

## Walker Pett

Department of Ecology, Evolution and Organismal Biology  
228 Bessey Hall  
Iowa State University  
Ames, Iowa

Email: [willpett@iastate.edu](mailto:willpett@iastate.edu)

## Current

---

### Postdoctoral Researcher

2016-Present

Department of Ecology, Evolution and Organismal Biology  
Iowa State University  
Principal Investigator: Tracy Heath

## Education

---

### PhD in Bioinformatics and Computational Biology

August 2014

Iowa State University  
Minor: statistics  
Advisors: Dennis Lavrov and Karin Dorman

### B.A. in Biology

May 2007

Bard College  
Annandale-on-Hudson, New York

## Research Positions

---

### Postdoctoral Researcher

2014-2016

Laboratoire de Biométrie et Biologie Évolutive  
Université Claude Bernard - Lyon 1  
Villeurbanne, France  
Principal Investigator: Nicolas Lartillot

### Graduate Research Assistant

2009-2014

Department of Ecology, Evolution and Organismal Biology  
Iowa State University  
Principal Investigator: Dennis Lavrov

## Refereed Publications

---

Diamantis Sellis, Frédéric Guérin, Olivier Arnaiz, **Walker Pett**, Emmanuelle Lerat, Nicole Boggetto, Sascha Krenek, Thomas Berendonk, Arnaud Couloux, Jean-Marc Aury, Karine Labadie, Sophie Malinsky, Simran Bhullar, Eric Meyer, Linda Sperling, Laurent Duret, and Sandra Duhaucourt (2021). “Massive colonization of protein-coding exons by selfish genetic elements in *Paramecium* germline genomes”. *bioRxiv*.

Daniel B Thomas, Alan J Tennyson, R Paul Scofield, Tracy A Heath, **Walker Pett**, and Daniel T. Ksepka (2020). “Ancient crested penguin constrains timing of recruitment into seabird hotspot”. *Proceedings of the Royal Society B: Biological Sciences* 287: 20201497.

- Walker Pett** and Tracy A Heath (2020). “Inferring the Timescale of Phylogenetic Trees from Fossil Data”. In: *Phylogenetics in the Genomic Era*. Ed. by Celine Scornavacca, Frédéric Delsuc, and Nicolas Galtier. No commercial publisher — Authors open access book, 5.1:1–5.1:18.
- Joëlle Barido-Sottani, **Walker Pett**, Joseph E O’Reilly, and Rachel CM Warnock (2019). “FOSSILSIM: an R package for simulating fossil occurrence data under mechanistic models of preservation and recovery”. *Methods in Ecology and Evolution* 10: 835–840.
- Walker Pett**, Maja Adamska, Marcin Adamski, Michael Eitel, Warren R Francis, Gert Wörheide, and Davide Pisani (2019). “The Role of Homology and Orthology in the Phylogenomic Analysis of Metazoan Gene Content”. *Molecular Biology and Evolution* 36: 643–649.
- James E Tarver, Richard S Taylor, Mark N Puttick, Graeme T Lloyd, **Walker Pett**, Bastian Fromm, Bettina E Schirrmeister, Davide Pisani, Kevin J Peterson, and Philip CJ Donoghue (2018). “Well-annotated microRNAomes do not evidence pervasive miRNA loss”. *Genome biology and evolution* 10: 1457–1470.
- Roberto Feuda, Martin Dohrmann, **Walker Pett**, Hervé Philippe, Omar Rota-Stabelli, Nicolas Lartillot, Gert Wörheide, and Davide Pisani (2017). “Improved Modeling of Compositional Heterogeneity Supports Sponges as Sister to All Other Animals”. *Current Biology* 27: 3864–3870.
- Dennis V Lavrov and **Walker Pett** (2016). “Animal mitochondrial DNA as we do not know it: mt-genome organization and evolution in nonbilaterian lineages”. *Genome biology and evolution* 8: 2896–2913.
- Davide Pisani, **Walker Pett**, Martin Dohrmann, Roberto Feuda, Omar Rota-Stabelli, Hervé Philippe, Nicolas Lartillot, and Gert Wörheide (2015). “Genomic data do not support comb jellies as the sister group to all other animals”. *Proceedings of the National Academy of Sciences* 112: 15402–15407.
- (February 9, 2016). “Reply to Halanych et al.: Ctenophore misplacement is corroborated by independent datasets”. *Proceedings of the National Academy of Sciences* 10.1073/pnas.1525718113.
- Walker Pett** and Dennis Lavrov (2015). “Cytonuclear interactions in the evolution of animal mitochondrial tRNA metabolism”. *Genome Biology and Evolution* 7: 2089–2101.
- Karri M Haen, **Walker Pett**, and Dennis Lavrov (2014). “Eight new mtDNA sequences of glass sponges reveal an extensive usage of +1 frameshifting in mitochondrial translation”. *Gene* 535: 336–44.
- Dennis V Lavrov, **Walker Pett**, Oliver Voigt, Gert Wörheide, Lise Forget, B Franz Lang, and Ehsan Kayal (2013). “Mitochondrial DNA of *Clathrina clathrus* (Calcarea, Calcinea): six linear chromosomes, fragmented rRNAs, tRNA editing, and a novel genetic code.” *Molecular Biology and Evolution* 30: 865–80.
- Walker Pett** and Dennis V Lavrov (2013). “The twin-arginine subunit C in *Oscarella*: origin, evolution, and potential functional significance.” *Integrative and Comparative Biology* 53: 495–502.
- Dennis V Lavrov, Olga O Maikova, **Walker Pett**, and Sergey I Belikov (2012). “Small inverted repeats drive mitochondrial genome evolution in Lake Baikal sponges.” *Gene* 505: 91–9.
- Walker Pett**, JF Ryan, Kevin Pang, James C Mullikin, Mark Q Martindale, Andreas D. Baxevanis, and Dennis V Lavrov (2011). “Extreme mitochondrial evolution in the ctenophore *Mnemiopsis leidyi*: Insight from mtDNA and the nuclear genome”. *Mitochondrial DNA* 22: 130–142.
- Romulo Segovia, **Walker Pett**, Steve Trewick, and Dennis V Lavrov (2011). “Extensive and evolutionarily persistent mitochondrial tRNA editing in Velvet Worms (phylum Onychophora).” *Molecular Biology and Evolution* 28: 2873–81.
- Karri M Haen, **Walker Pett**, and Dennis V Lavrov (2010). “Parallel Loss of Nuclear-Encoded Mitochondrial Aminoacyl-tRNA Synthetases and mtDNA-Encoded tRNAs in Cnidaria.” *Molecular Biology and Evolution* 27: 2216–9.

