frugiperda cellular immune response

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Auteur	Patrick Wincker
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Volume	59
Numéro	4
Pages	500-508
Publication	Journal of insect physiology
Date	Apr 2013
DOI	10.1016/j.jinsphys.2013.02.010
Résumé	An endoparasitic life style is widespread among Hymenoptera, and various different strategies allowing parasitoids to escape from the host encapsulation response have been reported. Species carrying polydnaviruses (PDVs), such as the ichneumonid Hyposoter didymator, generally rely on the viral symbionts to evade host immune responses. In this work, we show that H. didymator eggs can evade encapsulation by the host in the absence of calyx fluid (containing the viral particles), whereas protection of the larvae requires the presence of calyx fluid. This evasion by the eggs depends on proteins associated with the exochorion. This type of local passive strategy has been described for a few species carrying PDVs. Immune evasion by braconid eggs appears to be related to PDVs or proteins synthesized in the oviducts being associated with the egg. We report that in H. didymator, by contrast, proteins already present in the ovarian follicles are responsible for the eggs avoiding encapsulation. Mass spectrometry analysis of the egg surface proteins revealed the presence of host immune-related proteins, including one with similarities with apolipophorin-III, and also the presence of three viral proteins encoded by IVSPERs (Ichnovirus Structural Protein Encoding Regions).

Identification and Transcriptional Profiling of Differentially Expressed Genes Associated With Response to UVA Radiation in Drosophila melanogaster (Diptera: Drosophilidae)

Auteur	Li-Jun Zhou
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Auteur	Nicolas Desneux
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Volume	42
Numéro	5
Pages	1110-1117
Publication	Environmental Entomology
Date	2013-10-01T00:00:00///
DOI	10.1603/EN12319
Résumé	Ultraviolet A (UVA) radiation, the major component of solar ultraviolet (UV) radiation reaching the earth's surface, leads to negative effects in insects, such as oxidative stress, photoreceptor damage, and cell death. To better understand the molecular mechanisms of insect response to UVA radiation, suppression subtractive hybridization (SSH) and real-time quantitative polymerase chain reaction approaches were combined to reveal differential transcript expression in Drosophila melanogaster Meigen, 1830 (Diptera: Drosophilidae). In this study, two subtractive cDNA libraries were constructed and sequenced, obtaining 131 high-quality unique expressed sequence tags (ESTs) that were up- or downregulated in D. melanogaster exposed to UVA radiation for 0.5 h. Of the 131 ESTs, 102 unique ESTs were differentially expressed and classified into 10 functional categories. The results showed that UVA radiation induces expression of genes related to stress and defense response and metabolism. Potential transcription factor binding motifs upstream of these genes are associated with multiple signaling pathways that may help the insect cope with the stress of UVA radiation. To our knowledge, this is the first analysis of insect response to UVA radiation at the transcriptional level. Our results reveal that UVA radiation influences the expression profiles of stress-responsive genes and provide further insights into the mechanisms of adaptive response to UVA radiation stress.

Identification of Novel Target Genes for Safer and More Specific Control of Root-Knot Nematodes from a Pan-Genome Mining

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Auteur	Julie Guy
Auteur	François Artiguenave
Auteur	Pierre Abad
Volume	9
Numéro	10
Pages	e1003745
Publication	PLoS Pathog
Date	October 31, 2013
DOI	10.1371/journal.ppat.1003745
Résumé	Author SummaryPlant-parasitic nematodes are annually responsible for more than $100 billion crop yield loss worldwide and those considered as causing most of the damages are root-knot nematodes. These nematodes used to be controlled by chemicals that are now banned from use because of their poor specificity and high toxicity for the environment and human health. In the absence of sustainable alternative solutions, new control means, more specifically targeted against these nematodes and safe for the environment are needed. We searched in root-knot nematode genomes, genes conserved in various plant-damaging species while otherwise absent from the genomes of non target species such as those of chordates, plants, annelids, insect pollinators and mollusks. These genes are probably important for plant parasitism and their absence from non-target species make them interesting candidates for the development of more specific and safer control means. Further bioinformatics pruning of this set of genes yielded 16 novel candidates that could be biologically tested. Using RNA interference, we knocked down each of these 16 genes in a root-knot nematode and tested the effect on plant parasitism efficiency. Out of the 16 tested genes, 12 showed a significant and reproducible diminution of infestation when silenced and are thus particularly promising.

Identification of Reference Genes for Normalizing RNA Expression in Potato Roots Infected with Cyst Nematodes

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Auteur	Jawad Aarrouf
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Auteur	Didier Mugniéry
Auteur	Véronique Lefebvre
Auteur	Bernard Caromel
Volume	31
Numéro	4
Pages	936-945
Publication	Plant Molecular Biology Reporter
Date	2013/08/01
DOI	10.1007/s11105-013-0566-3
Résumé	Potato cyst nematodes induce changes in plant host gene expression following root invasion. For an accurate comparison of gene expression by reverse transcription quantitative real-time PCR (RT-qPCR), internal reference genes are necessary for transcript normalization. Very few experimental data on suitable reference genes are available for interactions between plant and root pathogens. In this study, we tested eight potential candidate reference genes for normalizing levels of potato gene transcripts by RT-qPCR after inoculation by nematodes. The ranking of candidate reference genes was performed using RefFinder WEB-based software. Four reference genes, RPN7 (26S proteasome regulatory subunit), UBP22 (ubiquitin-specific protease 22), OXA1 (OXA1 protein), and MST2 (mercaptopyruvate sulfurtransferase), were stably expressed in roots of susceptible or resistant potato plants, infected or uninfected by Globodera pallida. A normalization factor based on data from these four genes, highly homologous between potato and tomato, was used to normalize the expression of a chitinase gene, which was induced by nematodes in roots of potatoes carrying the resistance allele at a low-effect QTL, GpaXI spl .

Impact of the neonicotinoid acetamiprid on immature stages of the predator Eriopis connexa (Coleoptera: Coccinellidae)

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Auteur	Marcela Inés Schneider
Auteur	Nicolas Desneux
Auteur	Belén González
Auteur	Alicia E Ronco
Volume	22
Numéro	6
Pages	1063-1071
Publication	Ecotoxicology (London, England)
Date	Aug 2013
DOI	10.1007/s10646-013-1094-5
Résumé	Eriopis connexa is a native coccinelid predator in the Neotropical Region. In Argentina it is commonly found associated to sucking pests in several crops and among them aphids and whiteflies. These pests are usually controlled with newly developed systemic insecticides, such as the neonicotinoids. However, the compatibility between selective pesticides and natural enemies is required before incorporating them in integrated pest management (IPM) packages. Within this frame, the objective of this study was to evaluate the side effect of various concentrations/doses of one commonly used neonicotinoid in vegetal crops, acetamiprid, on immature stages of E. connexa by dipping or topical exposure for eggs and larvae, respectively. Acetamiprid reduced egg hatching from 34 to 100 %. Moreover, the embryogenesis was disrupted by insecticide at early embryo stage at all tested concentrations. Second larval instar was more susceptible to acetamiprid than the fourth one and this susceptibility was positively related with the tested concentrations. On the other hand, the survival reduction at larval stage reached 100 % from 20 mg a.i./L (10 % of maximum field concentration). Besides, the reproduction of the females developed from topical bioassays on fourth instar larvae was strongly affected, with reduction in fecundity and fertility from 22 to 44 % and from 37 to 45 %, respectively. Overall the results showed a high toxicity of acetamiprid on immature stages of E. connexa, demonstrating that this broadly used insecticide could reduce biocontrol services provided by this predator and could also likely disturb IPM programs.

Indigenous natural enemies attacking Tuta absoluta (Lepidoptera: Gelechiidae) in Southern France.

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Auteur	J. Lambion
Auteur	P. Han
Auteur	L. Zappalà
Auteur	N. Desneux
Volume	23
Numéro	1
Pages	117-121
Publication	Egyptian Journal of Biological Pest Control
Date	2013
Résumé	The South American tomato leafminer, Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae), is a serious worldwide threat to tomato industry. Since it has spread to the Afro-Eurasia, it was responsible of extensive damage and its control mainly relied on chemical insecticide applications. In this context, a survey of natural enemies attacking T. absoluta spontaneously was conducted in Southern France. Infested tomato leaves were collected from protected tomato crops in seasons 2011 and 2012. Three species of mirid predators [Macrolophus pygmaeus (Rambur), Nesidiocoris tenuis (Reuter) and Dicyphus sp.] were found preying on eggs and young larvae of the moth in both seasons of sampling. Eggs were also attacked by two trichogrammatid species, Trichogramma achaeae Nagaraja & Nagarkatti and Trichogramma sp. Whereas, T. absoluta larvae were parasitized by four parasitoid species belong to the families; Braconidae (Bracon nigricans Szepligeti), Eulophidae [Neochrysocharis formosa (Westwood), Stenomesius sp. near japonicus and Necremnus sp. near artynes]. Although further studies are needed to assess the actual role of these species in T. absoluta control, obtained results represent the first step towards developing biological and integrated management strategies against this pest in France. Furthermore, these results stress the need of conservation strategies of indigenous natural enemies to control the exotic pest species.

