

CURRICULUM VITAE

Jeffrey L. Boore

CURRENT POSITION

Director of Scientific Technology, Translational Systems Medicine, for Providence St. Joseph Health (January 2017-present). Providence is a large health care provider with 50 hospitals and 104,000 employees. This position reports to the Chief Science Officer (and Senior Vice-President) of Providence, and is responsible for forming and managing strategic partnerships among Providence clinicians and researchers, building outside collaborations, implementing technology for translational medicine, to include high-throughput genomics, proteomics, and single cell assays, developing commercial opportunities, leading an independent, externally-funded research program, and interfacing with the broader scientific community.

Affiliate of the Institute for Systems Biology (full-time consultant on Development, Technology, and Translational Medicine, Feb-Dec 2016, affiliate scientist Jan 2017-present)

Adjunct (Full) Professor, University of California Berkeley (December 2001-present)

CONTACT INFORMATION

Providence Health and Services and Institute for Systems Biology, 401 Terry Avenue N, Seattle, WA 98109, jeffrey.boore@providence.org or jboore@systemsbiology.org, cell phone (650) 776-5857

University of California Berkeley: <http://ib.berkeley.edu/faculty/boorej.html>, jlboore@berkeley.edu

Home: 809 Olive Way, #1502, Seattle WA 98101, jeffreyboore@gmail.com, cell phone (650) 776-5857

PREVIOUS SCIENTIFIC POSITIONS

2007-2015 Founder and Chief Executive Officer, Genome Project Solutions, Inc.
2007-2015 Guest researcher, DoE Joint Genome Institute (JGI) and Berkeley National Lab
2002-2007 Evolutionary Genomics Department Head, DOE Joint Genome Institute (JGI)
2000-2002 Comparative Genomics Group Leader, DOE Joint Genome Institute (JGI)
2000-2007 University of California Scientist, Lawrence Berkeley National Laboratory
1996-2000 Visiting Research Scientist, University of Michigan Department of Biology
1992-1996 NIH Postdoctoral Fellow, University of Minnesota Department of Cell Biology and Neuroanatomy

EDUCATION

1992-1996 Postdoctoral training, University of Minnesota
1992 Ph.D., Biology, University of Michigan
1980 B.S., Biology, Pennsylvania State University

Areas emphasized: Genetics, Molecular Biology, Biochemistry, Biotechnology, Genomics, Bioinformatics, Cell and Developmental Biology, Population Genetics, Evolutionary Biology, Genome Evolution, Biology of Invertebrates, and Systematics.

GRANT-FUNDED PROJECTS (Initial funding amounts are my portions, in some cases of larger, collaborative total awards)

1. \$86,002. National Science Foundation. Genomic Consequences of Asexuality. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the snail, *Potamopyrgus antipodarum*. P.I. is Maurine Neiman, University of Iowa, total funding \$263,530. 11/01/11-10/31/18.
2. \$200,000. Academy of Finland. Deep moss: phylogeny of the oldest moss lineages. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of many bryophyte plastid and mitochondrial genomes. P.I. is Jaakko Hyvonen, University of Helsinki. 1/01/09-12/31/14.
3. \$95,000. National Institutes of Health and the University of Würzburg, Germany. My role is to participate in the sequencing and interpretation and to lead the comparative analysis of the genome of the cancer-model platyfish, *Xiphophorus maculatus*. P.I.s Manfred Schartl, University of Würzburg, and Ronald Walter, Texas State University. 4/01/10-12/31/12.
4. \$30,000. Conoco-Phillips Research Foundation. Genome sequencing of the stramenopile, *Nannochloropsis gaditana*. My role is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the biofuels-producing candidate, *Nannochloropsis gaditana*. P.I. Matthew Posewitz, Colorado School of Mines and the National Renewable Energy Laboratory. 3/01/11-12/31/11.
5. \$30,000. Department of Energy. Genome Sequencing of the Chlorophyte Alga *Chlorella vulgaris* (UTEX strain #395). My role is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the biofuels-producing candidate, *Chlorella vulgaris*. P.I. Michael Guarnieri, National Renewable Energy Laboratory. 6/1/11-12/31/11.
6. \$176,312. National Institutes of Health. Circadian Clock: Differential Cryptochrome Functions. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the monarch butterfly, *Danaus plexippus*. P.I. Steve Reppert, University of Massachusetts Medical School, total funding \$802,601. 9/30/09-9/29/11. 3R01GM086794-02S1.
7. \$65,000. Solazyme, Inc. My role is to lead the complete sequencing, interpretation, and comparative analysis of the genome of a biofuels alga (unnamed because of corporate confidentiality needs). 5/1/2009-7/31/10.
8. \$66,840. National Science Foundation. Mobilome Genomics: Large Plasmids of Diverse Prokaryotic Groups. My role is to lead the complete sequencing and interpretation of multiple large plasmids toward an understanding of horizontal gene transfer. P.I. Anne Summers, total funding \$1,106,419. 1/01/07-12/31/09. MCB-0626940.
9. \$326,819. U.S. Dept of Agriculture and National Science Foundation. *Phytophthora sojae*: A High Quality Reference Sequence for the Oömycetes. My role as co-P.I. is to lead the finishing efforts on the genome of the oömycete plant pathogen, *Phytophthora sojae*, and to create a resource where all genes are interpreted phylogenetically across all available stramenopile genomes. P.I. Brett Tyler, Virginia Tech University, total funding \$2,130,000 (\$1,380,000 USDA and \$750,000 from NSF) (NSF/USDA Microbial Genome Sequencing Program.) 10/15/07-10/14/09. VAR-2007-04746.
10. \$351,000. National Science Foundation. P.I. on Genomic Analysis of Sexual Dimorphism in Stalk-eyed Flies (Diopsidae). 3/01/05-2/28/09. DEB-0445047.

