

Drosophila C Virus (DCV) and Cricket Paralysis Virus (CrPV) in *Drosophila*. By contrast, the other components of the pathway, including the regulatory subunit of the IKK β kinase, NEMO, do not appear to play a role in the resistance to infection by these viruses. Among the genes regulated by IKK β in virus-infected flies, we identified two genes involved in the resistance to viral infection. The first one is the homologue of the mammalian factor STING (Stimulator of Interferon Genes), and we could show that it acts upstream of IKK β and Relish in a new signaling pathway (Fig. 2). The second one encodes a new antiviral factor, that we called Nazo (meaning “enigma” in Japanese) [3]. The STING-IKK β -Relish signaling cassette controls inducible expression of Nazo in response to viral infection. Nazo results from a duplication of the gene CG3740 in *Drosophila* species from the *Sophophora* subgenus. Of note, CG3740 is not upregulated by viral infection, and ectopic expression of the gene has no effect on replication of DCV or CrPV, unlike expression of Nazo, which results in strong suppression of viral replication. The discovery of Nazo provides an excellent opportunity to decipher the genetics by which a cellular gene acquires a new function in antiviral immunity. Furthermore, the characterization of its mode of action against picorna-like viruses may reveal novel angles of attack against a family of viruses that include many serious human pathogens (e.g., poliovirus). In summary, the fantastic diversity of insects extends to the viruses they carry, and to the genetic mechanisms they evolved to control these viruses. This biodiversity provides a unique opportunity to extend the repertoire of known antiviral mechanisms and to identify weak spots in the replication cycles of viruses.

Disclosure of interest The author declares that he has no competing interest.

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15

Cassava mealybug biological control delivers multi-faceted societal benefits

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As core component of sustainable intensification, biological control constitutes a tailor-made solution for the long-term management of both endemic and invasive pests. Here, drawing upon the example of the cassava mealybug (*Phenacoccus manihoti*; Hemiptera), we illuminate the myriad benefits of insect biological control.

In 2008, the above mealybug invaded Asia, where it inflicted a 27% drop in aggregate cassava production and triggered a 260% surge in starch prices. Mealybug-induced shocks in Thailand's cassava output were offset by a 300,000-ha expansion of the agricultural frontier—accompanied with major loss of intact tropical forest. Mealybug outbreaks were permanently resolved through the release of the neotropical wasp *Anagyrus lopezi* (Hymenoptera). This minute parasitoid effectively suppressed *P. manihoti* at a continent-wide scale, restored food security, and delivered pest control services worth US\$ 200–700/ha. This same parasitic wasp had previously averted famine for ~ 20 million people in Africa. Our work emphasizes how beneficial (pest-controlling) insects

help meet food production needs while benefiting farmers' pockets, global commodity trade, and the environment.

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Further reading

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16

Insects and their microbial partners: The *Drosophila* case study

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Metazoans establish reciprocal interactions with their commensal bacterial communities. Despite recent progress, a clear view of the physiological benefits associated with host/microbiota relationship remains elusive. Hence the molecular mechanisms through which the microbiota exerts its beneficial influences are still largely undefined. In this line, we aim at deciphering the molecular dialogue governing the mutualistic interaction between intestinal bacteria and their host. To



Fig. 1 *Lactobacillus plantarum* (associated with blue food and feces) colonizes the host intestine (in both adults and larvae) and is transmitted vertically to progenies (note the contamination of an egg being laid) and promotes larval growth (note the size difference of *L. plantarum* associated individuals (larvae with blue intestine) vs. non colonized larvae (no blue in the intestine) when grown for six days on a low nutrient diet). © François Leulier.

this end, we are using a genetically tractable gnotobiotic animal model: *Drosophila melanogaster*, which is mono-associated with one of its natural dominant commensal, *Lactobacillus plantarum* (Fig. 1). We are developing multiscale functional approaches to identify the mechanisms that underlie their mutualistic relationship, which results in the promotion of host juvenile growth upon chronic undernutrition. Our approaches aim at identifying both the bacterial and host genetic networks required to sustain their mutualistic relationship.

Disclosure of interest The author declares that he has no competing interest.

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17

What five insects told us about how a native plant copes with real-world problems

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Five native insects have taught us about traits that are essential for the survival of a native tobacco plant, *Nicotiana attenuata*, which lives in the Great Basin Desert of the USA. The five insects come from different feeding guilds, attack different tissues at different developmental stages and have revealed different traits that are essential for plant survival. For example, this plant recognizes attack from a specialized Lepidopteran herbivore (*Manduca sexta*) by the particular chemistry of the herbivore's saliva, and uses this recognition to tailor a complicated 6-layered defense response that involves a remodeling of the plant's transcriptome, metabolome and proteome, as well as some of its life history traits. The plant traits revealed by the remaining four insects will be described below, and how these insects will be used as high-through-put (HTP) screeners of large plantations of transformed and recombinant inbred lines of this native plant, to reveal the function of genes required for survival in nature. Insects are some of the best plant biologists on our planet and it behooves plant biologists to rediscover the lost art of natural history discovery to take advantage of the unique skill-sets of insects.