Notes :

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Interactions insectes-plantes

Éditeur	Editions Quae
ISBN	9782759220182
Date	2013-08-19
Résumé	Cet ouvrage présente les grandes fonctions des insectes, leur fonctionnement individuel et collectif, leurs interactions plus ou moins intimes avec les composantes de l’écosystème, en particulier les plantes, en s’appuyant sur l’histoire évolutive à l’origine de ces interactions. Il décrit les multiples applications des recherches sur les insectes pour l’agriculture.
Nb de pages	818

Intraguild Predation on the Whitefly Parasitoid Eretmocerus eremicus by the Generalist Predator Geocoris punctipes: A Behavioral Approach

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Auteur	Ricardo Ramirez-Romero
Auteur	Lizette Cicero
Auteur	Claudia Michel-Rios
Auteur	Nicolas Desneux
Volume	8
Numéro	11
Pages	e80679
Publication	PLoS ONE
Date	November 19, 2013
DOI	10.1371/journal.pone.0080679
Résumé	Intraguild predation (IGP) takes place when natural enemies that use similar resources attack each other. The impact of IGP on biological control can be significant if the survival of natural enemy species is disrupted. In the present study, we assessed whether Geocoris punctipes (Hemiptera: Lygaeidae) engages in IGP on Eretmocerus eremicus (Hymenoptera: Aphelinidae) while developing on whitefly nymphs of Trialeurodes vaporariorum (Hemiptera: Aleyrodidae). In choice and non-choice tests, we exposed G. punctipes to parasitized and non-parasitized whitefly nymphs. We found that G. punctipes does practice IGP on E. eremicus. However, choice tests assessing G. punctipes consumption revealed a significant preference for non-parasitized T. vaporariorum nymphs. Subsequently, we investigated whether E. eremicus females modify their foraging behavior when exposed to conditions involving IGP risk. To assess this, we analyzed wasp foraging behavior under the following treatments: i) whitefly nymphs only (control = C), ii) whitefly nymphs previously exposed to a predator (= PEP) and, iii) whitefly nymphs and presence of a predator (= PP). In non-choice tests we found that E. eremicus did not significantly modify its number of attacks, attack duration, oviposition duration, or behavior sequences. However, E. eremicus oviposited significantly more eggs in the PEP treatment. In the PP treatment, G. punctipes also preyed upon adult E. eremicus wasps, significantly reducing their number of ovipositions and residence time. When the wasps were studied under choice tests, in which they were exposed simultaneously to all three treatments, the number of attacks and frequency of selection were similar under all treatments. These results indicate that under IGP risk, E. eremicus maintains several behavioral traits, but can also increase its number of ovipositions in the presence of IG-predator cues. We discuss these findings in the context of population dynamics and biological control.

Investigating the genetic load of an emblematic invasive species: the case of the invasive harlequin ladybird Harmonia axyridis

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Auteur	A Estoup
Auteur	R A Hufbauer
Auteur	V Ravigne
Auteur	I Goryacheva
Auteur	I A Zakharov
Auteur	E Lombaert
Auteur	B Facon
Volume	3
Numéro	4
Pages	864-871
Publication	Ecology and evolution
Date	Apr 2013
DOI	10.1002/ece3.490
Résumé	Introduction events can lead to admixture between genetically differentiated populations and bottlenecks in population size. These processes can alter the adaptive potential of invasive species by shaping genetic variation, but more importantly, they can also directly affect mean population fitness either increasing it or decreasing it. Which outcome is observed depends on the structure of the genetic load of the species. The ladybird Harmonia axyridis is a good example of invasive species where introduced populations have gone through admixture and bottleneck events. We used laboratory experiments to manipulate the relatedness among H. axyridis parental individuals to assess the possibility for heterosis or outbreeding depression in F1 generation offspring for two traits related to fitness (lifetime performance and generation time). We found that inter-populations crosses had no major impact on the lifetime performance of the offspring produced by individuals from either native or invasive populations. Significant outbreeding depression was observed only for crosses between native populations for generation time. The absence of observed heterosis is indicative of a low occurrence of fixed deleterious mutations within both the native and invasive populations of H. axyridis. The observed deterioration of fitness in native inter-population crosses most likely results from genetic incompatibilities between native genomic backgrounds. We discuss the implications of these results for the structure of genetic load in H. axyridis in the light of the available information regarding the introduction history of this species.

Is parasitoid virulence against multiple hosts adaptive or constrained by phylogeny? A study of Leptopilina spp. (Hymenoptera: Figitidae)/Drosophila (Diptera: Drosophilidae) interactions

Auteur	Stéphane Dupas
Auteur	Marylène Poirié
Auteur	Françoise Frey
Auteur	Yves Carton
Volume	49
Numéro	2
Pages	222-231
Publication	Annales de la Société entomologique de France (N.S.)
Date	2013
DOI	10.1080/00379271.2013.815045
Résumé	Summary. Some insects can develop immune resistance to koinobiont parasitoids. Reciprocally, adaptation to host immunology is critical for parasitoid success. Phylogenetic inertia and correlations between virulence against different hosts can act as constraints preventing these adaptations. Insights on these constraints may be obtained from the analysis of patterns of variations in the interactions at the species or genus level. Multivariate phylogenetic comparative methods were applied to virulence traits of 13 parasitoid strains of Leptopilina spp. (Hymenoptera: Figitidae) on five host strains of the Drosophila melanogaster species subgroup (Diptera Drosophilidae). Independent contrasts of virulence were calculated and principal component analysis (PCA) was performed on the independent contrasts to estimate the dimensionality of the interactions. Most of the variation of virulence was associated with the first component of the PCA (62.2%). But a significant proportion was explained by the second and third components, suggesting specific interactions. Strain–strain reciprocal specificity was observed in several pairs of host–parasitoid species. Significant phylogenetic inertia was observed on parasitoid virulence, but only at the genus level and only against hosts of intermediate resistance (phylogenetic R2 between 0.62 and 0.85). Some parts of the interaction matrix exhibited specific interactions and others were fixed due to ancestral non-specific virulence (or avirulence). The results were interpreted viewing virulence as a threshold trait determined by underlying liability. When liability is far from the threshold, virulence is fixed. When liability is close to the threshold, virulence varies specifically and reciprocal adaptations can take place. These phylogenetic constraints may lead to a scenario of escape and radiation coevolution in the host–parasitoid system.

Knocking-Down Meloidogyne incognita Proteases by Plant-Delivered dsRNA Has Negative Pleiotropic Effect on Nematode Vigor

Auteur	Jose Dijair Antonino de Souza Junior
Auteur	Roberta Ramos Coelho
Auteur	Isabela Tristan Lourenco
Auteur	Rodrigo da Rocha Fragoso
Auteur	Antonio Americo Barbosa Viana
Auteur	Leonardo Lima Pepino de Macedo
Auteur	Maria Cristina Mattar da Silva
Auteur	Regina Maria Gomes Carneiro
Auteur	Gilbert Engler
Auteur	Janice de Almeida-Engler
Auteur	Maria Fatima Grossi-de-Sa
Volume	8
Numéro	12
Publication	PLoS ONE
Date	2013-12-31
DOI	10.1371/journal.pone.0085364
Résumé	The root-knot nematode Meloidogyne incognita causes serious damage and yield losses in numerous important crops worldwide. Analysis of the M. incognita genome revealed a vast number of proteases belonging to five different catalytic classes. Several reports indicate that M. incognita proteases could play important roles in nematode parasitism, besides their function in ordinary digestion of giant cell contents for feeding. The precise roles of these proteins during parasitism however are still unknown, making them interesting targets for gene silencing to address protein function. In this study we have knocked-down an aspartic (Mi-asp-1), a serine (Mi-ser-1) and a cysteine protease (Mi-cpl-1) by RNAi interference to get an insight into the function of these enzymes during a host/nematode interaction. Tobacco lines expressing dsRNA for Mi-ser-1 (dsSER), Mi-cpl-1 (dsCPL) and for the three genes together (dsFusion) were generated. Histological analysis of galls did not show clear differences in giant cell morphology. Interestingly, nematodes that infected plants expressing dsRNA for proteases produced a reduced number of eggs. In addition, nematode progeny matured in dsSER plants had reduced success in egg hatching, while progeny resulting from dsCPL and dsFusion plants were less successful to infect wild-type host plants. Quantitative PCR analysis confirmed a reduction in transcripts for Mi-cpl-1 and Mi-ser-1 proteases. Our results indicate that these proteases are possibly involved in different processes throughout nematode development, like nutrition, reproduction and embryogenesis. A better understanding of nematode proteases and their possible role during a plant-nematode interaction might help to develop new tools for phytonematode control.

Le Psylle du Gommier rouge (Glycaspis brimblecombei Moore) introduit sur les eucalyptus de France (Hemiptera, Psyllidae)

Auteur	Christian Cocquempot
Auteur	Jean-Claude Malausa
Auteur	Marcel Thaon
Auteur	Lisa Brancaccio
Volume	117
Numéro	3
Pages	363-370
Publication	Bulletin de la Société entomologique de France
Date	2013

Lutte biologique contre le cynips du châtaignier : objectifs et enjeux de cette lutte biologique dite « classique »

Auteur	Borowiec N
Auteur	Thaon M
Auteur	Brancaccio L
Auteur	Warot S
Auteur	Risso S
Auteur	Bertoncello E
Auteur	Quacchia A
Auteur	Ris N,
Auteur	Malausa JC
Volume	662
Pages	32-35
Publication	Phytoma, la défense des végétaux
Date	2013

Methods for controlling Phytophthora in vegetable crops: inputs from microbial core collection in the plant breeding process

Auteur	Kuhn, M.-L.
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Auteur	Damidaux, R
Auteur	Gibowski, E.
Auteur	RUELLAN, Y.
Auteur	Lefebvre, V.
Auteur	Panabières, F.
Volume	27
Pages	47-58
Publication	Innovations Agronomiques
Date	2013

Modelling of immune response to a respiratory virus targeting pulmonary macrophages : exploration of the host susceptibility and viral virulence.

