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BOOK OF ABSTRACTS

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Cotesia chilonis (Hymenoptera: Braconidae) is the major larvae endoparasitoid wasp of striped stem borer, *Chilo suppressalis* (Lepidoptera: Crambidae), one of the most economically important rice pests in Asia, Northern Africa, and Southern Europe. The natural parasitism rates range from 10% to 30% and may be as high as 90%. This wasp is regarded as one of the most important natural enemies of *C. suppressalis*, and has great potential for pest biological control. Here, we present the draft genome of this endoparasitoid wasp. Adopting a whole-genome shotgun sequence strategy, we generated about 64.44 Gb of Illumina reads and 7.63 Gb of Pacbio reads. The filtered reads were assembled using ABySS to yield a 189.53 Mb assembly with an Contig N50 size and Scaffold N50 size of 1.22 Mb and 2.21 Mb, respectively. The GC content of the genome is 30.36%. The genome assembly is of high quality, as 237 out of 248 core eukaryotic genes mapping approach (CEGMA) genes are complete in the assembly; and 93% of 843 Single-Copy BUSCOs are full in length. We used Optimized Maker-based Insect Genome Annotation (OMIGA) pipeline to identify the protein coding genes and after integrating the evidences of RNA-Seq, *de novo* prediction and homolog protein alignment, an official gene set (OGS) of 14,142 genes of *C. chilonis* was obtained. We identified 16 small nucleolar RNA (snoRNA), 39 small nuclear RNA (snRNA), 144 transfer RNA (tRNA), 148 ribosome RNA (rRNA) and 111 microRNA (miRNA). We identified gene families with apparent expansions or contractions in *C. chilonis* by a comparison with other ten Hymenoptera insect genomes, and observed some gene families associated with parasitic behavior were significantly expanded in *C. chilonis*.

Keywords: *Cotesia chilonis*, genome, gene families, parasitic behavior, comparative genomics

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THE GENOME OF WASP *MACROCENTRUS CINGULUM* PROVIDES NEW INSIGHTS INTO POLYEMBRYONY AND IMMUNE EVASION

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Background: Parasitoid wasps are well-known natural enemies of major agricultural pests and arthropod borne diseases. The parasitoid wasp *Macrocentrus cingulum* has been widely used to control the notorious insect pests *Ostrinia furnacalis* (Asian Corn Borer) and *O. nubilalis* (European corn borer). One striking phenomenon exhibited by *M. cingulum* is polyembryony, the formation of multiple genetically identical offspring from a single zygote. Moreover, *M. cingulum* employs a passive parasitic strategy by preventing the host's immune system from recognizing the embryo as a foreign body. Thus, the embryos evade the host's immune system and are not encapsulated by host hemocytes. Unfortunately, the mechanism of both polyembryony and immune evasion remains largely unknown. Results: We report the genome of the parasitoid wasp *M. cingulum*. Comparative genomics analysis of *M. cingulum* and other five hymenopterans, two dipterans, two lepidopterans, one coleopteran, one hemipteran, and one mite species were conducted, finding some gene families with apparent expansion or contraction which might be linked to the parasitic behaviors or polyembryony of *M. cingulum*. Moreover, we present evidence that the microRNA miR-14b regulates the polyembryonic development of *M. cingulum* by targeting the c-Myc Promoter-binding Protein 1 (MBP-1), histone-lysine N-methyltransferase 2E (KMT2E) and segmentation protein Runt. In addition, Hemomucin, an O-glycosylated transmembrane protein, protects the wasp larvae from being encapsulated by host hemocytes. Motif and domain analysis showed that only the hemomucin in two endoparasitoids, *M. cingulum* and *Venturia canescens*, possessing the ability of passive immune evasion have intact mucin domain and have similar O-glycosylation patterns, indicating that the hemomucin is a key factor modulating the immune evasion. Conclusions: We provided the draft genome of an endoparasitoid wasp *M. cingulum*. The microRNA miR-14b participates in the regulation of polyembryonic development, and the O-glycosylation of the mucin domain in the hemomucin confers the passive immune evasion in this wasp. These key findings provide new insights into the polyembryony and immune evasion.

Keywords: *M. cingulum*, genome, polyembryony, immune evasion, comparative genomics.

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AFFINITIES AND DIVERGENCE OF Aedes MOSQUITOES USING BAYESIAN RELAXED CLOCKS AND COMPLEX MODELS OF EVOLUTION

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A detailed understanding of *Aedes* evolutionary affinities is important for at least three reasons: 1) it guides proper taxonomic classification of genus and species; 2) it aids planning comparative genomics by defining the sister-taxa of medical relevant species; 3) it provides a framework for estimating divergence and reconstructing paleo-ecological scenarios. Current knowledge of *Aedes* phylogeny and divergence is still based on fragmented molecular matrices and has never been explored using complex Bayesian inferences and relaxed clocks. Here we have blasted public databases and assembled a multi-gene alignment composed of mitochondrial coded COI, COII, NADH4, 16S and nuclear coded 28S, ITS, 18S, enolase and arginine kinase for a total of ~7500 nucleotide positions of 145 species, 100 *Aedes* species, 30 species from other Culicidae genera and 15 species from the Syrphidae family used to root the trees. Bayesian inferences indicate a poor resolution at the single gene level, while concatenation has higher resolution power; we compared our phylogenies using homogeneous and heterogeneous replacement models to define nodes that are susceptible to systematic errors. Our phylogenies revealed *A. falvopictus* and *A. japonicus* as the sister species of respectively *A. albopictus* and *A. koreicus* two species of growing interest in Europe. Our divergence estimates based on Bayesian relaxed clock reveal a strong among-genes heterogeneity of the evolutionary process, but overall indicate the origin of the Aedini tribe in the late Triassic and his radiation in the early Jurassic. Our study is the first attempt to provide a multi gene phylogeny of *Aedes* using heterogeneous replacement models and relaxed clock estimate of their divergence: results are relevant for clarifying some long lasting systematic issue and for providing a pleo-ecological scenario which may increase our understanding of *Aedes* biology and epidemiology.

Keywords: Mosquito, Phylogeny, *Aedes*, Clock

Evolution and Development of Functional Traits

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UNVEILING THE MOLECULAR GROUNDS OF AGGRESSIVE MIMICRY IN THE MYRMECOPHILOUS APHID *PARACLETUS CIMICIFORMIS*

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