11. \$1,583,708. U.S. Department of Agriculture. The Complete Sequence of the Glaucophyte alga *Cyanophora paradoxa*. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the glaucophyte alga, *Cyanophora paradoxa*. P.I. Debashish Bhattacharya, Rutgers University, total funding \$1,973,449. (NSF/USDA Microbial Genome Sequencing Program.) 10/01/06-9/30/08. EF-0625440.
12. \$306,690. National Science Foundation. Causes and Consequences of Recombination. My role as co-P.I. is to lead the development of a database plus query tools and a visualization system for the evolutionary interpretation of the complete genome of the crustacean, *Daphnia pulex* (a genome for which I had led the sequencing and analysis efforts in my capacity as Head of Evolutionary Genomics at the DOE Joint Genome Institute). P.I. Michael Lynch, Indiana University, total funding \$5,000,627. 9/01/03-8/31/08. EF 0328516.
13. \$300,000. National Institutes of Health and the University of Massachusetts Medical School. P.I. on this project for light-coverage (1X) preliminary sequence and its interpretation of the genome of the monarch butterfly, *Danaus plexippus*. 6/01/07-12/31/07.
14. \$1,049,000. National Science Foundation. Genomics of the Compositae. My role is to lead the complete sequencing and analysis of the transcriptome sequences of many plants from the group Compositae (generally of agricultural importance). P.I. Loren Reiseberg, Indiana University, total funding \$5,584,982. 8/1/04-7/31/07. DBI 0421630.
15. \$26,000. National Science Foundation. Molecular Systematics of Arachnids Using Whole Mitochondrial Genomes. My role as co-P.I. is to lead the complete sequencing and assist in the interpretation and comparative analysis of the mitochondrial genomes of many phylogenetically diverse arachnids. P.I. Susan Masta, Portland State University, total funding \$317,548. 7/1/04-6/30/07. DEB-0416628.
16. \$1,789,842. U.S. Department of Agriculture. Genome Sequence of *Phakopsora pachyrhizi* and *Phakopsora meibomia*. P.I. for the complete sequencing and interpretation of the genome of the plant pathogen, *Phakopsora pachyrhizi* and its non-pathogenic congener, *Phakopsora meibomia*. 10/01/02-12/31/06.
17. \$551,476. National Science Foundation. A Combined Strategy for Resolving Difficulties in Basal Green Plant Phylogeny. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the plastid genomes of many phylogenetically diverse plants. P.I. Charles O'Kelly, Bigelow Marine Laboratories, total funding \$2,945,292. 10/01/02-9/30/06.
18. \$201,109. National Science Foundation. Wormnet: Reconstructing the Early Evolution of Segmented Annelid Worms. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the mitochondrial genomes of many phylogenetically diverse annelids. P.I. K. Halanych, Auburn University, total funding \$1,350,000. 9/15/01-9/15/06.
19. \$404,777. National Science Foundation. Comparative Chloroplast Genomics: Integrating Computational Methods, Molecular Evolution, and Phylogeny. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the plastid genomes of many phylogenetically diverse plants. P.I. Robert Jansen, University of Texas, total funding \$1,350,000. 9/15/01-9/15/06.
20. \$200,000. National Institute of Health. Genomics, Cis-Regulation and Genetic Variation (Comparative Genome Analysis and Interpretation). I served as co-P.I. on this project to

