Untangling the evolution of the twisted-wing parasites (Strepsiptera)

Sequencing the whole genome of *Xenos peckii* (Strepsiptera: Xenidae)

RJ Millena, Ethan Tolman, Jessica Ware

American Museum
of Natural History

Outline

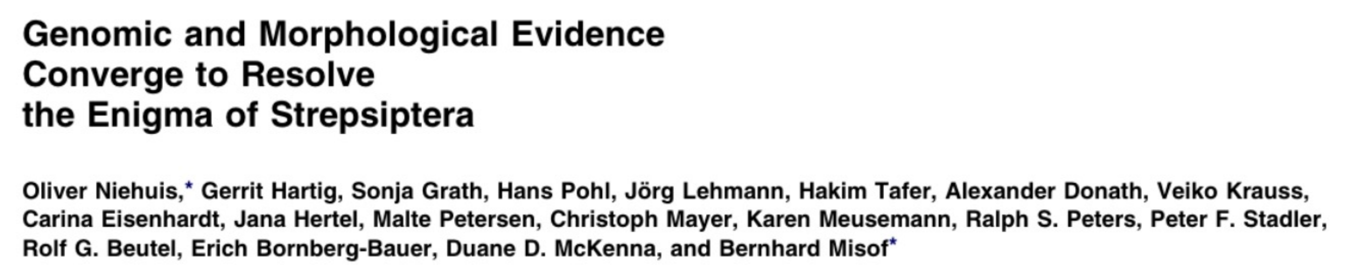
01. History

02. Aims

03. Genome

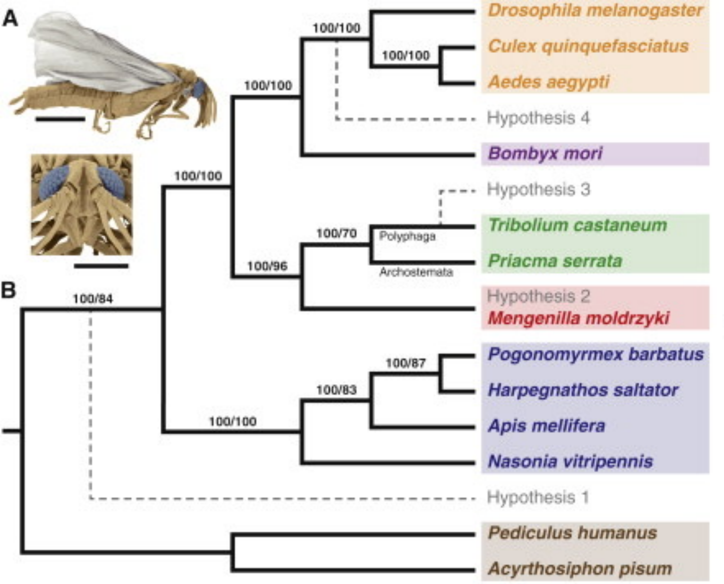
04. Plans

What is Strepsiptera?



Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera

Oliver Niehuis,* Gerrit Hartig, Sonja Grath, Hans Pohl, Jörg Lehmann, Hakim Tafer, Alexander Donath, Veiko Krauss, Carina Eisenhardt, Jana Hertel, Malte Petersen, Christoph Mayer, Karen Meusemann, Ralph S. Peters, Peter F. Stadler, Rolf G. Beutel, Erich Bornberg-Bauer, Duane D. McKenna, and Bernhard Misof*



Previous Work

Whole genome

- One species (*Mengenilla moldrzyki*)
  - Niehuis et al., 2012
- Sequenced from 15 males
- For use only in context of insect radiation

Mitochondrial genome

- Four species across three families; Xenidae, Mengenillidae, Halictophagidae
- Odd rearrangements of sequence and structure

Transcriptome

- Two species (*Stylops melittae*, *Xenos vesparum*); 2015, 2019
  - Misof et al., 2014

