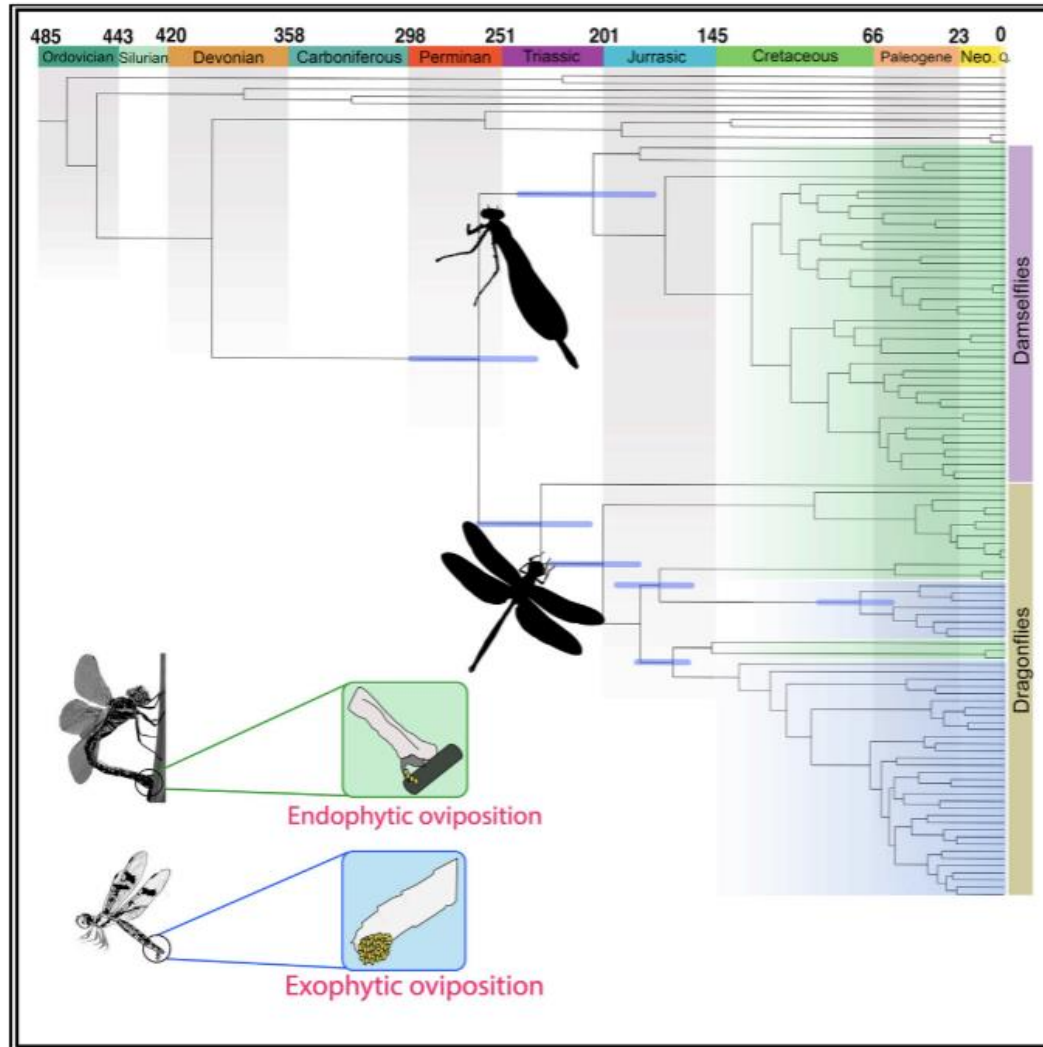


## Article

# Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics



Manpreet Kohli,  
Harald Letsch,  
Carola Greve, ...,  
Xin Yu, Bernhard  
Misof, Jessica  
Ware

[mkohli@amnh.org](mailto:mkohli@amnh.org)

