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**Title:** Strepsiptera, Phylogenomics and the Long Branch Attraction Problem

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**Source:** PLOS ONE **Volume:** 9 **Issue:** 10 **Article Number:** e107709 **DOI:** 10.1371/journal.pone.0107709 **Published:** OCT 1 2014

**Times Cited in Web of Science Core Collection:** 17

**Total Times Cited:** 17

**Usage Count (Last 180 days):** 2

**Usage Count (Since 2013):** 30

**Cited Reference Count:** 70

**Abstract:** Insect phylogeny has recently been the focus of renewed interest as advances in sequencing techniques make it possible to rapidly generate large amounts of genomic or transcriptomic data for a species of interest. However, large numbers of markers are not sufficient to guarantee accurate phylogenetic reconstruction, and the choice of the model of sequence evolution as well as adequate taxonomic sampling are as important for phylogenomic studies as they are for single-gene phylogenies. Recently, the sequence of the genome of a strepsipteran has been published and used to place Strepsiptera as sister group to Coleoptera. However, this conclusion relied on a data set that did not include representatives of Neuropterida or of coleopteran lineages formerly proposed to be related to Strepsiptera. Furthermore, it did not use models that are robust against the long branch attraction artifact. Here we have sequenced the transcriptomes of seven key species to complete a data set comprising 36 species to study the higher level phylogeny of insects, with a particular focus on Neuropteroidea (Coleoptera, Strepsiptera, Neuropterida), especially on coleopteran taxa considered as potential close relatives of Strepsiptera. Using models robust against the long branch attraction artifact we find a highly resolved phylogeny that confirms the position of Strepsiptera as a sister group to Coleoptera, rather than as an internal clade of Coleoptera, and sheds new light onto the phylogeny of Neuropteroidea.

**Accession Number:** WOS:000343729600018

**PubMed ID:** 25272037

**Language:** English

**Document Type:** Article

**KeyWords Plus:** PHYLOGENETIC METHODS; HOLOMETABOLOUS INSECTS; MAXIMUM-LIKELIHOOD; EVOLUTIONARY TREES; MODEL; GENES; SEQUENCE; ORDERS; 18S; UNCERTAINTY

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**Publisher:** PUBLIC LIBRARY SCIENCE

**Publisher Address:** 1160 BATTERY STREET, STE 100, SAN FRANCISCO, CA 94111 USA

**Web of Science Categories:** Multidisciplinary Sciences

**Research Areas:** Science & Technology - Other Topics

**IDS Number:** AR6ZM

**ISSN:** 1932-6203

**29-char Source Abbrev.:** PLOS ONE

**ISO Source Abbrev.:** PLoS One

**Source Item Page Count:** 9

**Funding:**

Funding Agency	Grant Number
NSF	DEB-0445453
NIH	GM-069801
	GM076007
	GM093182
Packard Fellowship	
Human Frontier Science Program	
CNRS	

This research was supported by grants from the NSF (DEB-0445453) and NIH (GM-069801) awarded to J.P.H. and NIH (GM076007 and GM093182), and a Packard Fellowship awarded to D.B.B.B. was supported by a Human Frontier Science Program post-doctoral fellowship and the CNRS. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Open Access:** gold

**Output Date:** 2017-07-31

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