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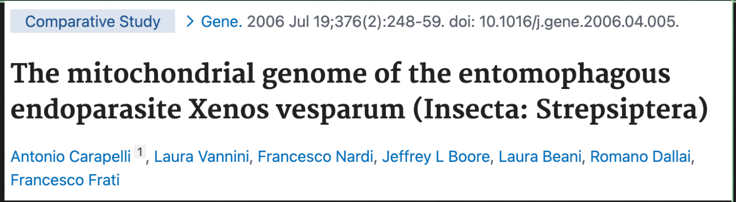
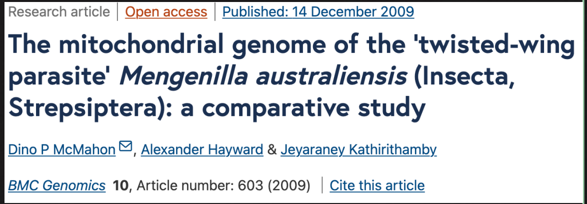


Comparative Study > Gene. 2006 Jul 19;376(2):248-59. doi: 10.1016/j.gene.2006.04.005.

The mitochondrial genome of the entomophagous endoparasite Xenos vesparum (Insecta: Strepsiptera)

Antonio Carapelli [1], Laura Vannini, Francesco Nardi, Jeffrey L Boore, Laura Beani, Romano Dallai, Francesco Frati

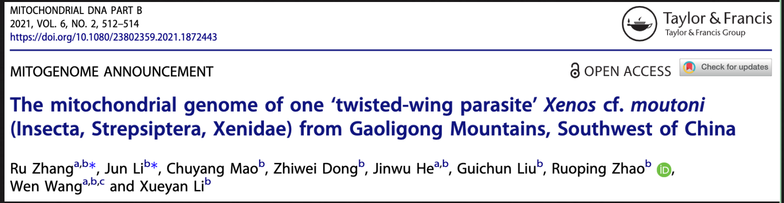


Research article | Open access | Published: 14 December 2009

The mitochondrial genome of the 'twisted-wing parasite' *Mengenilla australiensis* (Insecta, Strepsiptera): a comparative study

Dino P McMahon, Alexander Hayward & Jeyaraney Kathirithamby

BMC Genomics **10**, Article number: 603 (2009) | Cite this article



MITOCHONDRIAL DNA PART B
2021, VOL. 6, NO. 2, 512–514
https://doi.org/10.1080/23802359.2021.1872443

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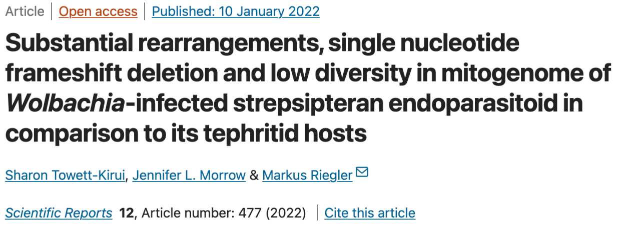
MITOGENOME ANNOUNCEMENT

OPEN ACCESS

Check for updates

The mitochondrial genome of one 'twisted-wing parasite' *Xenos* cf. *moutoni* (Insecta, Strepsiptera, Xenidae) from Gaoligong Mountains, Southwest of China

Ru Zhang[a,b*], Jun Li[b*], Chuyang Mao[b], Zhiwei Dong[b], Jinwu He[a,b], Guichun Liu[b], Ruoping Zhao[b], Wen Wang[a,b,c] and Xueyan Li[b]



Article | Open access | Published: 10 January 2022

Substantial rearrangements, single nucleotide frameshift deletion and low diversity in mitogenome of *Wolbachia*-infected strepsipteran endoparasitoid in comparison to its tephritid hosts

Sharon Towett-Kirui, Jennifer L. Morrow & Markus Riegler

Scientific Reports **12**, Article number: 477 (2022) | Cite this article

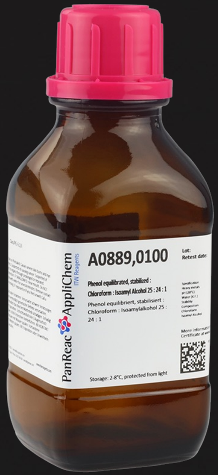
Aims

This project:

- Sequence the whole genome of *Xenos peckii*
- Investigate structural elements of this genome

Big picture:

- Evolution of the strepsipteran genome
- "The Strepsiptera Problem"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Phenol equilibrated, stabilized :
Chloroform : Isoamyl Alcohol 25 : 24 : 1
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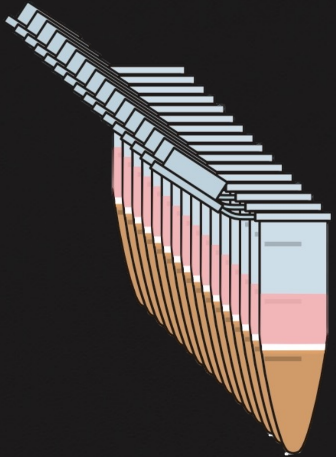
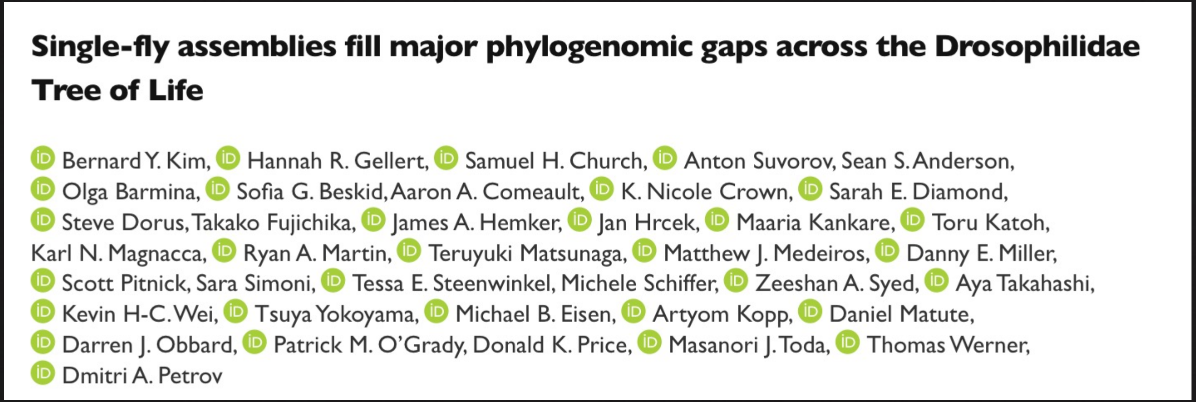
Chloroform : Isoamylalkohol 25 : 24 : 1
Storage: 2-8°C, protected from light


FLAMMABLE
KEEP FIRE
AWAY



Highly contiguous assemblies of 101 drosophilid genomes

Bernard Y Kim[1†*], Jeremy R Wang[2†], Danny E Miller[3], Olga Barmina[4], Emily Delaney[4], Ammon Thompson[4], Aaron A Comeault[5], David Peede[6], Emmanuel RR D'Agostino[6], Julianne Pelaez[7], Jessica M Aguilar[7], Diler Haji[7], Teruyuki Matsunaga[7], Ellie E Armstrong[1], Molly Zych[8], Yoshitaka Ogawa[9], Marina Stamenković-Radak[10], Mihailo Jelić[10], Marija Savić Veselinović[10], Marija Tanasković[11], Pavle Erić[11], Jian-Jun Gao[12], Takehiro K Katoh[12], Masanori J Toda[13], Hideaki Watabe[14], Masayoshi Watada[15], Jeremy S Davis[16], Leonie C Moyle[17], Giulia Manoli[18], Enrico Bertolini[18], Vladimír Koštál[19], R Scott Hawley[20], Aya Takahashi[9], Corbin D Jones[6], Donald K Price[21], Noah Whiteman[7], Artyom Kopp[4], Daniel R Matute[6†*], Dmitri A Petrov[1†*]



Single-fly assemblies fill major phylogenomic gaps across the Drosophilidae Tree of Life