### Highlights

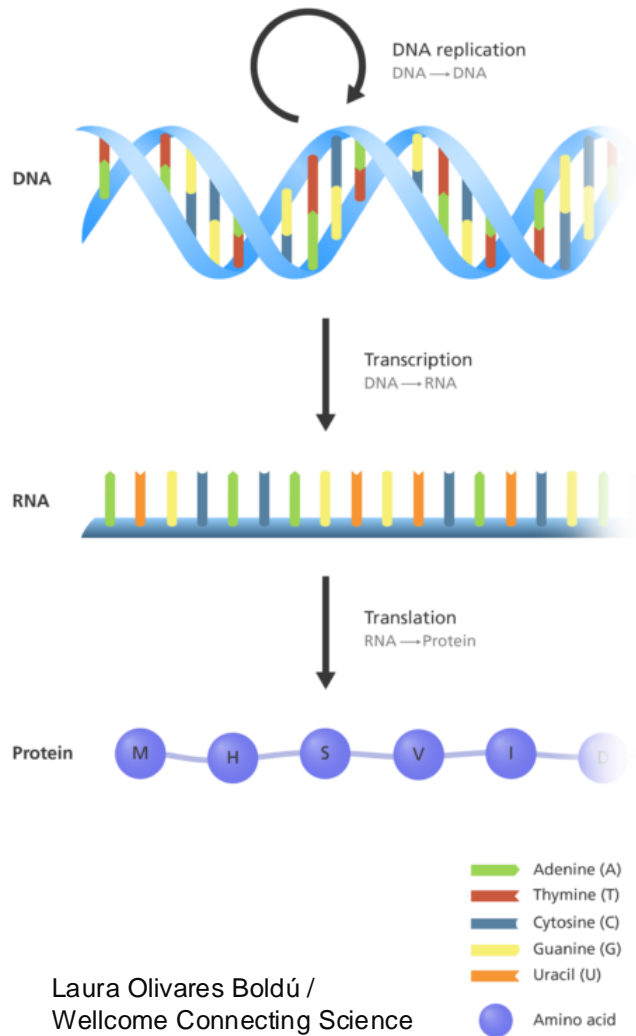
Relationships of  
dragonflies and  
damselflies are unraveled  
using transcriptomes

Earliest flying insects –  
Odonata and extinct  
relatives – date back to  
Permian period