- train scientists in genomics and bioinformatics. P.I. Richard Karp, University of California Berkeley, total funding \$750,000. 7/01/03-6/30/06.
21. \$142,163. National Science Foundation. The Molluscan Mitochondrial Genome Project: Phylogenetic Analysis, Evaluation, and Enrichment. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the mitochondrial genomes of many phylogenetically diverse mollusks. P.I. David Lindberg, University of California Berkeley, total funding \$285,900. 6/01/02-5/31/05.
 22. \$98,264. National Institutes of Health. P.I. Sponsor for National Research Service Award (postdoctoral study) for Rick Baker, "Phylogenomics of Head Development Genes in Diopsid Flies". 4/01/03-3/31/05.
 23. \$200,000. Department of Energy. P.I. on Evolutionary Genomics Studies. 10/01/04-10/01/05.
 24. \$1,848,000. National Science Foundation/U.S. Department of Agriculture. Genome Sequence of *Phytophthora sojae*. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the genome of the oomycete plant pathogen, *Phytophthora sojae*. P.I. Brett Tyler, total funding \$2,350,000. 10/01/02-9/30/05.
 25. \$1,500,000. U.S. Department of Energy. P.I. on Genome Sequence of *Phytophthora ramorum*, causative agent of "Sudden Oak Death" and related pathologies. 10/01/02-9/30/05.
 26. \$663,000. Department of Energy. P.I. on Evolutionary Genomics Studies. 10/01/03-10/01/04.
 27. \$186,000. NASA. Microbial Life at Low Temperatures. My role is to lead the sequencing and interpretation of several prokaryotic genomes that are adapted to life at very cold temperatures. P.I. James Tiedje, Michigan State University. 10/01/01-9/30/04.
 28. \$30,000. National Science Foundation. Flatworm cDNA Sequencing. My role is to lead the sequencing and interpretation of the complete transcriptomes of several phylogenetically diverse platyhelminths. 9/01/03-8/31/04.
 29. \$743,000. Department of Energy. P.I. on Evolutionary Genomics Studies. 10/01/02-10/01/03.
 30. \$936,000. Department of Energy. P.I. on Genomic Diversity Studies. 10/01/01-9/30/02.
 31. \$30,000. U.S. Department of Agriculture. Sequence of 10,000 Moss cDNA Clones. My role is to lead the sequencing and interpretation of the complete transcriptomes of several phylogenetically diverse bryophytes. 9/10/01-8/31/02.
 32. \$558,030. U.S. Department of Energy, P.I. on Mitochondrial Genomics and P.I. on Evolution of Gene Families. 10/01/00-9/30/01.
 33. \$200,000. National Science Foundation. A Phylogeny of Major Metazoan Radiations. 9/01/98-09/01/01. My role as co-P.I. is to lead the complete sequencing, interpretation, and comparative analysis of the mitochondrial genomes of many phylogenetically diverse animals with a goal of understanding early metazoan radiations based on patterns of gene rearrangements. P.I. Wesley Brown, University of Michigan.
 34. \$70,000. National Institutes of Health. National Research Service Award. Dorsal-Ventral Patterning in the Frog *Xenopus laevis*. 11/01/92-3/31/96.
 35. \$21,669. Rackham Research Partnership Program. 9/1/91-8/31/92.

PROFESSIONAL EXPERIENCE, SERVICE, FELLOWSHIPS, AND HONORS

- 2014 Distinguished Visiting Fellow of the Institute for Advanced Studies, University of Birmingham, United Kingdom (8 weeks)
- 2012-present Associate Editor of the journal *BMC Genomics*
- 2012 Advisory Panel to the Chancellor of Louisiana State University regarding their programs in genomics and bioinformatics, including those at Pennington Biomedical Research Center
- 2008 Advisory Panel to NSF regarding their program Assembling the Tree of Life
- 2008 NSF Grant Review Panel for the Assembling the Tree of Life Program
- 2005-2010 Member, Genome Standards Consortium
- 2005 Invited member of a panel on “eGenomics”, European Bioinformatics Institute (EBI), Hinxton, United Kingdom
- 2005 Advisory Panel to the National Evolutionary Synthesis Center (NESCent) on database development
- 2005-2008 NIH Study Section for “Instrumentation and Systems Development”
- 2005-2007 Elected member of the Society for Systematic Biology Council
- 2004-present Developed and maintain the “PHRINGE” (“Phylogenetic Resources for the Interpretation of Genomes) system, an advanced tool for interpreting patterns of genome evolution and for inferring gene function
- 2003-2004 Led the development of the “JGI Community Sequencing Program” which allocates ~60% of JGI’s capacity (~\$20,000,000 / year).
- 2004-2006 Steering Committee for “Protist Genomics Initiative”
- 2004 Invited participant in NSF Protist Genomes Workshop
- 2002-2004 Advisor to the All Species Foundation
- 2002 Steering Committee for “New Academic Initiatives”, UC Berkeley
- 2002 Advisory Board on Technology Development to the All Species Foundation
- 2001-2007 Lawrence Berkeley National Laboratory Institutional Biosafety Committee
- 2002 Search committee, Department of Plant and Microbial Biology, UC Berkeley
- 2001-2004 Editorial Board for *Genome Letters*
- 2001-2004 Planning committee for Bay Area Biosystematists Group
- 2000 Advisory board to the NSF Tree of Life Initiative, Austin, TX
- 1999 Planned and led a symposium on “Mitochondrial Genomics” at the annual meetings of the Society for Molecular Biology and Evolution and the Genetics Society of Australia, Brisbane, Australia
- 1999 Gordon Research Conference Travel Fellowship to Japan
- 1992-96 NIH Postdoctoral Fellowship, University of Minnesota
- 1995 NSF-Sponsored Travel Fellowship to Japan
- 1991 Rackham Dissertation Fellowship, grad school tuition and stipend for 1 year
- 1989-91 University of Michigan Competitive Graduate Student Grants, nine awards
- 1987-90 NIH Genetics Traineeship, tuition and stipend, four years

