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Insect-vectored plant viruses represent a major threat in agriculture causing significant yield losses worldwide. To fight these crop pests, insecticides are widely applied to reduce insect populations and therefore limit virus dispersion. A better understanding of the tripartite interactions between the virus, the vector and the host plant is needed to develop innovative alternatives to these chemical treatments. Recent studies have shown that vector-borne viruses can alter the phenotype of their host plants in such ways that the behavior of their vectors is modified, thus impacting their transmission. This project explores whether an aphid-transmitted virus can manipulate the plant response to its vector in order to influence its own transmission. The pathosystem is composed of the model plant *Arabidopsis thaliana*, the Turnip yellows virus (TuYV), a polerovirus which is efficiently transmitted by the aphid *Myzus persicae* in a circulative mode. A transcriptomic analysis was conducted on TuYV-infected or non-infected plants infested for 0, 6 or 72h with non-viruliferous *M. persicae*. The samples were subjected to non-targeted and targeted metabolomic analyses. We observed a dramatic effect of virus infection on the plant's response to aphids. Indeed, most of the 3,000 genes deregulated in healthy plants after aphid infestation remained unaffected when the virus was present. Only a small proportion of deregulated transcripts were common between healthy and infected plants upon aphid infestation. We also observed that more metabolomic modifications were induced by aphids rather than by the virus. Viral infection however modified the metabolite profiles of plants infested with aphids. All together, these data indicate that TuYV-infection lowers the plant's response to aphids, which may favor virus transmission.

Keywords: Polerovirus, Aphid, Arabidopsis, Transcriptomics, Metabolomics,

CO448

DISRUPTING INSECT-MEDIATED TRANSMISSION OF PLANT VIRUSES

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Crop yields are threatened by pathogens, of which plant viruses represent the major emerging group. Many viruses are vectored by hemipteran insects (aphids, whiteflies) that feed using specialised piercing mouthparts called stylets. In certain hosts such as *Arabidopsis thaliana* (Col-0) the aphid-transmitted virus cucumber mosaic virus (CMV) induces aphid feeding deterrence that inhibits settling of the aphids and encourages them to move to other hosts promoting virus transmission (Westwood *et al.* 2013). We investigated the effects of CMV infection on host-vector interactions in various Arabidopsis accessions. Aphid growth rate on CMV infected Arabidopsis accessions displays a continuum of responses from aphid resistance to aphid susceptibility. The innate attraction of aphids towards certain hosts can be used to manipulate virus-vector-host dynamics to decrease virus spread. We screened for Arabidopsis accessions that were aphid attractive hosts to be engineered as virus resistant plants using a hairpin RNA construct targeting the 2b CMV region. Using Arabidopsis 'microcosms', we evaluated the effects of mixing various proportions of aphid attractive and less attractive plants, as well as virus-resistant plants, on aphid-mediated transmission of viruses. We found that mixing specific proportions of virus resistant plants and susceptible plants disrupted transmission of CMV by aphids. Thus, virus-vector-host interactions can be manipulated to limit aphid mediated virus spread.

Keywords: plant virus, *Myzus persicae*, Arabidopsis, insect vector, CMV

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INSIGHTS INTO THE TRANSMISSION DYNAMICS OF BEETLE-BORNE VIRUSES

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Beetle-borne viruses have a unique mode of transmission, though their interactions with host plants and vectors remain poorly understood. Mexican bean beetles (*Epilachna varivestis*) are efficient vectors of several soybean-infecting viruses, including Bean pod mottle virus (BPMV). In these studies, we describe how BPMV-induced changes to plant physiology alter beetle feeding preferences in a way that likely facilitates virus spread. In addition, we describe the composition of oral secretions that feeding beetles regurgitate onto host plants, and how these secretions may play a fundamental role in beetle-borne virus specificity.

Keywords: Beetles, Viruses, Transmission

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TRANSMISSION OF THE CODIRO STRAIN OF XYLELLA FASTIDIOSA BY DIFFERENT INSECT SPECIES

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Most of the diseases associated to the insect-transmitted bacterium *Xylella fastidiosa* (Xf) have been described in North and South America, but in the last five years widespread infections were reported in a restricted area of the Apulia region (southern Italy), on olives suffering a severe disease denoted "olive quick decline syndrome - OQDS". Following this first report, several outbreaks have been reported in Corsica and Balearic Islands, and some in mainland France and Spain. Because many xylem sap-feeding insects can function as vectors for the transmission of this exotic pathogen in EU, several research programs are ongoing to assess the role of candidate vectors in the spread of the infections. Initial investigations identified *Philaenus spumarius* as the predominant vector species in the olive orchards affected by the OQDS. Additional experiments carried out over the past two years included, the spittlebugs *Philaenus italosignus* and *Neophilaenus campestris*, and of the planthopper *Latilica tunetana* (Hemiptera Issidae). Adults have been tested in transmission experiments to assess their ability to acquire the bacterium from infected olives and to infect different susceptible plant species. Acquisition rates determined by testing individual insects in quantitative PCR assays, ranged from 4,9% in *N. campestris* to 22% in *P. italosignus*, whereas no acquisition was recorded for *L. tunetana*. Successful transmissions were detected in some of the plant species exposed to *P. italosignus* or *N. campestris*, whereas *L. tunetana* did not transmit, even when adults were collected directly from the canopies of field-infected trees and tested positive in qPCR (1,4%). The ecological and epidemiological relevance of these findings are discussed. Although still limited, the data so far collected on the candidate vectors of Xf in Europe remark the major, if not exclusive, role of spittlebugs in the spread of this emerging pathogen.