Présentateur	Natacha Go
Présentateur	Caroline Bidot
Présentateur	Catherine Belloc
Présentateur	Suzanne Touzeau
Date	13/05/2013
Type	Oral presentation
Intitulé de la réunion	Systems Biology Approach to Infectious Processes (SBIP 2013)
Résumé	Respiratory viruses are responsible for tissue damages and local inflammation. The best strategy to control their severity is to limit the infection while maintaining an efficient immune response. Given this context, the case when the macrophage is the target cell of infection is of interest. Indeed, pulmonary macrophages (i) are responsible for inflammation and viral destruction by phagocytosis and (ii) participate in the induction and orientation of the adaptive immune response. Consequently, macrophage infection hampers the whole immune response. The interaction between macrophages and virus during the first steps of infection has not been throughly investigated in experimentale studies and is not detailed in models of immune response. Consequently, the influence of macrophage – virus interactions on the infection resolution is unknown. Here, we propose an original model of the immune response centred on the macrophage – virus interactions. We represent all macrophage infectious statuses, their immune functions, and the interactions between innate and adaptive responses taking into account the cytokines regulations. We use the model to study the relative influence of macrophage – virus interactions on the infection resolution by a multivatiate sensitivity analysis. Then, we explore the influence of macrophage immune functions by considering two levels of host susceptibility and viral virulence. We conclude that both repilication rate of the virus and host capacity to synthetize anti-viral cytokines are key for infection resolution.

Multiyear evaluation of the durability of the resistance conferred by Ma and RMia genes to Meloidogyne incognita in Prunus under controlled conditions

Auteur	Samira Khallouk
Auteur	Roger Voisin
Auteur	Ulysse Portier
Auteur	Joel Polidori
Auteur	Cyril Van-Ghelder
Auteur	Daniel Esmenjaud
Publication	Phytopathology
Date	Feb 20, 2013
DOI	10.1094/PHYTO-09-12-0228-R
Résumé	Root-knot nematodes (RKN) Meloidogyne spp. are highly polyphagous pests that parasitize Prunus crops in Mediterranean climates. Breeding for RKN-resistant Prunus cultivars, as an alternative to the now-banned use of nematicides, is a real challenge, as the perennial nature of these trees increases the risk of resistance breakdown. The Ma plum resistance (R) gene, with a complete spectrum, and the RMia peach R gene, with a more restricted spectrum, both provide total control of M. incognita, the model parthenogenetic species of the genus and the most important RKN in terms of economic losses. We investigated the durability of the resistance to this nematode conferred by these genes, comparing the results obtained with those for the tomato Mi-1 reference gene. In multiyear experiments, we applied a high and continuous nematode inoculum pressure, by cultivating nematode-infested susceptible tomato plants with either Prunus accessions carrying Ma and/or RMia R genes, or with R tomato plants carrying the Mi-1 gene. Suitable conditions for Prunus development were achieved by carrying out the studies in a glasshouse, in controlled conditions allowing a short winter leaf fall and dormancy. We first assessed the plum accession 'P.2175', which is heterozygous for the Ma gene, in two successive two-year evaluations, for resistance to two M. incognita isolates. Whatever the isolate used, no nematodes reproducing on 'P.2175' were detected, whereas galls and nematodes reproducing on tomato plants carrying Mi-1 were observed. In a second experiment with the most aggressive isolate, interspecific full-sib material ['P.2175' x ('Garfi' almond x 'Nemared' peach)], carrying either Ma or RMia (from Nemared) or both (in the heterozygous state) or neither of these genes, was evaluated for four years. No virulent nematodes developed on Prunus carrying R genes, whereas galling and virulent individuals were observed on Mi-1 resistant tomato plants. Thus, the resistance to M. incognita conferred by Ma in Prunus material in both a pure-plum and an interspecific genetic background, or by RMia in an interspecific background, appears to be durable, highlighting the value of these two genes for the creation of Prunus rootstock material.

Natural enemies of the South American moth, Tuta absoluta, in Europe, North Africa and Middle East, and their potential use in pest control strategies

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Auteur	Antonio Biondi
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Auteur	Gaetano Siscaro
Auteur	Menelaos Stavrinides
Auteur	Luciana Tavella
Auteur	Rosa Vercher Aznar
Auteur	Alberto Urbaneja
Auteur	Nicolas Desneux
Volume	86
Numéro	4
Pages	635-647
Publication	Journal of Pest Science
Date	2013/12/01
DOI	10.1007/s10340-013-0531-9
Résumé	The South American tomato leafminer, Tuta absoluta Meyrick (Lepidoptera: Gelechiidae), is an invasive Neotropical pest. After its first detection in Europe, it rapidly invaded more than 30 Western Palaearctic countries becoming a serious agricultural threat to tomato production in both protected and open-field crops. Among the pest control tactics against exotic pests, biological control using indigenous natural enemies is one of the most promising. Here, available data on the Afro-Eurasian natural enemies of T. absoluta are compiled. Then, their potential for inclusion in sustainable pest control packages is discussed providing relevant examples. Collections were conducted in 12 countries, both in open-field and protected susceptible crops, as well as in wild flora and/or using infested sentinel plants. More than 70 arthropod species, 20 % predators and 80 % parasitoids, were recorded attacking the new pest so far. Among the recovered indigenous natural enemies, only few parasitoid species, namely, some eulophid and braconid wasps, and especially mirid predators, have promising potential to be included in effective and environmentally friendly management strategies for the pest in the newly invaded areas. Finally, a brief outlook of the future research and applications of indigenous T. absoluta biological control agents are provided.

Nematode feeding sites: unique organs in plant roots

Auteur	Tina Kyndt
Auteur	Paulo Vieira
Auteur	Godelieve Gheysen
Auteur	Janice de Almeida-Engler
Volume	238
Numéro	5
Pages	807-818
Publication	Planta
Date	2013/11/01
DOI	10.1007/s00425-013-1923-z
Résumé	Although generally unnoticed, nearly all crop plants have one or more species of nematodes that feed on their roots, frequently causing tremendous yield losses. The group of sedentary nematodes, which are among the most damaging plant-parasitic nematodes, cause the formation of special organs called nematode feeding sites (NFS) in the root tissue. In this review we discuss key metabolic and cellular changes correlated with NFS development, and similarities and discrepancies between different types of NFS are highlighted.

Nematode-induced endoreduplication in plant host cells: why and how?

Auteur	Janice de Almeida Engler
Auteur	Godelieve Gheysen
Volume	26
Numéro	1
Pages	17-24
Publication	Molecular plant-microbe interactions: MPMI
Date	Jan 2013
DOI	10.1094/MPMI-05-12-0128-CR
Résumé	Plant-parasitic root-knot and cyst nematodes have acquired the ability to induce remarkable changes in host cells during the formation of feeding sites. Root-knot nematodes induce several multinucleate giant cells inside a gall whereas cyst nematodes provoke the formation of a multinucleate syncytium. Both strategies impinge on the deregulation of the cell cycle, involving a major role for endoreduplication. This review will first describe the current knowledge on the control of normal and aberrant cell cycles. Thereafter, we will focus on the role of both cell-cycle routes in the transformation process of root cells into large and highly differentiated feeding sites as induced by the phytoparasitic root-knot and cyst nematodes.

Nuclear receptors HR96 and Ultraspiracle from the fall armyworm (Spodoptera frugiperda), developmental expression and induction by xenobiotics

Auteur	Maeva Giraudo
Auteur	Pascaline Audant
Auteur	René Feyereisen
Auteur	Gaëlle Le Goff
Publication	Journal of insect physiology
Date	Mar 19, 2013
DOI	10.1016/j.jinsphys.2013.03.003
Résumé	The fall armyworm Spodoptera frugiperda is a major polyphagous pest in agriculture and little is known on how this insect can adapt to the diverse and potentially toxic plant allelochemicals that they ingest or to insecticides. To investigate the involvement of nuclear receptors in the response of Spodoptera frugiperda to its chemical environment, we cloned SfHR96, a nuclear receptor orthologous to the mammalian xenobiotic receptors, pregnane X receptor (PXR) and constitutive androstane receptor (CAR). We also cloned Ultraspiracle (USP), the ortholog of retinoid X receptor (RXR) that serves as partner of dimerization of PXR and CAR. Cloning of SfUSP revealed the presence of two isoforms, SfUSP-1 and SfUSP-2 in this species, that differ in their N-terminal region. The expression of these receptors as well as the ecdysone receptor was studied during specific steps of development in different tissues. SfHR96 was constitutively expressed in larval midgut, fat body and Malpighian tubules throughout the last two instars and pupal stage, as well as in Sf9 cells. EcR and SfUSP-2 showed peaks of expression before larval moults and during metamorphosis, whereas SfUSP-1 was mainly expressed in the pre-pupal stage. Receptor induction was followed after exposure of larvae or cells to eleven chemicals compounds. SfHR96 was not inducible by the tested compounds. EcR was significantly induced by the 20- hydroxyecdysone agonist, methoxyfenozide, and SfUSP showed an increase expression when exposed to the juvenile hormone analog, methoprene. The cloning of these nuclear receptors is a first step in the understanding of the important capacities of adaptation of this insect pest.