Researchers supervised

Staff: Pilar Francino (Ph.D.-level scientist), Mónica Medina (Ph.D.-level scientist), J. Robert Macey (Ph.D.-level scientist), H. Matthew Fourcade (Senior Research Associate [SRA]), Jenna Morgan (SRA), Jeff Froula (SRA), Jennifer Kuehl (RA), David Engle (RA), Nila Bala (intern), Allen Haim (software developer)

Postdoctoral scholars: Susan Masta, Douda Bensasson, Paramvir Dehal, Brian Simison, Martha Lucia-Posada, Jim Parham, Jodi Schwarz (under Medina), Parag Vaishampayan (under Francino), Araceli Huerta (under Francino), Richard Baker

Graduate students: Kevin Helfenbein (Ph.D. September 2002), Rachel Mueller (with David Wake; Ph.D. December 2004), Kirsten Swinstrom (with Roy Caldwell; Ph.D. May 2004), Yvonne Vallès (Ph.D. May 2007), Jonathan Fong (with James McGuire; Ph.D. May 2011)

Undergraduate students: Shavon Crawford, Marco Espinoza, Tori Takaoka, Alexandre Xue, Ramendeeep Kaur

Dissertation committees: Dennis Lavrov, Russell Watkins, Stacia Wyman, Matthew Fujita, Wes Savage, Scott Fay, Rebecca Welch

Graduate student exam committees: Renfu Shao, Gene Tyson, Guinevere Wogan, Rebecca Welch, Susan Tremblay

Guest researchers (on sabbatical or similar arrangements): Prof. Axel Meyer (U of Konstanz, 7 mo), Inaki Ruiz-Trillo (U of Barcelona, 3 mo), Prof. Jim Garey (U of South Florida, 1 wk), Prof. Eric Knox (Rutgers U, 3 wk), Dr. Marty Wojciechowski (Berkeley, 3 mo), Alek Bituin (UC Berkeley, 3 mo), Dr. William Eddie (U of Texas, 3 mo), Renfu Shao (U of Queensland, 2 mo), Dr. Marco Passamonti (U of Bologna, 9 mo), Dr. Mike Atkins (Woods Hole Marine Biology Lab, 1 month), Karen Slon (U of Connecticut, 1 month), David DeGusta (Berkeley, 6 mo), Martin Jaekel (Berkeley, 1 year), Dr. Hsiao-Pei Yang (UC Davis, 4 mo), Lisa Lee (U of Southern California, 4 mo), Prof. Richard Thomas (Natural History Museum, London, 6 mo), Stacia Wyman (U of Texas, 3 mo), Prof. Hiroshi Akashi (Penn State U, 2 wk), Nikoletta Danos (Berkeley, 1 yr), Dr. Marcos Perez-Losada (Brigham Young U, 2 wk), Dr. Kelly Ivors (Berkeley, 2 wk), Rebekah Andrus (Utah State U, 1 wk), Romey Haberle (U of Texas, 3 wk), Dr. Yau-Wen Yang (Academia Sinica, Taiwan, 6 mo), Ernesto Recuero (National Museum, Madrid, Spain, 2 mo), Dr. Gabriela Parra (National Autonomous University of Mexico, 1 mo), Miriam Satler (U of Vienna, 1 mo), Ron Bonett (U of Texas Arlington, 1 year), Natasha Sankovic (U of Melbourne, 3 mo), Ruth Timme (U of Texas, 1 mo), Ana-Claudia Lessinger (Campinas, Brazil, 1 wk), Shruti Lal (UC Merced, 1 mo), Dan Mulcahy (Utah State U, 3 years), Wes Savage (UC Davis, 3 years), Matthias Stoeck (UC Berkeley, 2 years).