Bernard Y. Kim, Hannah R. Gellert, Samuel H. Church, Anton Suvorov, Sean S. Anderson, Olga Barmina, Sofia G. Beskid, Aaron A. Comeault, K. Nicole Crown, Sarah E. Diamond, Steve Dorus, Takako Fujichika, James A. Hemker, Jan Hrcek, Maaria Kankare, Toru Katoh, Karl N. Magnacca, Ryan A. Martin, Teruyuki Matsunaga, Matthew J. Medeiros, Danny E. Miller, Scott Pitnick, Sara Simoni, Tessa E. Steenwinkel, Michele Schiffer, Zeeshan A. Syed, Aya Takahashi, Kevin H-C. Wei, Tsuya Yokoyama, Michael B. Eisen, Artyom Kopp, Daniel Matute, Darren J. Obbard, Patrick M. O'Grady, Donald K. Price, Masanori J. Toda, Thomas Werner, Dmitri A. Petrov

Assembly Statistics

	BUSCO	N50	Size	Sequencer	Assembly
Xenos peckii	84.2%	421 kb	≤100Mb	ONT MinION + Illumina NovaSeq	Flye 2.9.1, w/AUGUSTUS (Mikhail et al., 2020, Stanke et al., 2006)
Mengenilla moldrzyki (Niehuis et al., 2012)	16.3%	4 kb	155.7 Mb	Roche 454 GS-FLX Titanium	Newbler v. 2.3 (Genivaldo et al., 2013)

	BUSCO	Sequencer	Assembly
Stylops melittae (Misof et al., 2014)	82.4%	Illumina	SOAPdenovo-Trans-31kmer 1.01 (Xie et al., 2014)
Xenos vesparum (Misof et al., 2014)	80.4%	Illumina	SOAPdenovo-Trans-31kmer 1.01 (Xie et al., 2014)