Optimal within-patch movement strategies for optimising patch residence time: an agent-based modelling approach

Auteur	E. Wajnberg
Auteur	T. S. Hoffmeister
Auteur	P. Coquillard
Volume	67
Numéro	12
Pages	2053-2063
Publication	Behavioral Ecology and Sociobiology
Date	2013/12/01
DOI	10.1007/s00265-013-1615-5
Résumé	Several optimisation models, like the marginal value theorem (MVT), have been proposed to predict the optimal time foraging animals should remain on patches of resources. These models do not clearly indicate, however, how animals can follow the corresponding predictions. Hence, several proximate patch-leaving decision rules have been proposed. Most if not all of these are based on the animals’ motivation to remain on the patches, but the real behaviours involved in such motivation actually still remain to be identified. Since animals are usually exploiting patches of resources by walking, we developed a model simulating the intra-patch movement decisions of time-limited animals exploiting resources distributed in delimited patches in environments with different resource abundances and distributions. The values of the model parameters were optimised in the different environments by means of a genetic algorithm. Results indicate that simple modifications of the walking pattern of the foraging animals when resources are discovered can lead to patch residence times that appear consistent with the predictions of the MVT. These results provide a more concrete understanding of the optimal patch-leaving decision rules animals should adopt in different environments.

Origins of P450 diversity

Auteur	Hideki Sezutsu
Auteur	Gaëlle Le Goff
Auteur	René Feyereisen
Volume	368
Numéro	1612
Publication	Philosophical Transactions of the Royal Society B: Biological Sciences
Date	02/19/2013
DOI	10.1098/rstb.2012.0428
Résumé	The P450 enzymes maintain a conserved P450 fold despite a considerable variation in sequence. The P450 family even includes proteins that lack the single conserved cysteine and are therefore no longer haem-thiolate proteins. The mechanisms of successive gene duplications leading to large families in plants and animals are well established. Comparisons of P450 CYP gene clusters in related species illustrate the rapid changes in CYPome sizes. Examples of CYP copy number variation with effects on fitness are emerging, and these provide an opportunity to study the proximal causes of duplication or pseudogenization. Birth and death models can explain the proliferation of CYP genes that is amply illustrated by the sequence of every new genome. Thus, the distribution of P450 diversity within the CYPome of plants and animals, a few families with many genes (P450 blooms) and many families with few genes, follows similar power laws in both groups. A closer look at some families with few genes shows that these, often single member families, are not stable during evolution. The enzymatic prowess of P450 may predispose them to switch back and forth between metabolism of critical structural or signal molecules and metabolism dedicated to environmental response.

Parental Transfer of the Antimicrobial Protein LBP/BPI Protects Biomphalaria glabrata Eggs against Oomycete Infections

Auteur	Olga Lucia Baron
Auteur	Pieter van West
Auteur	Benoit Industri
Auteur	Michel Ponchet
Auteur	Géraldine Dubreuil
Auteur	Benjamin Gourbal
Auteur	Jean-Marc Reichhart
Auteur	Christine Coustau
Volume	9
Numéro	12
Pages	e1003792
Publication	PLoS Pathog
Date	December 19, 2013
DOI	10.1371/journal.ppat.1003792
Résumé	Author SummaryVertebrate immune systems not only protect adult organisms against infections but also increase survival of offspring through parental transfer of innate and adaptive immune factors via the placenta, colostrum and milk or via the egg yolk. This maternal transfer of immunity is critical for species survival as embryos and neonates are immunologically immature and unable to fight off infections at early life stages. Parental immune protection is poorly documented in invertebrates and how the estimated 1.3 million of invertebrate species protect their eggs against pathogens remains an intriguing question. Here, we show that a fresh-water snail, Biomphalaria glabrata massively loads its eggs with a lipopolysaccharide binding protein/bactericidal permeability increasing protein (LBP/BPI) displaying expected antibacterial activities. Remarkably, this snail LBP/BPI also displayed a strong biocidal activity against water molds (oomycetes). This yet unsuspected activity is conserved in human BPI. Gene expression knock-down resulted in the reduction of snail reproductive success and massive death of eggs after water mold infections. This work reveals a novel and conserved biocidal activity for LBP/BPI family members and demonstrates that the snail LBP/BPI represents a major fitness-related protein transferred from parents to their clutches and protecting them from widespread and lethal oomycete infections.

Peribacteriod space acidification: a marker of mature bacteroid functioning in Medicago truncatula nodules

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Auteur	Eric Boncompagni
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Publication	Plant, cell & environment
Date	Apr 16, 2013
DOI	10.1111/pce.12116
Résumé	Legumes form a symbiotic interaction with Rhizobiacea bacteria which differentiate into nitrogen fixing bacteroids within nodules.. Here, we investigated in vivo the pH of the peribacteroid space (PBS) surrounding the bacteroid and pH variation throughout symbiosis. In vivo confocal microscopy investigations, using acidotropic probes, demonstrated the acidic state of the PBS. In planta analysis of nodule senescence induced by distinct biological processes drastically increased PBS pH in the N2 fixing zone (zone III). Therefore, the PBS acidification observed in mature bacteroids can be considered as a marker of bacteroids N2 fixation. Using a pH sensitive ratiometric probe, PBS pH was measured in vivo during the whole symbiotic process. We showed a progressive acidification of the PBS between the bacteroid release up to the onset of N2 fixation. Genetic and pharmacological approaches were conducted and lead to disruption of the PBS acidification. Altogether, our findings shed light on the role of PBS pH of mature bacteroids in nodule functioning, providing new tools to monitor in vivo bacteroid physiology.

Plant parasitic nematode effectors target host defense and nuclear functions to establish feeding cells

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Volume	4
Pages	53
Publication	Frontiers in plant science
Date	2013
DOI	10.3389/fpls.2013.00053
Résumé	Plant parasitic nematodes are microscopic worms, the most damaging species of which have adopted a sedentary lifestyle within their hosts. These obligate endoparasites have a biotrophic relationship with plants, in which they induce the differentiation of root cells into hypertrophied, multinucleate feeding cells (FCs). Effectors synthesized in the esophageal glands of the nematode are injected into the plant cells via the syringe-like stylet and play a key role in manipulating the host machinery. The establishment of specialized FCs requires these effectors to modulate many aspects of plant cell morphogenesis and physiology, including defense responses. This cell reprogramming requires changes to host nuclear processes. Some proteins encoded by parasitism genes target host nuclei. Several of these proteins were immunolocalized within FC nuclei or shown to interact with host nuclear proteins. Comparative genomics and functional analyses are gradually revealing the roles of nematode effectors. We describe here these effectors and their hypothesized roles in the unique feeding behavior of these pests.

Potential for combined use of parasitoids and generalist predators for biological control of the key invasive tomato pest Tuta absoluta

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Auteur	Edwige Amiens-Desneux
Auteur	Ricardo Ramirez-Romero
Auteur	Nicolas Desneux
Volume	86
Numéro	3
Pages	533-541
Publication	Journal of Pest Science
Date	2013/09/01
DOI	10.1007/s10340-013-0498-6
Résumé	The tomato leafminer Tuta absoluta (Meyrick) (Lepidoptera: Gelechiidae) has recently invaded Mediterranean countries and is a major pest in tomato crops. Trichogrammatid oophagous parasitoids have shown promising potential for controlling the pest before the yield decreases in the greenhouse. In protected tomato crops (greenhouse), mirid predators are commonly used for biological control of whiteflies and they also prey on T. absoluta. These predators do not attack Trichogramma adults but they may partially decrease the overall impact of parasitoids on T. absoluta if intraguild predation (IGP) occurs on parasitized eggs. Under laboratory conditions, we tested if the mirid predator Macrolophus pygmaeus shows preference between parasitized and unparasitized T. absoluta eggs. We also tested if the predator reduces the number of parasitized eggs on caged tomato plants (microcosms) and assessed the efficacy of natural enemies used alone or together in limiting T. absoluta populations. We found that IGP is inflicted on the parasitoid Trichogramma achaeae by M. pygmaeus and that the risk of IGP depends on the developmental stage of T. achaeae inside the egg because the larva is at risk mostly early in its development (when parasitized egg is still yellow). In addition, we observed that non-consumptive events, likely probing of the predator on parasitized eggs, may induce mortality in parasitoid offspring without actual feeding on parasitized eggs. However, both IGP and non-consumptive events decreased when the predator was not confined with parasitized eggs in small arenas. Despite negative effects of the predator to the parasitoid, results demonstrate that adding Trichogramma parasitoids may significantly increase the level of control of the pest over what could be attained when only the mirid predator M. pygmaeus is present on tomato. Implications of results are discussed regarding potential of these natural enemies for biological control of T. absoluta in greenhouse tomato crops.