The plant and its insect herbivore community

Nicotiana attenuata (coyote tobacco: Solanales: Solanaceae) is a diploid tobacco native to the Great Basin Desert of North America. It enjoys a unique position scientifically, because hundreds of transgenic lines have been studied over the past two decades to understand the fitness consequences of precisely defined changes in gene expression for plants growing in their native habitats. For more than 30 years, the plant has been an ecological model system to study the complex plant-mediated interactions that occur in nature and to elucidate the genetic basis of traits important for the Darwinian fitness of plants. The choice of this diploid, largely selfing plant as a model system is grounded in its natural history and unusual germination behavior. Dormant seeds, survivors of decades or even cen-

turies of microbial challenges in soil, germinate synchronously into the nitrogen-rich, competition-free environments that are commonly found after fires. Dense *N. attenuata* populations then develop, in which plants are exposed not only to intense conspecific competition, but also to attack from as many as 34 different herbivore and pathogen taxa that colonize these post-fire populations from adjacent unburned areas.

These are the ecological conditions in which agriculture started, as slash-and-burn agriculture, and are the conditions that all our crops face. However, most crop taxa have not originated from post-fire adapted native species and are unlikely to be pre-adapted to the conditions of the agricultural niche. By understanding the specific traits that this native tobacco plant has evolved to optimize its fitness in the post-fire environment in which it times its germination and growth from long-lived seedbanks, we hope to learn what will be required to make our crop plants more self-sufficient, less dependent on agricultural inputs.

Nicotiana attenuata hosts a diverse insect herbivore community that includes several specialists on the Solanaceae: *Corime-laena extensa* (Hemiptera: Thyreocoridae), *Epitrix hirtipennis*, and *E. subcrintia* (Coleoptera: Chrysomelidae), two sympatric sibling species of *Trichobaris*, *T. compacta*, and *T. mucorea* (Coleoptera: Curculionidae), *Tupiocoris notatus*, (Hemiptera: Miridae), *Manduca quinquemaculata*, and *M. sexta* (Lepidoptera: Sphingidae) as well as the generalist herbivores *Spodoptera* spp. (Lepidoptera: Noctuidae), *Trimerotropis* spp. (Orthoptera: Acrididae), and *Oecanthus* spp. tree crickets (Orthoptera: Gryllidae) and the opportunistic generalist herbivores *Empoasca* spp. (Hemiptera: Cicadellidae) and *Heliothis* spp. (Lepidoptera: Noctuidae). *Geocoris pallens* is a common predator of herbivores on *N. attenuata*.

Five of these insects (four herbivores and one predator) have proven to be very useful in eliciting and responding to plant traits, characteristics that make them very useful as High-Through-Put (HTP) screeners and sentinel insects for large forward-genetic Recombinant Inbred Line (RIL) populations that will be described after these five insects are introduced.

The herbivores: *Manduca*, *Empoasca*, *Tupiochorus*, and *Trichobaris* spp

Manduca spp. The tobacco and tomato hornworms (*M. sexta* and *M. quinquemaculata*) have evolved an unprecedented capacity to detoxify the signature defense metabolite of the genus, *Nicotiana*, namely: nicotine. These nicotine-adapted larvae excrete the vast majority of the nicotine that they ingest with their food, but also co-opt a small fraction of the ingested nicotine for their own defense [1]. *M. sexta* larvae are found on *N. attenuata* plants because the adult moths oviposit while nectaring on the flowers. Hence, this insect plays dual roles in the lives of *N. attenuata* plants, as a devastating herbivore during the larval stages and as an important pollinator as an adult, vectoring gametes among the spatially separated plant populations that occur after fires, likely adding important genetic diversity to the seeds that must survive the decades of dormancy in the seed banks. Attack from these nicotine-adapted larvae is specifically recognized by the plant, when fatty acid amino acid conjugates (FACs) in the larval oral secretions are introduced into wounds when the larvae feed. This FAC-mediated recognition by the plant results in a six-layered suite of defense, avoidance, and tolerance responses (summarized in an iBiology talk available at <https://www.ibiology.org/plant-biology/studying-plants-ecological-interactions-genomics-era-story-nicotiana-attenuata/#part-2>), which engages all aspects of the plant's physiology. As such, *Manduca* larvae are ideal elicitors of ecologically important plant phenotypes and these phenotypes can be elicited by introducing larval oral secretions into plant wounds, a treatment that can be readily accomplished in a HTP manner for the large numbers of plants in a MAGIC population.

Empoasca spp. These piercing-sucking leafhoppers "eavesdrop" on the jasmonate (JA)-mediated signaling capacities of their host plants, preferentially selecting those hosts that are deficient in jasmonate accumulations [2]. Given that JA signaling mediates the vast majority of plant defenses, it is particularly intriguing that this natural phenotyping "bloodhound" specif-