RESEARCH EXPERIENCE

Main conceptual areas of my research program:

Human biology, translational medicine, human genetics, genotype-phenotype associations
Biotechnology, especially as related to the study of genes, genomes, gene expression, and protein analysis
Large-scale DNA sequencing project management
High throughput techniques for genome sequencing and interpretation
Gene expression measures and analysis
Databases and software for analyzing and comparing genomes and visualizing the results
Genome assembly, annotation, and analysis
Genome duplications
Evolutionary transfer of genes among organisms and intracellular compartments
Modeling of genome rearrangements and systematics theory and practice
Phylogenetic analysis using gene rearrangements and of DNA and amino acid sequences
Genomics of mitochondria and chloroplasts
Other past research areas: RNA editing, comparative developmental biology

Laboratory techniques that have been emphasized in my research program:

Management of a DNA sequencing “factory”, including the use of robots in a high throughput environment and an integrated work flow system for project tracking, quality control, assembly, and annotation of genomic sequence
DNA sequencing using manual methods, ABI 310, ABI 377, ABI 3730XL, MegaBace1000/4000/4500, Illumina GAIIX, Illumina MiSeq, Illumina HiSeq2500/4000/X, Roche (454), Ion Torrent PGS, and PacBio RSII/Sequel sequencers
Isolation and analysis of DNA, RNA, and proteins, including Southern, Northern, and Western hybridization; nucleic acid solution hybridization
PCR, quantitative PCR, including quantitative RT-PCR
Whole genome amplification
cDNA and genomic library (plasmid, phage, cosmid/fosmid, BAC) construction and screening; transposon-mediated cloning
In situ hybridization and immunohistochemistry
Bacterial culture and selection; radioactive and biohazard material handling and disposal
Microscopy, microdissection of embryos, histology

Bioinformatics techniques that have been emphasized in my research program:

Genome assembly and its evaluation
Identifying and annotating gene structures
Inferring gene function
Use and development of online tools and databases for genome research
Gene expression measurements and comparisons
Genome structure comparisons
Construction of databases and query tools and their web-based presentations
Graphic design software
Phylogenetic analysis software

MANAGEMENT TRAINING AND EXPERIENCE

Scientific

2006-2015	CEO, Genome Project Solutions
1996-2007	Led a scientific team of ~25 researchers, targeting >25 scientific projects
2000-2007	Joint Genome Institute Senior Management Committee
2001-2002	Training in Leadership and Management Principles, Berkeley National Lab (~ 50 classroom hours)
2000	Training in Leadership and Management Principles, Lawrence Livermore National Lab (~40 classroom hours)

Military (Air Force and Air National Guard)

1998-2000	Flight Commander and Chief Navigator, supervising about 20 officers
1995-1997	Air Command and Staff College, an advanced course in communication, management theory, and political science considered to be the equivalent of a Master's degree
1990-1994	Commander of one branch of aircraft maintenance for an F-16 fighter squadron, supervising about 100 highly skilled technicians of diverse specialties. Officer-in-charge for several international deployments
1986	Survival training class leader (200 students)
1985-1986	Flight training class leader (66 students)
1982-1984	Squadron Officers' School, a course in communication, management theory, and political science considered to be the equivalent of a Master's degree
1982-1984	Air Force Officers' Leadership and Management Seminar Program
1981-1984	Deputy Commander, then Commander, of a nuclear ICBM site and the Commander of the Base Alternate Command Post. Responsible for a nine-story underground complex, crew, oversight of missile complex maintenance and repair, nuclear employment, safety, and surety.
1976-1980	Reserve Officer Training Corps, Pennsylvania State University. 18 credit hours in Management Principles and Leadership Training. Cadet Corps Leader for the largest ROTC unit in the country.

LEGAL CONSULTING EXPERIENCE

Expert witness for judicial (i.e., Frye) hearing to determine the admissibility of mitochondrial DNA forensic evidence in the state of Michigan.

Expert witness in the case of "People of the State of Michigan vs. Kevin Holtzer" (trial for the crime of murder) including the first use of mitochondrial DNA forensic evidence in the state of Michigan.

Expert witness in the case of "People of the State of Maryland vs. Hadden Clark", judicial hearing to determine the admissibility of mitochondrial DNA forensic evidence in the state of Maryland.

Expert witness in the case of "People of the State of Maryland vs. Russell Wagner" (trial for the crime of murder).