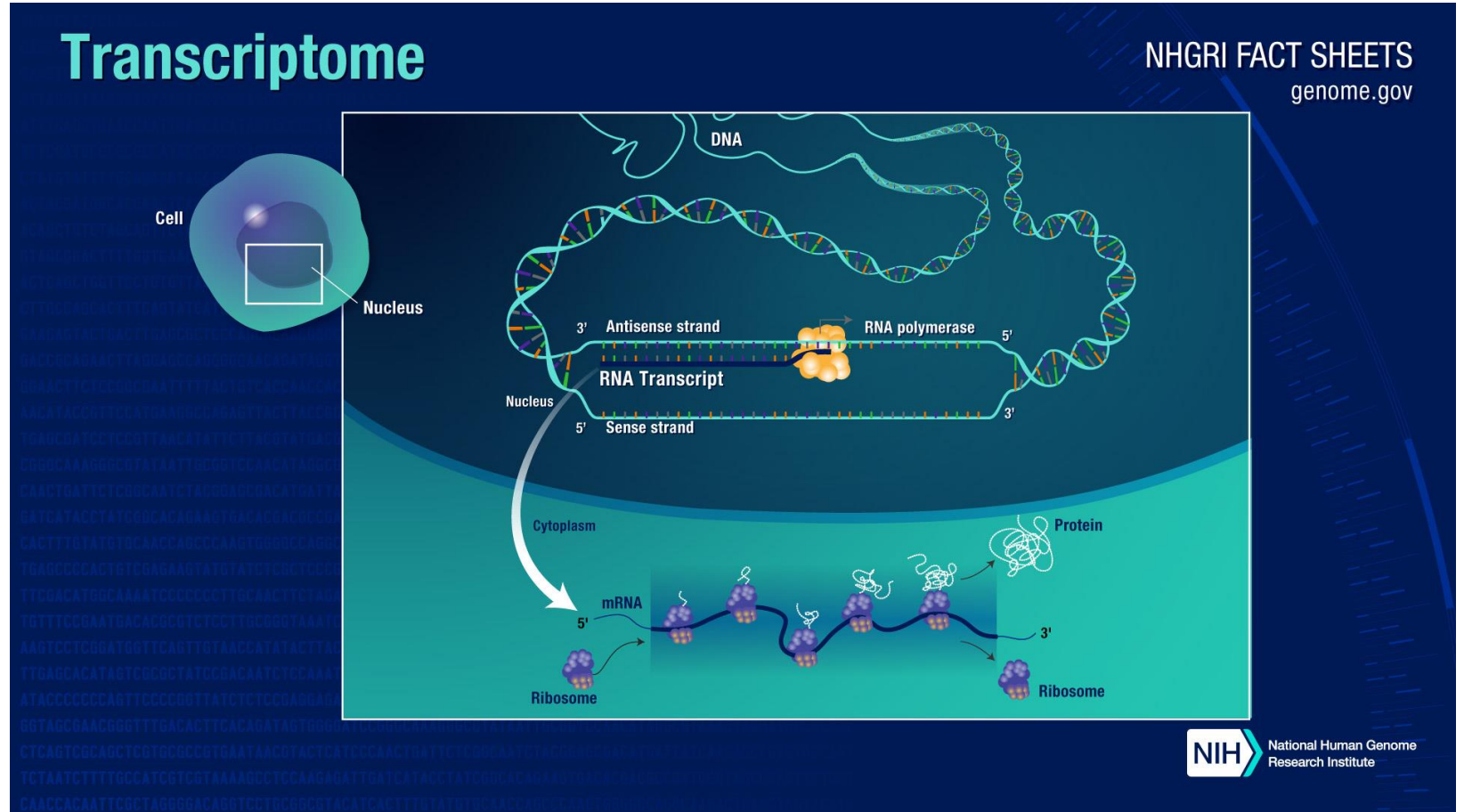
Both extant dragonflies  
and damselflies started  
diverging in the Triassic  
period

An overview  
Kate Montana  
Comparative Genomics 2  
RGGs AMNH  
October 10, 2024

# What is a transcriptome?



Laura Olivares Boldú /  
Wellcome Connecting Science



## STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE
- RESOURCE AVAILABILITY
  - Lead contact
  - Materials availability
  - Data and code availability
- EXPERIMENTAL MODELS AND SUBJECT DETAILS
- METHOD DETAILS
  - Taxa selection and transcriptomics
  - Specimen collection, sequencing, and taxon sampling
  - Orthology assignment
  - Multiple sequence alignments
  - Protein domain identification, alignment masking, optimizing datasets
  - Dataset diagnostics and dataset optimization
  - Selecting optimal partition schemes and model selection
  - Rogue taxon analyses
  - Maximum likelihood tree inference and statistical support
  - Multispecies coalescence
  - Gene and site concordance factor
  - Hypothesis testing with four-cluster likelihood mapping (FcLM) for alternative and putatively confounding signal
  - Fossil selection and divergence time estimation
  - Crown-Ephemeroptera
  - Crown-Zygoptera
  - Crown-Anisoptera

## Transcriptome sequencing + taxon sampling

illumina

HiSeq 2000

102 odonate sp + 150 bp paired-end --> ca. 2.6 Gb/sample  
2 mayfly sp

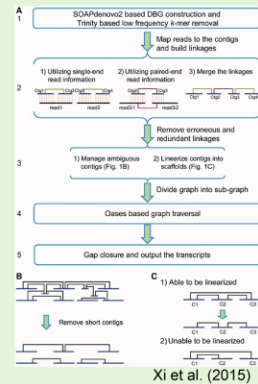
7 odonate sp 90 bp paired-end

+ Existing seqs:  
3 Odonata  
2 Ephemeroptera  
3 Zygentoma  
2 Archaeognatha

120 taxa

## Read assembly

SOAPdenovo-Trans-31kmer



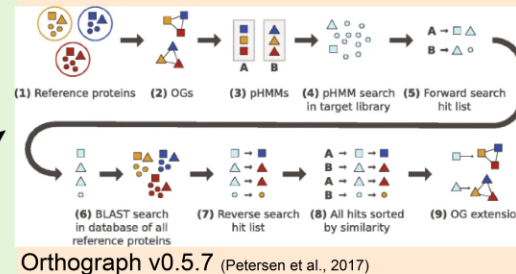
Filter for contaminants

+ Submit to NCBI Sequence Read Archive (SRA) and the Transcriptome Shotgun Assembly (TSA) database