Preference and Prey Switching in a Generalist Predator Attacking Local and Invasive Alien Pests

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Auteur	Edwige Amiens-Desneux
Auteur	Nicolas Desneux
Éditeur	Joseph Clifton Dickens
Volume	8
Numéro	12
Pages	e82231
Publication	PLoS ONE
Date	2013-12-2
DOI	10.1371/journal.pone.0082231

Pupal diapause development and termination is driven by low temperature chilling in Bactrocera minax

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Auteur	Rui Pereira
Auteur	Nicolas Desneux
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Volume	86
Numéro	3
Pages	429-436
Publication	Journal of Pest Science
Date	2013/09/01
DOI	10.1007/s10340-013-0493-y
Résumé	Bactrocera minax is a major citrus pest in China, Bhutan, and India. It is univoltine and exhibits pupal diapause during winter. To better understand pupal diapause in this pest, we investigated pupal survival and pupal developmental duration under field and laboratory conditions. Specifically, we tested if pupal chilling was required for diapause development and termination. Nearly all mature larvae collected at the end of the citrus season entered pupal diapause. For pupae exposed in the field, natural chilling for less than 3 months resulted in more than 70 % mortality. However, exposure to winter conditions for 3 months or more both decreased pupal mortality and developmental duration when pupae were returned to the laboratory and held under constant temperature (25 °C). When pupae were gathered from the field in November and exposed to different chilling regimes in the laboratory, the chilling duration (30 vs 60 days) had significantly more impact on pupal survival than the specific chilling temperature (6, 8, 10, or 12 °C constant). However, both chilling duration and chilling temperature impacted on the pupal developmental duration, with longer chilling duration and higher temperatures decreasing pupal developmental duration. In conclusion, we demonstrated that pupal diapause development and termination in B. minax is strongly influenced by chilling conditions. Increasing cold exposure led to significantly and consistently faster adult eclosion and improved synchronization of adult emergence. This knowledge will help with the laboratory rearing of B. minax, an essential step in the long-term management of this pest.

Refounding of the activity concept? Towards a federative paradigm for modeling and simulation

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Auteur	P. Caillou
Auteur	O. Michel
Auteur	D. R. Hill
Volume	89
Numéro	2
Pages	156-177
Publication	SIMULATION
Date	2013
DOI	10.1177/0037549712457852

RNAi Silencing of the HaHMG-CoA Reductase Gene Inhibits Oviposition in the Helicoverpa armigera Cotton Bollworm

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Volume	8
Numéro	7
Pages	e67732
Publication	PLoS ONE
Date	July 2, 2013
DOI	10.1371/journal.pone.0067732
Résumé	RNA interference (RNAi) has considerable promise for developing novel pest control techniques, especially because of the threat of the development of resistance against current strategies. For this purpose, the key is to select pest control genes with the greatest potential for developing effective pest control treatments. The present study demonstrated that the 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase; HMGR) gene is a potential target for insect control using RNAi. HMGR is a key enzyme in the mevalonate pathway in insects. A complete cDNA encoding full length HMGR (encoding an 837-aa protein) was cloned from Helicoverpa armigera (Lepidoptera: Noctuidae). The HaHMGR (H. armigera HMGR) knockdown using systemic RNAi in vivo inhibited the fecundity of the females, effectively inhibited ovipostion, and significantly reduced vitellogenin (Vg) mRNA levels. Moreover, the oviposition rate of the female moths was reduced by 98% by silencing HaHMGR compared to the control groups. One-pair experiments showed that both the proportions of valid mating and fecundity were zero. Furthermore, the HaHMGR-silenced females failed to lay eggs (approximate 99% decrease in oviposition) in the semi-field cage performance. The present study demonstrated the potential implications for developing novel pest management strategies using HaHMGR RNAi in the control of H. armigera and other insect pests.

Role of a gamma-aminobutryic acid (GABA) receptor mutation in the evolution and spread of Diabrotica virgifera virgifera resistance to cyclodiene insecticides

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Volume	22
Numéro	5
Pages	473-484
Publication	Insect molecular biology
Date	Oct 2013
DOI	10.1111/imb.12037
Résumé	The western corn rootworm, Diabrotica virgifera virgifera, is a damaging pest of cultivated corn that was controlled by applications of cyclodiene insecticides from the late 1940s until resistance evolved ∼10 years later. Range expansion from the western plains into eastern USA coincides with resistance development. An alanine to serine amino acid substitution within the Rdl subunit of the gamma-aminobutyric acid (GABA) receptor confers resistance to cyclodiene insecticides in many species. We found that the non-synonymous single nucleotide polymorphism (SNP) G/T at the GABA receptor cDNA position 838 (G/T(838)) of D. v. virgifera resulted in the alanine to serine change, and the codominant SNP allele T(838) was genetically linked to survival of beetles in aldrin bioassays. A phenotypic gradient of decreasing susceptibility from west to east was correlated with higher frequencies of the resistance-conferring T(838) allele in the eastern-most populations. This pattern exists in opposition to perceived selective pressures since the more eastern and most resistant populations probably experienced reduced exposure. The reasons for the observed distribution are uncertain, but historical records of the range expansion combined with the distribution of susceptible and resistant phenotypes and genotypes provide an opportunity to better understand factors affecting the species' range expansion.

Sharing a predator: can an invasive alien pest affect the predation on a local pest?

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Auteur	Coline C. Jaworski
Auteur	Philippe Bearez
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Volume	55
Numéro	3
Pages	433-440
Publication	Population Ecology
Date	2013/07/01
DOI	10.1007/s10144-013-0371-8
Résumé	Invasive species can strongly affect biotic interactions in ecosystems, interacting both directly and indirectly with local species. In European tomato greenhouses, the invasive alien pest Tuta absoluta may impact the population dynamics of other pests like whiteflies. Besides inducing damages to the host plant and competing for resources with local pests, this alien species may exert a predator-mediated interaction on local pests sharing common natural enemies. Biocontrol agents usually used against whiteflies may also prey upon T. absoluta and this could alter the dynamics of local pest populations. We evaluated possible resource competition and predator-mediated interactions in a system involving one mirid predator Macrolophus pygmaeus and two pests, T. absoluta and a local whitefly, Bemisia tabaci, on greenhouse tomatoes. Results showed that both resource competition and predator-mediated interactions occurred simultaneously. In the presence of the shared predator, there was a short-term positive effect of T. absoluta on B. tabaci [up to 5.9-fold increase of B. tabaci juveniles (egg + larvae) after four weeks]. However, in the long-term there was a negative predator-mediated interaction of T. absoluta on B. tabaci, i.e., after ten weeks the density of B. tabaci was 7.3-fold lower in the presence of the invasive pest. We emphasize the critical role of generalist predators in managing both local and invasive alien pest populations and that the strength and direction of predator-mediated indirect interactions can depend on the time scale considered.

Solanidine isolation from Solanum tuberosum by centrifugal partition chromatography

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Volume	36
Numéro	14
Pages	2379-2385
Publication	Journal of separation science
Date	Jul 2013
DOI	10.1002/jssc.201300188
Résumé	The aim of this investigation was the preparative isolation of solanidine (aglycone of the two main potato glycoalkaloids: α-chaconine and α-solanine) from fresh Solanum tuberosum (cv. Pompadour) material by implementing a new preparation scheme using centrifugal partition chromatography (CPC). A setup for obtaining solanidine by hydrolysis of the glycoalkaloids found in the skin and sprouts of S. tuberosum was first developed. Then its isolation was carried out by the development of CPC conditions: the solvent system used for separation was ethyl acetate/butanol/water in the ratio 42.5:7.5:50 v/v/v, 0.6 g of crude extract were separated with a 8 mL/min flow rate of mobile phase while rotating at 2500 rpm. A run yielded 98 mg of solanidine (86.7 % recovery from the crude extract) in a one-step separation. The purity of the isolated solanidine was over 98%. Thus, CPC has proven to be the method of choice to get solanidine of very high purity from S. tuberosum biomass in large quantities.

Spatiotemporal patterns of induced resistance and susceptibility linking diverse plant parasites

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Auteur	Ian Kaplan
Auteur	Philippe Bearez
Auteur	Edwige Amiens-Desneux
Auteur	Nicolas Desneux
Volume	173
Numéro	4
Pages	1379-1386
Publication	Oecologia
Date	2013/12/01
DOI	10.1007/s00442-013-2716-6
Résumé	Induced defenses mediate interactions between parasites sharing the same host plant, but the outcomes of these interactions are challenging to predict because of spatiotemporal variation in plant responses and differences in defense pathways elicited by herbivores or pathogens. Dissecting these mediating factors necessitates an approach that encompasses a diversity of parasitic feeding styles and tracks interactions over space and time. We tested indirect plant-mediated relationships across three tomato (Solanum lycopersicum) consumers: (1) the fungal pathogen—powdery mildew, Oidium neolycopersici; (2) a sap-feeding insect—silverleaf whitefly, Bemisia tabaci; and (3) a chewing insect—the leaf miner, Tuta absoluta. Further, we evaluated insect/pathogen responses on local vs. systemic leaves and over short (1 day) vs. long (4 days) time scales. Overall, we documented: (1) a bi-directional negative effect between O. neolycopersici and B. tabaci; (2) an asymmetrical negative effect of B. tabaci on T. absoluta; and (3) an asymmetrical positive effect of T. absoluta on O. neolycopersici. Spatiotemporal patterns varied depending on the species pair (e.g., whitefly effects on leaf miner performance were highly localized to the induced leaf, whereas effects on pathogen growth were both local and systemic). These results highlight the context-dependent effects of induced defenses on a diverse community of tomato parasites. Notably, the outcomes correspond to those predicted by phytohormonal theory based on feeding guild differences with key implications for the recent European invasion by T. absoluta.