TEACHING EXPERIENCE

EVOLUTION (IB 160), UC Berkeley, Fall semester 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013 (with Kevin Padian and Craig Moritz or Ellen Simms).
EVOLUTION OF MITOCHONDRIAL GENOMES, UC Berkeley, Winter 2002.
GSI, U of Michigan, GENETICS (winter 1991) and EVOLUTION (Fall 1990).

Formal training in instructional methods: In preparation for my assignment as an Air Force instructor in 1982, I received formal training in teaching theory and methods, including many critiqued exercises. For 18 months, then, I performed daily instruction in the classroom and in practical, hands-on settings, teaching such diverse topics as electronics, space physics, and management theory. I wrote hundreds of pages of instructional materials, workbooks, and tests.

MILITARY SERVICE

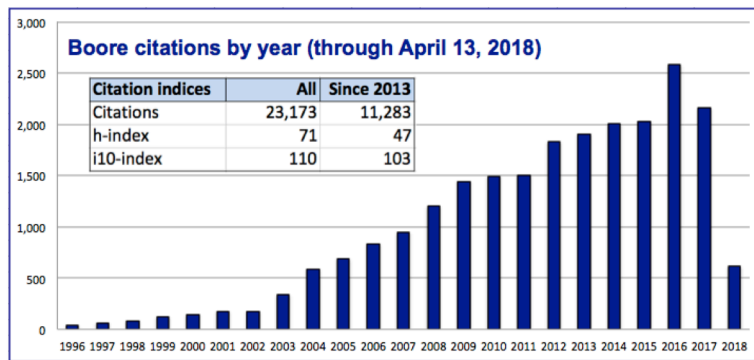
Branch:	US Air Force, Air National Guard
Rank:	Lieutenant Colonel (retired)
Dates of service	October 1980-December 1984 (USAF) January 1985-August 2000 (ANG)
Aeronautical rating:	Senior Navigator
Most recent position:	Flight Commander, Chief Navigator
Security clearance:	Top Secret

Career Highlights:

Flight Commander and Chief Navigator, Selfridge ANGB, MI, 1/98-8/00
Air Command and Staff College, by correspondence, 3/95-5/97
C-130 Navigator, Selfridge ANGB, MI, 1/95-8/00
C-130 Training, Little Rock AFB, AR, 9/94-12/94, Distinguished Graduate
Officer-in-Charge, F-16 Fighter Aircraft Maintenance, Selfridge ANGB, MI, 7/90-8/94,
Supervising approx. 100 technicians, Officer-in-Charge for several international
deployments
Aircraft Maintenance Officer School, Chanaute AFB, IL, 5/90-6/90, Distinguished Graduate
Operated the F-4 Phantom II fighter in its role as an air defense interceptor, Weapon Systems
Officer, Tactics Officer, Selfridge ANGB, MI, 8/86-6/90
F-4 Fighter-Interceptor Training, Kingsley Field, OR, 3/86-8/86
Tactical Navigation Training, Mather AFB, CA, 8/85-9/85, "Top Gun" Trophy
Undergraduate Navigator Training, Mather AFB, CA, ATC Commander's Trophy, Ira Husik
Memorial Trophy, Distinguished Graduate
Squadron Officers' School, by correspondence, 12/82-3/84
Missile Crew Commander, McConnell AFB, KS, 2/84-11/84, Responsible for a nine-story
underground complex, nuclear employment, safety and surety
Missile Launch Officer Instructor, McConnell AFB, KS, 12/82-11/83, Teaching electronics,
space physics, management theory, nuclear safety and surety requirements
Deputy Missile Crew Commander, McConnell AFB, KS, 3/82-12/82
Missile Launch Officer Training, Sheppard AFB, TX, Vandenberg AFB, CA, 8/81-3/82
4-year Air Force Scholarship, Pennsylvania State University, 1976-1980

PUBLICATIONS

Statistics from Google Scholar, updated April 13, 2018:



“**h-index**” shows that 71 of my publications have been cited at least 71 times each (47 cited at least 47 times each in the last 5 years)

“**i10-index**” shows that 110 of my publications have been cited at least 10 times each (103 cited at least 10 times each in the last 5 years)

(Note that these are **annual**, not cumulative citations).

