

PREFACE

Leap forward with insect genomics

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Insects comprise the largest animal group in the world. More than a million insect species have been identified, leaving possibly two to three times more to be discovered. Systematic understanding of the genetic content of an insect species began more than 15 years ago when the genome sequence of the fruit fly, *Drosophila melanogaster* was reported (Adams *et al.*, 2000). For the first time, scientists were able to glean unprecedented insights into the genetic blueprint of a model insect, presenting its 13 600 protein coding genes. Such fundamental information opened a floodgate for comparative and functional analysis of these genes and enabled systems approaches to comparative, evolutionary and population genomic studies. In recent years, next-generation and third-generation sequencing platforms brought genome sequencing to more than a hundred insect species, reaching far beyond the few well-studied model organisms. The international consortium for insect genomes is working toward an ambitious goal to sequence 5000 species of insects.

The discovery of genes from insect genomes has facilitated many fields of insect science: revealing the mechanism of development and metamorphosis, providing new tools for pest control and promoting the use of beneficial insects, just to name a few. For example, the genome sequence of the monarch butterfly uncovered the potential genetic determinant of its long-distance migration (Zhan *et al.*, 2011); the male-determining factor (M factor) that

eluded scientists for approximately 70 years was identified through mosquito genome analysis (Hall *et al.*, 2015). The completion of the plant hopper genome sequence enabled the identification of key genes and pathways that regulate wing development (Xue *et al.*, 2014), and sequencing of the gigantic genome of the migratory locust enabled scientists to address many questions, including the transformation from solitary to gregarious phase (Wang *et al.*, 2014). These few examples of applications of insect genomics bode well for a bright future for insect science. Research described in this special issue is further evidence of the vibrant and exciting field of insect genomics. This collection stems from the 2nd International Conference on Insect Genomics, which was organized by Professor Bin Chen of Chongqing Normal University, China. The meeting was held in Chongqing, September 18–20, 2015, with more than 250 participants. At the suggestion of the Editor-in-Chief, Professor Le Kang and the Executive Editor, Dr. Yun Xian Zhao of *Insect Science*, the meeting organization committee compiled two special issues that include invited and contributed manuscripts, all of which were peer-reviewed according to the regulations of *Insect Science*. Here, we briefly summarize these articles.

Transcriptome data are powerful tools for direct identification of genes and analysis of global gene expression profiles. Liu *et al.* reported an integrated analysis of micro RNAs (miRNAs) and transcriptomes in the midgut of *Aedes albopictus* (Liu *et al.*, 2016a). They showed differential expression profiles of immune-related genes during infection by dengue virus serotype-2. Liu *et al.* from another group presented metatranscriptome data that indicated variation of the protistan community in *Reticulitermes flaviceps*, after treatment of the juvenile hormone analogues fenoxycarb to induce development of termite workers (Liu *et al.*, 2016b). Yu *et al.* focused on genes and proteins that may explain the supercooling ability of

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the Chinese white wax scale insect (Yu *et al.*, 2016). They identified a gene named *epAFP* that exhibited thermal hysteresis activity. He *et al.* identified and characterized 64 odorant-binding protein (OBP) genes in the malaria vector, *Anopheles sinensis*, from a whole genome analysis (He *et al.*, 2016). Zhang *et al.* used transcriptome profiling to identify the olfactory genes of a tiny insect parasitoid wasp of *Dendrolimus punctatus* (Zhang *et al.*, 2016). Hao *et al.* investigated a possible mechanism of summer diapause of *Delia antiqua* through digital gene expression analysis (Hao *et al.*, 2016). In addition, Cheng *et al.* identified toxins in the venom gland of Chinese bird spider at the whole genome level (Cheng *et al.*, 2016).

Cloning, expression and function analysis of genes becomes much easier with the help of genome and transcriptome information. Li *et al.* demonstrated that the two duplicated Cht5s (LmCht5-1 and LmCht5-2) from the migratory locust, *Locusta migratoria*, have distinct molecular characteristics and biological roles (Li *et al.*, 2016). In the same species, Song *et al.* reported the critical importance of a cuticle protein LmTwdl1 in molt development (Song *et al.*, 2016). Zhou *et al.* identified the *MBF2* family of genes in silkworm, and provided insights into the evolution of these genes in response to *Bacillus bombysepticus* infection (Zhou *et al.*, 2016). Huang *et al.* cloned a specific helitron, Bmhel-8, from the *sericin-1* gene promoter sequence and showed that Bmhel-8 exhibits enhancer activity in a *sericin-1* promoter-driven gene expression system, but does not influence tissue-specific expression of *sericin-1* (Huang *et al.*, 2016). Lu *et al.* discovered genes associated with new green cocoon through microarray analysis in the silkworm (Lu *et al.*, 2016). Chen *et al.* reviewed the *Distal-less* (*Dll*) genes in both insects and spiders (Chen *et al.*, 2016). Chang *et al.* identified and characterized miRNAs in the white-backed planthopper, *Sogatella furcifera* (Chang *et al.*, 2016). They identified 382 miRNAs from veruliferous and non-veruliferous populations. Lemonds *et al.* focused on the melanin pathway that affects overall body pigmentation during ontogenesis of *Periplaneta americana*. Their results showed that genetic mechanisms of coloration can change during ontogenesis (Lemonds *et al.*, 2016).

Mitochondrial genome (mtgenome) information can provide unique evolutionary insights. Hua *et al.* sequenced the complete mtgenome of *Anopheles minimus* and constructed a phylogenetic tree that included 18 other *Anopheles* species (Hua *et al.*, 2016). Their results showed that the subgenera, *Cellia* and *Anopheles*, and *Nyssorhynchus* and *Kerteszia*, have mutually close relationships, respectively.

Genome editing is a recent development that is revolutionizing many aspects of biological research. Bi *et al.*

reported their latest results of CRISPR/Cas9-mediated mutagenesis in *Spodoptera litura*. Direct injection of Cas9 mRNA and SlAbd-A-specific single guide RNA (sgRNA) into *S. litura* embryos successfully induced the typical Abd-A deficient phenotype (Bi *et al.*, 2016).

Insect and microbial interaction is another rapidly expanding field. High-throughput DNA or RNA sequences could be directly used to evaluate species abundance as well as gene expression profiles. Fan *et al.* reported the draft genome of a facultative endosymbiont of the brown planthopper (Fan *et al.*, 2016). They suggest that microbial gene horizontal transmission may play crucial roles in vitamin metabolic function. Zhu *et al.* sequenced the *Rickettsia* genomes from the whitefly and revealed genes that are potentially involved in symbiosis (Zhu *et al.*, 2016).

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Disclosure

The authors declare that they have no conflicts of interest.

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