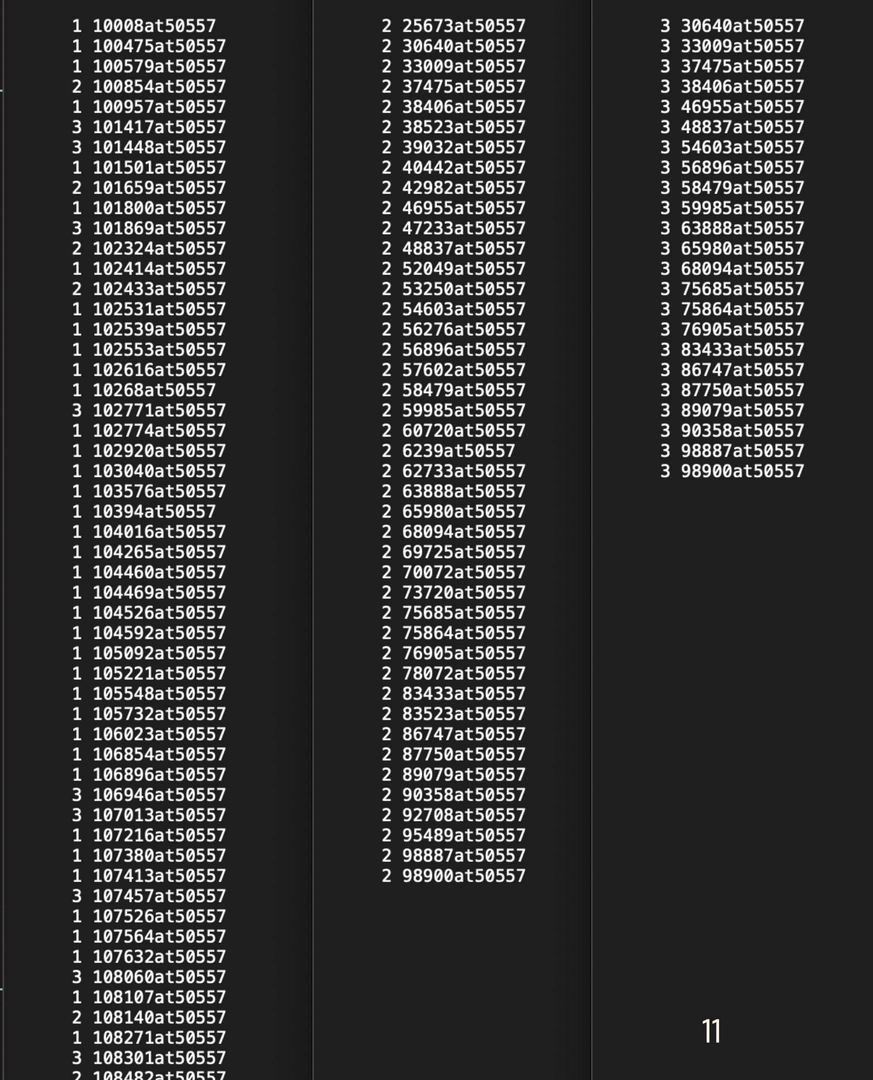
Preliminary Comparisons

Missing BUSCO genes

- *Stylops melittae* and *Xenos vesparum*: 43
  - *Stylops*: 43/153, 28%
  - *Xenos*: 43/173, 25%
- Transcriptomes + *Xenos peckii*: 23

Hypothesis

- The BUSCO genes are still there, just difficult to assemble or identify!
- Unclassified repeats



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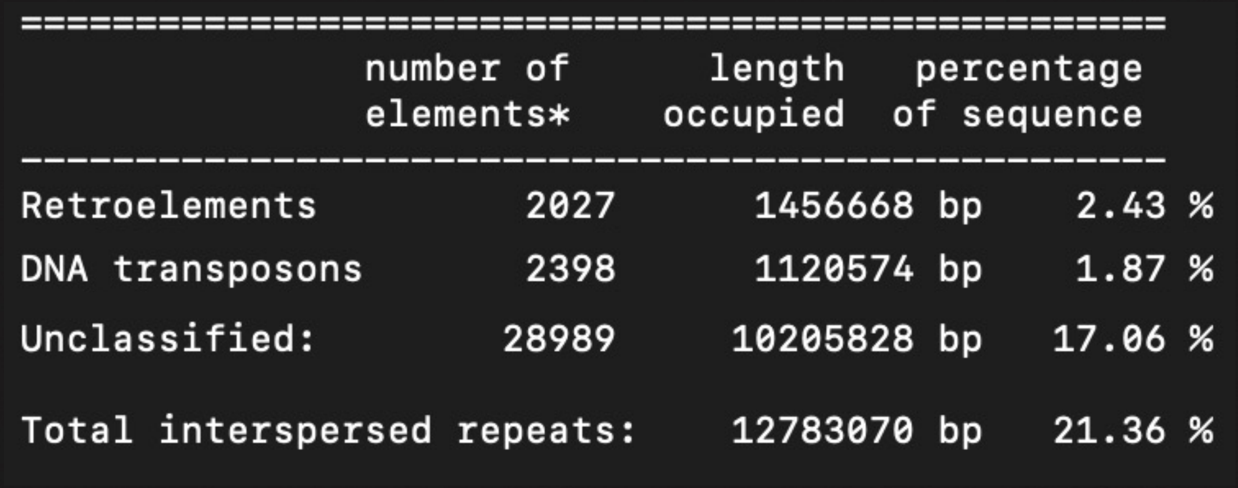
Repeats



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                    number of       length   percentage
                    elements*     occupied  of sequence
--------------------------------------------------
Retroelements             2027      1456668 bp    2.43 %
DNA transposons           2398      1120574 bp    1.87 %
Unclassified:            28989     10205828 bp   17.06 %

Total interspersed repeats:    12783070 bp   21.36 %
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RepeatMasker v. 4.1.2 (Smit et al., 2013-2015)

Next Steps

Polishing, annotation
- Illumina reads
- reads2tree

More genomes with PacBio
- *Elenchus koebelei* (Florida, USA)
- *Caenocholax fenyesi* (Veracruz, Mexico)
- Resolution of repetitive elements

Genomic collinearity analyses
- Intraordinal (Stylops, Mengenilla)
- Interordinal (Neuropterida, Coleopterida)

Thanks!

Questions?

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rjmillena.com

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