- Hoffmann, R. J., J. L. Boore and W. M. Brown, 1992 A novel mitochondrial genome organization for the Blue Mussel, *Mytilus edulis*. *Genetics* **131**: 397-412.
- Boore, J. L. and W. M. Brown, 1994 Mitochondrial genomes and the phylogeny of mollusks. *Nautilus* **108 (suppl. 2)**: 61-78.
- Boore, J. L. and W. M. Brown, 1994 The complete DNA sequence of the mitochondrial genome of the Black Chiton *Katharina tunicata*. *Genetics* **138**: 423-443.
- Boore, J. L., T. M. Collins, D. Stanton, L. L. Daehler and W. M. Brown, 1995 Deducing arthropod phylogeny from mitochondrial DNA rearrangements. *Nature* **376**: 163-165.
- Boore, J. L. and W. M. Brown, 1995 The complete DNA sequence of the mitochondrial genome of the annelid worm *Lumbricus terrestris*. *Genetics* **141**:305-319.
- Yost, H. J., C. R. Phillips, J. L. Boore, J. Bertman, B. Whalen and M. V. Danilchik, 1995 Relocation of mitochondrial RNA to the prospective dorsal midline during *Xenopus* embryogenesis. *Developmental Biology* **170**: 83-90.
- Boore, J. L., 1996 Ancient patterns of arthropod evolution are recorded in mitochondrial genome rearrangements. In *Current Topics on Molecular Evolution: Proceedings of the U.S.-Japan Workshop on Molecular Evolution* (M. Nei and N. Takahata, eds.). Mishima, Japan, pp. 69-78.
- Boore, J. L., 1997 Transmission of mitochondrial DNA—Playing favorites? *Bioessays* **19(9)**: 751-753.
- Boore, J. L., D. Lavrov and W. M. Brown, 1998 Gene translocation links insects and crustaceans. *Nature* **392**: 667-668.
- Boore, J. L., and W. M. Brown, 1998 Big trees from little genomes: Mitochondrial gene order as a phylogenetic tool. *Current Opinion in Genetics and Development* **8(6)**: 668-674.
- Boore, J. L., L. L. Daehler and W. M. Brown, 1999 Complete sequence, gene arrangement and genetic code of mitochondrial DNA of the cephalochordate *Branchiostoma floridae* (“Amphioxus”). *Molecular Biology and Evolution* **16(3)**: 410-418.

12. Boore, J. L., 1999 Animal mitochondrial genomes. *Nucleic Acids Research* **27(8)**: 1767-1780.
13. Boore, J. L. and S. I Fuerstenberg, 1999 *Entamoeba histolytica*—A derived mitochondriate eukaryote? *Trends in Microbiology* **7(11)**: 426-428.
14. Boore, J. L., 1999 Phylogenies derived from rearrangements of the mitochondrial genome. In *Proceedings of the International Institute for Advanced Studies Symposium on Biodiversity* (N. Saitou, ed.). Kyoto, Japan, pp. 9-20.
15. Boore, J. L., and W. M. Brown, 2000 Mitochondrial genomes of *Galathealinum*, *Helobdella*, and *Platynereis*: Sequence and gene arrangement comparisons indicate that Pogonophora is not a phylum and Annelida and Arthropoda are not sister taxa. *Molecular Biology and Evolution* **17(1)**: 87-106.
16. Lavrov, D., J. L. Boore and W. M. Brown, 2000 The complete mitochondrial DNA sequence of the horseshoe crab *Limulus polyphemus*. *Molecular Biology and Evolution* **17(5)**: 813-824.
17. Boore, J. L., 2000 The duplication/random loss model for gene rearrangement exemplified by mitochondrial genomes of deuterostome animals. In *Comparative Genomics* (D. Sankoff and J. Nadeau, eds.). Computational Biology Series vol 1, Kluwer Academic Publishers, Dordrecht, Netherlands, pp. 133-147.
18. Lavrov, D., W. M. Brown, and J. L. Boore, 2000 A novel type of RNA editing occurs in the mitochondrial tRNAs of the centipede *Lithobius forficatus*. *Proceedings of the National Academy of Sciences USA* **97(25)**: 13738-13742.
19. Nickisch-Roseneck, M. von, W. M. Brown and J. L. Boore, 2001 Sequence and structure of the mitochondrial genome of the tapeworm *Hymenolepis diminuta*: Gene arrangement indicates that platyhelminths are derived eutrochozoans. *Molecular Biology and Evolution* **18(5)**: 721-730.
20. Boore, J. L., 2001 Complete mitochondrial genome sequence of the polychaete annelid *Platynereis dumerilii*. *Molecular Biology and Evolution* **18(7)**: 1413-1416.
21. Helfenbein, K. G., W. M. Brown and J. L. Boore, 2001 The complete mitochondrial genome of a lophophorate, the brachiopod *Terebratalia transversa*. *Molecular Biology and Evolution* **18(9)**: 1734-1744.
22. Wollscheid-Lengeling, E., J. L. Boore, W. M. Brown, and H. Wägele, 2001 The phylogeny of Nudibranchia (Opisthobranchia, Gastropoda, Mollusca) reconstructed by three molecular markers. *Organisms, Diversity and Evolution* **1(4)**: 241-256.
23. Boore, J. L., and J. Staton, 2002 The mitochondrial genome of the sipunculid *Phascolopsis gouldii* supports its association with Annelida rather than Mollusca. *Molecular Biology and Evolution* **19(2)**: 127-137.
24. Lavrov, D. V., J. L. Boore and W. M. Brown, 2002 Complete mtDNA sequences of two millipedes suggest a new model for mitochondrial gene rearrangements: Duplication and non-random loss. *Molecular Biology and Evolution* **19(2)**: 163-169.
25. Dehal, P., Y. Satou, R. Campbell, J. Chapman, B. Degnan, A. DeTomaso, B. Davidson, A. DiGregorio, M. Gelpke, D. Goodstein, N. Harafuji, K. Hastings, I. Ho, K. Hotta, W. Huang,

