Published in final edited form as:

Curr Opin Insect Sci. 2018 October ; 29: vi–viii. doi:10.1016/j.cois.2018.08.004.

Editorial overview: Molecular physiology: from omics data encyclopedia to physiology ‘short stories’

Fernando G Noriega and

Department of Biological Sciences and Biomolecular Sciences Institute, Florida International University, United States

Pedro L Oliveira

Instituto de Bioquímica Médica Leopoldo de Meis, Universidade Federal do Rio de Janeiro, Brazil

‘Omics’ approaches are rapidly growing fields of science that study large sets of biological molecules [1]. In the post-genomics era, all-inclusive analyses using functional ‘omics’ technologies such as transcriptomics, proteomics and metabolomics have increased our understanding of insect physiology. Insect science gained a new molecular dimension thanks to this *omics* tide, affecting all areas of biological knowledge and blurring disciplinary fields. The drive for developing an integrative view of an organism is part of the intrinsic nature of physiology, as observed already in the Introduction of Wigglesworth classic book ‘The Principles of Insect Physiology’, who pointed that “every anatomical peculiarity, every ecological specialization, has indeed its physiological counterpart. In that sense, anatomy, physiology and ecology are not separable” [1]. Nowadays, the enormous amount of raw analytical data is driving a synthetic movement of science from a descriptive huge collection of omics towards integration of molecular details into a physiological context.

The very simple idea behind this volume was to ask contributors to make their personal account of the molecular mechanisms that are behind some of the most classical topics of insect physiology, with emphasis on the view provided by recent omics data from all kinds.

Perhaps the best example of how the high throughput approach is changing basic concepts in biology is the unraveling of a microbial world of previously unsuspected size and diversity. [Angela Douglas](#) review describes general outlines of how this avalanche of data is now allowing proposition of novel hypotheses regarding the interaction of microbial communities with their insect hosts, emphasizing the need for solid experimental designs towards testing these hypotheses.

The most intensively studied aspect of the interaction between hosts and microorganisms is by far the immune response elicited by pathogens that is directed to elimination of disease-causing organisms. Disease is a condition characterized by deviation from homeostasis due to damage to the host, determined both by the action of the pathogen, as well as self-inflicted damage due to the immune response. [Lissner and Schneider](#) comment on a frequently overlooked essential aspect of disease biology, which is how organisms can

tolerate infection and damage by triggering an adaptive repair program. Recent data reviewed here indicate that stress response and immune-metabolic regulation work towards recovering of homeostasis and are critical to make the choice between survival and death.

The cell physiology changes that occur after infection are further discussed in the review by [Lee and Lee](#). They dissect the reciprocal regulatory loops between metabolism and immune signaling. These two areas were classically treated as essentially unrelated fields, but recent evidence has now revealed that not only immune pathways have profound implications on energy metabolic pathways, but that regulation of metabolism has previously unsuspected signaling connections that modulate immunity.

The capacity of obtain certain types of food encompasses traits that are key adaptations of insects to specific ecological niches. Here, [Arca and Ribeiro](#) show that the anti-hemostatic and immunomodulatory components of the saliva of hematophagous insects are the product of a 200 million years Red Queen dynamics involving an arms race between vertebrates and insects. They discuss that abundant omics data reveal that complex sialomes bearing those activities appeared independently several times in the evolution of insects. Still, some common patterns appeared, such as extensive duplications within specific gene families, as well as the use of protein inhibitors (called kratagonists) that act through binding small molecule agonists to interfere on vertebrate host hemostasis. They also highlight some recent advances in sialome research, specifically the discovery of complement inhibitors and the presence of microRNAs in insect saliva that may play a role in host manipulation, but can also act on pathogen transmission by insect vectors.

The regulation of many physiological processes in insects involves G protein-coupled receptors (GPCRs). Also known as seven transmembrane region (7TM) receptors, these cell surface receptors and integral membrane proteins transduce signals across cell membranes. [Pietrantonio et al.](#) summarize key points about GPCRs and signaling, and emphasize the most recent developments in the pharmacology of arthropod neuropeptide GPCRs; discussing omics' contributions to the advancement of this field; including the improvement of GPCR deorphanization and characterization. In addition, the recent incorporation of computational structural biology to modelling of arthropod GPCRs and peptidomimetic design is accelerating the efforts of insect physiologists and chemists to design more potent and stable receptor ligands. In the future, further functional analyses of diverse insect GPCR sequences will provide a clearer picture of constraints, commonalities and behaviors of these receptors between vertebrates and invertebrates.

