

Emerging Psyllid Genomes- Increasing RNAi Targets for Insect Management

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Abstract:

Genomics has changed the strategies used to manage insects and diseases. The ability to effect a change in proteins, and transcripts, through RNA-interference, RNAi, has produced a rush towards the development of the most state-of-the-art pest suppression strategy available. To rapidly advance these efforts, we established the "International Psyllid Genome Consortium" to bring together researchers interested in psyllid genomics. The first psyllid species being sequenced is the Asian Citrus Psyllid, *Diaphorina citri*, (~550 Mb) first draft DIACI_v1.0 (Illumina, by 2010) being led by Wayne Hunter, with Robert Shatters, and David Hall, of the USDA, Subtropical Research Insects Unit, Ft. Pierce, FL. The second psyllid species planned for sequencing is the potato psyllid, *Bacterocera cockerelli*, (~620 Mb) being led by Dr. Bextine, University of Texas at Tyler, together these efforts form the main working group with other members involved listed under the "The International Psyllid Genome Consortium" working group website: <http://www.uttyler.edu/psyllidgenomics/Home.html>.

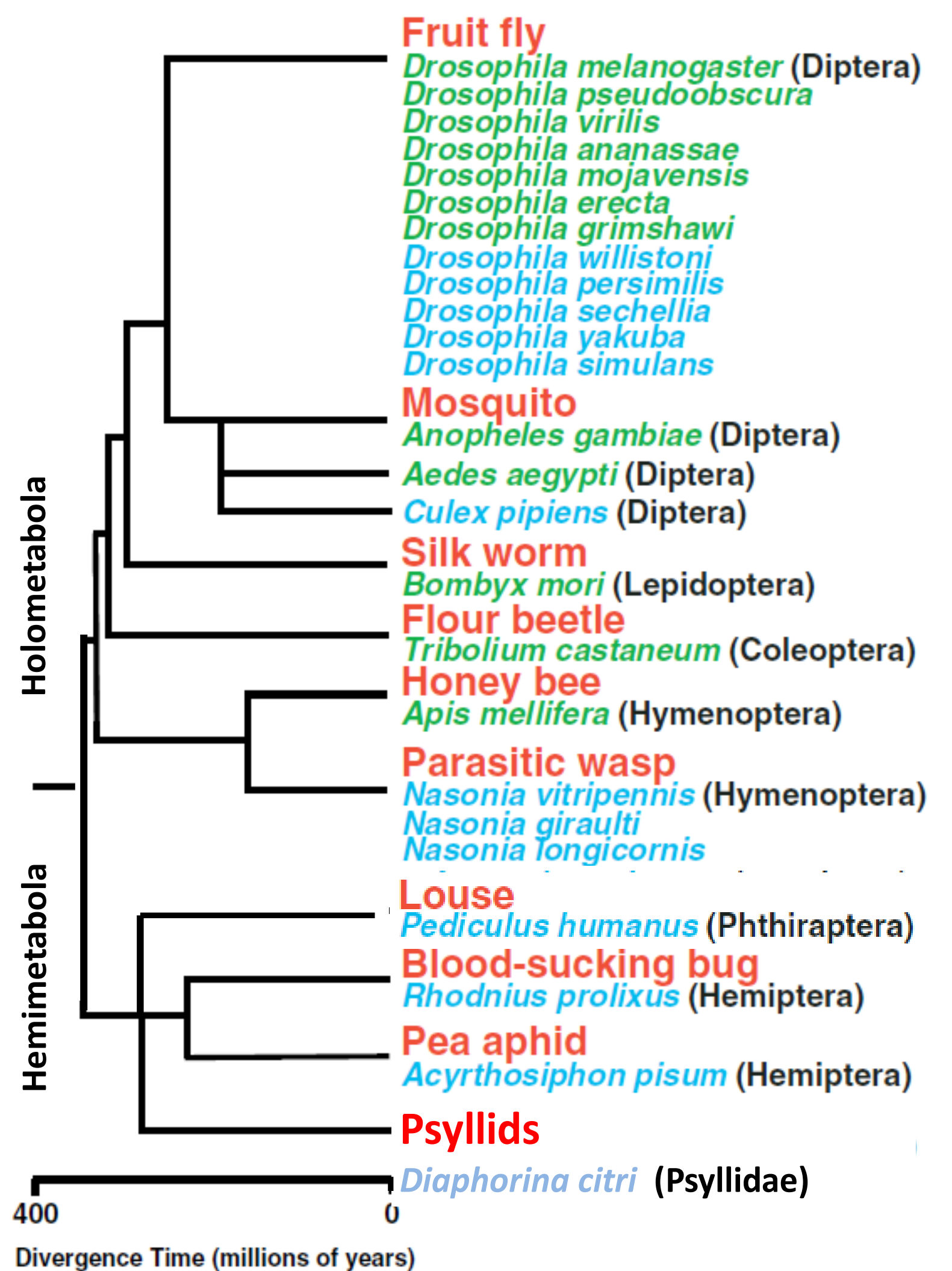
Current and future data on Asian citrus psyllid genome are available at NCBI homepage:

<http://www.ncbi.nlm.nih.gov/sites/entrez?Db=genomeprj&cmd=ShowDetailView&TermToSearch=29473>

The genome from *D. citri* will act as the reference genome for future sequencing projects and will provide the transcriptome, plus a gene list of predicted genes in psyllids. With this information, the research community can now work in full light of specific genes of interest. Combining this with research on RNAi delivery, construction, and development, we propose that specific psyllid transcripts can be used to reduce and suppress psyllids within an area-wide program using RNAi strategies.



Figure 1. The evolutionary relationships of insects for which genome projects exist. Insects whose genome has been completely sequenced (to at least 8–9 times coverage) are highlighted in green. Insects for which the genome sequence is still incomplete (less than 8–9 times coverage, as of February 2007) are highlighted in blue. The divergence times (the evolutionary distances in time between each species and the common ancestor with its neighbor in this figure) are the horizontal bars. The Asian citrus psyllid, *Diaphorina citri*, genome project has just begun.



CONCLUSIONS

The emergence of a large number of insect genome projects during the last 4 years (Fig. 1), includes over 30 insect species. Genomics has revolutionized insect research, as large amounts of new data are rapidly becoming available. Among the insects which have been sequenced are two agricultural pests (red flour beetle: *T. castaneum* and Pea aphid: *A. pisum*) and three parasitic wasps that can be used for biological pest control. The addition of the two psyllid species proposed will expand what is currently understood about hemipteran pests overall and will set the foundation for psyllid genomics. With this information in place insect pest management has entered the genomic era which will surely provide researchers and agricultural industries with more opportunities to reduce pests and diseases.

General information on psyllids and other insect genomes available at:

Arthropod Genomes: http://arthropodgenomes.org/wiki/Diaphorina_citri

Psyllids.org, Diana M. Percy: <http://www.psyllids.org/>

Wikipedia: http://en.wikipedia.org/wiki/Jumping_plant_louse