## Orthology assignment

Official gene sets from 4 species from OrthoDB v8:

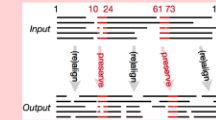
*Daphnia pulex* OGS v1.22  
*Zootermopsis nevadensis* OGBv2.2  
*Ephemera danica* OGB v0.5.3  
*Ladona fulva* OGSv0.5.3



2,980 genes for 115 sp

## Multiple sequence alignment + partitioning + model selection

Alignment via MAFFT v7.123



Protein domain ID + assesement via:  
Domain-identification-v1.3  
Domain-parser-v1.4.1  
PFAM\_SCAN.PL v1.5  
HMMSCAN from HMMER  
MARE v0.1.2-rc

PartitionFinder v2.0.0 = 1217 partitions  
RaxML v8.2.8 restricted to GTR models

## Analyses

Maximum likelihood tree inference  
IQ-TREE v1.5.1

Multispecies coalescence  
Amino acids as data, genes as partitions  
IQ-TREE → ASTRAL III species tree

Gene and site concordance factor  
IQ-TREE -gcf, -scf

Four-cluster likelihood mapping  
IQ-TREE for certain phylogenetic relationships



# Transcriptome sequencing + taxon sampling

illumina

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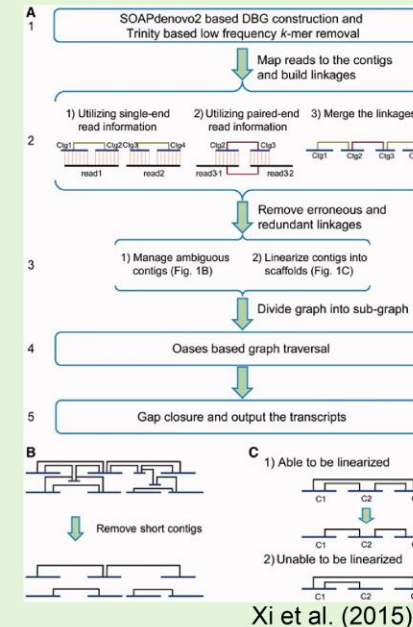
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## Orthology assignment

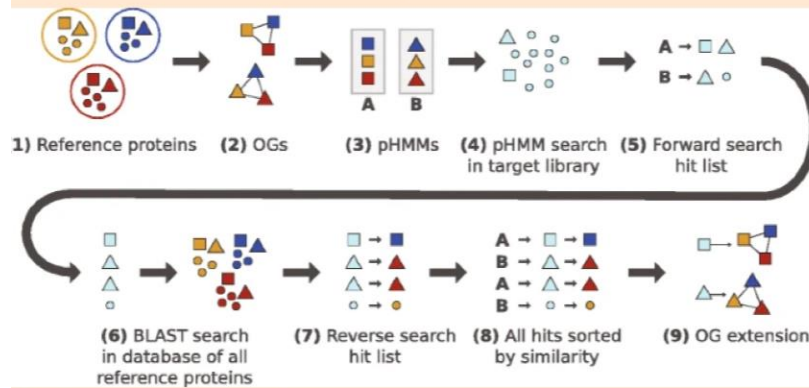
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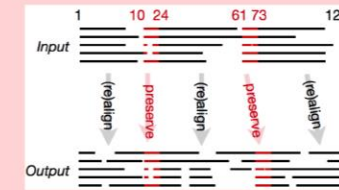


Orthograph v0.5.7 (Petersen et al., 2017)

2,980 genes for 115 sp

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## Four-cluster likelihood mapping

## IQ-TREE for certain phylogenetic relationships