The Malpighian tubule (MT) is a key component of the insect excretory and osmoregulatory systems that contributes to the success of insects in exploiting the widest range of habitats. [Dow et al.](#) discuss that modern functional genomics approaches have transformed our understanding of MT physiology. Initially, this was based largely on data mining of the newly sequenced *Drosophila melanogaster* genome, and associated transcriptomics. However, in the last years, multiple new omics studies from insects others than *Drosophila* have widener our knowledge of the physiology of this critical system. This review provides an overview on the influence of next generation sequencing (NGS) on genomics and transcriptomics studies; as well as the influence of proteomics and metabolomics profiling

studies on the understanding of new aspects of MT physiology. Finally, integrative data analysis and meta-analysis are currently used to analyse high-throughput data from transcriptomics, proteomics and metabolomics to provide an integrative comprehensive view of the MT biology.

Insects utilize an open circulatory system to transport nutrients, waste, hormones and immune factors throughout the hemocoel. The primary organ that drives hemolymph circulation is the dorsal vessel, which is a muscular tube that traverses the length of the body and is divided into an aorta in the head and thorax, and a heart in the abdomen. The dorsal vessel is myogenic; it does not require neural or hormonal input for contractions to take place. However, the rhythmicity of the dorsal vessel is modulated by neuropeptides and neurotransmitters. Hyllner's review summarizes how neuropeptides such as crustacean cardioactive peptide (CCAP), FMRamide-like peptides, proctolin, allatotropin and allatostatin modulate the heart contraction rate and the directionality of heart contractions. Likewise, it discusses how neurotransmitters such as serotonin, octopamine, glutamate and nitric oxide influence the heart rate, and how transcriptomics and proteomics approaches have been used to advance our understanding of insect circulatory physiology. Finally, this review argues that the immune system may modulate heart rhythmicity, and discusses evidence showing that the myotropic activity of cardioactive factors extends to the accessory pulsatile organs, such as the auxiliary hearts of the antennae.

Terra et al. propose that the discovery of new insect midgut features has been made possible by the recent availability of transcriptome datasets. These data uncovered the existence of a true mucous layer, derived from the preferential expression of mucus-forming mucins either at midgut regions that require protection or at sites of enzyme immobilization, particularly around the peritrophic membrane. Omics studies have highlighted that Coleoptera lysosomal peptidases are directed to midgut lumen by a mechanism other than the mannose-dependent pathway, a feature that is likely conserved across Annelida, Mollusca, Nematoda, and Arthropoda. Moreover, midgut transcriptomes of distantly related species have exposed a general overexpression of xenobiotic detoxification pathways to attenuate toxicity of plant-derived compounds and insecticides, exposing a role for these detoxification pathways in regulating host-microbiota interactions by metabolizing bacterial secondary metabolites.

The juvenile hormones (JHs) are a family of insect acyclic sesquiterpenoids produced by the *corpora allata* (CA), a pair of endocrine glands connected to the brain. They are involved in the regulation of development, reproduction, behavior, caste determination, diapause, stress response, and numerous polyphenisms. Nouzova et al. describe that in the post-genomics era, comprehensive analyses using functional 'omics' technologies such as transcriptomics, proteomics and metabolomics have increased our understanding of the activity of the minute CA. This review summarizes some of the 'omics' studies that have contributed to further understand JH synthesis in insects, with an emphasis on research on the mosquito *Aedes aegypti*. In the post-genomics era, important progresses have been made in our understanding of the regulation of JH synthesis. Among them, the authors highlighted the identification of all the enzymes involved in the JH synthesis pathway, as well as the measurement of changes in transcripts, JH precursor metabolites and enzymatic activities in the minute CA of insects. 'Omics' approaches also helped in the identification of new

allatoregulatory molecules and their receptors, as well as provided insights into their mechanisms of action. Early work in each omics area is beginning to illustrate that there is still much more to learn about the intricate regulation of JH synthesis.

We hope that the reviews in this section, written by authoritative authors in their fields, will provide the reader a glimpse on the impact and use of the omics approach towards integration of molecular data into tissue and organismal level physiology.

Biographies

Fernando G Noriega

Fernando G Noriega is a Professor in the Department of Biological Sciences at Florida International University. His research group employs an integrative approach that combines experiments at the organismal, cellular and molecular level to understand the regulation of Juvenile Hormone (JH) synthesis in mosquitoes. By integrating metabolomics, genomics and proteomics tools, he is uncovering that mosquito regulation of hormone synthesis has unique features that are related to the adaptation to blood-feeding and the cyclic maturation of ovarian development.

Pedro L Oliveira

Pedro L Oliveira is a Professor in the Instituto de Bioquímica Médica Leopoldo de Meis, Biochemistry at the Universidade Federal do Rio de Janeiro, Brazil. His research is concentrated on the study of adaptations of blood sucking insects to hematophagy. More specifically, he focus on how these animals tolerate a high intake of heme and aminoacids that occur as a consequence of a blood meal.

References

1. Wigglesworth VB: The Principles of Insect Physiology. London: Chapman and Hall; 1972.