SP-Designer: a user-friendly program for designing species-specific primer pairs from DNA sequence alignments

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Auteur	Thibaut Malausa
Volume	13
Numéro	4
Pages	755-758
Publication	Molecular ecology resources
Date	Jul 2013
DOI	10.1111/1755-0998.12116
Résumé	SP-Designer is an open-source program providing a user-friendly tool for the design of specific PCR primer pairs from a DNA sequence alignment containing sequences from various taxa. SP-Designer selects PCR primer pairs for the amplification of DNA from a target species on the basis of several criteria: (i) primer specificity, as assessed by interspecific sequence polymorphism in the annealing regions, (ii) the biochemical characteristics of the primers and (iii) the intended PCR conditions. SP-Designer generates tables, detailing the primer pair and PCR characteristics, and a FASTA file locating the primer sequences in the original sequence alignment. SP-Designer is Windows-compatible and freely available from http://www2.sophia.inra.fr/urih/sophia_mart/sp_designer/info_sp_designer.php.

Species-specific DNA markers for identification of two root-knot nematodes of coffee: Meloidogyne arabicida and M. izalcoensis

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Auteur	José Ricardo Peixoto
Auteur	Philippe Castagnone-Sereno
Auteur	Regina Maria Dechechi Gomes Carneiro
Volume	137
Numéro	2
Pages	305-313
Publication	European Journal of Plant Pathology
Date	2013/10/01
DOI	10.1007/s10658-013-0242-3
Résumé	Seven root-knot nematodes (RKN), including Meloidogyne exigua, M. incognita, M. paranaensis, M. enterolobii, M. arabicida, M. izalcoensis and M. arenaria are major pathogens of coffee crop in the Americas. Species-specific primers for their identification have been developed for five of them and constitute a fast and reliable method of identification. Here we report a PCR-based assay for specific detection of M. arabicida and M. izalcoensis. Random Amplified Polymorphic DNA fragments specific for these two species were converted into sequence characterized amplified region (SCAR) markers. PCR amplification using the SCAR primers produced a specific fragment of 300 bp and 670 bp for M. arabicida and M. izalcoensis, respectively, which were absent in other coffee-associated Meloidogyne spp. tested. SCAR primers also allowed successful amplification of DNA from single second-stage juveniles (J2), males and females. In addition, these primers were able to unambiguously detect the target species in nematode suspensions extracted from soil and roots samples, in different isolates of the same species or when used in multiplex PCR reactions containing mixtures of species. These results demonstrated the effectiveness of these SCAR markers and their multiplex use with those previously developed for M. exigua, M. incognita, M. paranaensis, M. enterolobii and M. arenaria constitute an essential detection tool. This diagnostic kit will contribute for specific J2 identification of the major RKN infecting coffee from field samples in the Americas.

Spider mite control and resistance management: does a genome help?

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Auteur	Luc Tirry
Auteur	René Feyereisen
Volume	69
Numéro	2
Pages	156–159
Publication	Pest Management Science
Date	2013
DOI	10.1002/ps.3335
Résumé	The complete genome of the two-spotted spider mite, Tetranychus urticae, has been reported. This is the first sequenced genome of a highly polyphagous and resistant agricultural pest. The question as to what the genome offers the community working on spider mite control is addressed. Copyright © 2012 Society of Chemical Industry

Sublethal and transgenerational effects of chlorantraniliprole on biological traits of the diamondback moth, Plutella xylostella L.

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Auteur	Pei Liang
Auteur	Peng Han
Auteur	Xi-Wu Gao
Volume	48
Pages	29-34
Publication	Crop Protection
Date	June 2013
DOI	10.1016/j.cropro.2013.02.009
Résumé	The diamondback moth, Plutella xylostella (L.), is an important international pest of cruciferous vegetables. The effects of the new diamide insecticide chlorantraniliprole, at a lethal concentration inducing only 25% mortality (LC25), were assessed on the development and reproductive parameters of P. xylostella under laboratory conditions. In addition, effects on development time, pupation rate, larval and pupae weight, fertility, and survival in the parent and F1 generations were assessed. When 4th instar P. xylostella larvae were exposed to LC25 of chlorantraniliprole on a cabbage (Brassica oleracea var. capitata L.) leaf for 96 h, we observed increased developmental time for 4th instar larval to pupa period (4.27 days vs. 3.34 days in the control), lower pupal weight (3.58 mg vs. 4.17 mg in the control) and decreased adult fecundity (by 42%). F1 generation underwent transgenerational effects, i.e. higher developmental time from egg to pre-pupae and lower egg hatching rate occurred. Demographic growth parameters, such as the net reproductive rate (R0), the intrinsic rate of increase (rm), and finite rate of increase (λ) were significantly lower for the LC25 chlorantraniliprole treated group than for the untreated control. Our results suggest that exposure to LC25 of chlorantraniliprole may have negative effects both on exposed individuals and on subsequent generations in P. xylostella.

Suitability of the Pest-Plant System Tuta absoluta (Lepidoptera: Gelechiidae)-Tomato for Trichogramma (Hymenoptera: Trichogrammatidae) Parasitoids and Insights for Biological Control

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Auteur	Peng Han
Auteur	Elisabeth Tabone
Auteur	Nicolas Desneux
Volume	106
Numéro	6
Pages	2310-2321
Publication	Journal of Economic Entomology
Date	2013-12-01T00:00:00///
DOI	10.1603/EC13092
Résumé	The South American tomato leafminer, Tuta absoluta Meyrick (Lepidoptera: Gelechiidae), is a major pest that has recently invaded Afro-Eurasia. Biological control, especially by Trichogramma parasitoids, is considered to be promising as a management tool for this pest. However, further development of Trichogramma-based biocontrol strategies would benefit from assessing the impact of released parasitoid offspring on the pest. Under laboratory conditions, we 1) compared the parasitism of five Trichogramma species-strains on the pest-plant system T. absoluta-tomato, and 2) assessed various biological traits of parasitoids, mass-reared on a factitious host (Ephestia kuehniella Zeller), when developing on T. absoluta. In addition, we evaluated the overall efficiency of two specific Trichogramma species when released under greenhouse conditions in combination with a common natural enemy in tomato crop, the predator Macrolophus pygmaeus Rambur. Parasitoids emerging from T. absoluta on tomato showed lower parasitism rates and poor biological traits, for example, wing deformations, reduced longevity, when compared with the control reared on the factitious host. Under greenhouse conditions, the parasitoids that developed on T. absoluta after initial releases contributed little to biological control of T. absoluta, and parasitism tended to be lower when the predator was present. However, a slightly higher T. absoluta control level was achieved by combining the predator and release of the parasitoid Trichogramma achaeae Nagaraja and Nagarkatti. This study shows that Trichogramma parasitoids may not build up populations on the T. absoluta-tomato system, but that Trichogramma parasitoids can be used in combination with M. pygmaeus to enhance biological control of the pest in tomato crops.

Testing banker plants for biological control of mites on roses

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Auteur	Nicolas Desneux
Auteur	Christine Poncet
Volume	41
Numéro	3
Pages	249-262
Publication	Phytoparasitica
Date	2013/07/01
DOI	10.1007/s12600-012-0285-6
Résumé	We tested whether plant species used in a banker plant system influence the success of a biological control program with predatory mites. Banker plants (BP) may sustain a reproducing population of predators and provide long-term pest suppression. In an experiment lasting 12 weeks, we analyzed the responses of the predatory mite Amblyseius californicus and the pest mite Tetranychus urticae to eight species of potential BP with different morphological structures. Every BP was paired with a rose plant and infested with pest and predatory mites. The measured parameters were vitality and growth of the plants and numbers of predators, pests and their eggs. Reproduction and establishment of the pest and predatory mites differed among plant species as well as plant growth and vitality. Vitis riparia and Viburnum tinus were the most efficient BP in this combination of pest–predator species. Their presence resulted in best health of the rose crops, highest number of predatory mites and lowest number of pests. Both these BP possess domatia which may be responsible for the efficiency in hosting predatory mites. Overall, the species which fulfilled the requirements of a BP best was the local shrub V, tinus, which bore no pests and a very large number of predators and has a compact growth form suited for application in greenhouses. Although our study gives only evidence for an artificial system with a high BP:crop ratio, high numbers of introduced predators and short distances between plants, this study contributes to knowledge of BP systems and to improve the understanding of the criteria for the choice of local plant species to be used as BP for biological control in IPM.

The effect of mating system on invasiveness: some genetic load may be advantageous when invading new environments

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Auteur	Benoît Facon
Auteur	Jean Carlier
Auteur	Virginie Ravigné
Volume	16
Numéro	4
Pages	875-886
Publication	Biological Invasions
Date	2013/09/13
DOI	10.1007/s10530-013-0544-6
Résumé	The role of adaptation in determining invasion success has been acknowledged recently, notably through the accumulation of case studies of rapid evolution during bioinvasions. Despite this growing body of empirical evidence, there is still a need to develop the theoretical background of invasions with adaptation. Specifically, the impact of mating system on the dynamics of adaptation during invasion of a new environment remains only partially understood. Here, we analyze a simulation demo-genetic model of bioinvasion accounting for partial asexuality rates. We simulate two levels of recurrent immigration from a source population at mutation–drift–selection equilibrium to a new empty environment with a different adaptive landscape (black-hole sink). Adaptation relies on a quantitative trait coded explicitly by 10 loci under mutation, selection and genetic drift. Using this model, we confirm previous results on the positive effects on invasiveness of migration, mutation and similarity of local phenotypic optima. We further show how the invasion dynamics of the introduced population is affected by the rate of asexuality. Purely asexual species have lower invasion success in terms of probability and time to invasion than species with other mating systems. Among species with mixed mating systems, the greatest invasiveness is observed for species with high asexual rates. We suggest that this pattern is due to inflated genetic variance in the source population through the Hill-Robertson effect (i.e., clonal interference). An interesting consequence is that species with the highest genetic load in their source environment have greatest invasiveness in the new environment.