Keywords: Spittlebugs, *Philaenus italosignus*, *Neophilaenus campestris*, Aphrophoridae, OQDS

CO451

VECTORS OF XF IN EUROPE: BEHAVIORAL ASPECTS INVOLVED IN TRANSMISSION

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Vector-borne plant pathogens spread is mediated by a continuum of interactions among three main components: the pathogen, the host, and the vector. Considering the bacterium *Xylella fastidiosa*, one of the most frightful pathogens threatening Europe, many steps have been done toward the direction of a complete understanding of the pathosystem's components and reciprocal interactions. Nevertheless, despite decades of efforts, a fundamental question remains unsolved: which specific vector behavior is associated with bacterium transmission? Previous research definitely proved that *X. fastidiosa* transmission is a mechanism driven by an active vector behavior, such as the previously proposed salivation-egestion hypothesis. However, to date conclusive evidences about salivation-egestion and its possible involvement in bacterial cells delivery to the plant are still missing. Moreover, the applicability in the European scenario of the background about *X. fastidiosa* transmission is hampered by the fact that all the previous studies were carried out with sharpshooters (Hemiptera: Cicadellidae), the main American vectors. On the other side, the spittlebug *Philaenus spumarius* (Hemiptera: Aphrophoridae), to date considered the most important European vector of the bacterium, has shown elements of novelty compared to sharpshooter in respect to its relationship with the bacterium. Therefore, part of the outline valid for sharpshooters should be questioned and further validated for those vector families widespread in Europe, and disregarded in previously studied outbreaks, such as spittlebugs and cicadas. Here we briefly review evidences and theories about the mechanism related to *X. fastidiosa* transmission, with a special focus on *P. spumarius* feeding behavior and its likely role in the epidemiology of *X. fastidiosa*-related diseases in Europe.

Keywords: *Xylella fastidiosa*, vectors, transmission, EPG

CO452

PHYTOPLASMA VIRULENCE PROTEINS ALTER PLANT DEVELOPMENT AND PROMOTE COLONIZATION OF INSECT VECTORS

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One of the most spectacular phenomena in biology is the complete hijacking of hosts by parasites such that these hosts become 'zombies' destined to advance survival of the parasites often to the detriment of the hosts. Phytoplasmas are obligate intracellular bacterial parasites of plants that induce dramatic changes in plant development, including proliferation of stems (witch's brooms) and the reversion of flowers into leaf-like structures (phyllody). These bacterial parasites produce two virulence proteins (effectors), named SAP11 and SAP54, that promote the degradation of plant TCP and MADS-box transcription factors, respectively, thus altering leaf and flower development. Phytoplasmas are dependent on sap-feeding insects for transmission to plants. Interestingly, SAP11 and SAP54 also convert plants into more attractive hosts for egg laying and reproduction of the insect vectors. Thus, phytoplasma effectors interfere with key plant developmental processes. Moreover, these effectors increase the colonization of plants by insect vectors thereby promoting transmission of the obligate phytoplasmas to new plant hosts.

Keywords: Symbiont, symbiosis, bacteria, phytoplasma, Hemiptera, pathogen, insect vector, leafhopper, aphid, virulence, effector, molecular mechanism, functional genomics, metagenomics, insect behavior, plant defense, insect-plant interactions, insect-microbe interactions, plant-microbe interactions, plant development, transcription factor, parasite

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EVOLUTIONARY DETERMINANTS OF HOST AND VECTOR MANIPULATION BY PLANT VIRUSES

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Plant viruses possess adaptations for facilitating acquisition, retention, and inoculation by vectors. Until recently, it was hypothesized that these adaptations are limited to virus proteins that enable virions to bind to vector mouthparts or invade their internal tissues. However, increasing evidence suggests that viruses can also manipulate host plant phenotypes and vector behaviors in ways that enhance their own transmission. Manipulation of vector-host interactions occurs through virus effects on host cues that mediate vector orientation, feeding, and dispersal behaviors, and thereby, the probability of virus transmission. Effects on host phenotypes vary by pathosystem but show a remarkable degree of convergence among unrelated viruses whose transmission is favored by the same vector behaviors. Convergence based on transmission mechanism, rather than phylogeny, supports the hypothesis that virus effects are adaptive and not just by-products of infection. Based on this, it has been proposed that viruses manipulate hosts through multifunctional proteins that facilitate exploitation of host resources and elicitation of specific changes in host phenotypes. But this proposition is rarely discussed in the context of the numerous constraints on virus evolution imposed by molecular and environmental factors, which figure prominently in research on virus-host interactions not dealing with host manipulation. To explore the implications of this oversight, we synthesized available literature to identify patterns in virus effects among pathogens with shared transmission mechanisms and discussed the results of this synthesis in the context of molecular and environmental constraints on virus evolution, limitations of existing studies, and prospects for future research.

Keywords: Host phenotype manipulation, vector behavior, disease ecology, chemical ecology, virus evolution, fitness, adaptation, generalist vs specialist, host diversity, landscape heterogeneity