## Awards

---

Research Excellence Award, ISU	2014
Cornette Fellowship, ISU	2012
EEOB Graduate Student Research Award, ISU	2012
BCB Student Seminar Award, ISU	2010

## Teaching – Courses

---

### Iowa State University

BIOL 315: Evolution	2014
BIOL 212L: Principles of Biology Lab	2014
BIOL 255L: Human Anatomy Lab	2013
BIOL 211L: Introduction to Biodiversity Lab	2012-2013
BCB 570: Computational Functional Genomics and Systems Biology	2012
EEOB 536: Molecular Phylogenetics	2011

## Teaching – Workshops

---

### Stay-at-Home RevBayes Workshop

Online	April 21, 2021
--------	----------------

### Stay-at-Home RevBayes Workshop

Online	July 13, 2020
--------	---------------

### Analysing Macroevoolutionary Processes using RevBayes

Bristol, United Kingdom	May 1-3, 2018
-------------------------	---------------

### Introduction to Bayesian phylogenetic inference in RevBayes

University of Gothenburg and ForBio workshop Gothenburg, Sweden	Oct 23-27, 2017
--	-----------------

### Introduction to Bayesian phylogenetic inference in RevBayes

Meeting of International Biogeography Society Bangalore, India	Sep 25-26, 2017
---	-----------------

### Introduction to Bayesian phylogenetic inference in RevBayes

Ames, Iowa	Aug 14-15, 2017
------------	-----------------

### Analysis of Fossil and Molecular Data in RevBayes

Baton Rouge, Louisiana	Jan 8, 2017
------------------------	-------------

## Invited Talks

---

### A morphospeciation model for integrating fossil character evolution and stratigraphic range data

Evolution, Spotlight Session, Providence, Rhode Island	2019
--	------

<b>Beyond supermatrix resolution: deep metazoan phylogeny from gene content</b> Evolution, Spotlight Session, Portland, Oregon	2017
---	------

## Contributed Talks and Posters

---

<b>Integrating models of fossil character evolution and stratigraphic range data</b> Evolution, Talk Montpellier, France	2018
--	------

<b>Ascertainment bias in gene family data and metazoan phylogenomics</b> Ancestron Project Annual Meeting, Talk Paris, France	2015
---	------

<b>Genomic data do not support comb jellies as the sister group to all other animals</b> Society of Molecular Biology and Evolution, Poster Vienna, Austria	2015
---	------

<b>Deep metazoan phylogeny and the position of Ctenophora</b> Ancestron Project Annual Meeting, Talk Saint-Martin-de-Londres, France	2014
--	------

<b>A mitochondrial gene unique among animals: the evolution of the Tat pathway in <i>Oscarella</i></b> Society for Integrative and Comparative Biology, Talk San Francisco, CA	2013
--	------

<b>The Coevolving Histories of mt-tRNAs and aminoacyl-tRNA synthetases</b> Society of Molecular Biology and Evolution, Poster Kyoto, Japan	2011
--	------

<b>Reconstructing Patterns of Rearrangements in Animal Mitochondrial DNA</b> New Mexico Bioinformatics Symposium, Poster Santa Fe, NM	2011
---	------

<b>Mitochondrial Genome Rearrangements in Animals</b> Society for Integrative and Comparative Biology, Talk Seattle, WA	2010
---	------

## Experience

---

<b>Smithsonian Tropical Research Institute</b> , Bocas del Toro, Panama Taxonomy and Ecology of Caribbean Sponges (course)	2012
---	------

<b>Point Reyes Bird Observatory</b> , Point Reyes, CA Resident species nest-searching, and neotropical migrant banding internships	2008
---	------

<b>Hudsonia, Ltd.</b> , Red Hook, NY Blanding's turtle conservation and monitoring internship	2007
--	------

## Service

---

**BCB Curriculum Committee**, student representative

2012-2013

## Languages

---

C++, R, Perl, Python, Ruby, SQL, bash, L<sup>A</sup>T<sub>E</sub>X, Mathematica, JavaScript

## Software

---

**biphy**: Phylogenetic analysis of binary character data (sole author)

**RevBayes**: An interactive statistical environment for Bayesian phylogenetics (core developer)