The Phytophthora parasitica RXLR effector penetration-specific effector 1 favours Arabidopsis thaliana infection by interfering with auxin physiology

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Volume	199
Numéro	2
Pages	476-489
Publication	The New phytologist
Date	Jul 2013
DOI	10.1111/nph.12270
Résumé	Pathogenic oomycetes have evolved RXLR effectors to thwart plant defense mechanisms and invade host tissues. We analysed the function of one of these effectors (Penetration-Specific Effector 1 (PSE1)) whose transcript is transiently accumulated during penetration of host roots by the oomycete Phytophthora parasitica. Expression of PSE1 protein in tobacco (Nicotiana tabacum and Nicotiana benthamiana) leaves and in Arabidopsis thaliana plants was used to assess the role of this effector in plant physiology and in interactions with pathogens. A pharmacological approach and marker lines were used to charcterize the A. thaliana phenotypes. Expression of PSE1 in A. thaliana led to developmental perturbations associated with low concentrations of auxin at the root apex. This modification of auxin content was associated with an altered distribution of the PIN4 and PIN7 auxin efflux carriers. The PSE1 protein facilitated plant infection: it suppressed plant cell death activated by Pseudomonas syringae avirulence gene AvrPto and Phytophthora cryptogea elicitin cryptogein in tobacco and exacerbated disease symptoms upon inoculation of transgenic A. thaliana plantlets with P. parasitica in an auxin-dependant manner. We propose that P. parasitica secretes the PSE1 protein during the penetration process to favour the infection by locally modulating the auxin content. These results support the hypothesis that effectors from plant pathogens may act on a limited set of targets, including hormones.

The plant genetic background affects the efficiency of the pepper major nematode resistance genes Me1 and Me3

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Pages	1-9
Publication	Theoretical and Applied Genetics
Date	2013
DOI	10.1007/s00122-013-2235-1
Résumé	Key message The plant genetic background influences the efficiency of major resistance genes to root-knot nematodes in pepper and has to be considered in breeding strategies. Abstract Root-knot nematodes (RKNs), Meloidogyne spp., are extremely polyphagous plant parasites worldwide. Since the use of most chemical nematicides is being prohibited, genetic resistance is an efficient alternative way to protect crops against these pests. However, nematode populations proved able to breakdown plant resistance, and genetic resources in terms of resistance genes (R-genes) are limited. Sustainable management of these valuable resources is thus a key point of R-gene durability. In pepper, Me1 and Me3 are two dominant major R-genes, currently used in breeding programs to control M. arenaria, M. incognita and M. javanica, the three main RKN species. These two genes differ in the hypersensitive response induced by nematode infection. In this study, they were introgressed in either a susceptible or a partially resistant genetic background, in either homozygous or heterozygous allelic status. Challenging these genotypes with an avirulent M. incognita isolate demonstrated that (1) the efficiency of the R-genes in reducing the reproductive potential of RKNs is strongly affected by the plant genetic background, (2) the allelic status of the R-genes has no effect on nematode reproduction. These results highlight the primary importance of the choice of both the R-gene and the genetic background into which it is introgressed during the selection of new elite cultivars by plant breeders.

The root-knot nematode calreticulin Mi-CRT is a key effector in plant defense suppression

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Volume	26
Numéro	1
Pages	97-105
Publication	Molecular plant-microbe interactions: MPMI
Date	Jan 2013
DOI	10.1094/MPMI-05-12-0130-R
Résumé	Root-knot nematodes (RKN) are obligate biotrophic parasites that settle close to the vascular tissues in roots, where they induce the differentiation of specialized feeding cells and maintain a compatible interaction for 3 to 8 weeks. Transcriptome analyses of the plant response to parasitic infection have shown that plant defenses are strictly controlled during the interaction. This suggests that, similar to other pathogens, RKN secrete effectors that suppress host defenses. We show here that Mi-CRT, a calreticulin (CRT) secreted by the nematode into the apoplasm of infected tissues, plays an important role in infection success, because Mi-CRT knockdown by RNA interference affected the ability of the nematodes to infect plants. Stably transformed Arabidopsis thaliana plants producing the secreted form of Mi-CRT were more susceptible to nematode infection than wild-type plants. They were also more susceptible to infection with another root pathogen, the oomycete Phytophthora parasitica. Mi-CRT overexpression in A. thaliana suppressed the induction of defense marker genes and callose deposition after treatment with the pathogen-associated molecular pattern elf18. Our results show that Mi-CRT secreted in the apoplasm by the nematode has a role in the suppression of plant basal defenses during the interaction.

The tyrosine-sulfated peptide receptors PSKR1 and PSY1R modify the immunity of Arabidopsis to biotrophic and necrotrophic pathogens in an antagonistic manner

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Volume	73
Numéro	3
Pages	469-482
Publication	The Plant journal: for cell and molecular biology
Date	Feb 2013
DOI	10.1111/tpj.12050
Résumé	The tyrosine-sulfated peptides PSKα and PSY1 bind to specific leucine-rich repeat surface receptor kinases and control cell proliferation in plants. In a reverse genetic screen, we identified the phytosulfokine (PSK) receptor PSKR1 as an important component of plant defense. Multiple independent loss-of-function mutants in PSKR1 are more resistant to biotrophic bacteria, show enhanced pathogen-associated molecular pattern responses and less lesion formation after infection with the bacterial pathogen Pseudomonas syringae pv. tomato DC3000. By contrast, pskr1 mutants are more susceptible to necrotrophic fungal infection with Alternaria brassicicola, show more lesion formation and fungal growth which is not observed on wild-type plants. The antagonistic effect on biotrophic and necrotrophic pathogen resistance is reflected by enhanced salicylate and reduced jasmonate responses in the mutants, suggesting that PSKR1 suppresses salicylate-dependent defense responses. Detailed analysis of single and multiple mutations in the three paralogous genes PSKR1, -2 and PSY1-receptor (PSY1R) determined that PSKR1 and PSY1R, but not PSKR2, have a partially redundant effect on plant immunity. In animals and plants, peptide sulfation is catalyzed by a tyrosylprotein sulfotransferase (TPST). Mutants lacking TPST show increased resistance to bacterial infection and increased susceptibility to fungal infection, mimicking the triple receptor mutant phenotypes. Feeding experiments with PSKα in tpst-1 mutants partially restore the defense-related phenotypes, indicating that perception of the PSKα peptide has a direct effect on plant defense. These results suggest that the PSKR subfamily integrates growth-promoting and defense signals mediated by sulfated peptides and modulates cellular plasticity to allow flexible adjustment to environmental changes.

Thiol-based redox signaling in the nitrogen-fixing symbiosis

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Volume	4
Pages	376
Publication	Frontiers in Plant Physiology
Date	2013
DOI	10.3389/fpls.2013.00376
Résumé	In nitrogen poor soils legumes establish a symbiotic interaction with rhizobia that results in the formation of root nodules. These are unique plant organs where bacteria differentiate into bacteroids, which express the nitrogenase enzyme complex that reduces atmospheric N2 to ammonia. Nodule metabolism requires a tight control of the concentrations of reactive oxygen and nitrogen species (RONS) so that they can perform useful signaling roles while avoiding nitro-oxidative damage. In nodules a thiol-dependent regulatory network that senses, transmits and responds to redox changes is starting to be elucidated. A combination of enzymatic, immunological, pharmacological and molecular analyses has allowed us to conclude that glutathione and its legume-specific homolog, homoglutathione, are abundant in meristematic and infected cells, that their spatio-temporally distribution is correlated with the corresponding (homo)glutathione synthetase activities, and that they are crucial for nodule development and function. Glutathione is at high concentrations in the bacteroids and at moderate amounts in the mitochondria, cytosol and nuclei. Less information is available on other components of the network. The expression of multiple isoforms of glutathione peroxidases, peroxiredoxins, thioredoxins, glutaredoxins and NADPH-thioredoxin reductases has been detected in nodule cells using antibodies and proteomics. Peroxiredoxins and thioredoxins are essential to regulate and in some cases to detoxify RONS in nodules. Further research is necessary to clarify the regulation of the expression and activity of thiol redox-active proteins in response to abiotic, biotic and developmental cues, their interactions with downstream targets by disulfide-exchange reactions, and their participation in signaling cascades. The availability of mutants and transgenic lines will be crucial to facilitate systematic investigations into the function of the various proteins in the legume-rhizobial symbiosis.

Time-lag in extinction dynamics in experimental populations: evidence for a genetic Allee effect?

