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 IKKβ kinase, NEMO, do not appear to play a role in the resistance to infection by these viruses. Among the genes regulated by IKKβ 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 IKKβ 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-IKKβ-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.

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References

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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 losses 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.

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

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
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.

**Further reading**

M.E. Martino, P. Joncour, R. Leenay, H. Gervais, M. Shah, S. Hughes, B. Gillet, C. Beisel, F. Leulier, Bacterial Adaptation to the Host’s Diet Is a Key Evolutionary Force Shaping *Drosophila-Lactobacillus* Symbiosis. Cell Host Microbe 24. Published online 28 June 2018. 10.1016/j.chost.2018.06.001


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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 (*Mandrau sexta*) by the particular chemistry of the herbivore’s saliva, and uses this recognition to tailor a complex 6-layered 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 scientifially, 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 coyote tobacco is 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 centuries 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 are develop, in which 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: *Corineura sericea* (Hemiptera), *Nicta tile* (Hemiptera), *nicotiana*. 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 fitness of *N. attenuata*: as a devastating herbivore, it often colonizes 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 iBioLogic 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, *Mandrau* larvae are ideal elicitors of ecologically important plant phenotypes and these phenotypes can be elicited by introducing larval oral secretions into the plant wounds by treatment that can be readily accomplished in a HTP manner for the large numbers of plants in a MAGIC population.

*Emepoa* spp. These piercing–sucking leafhoppers “eavesdrop” on the jasmonate (JA)-mediated signaling capacities of their host plants, preferring to select 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-