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Auteur	Nicolas Ris
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Auteur	Xavier Fauvergue
Publication	The Journal of animal ecology
Date	Feb 7, 2013
DOI	10.1111/1365-2656.12051
Résumé	Propagule pressure, i.e. the number of individuals introduced, is thought to be a major predictor of the establishment success of introduced populations in the field. Its influence in laboratory experimental systems has however been questioned. In fact, other factors involved in long-term population persistence, like habitat size, were usually found to explain most of the dynamics of experimental populations. To better understand the respective influence of short- and long-term factors and their potential interaction on extinction dynamics in experimental systems, we investigated the influence of propagule pressure, habitat size and genetic background on the early dynamics of laboratory-based populations of a hymenopteran parasitoid. The amount of demographic variance differed between establishment and persistence phase and was influenced by habitat size and genetic background (geographic strain), but independent of propagule pressure. In contrast, the probability of extinction within five generations depended on the genetic background and on the interaction between propagule pressure and habitat size. Vulnerability to extinction in small size habitats was increased when populations were founded with a small number of individuals, but this effect was delayed until the third to fifth generations. These results indicate that demographic stochasticity is influential during population establishment, but is not affected by the genetic variability of propagules. On the other hand, extinction might be influenced by a genetic Allee effect triggered by the combination of low propagule pressure and genetic drift. Finally, we documented consistent differences between genetic backgrounds in both deterministic and stochastic population dynamics patterns, with major consequences on extinction risk and ultimately population establishment.

Top 10 plant-parasitic nematodes in molecular plant pathology

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Auteur	Johannes Helder
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Auteur	Juan E. Palomares-Rius
Auteur	Wim M. L. Wesemael
Auteur	Roland N. Perry
Pages	n/a–n/a
Publication	Molecular Plant Pathology
Date	2013
DOI	10.1111/mpp.12057
Résumé	The aim of this review was to undertake a survey of researchers working with plant-parasitic nematodes in order to determine a ‘top 10’ list of these pathogens based on scientific and economic importance. Any such list will not be definitive as economic importance will vary depending on the region of the world in which a researcher is based. However, care was taken to include researchers from as many parts of the world as possible when carrying out the survey. The top 10 list emerging from the survey is composed of: (1) root-knot nematodes (Meloidogyne spp.); (2) cyst nematodes (Heterodera and Globodera spp.); (3) root lesion nematodes (Pratylenchus spp.); (4) the burrowing nematode Radopholus similis; (5) Ditylenchus dipsaci; (6) the pine wilt nematode Bursaphelenchus xylophilus; (7) the reniform nematode Rotylenchulus reniformis; (8) Xiphinema index (the only virus vector nematode to make the list); (9) Nacobbus aberrans; and (10) Aphelenchoides besseyi. The biology of each nematode (or nematode group) is reviewed briefly.

Transcriptome profiling of Chironomus kiinensis under phenol stress using Solexa sequencing technology

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Volume	8
Numéro	3
Pages	e58914
Publication	PloS one
Date	2013
DOI	10.1371/journal.pone.0058914
Résumé	Phenol is a major pollutant in aquatic ecosystems due to its chemical stability, water solubility and environmental mobility. To date, little is known about the molecular modifications of invertebrates under phenol stress. In the present study, we used Solexa sequencing technology to investigate the transcriptome and differentially expressed genes (DEGs) of midges (Chironomus kiinensis) in response to phenol stress. A total of 51,518,972 and 51,150,832 clean reads in the phenol-treated and control libraries, respectively, were obtained and assembled into 51,014 non-redundant (Nr) consensus sequences. A total of 6,032 unigenes were classified by Gene Ontology (GO), and 18,366 unigenes were categorized into 238 Kyoto Encyclopedia of Genes and Genomes (KEGG) categories. These genes included representatives from almost all functional categories. A total of 10,724 differentially expressed genes (P value <0.05) were detected in a comparative analysis of the expression profiles between phenol-treated and control C. kiinensis including 8,390 upregulated and 2,334 downregulated genes. The expression levels of 20 differentially expressed genes were confirmed by real-time RT-PCR, and the trends in gene expression that were observed matched the Solexa expression profiles, although the magnitude of the variations was different. Through pathway enrichment analysis, significantly enriched pathways were identified for the DEGs, including metabolic pathways, aryl hydrocarbon receptor (AhR), pancreatic secretion and neuroactive ligand-receptor interaction pathways, which may be associated with the phenol responses of C. kiinensis. Using Solexa sequencing technology, we identified several groups of key candidate genes as well as important biological pathways involved in the molecular modifications of chironomids under phenol stress.

Two Sinorhizobium meliloti glutaredoxins regulate iron metabolism and symbiotic bacteroid differentiation

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Volume	15
Numéro	3
Pages	795–810
Publication	Environmental Microbiology
Date	2013
DOI	10.1111/j.1462-2920.2012.02835.x
Résumé	Legumes interact symbiotically with bacteria of the Rhizobiaceae to form nitrogen-fixing root nodules. We investigated the contribution of the three glutaredoxin (Grx)-encoding genes present in the Sinorhizobium meliloti genome to this symbiosis. SmGRX1 (CGYC active site) and SmGRX3 (CPYG) recombinant proteins displayed deglutathionylation activity in the 2-hydroethyldisulfide assay, whereas SmGRX2 (CGFS) did not. Mutation of SmGRX3 did not affect S. meliloti growth or symbiotic capacities. In contrast, SmGRX1 and SmGRX2 mutations decreased the growth of free-living bacteria and the nitrogen fixation capacity of bacteroids. Mutation of SmGRX1 led to nodule abortion and an absence of bacteroid differentiation, whereas SmGRX2 mutation decreased nodule development without modifying bacteroid development. The higher sensitivity of the Smgrx1 mutant strain as compared with wild-type strain to oxidative stress was associated with larger amounts of glutathionylated proteins. The Smgrx2 mutant strain displayed significantly lower levels of activity than the wild type for two iron-sulfur-containing enzymes, aconitase and succinate dehydrogenase. This lower level of activity could be associated with deregulation of the transcriptional activity of the RirA iron regulator and higher intracellular iron content. Thus, two S. meliloti Grx proteins are essential for symbiotic nitrogen fixation, playing independent roles in bacterial differentiation and the regulation of iron metabolism.

Une carte de la science basée sur les flux de soumission d’articles

Auteur	Vincent Calcagno
Auteur	Émilie Demoinet
Volume	17
Numéro	2
Pages	51-53
Publication	Virologie
Date	2013-03-01
DOI	10.1684/vir.2013.0478

Un monde sans moustiques ni cafards est-il possible?

Auteur	Denis Bourguet
Auteur	Thomas Guillemaud
Édition	LE POMMIER
ISBN	978-2-7465-0562-9
Date	2013

Venom gland extract is not required for successful parasitism in the polydnavirus-associated endoparasitoid Hyposoter didymator (Hym. Ichneumonidae) despite the presence of numerous novel and conserved venom proteins

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Auteur	Isabelle Darboux
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Auteur	Jean-Luc Gatti
Auteur	Marylène Poirié
Auteur	Anne-Nathalie Volkoff
Volume	43
Numéro	3
Pages	292-307
Publication	Insect biochemistry and molecular biology
Date	Mar 2013
DOI	10.1016/j.ibmb.2012.12.010
Résumé	The venom gland is a conserved organ in Hymenoptera that shows adaptations associated with life-style diversification. Few studies have investigated venom components and function in the highly diverse parasitic wasps and all suggest that the venom regulates host physiology. We explored the venom of the endoparasitoid Hyposoter didymator (Campopleginae), a species with an associated polydnavirus produced in the ovarian tissue. We investigated the effects of the H. didymator venom on two physiological traits of the host Spodoptera frugiperda (Noctuidae): encapsulation response and growth rate. We found that H. didymator venom had no significant effect on host cellular immunity or development, suggesting that it does not contribute to parasitism success. The host physiology seemed to be modified essentially by the ovarian fluid containing the symbiotic polydnaviruses. Proteomic analyses indicated that the H. didymator venom gland produces a large variety of proteins, consistent with the classical hymenopteran venom protein signature, including: reprolysin-like, dipeptidyl peptidase IV, hyaluronidase, arginine kinase or allergen proteins. The venom extracts also contained novel proteins, encoded by venom genes conserved in Campopleginae ichneumonids, and proteins with similarities to active molecules identified in other parasitoid species, such as calreticulin, reprolysin, superoxide dismutase and serpin. However, some of these proteins appear to be produced only in small amounts or to not be secreted. Possibly, in Campopleginae carrying polydnaviruses, the host-modifying activities of venom became redundant following the acquisition of polydnaviruses by the lineage.

Which role for nitric oxide in symbiotic N2-fixing nodules: toxic by-product or useful signaling/metabolic intermediate?

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Volume	4
Pages	384
Publication	Frontiers in Plant Physiology
Date	2013
DOI	10.3389/fpls.2013.00384
Résumé	The interaction between legumes and rhizobia leads to the establishment of a symbiotic relationship characterized by the formation of new organs called nodules, in which bacteria have the ability to fix atmospheric nitrogen (N2) via the nitrogenase activity. Significant nitric oxide (NO) production was evidenced in the N2-fixing nodules suggesting that it may impact the symbiotic process. Indeed, NO was shown to be a potent inhibitor of nitrogenase activity and symbiotic N2 fixation. It has also been shown that NO production is increased in hypoxic nodules and this production was supposed to be linked – via a nitrate/NO respiration process – with improved capacity of the nodules to maintain their energy status under hypoxic conditions. Other data suggest that NO might be a developmental signal involved in the induction of nodule senescence. Hence, the questions were raised of the toxic effects versus signaling/metabolic functions of NO, and of the regulation of NO levels compatible with nitrogenase activity. The present review analyses the different roles of NO in functioning nodules, and discusses the role of plant and bacterial (flavo)hemoglobins in the control of NO level in nodules.