- T. Kawashima, P. Lemaire, D. Martinez, I. Meinertzhagen, S. Necula, M. Nonaka, N. Putnam, S. Rash, H. Saiga, M. Satake, A. Terry, L. Yamada, H.-G. Wang, S. Awazu, K. Azumi, J. L. Boore, M. Branno, S. Chin-bow, R. DeSantis, S. Doyle, P. Francino, D. Keys, S. Haga, H. Hayashi, K. Hino, K. Imai, K. Inaba, S. Kano, K. Kobayashi, M. Kobayashi, B.-I. Lee, K. Makabe, C. Manohar, G. Matassi, M. Medina, Y. Mochizuki, S. Mount, T. Morishita, S. Miura, A. Nakayama, S. Nishizaka, H. Nomoto, F. Ohta, K. Oishi, I. Rigoutsos, M. Sano, A. Sasaki, Y. Sasakura, E. Shoguchi, T. Sin-I, A. Spagnuolo, D. Stainier, M. Suzuki, O. Tassy, N. Takatori, M. Tokuoka, K. Yagi, F. Yoshizaki, S. Wada, C. Zhang, P. D. Hyatt, F. Larimer, C. Detter, N. Doggett, T. Glavina, T. Hawkins, P. Richardson, S. Lucas, Y. Kohara, M. Levine, N. Satoh and D. Rokhsar, 2002 The draft Genome of *Ciona intestinalis*: Insights into chordate and vertebrate origins. *Science* **298** (5601): 2157-2167.
26. Nardi, F., G. Spinsanti, J. L. Boore, A. Carapelli, R. Dallai and F. Frati, 2003 Hexapod origins, monophyletic or paraphyletic? *Science* **299**: 1887-1889.
 27. Passamonti, M., J. L. Boore and V. Scali, 2003 Molecular evolution and recombination in gender-associated mitochondrial DNAs of the Manila clam *Tapes philippinarum*. *Genetics* **164**: 603–611.
 28. Santini, S., J. L. Boore and A. Meyer, 2003 Evolutionary conservation of regulatory elements in vertebrate *HOX* gene clusters. *Genome Research* **13**: 1111-1122.
 29. Nardi, F., G. Spinsanti, J. L. Boore, A. Carapelli, R. Dallai and F. Frati, 2003 Technical Comment: Response to Comment on "Hexapod Origins: Monophyletic or Paraphyletic?", *Science* **301**: 1482e.
 30. Wyman, S. K., and J. L. Boore, 2003 Annotating animal mitochondrial tRNAs: An experimental evaluation of four methods. In *Proceedings of the European Conference on Computational Biology* (ECCB), pp. 44-46.
 31. Lavrov, D., W. M. Brown and J. L. Boore, 2004 Phylogenetic position of the Pentastomida and (pan)crustacean relationships. *Proceedings of the Royal Society of London B* **271**(1538): 537-544.
 32. Helfenbein, K. G., and J. L. Boore, 2004 The mitochondrial genome of *Phoronis architecta*—Comparisons demonstrate that phoronids are lophotrochozoan protostomes. *Molecular Biology and Evolution* **21**(1): 153-157.
 33. Masta, S. E., and J. L. Boore, 2004 The complete mitochondrial genome sequence of the spider *Habronattus oregonensis* reveals rearranged and extremely truncated tRNAs. *Molecular Biology and Evolution* **21**: 893-902.
 34. Bensasson, D., J. L. Boore and K. M. Nielsen, 2004 Genes without frontiers? *Journal of Heredity* **92**: 483-489.
 35. Boore, J. L., M. Medina and L. A. Rosenberg, 2004 Complete sequences of two highly rearranged molluscan mitochondrial genomes, those of the scaphopod *Graptacme eborea* and of the bivalve *Mytilus edulis*. *Molecular Biology and Evolution* **21**(8): 1492–1503.
 36. Helfenbein, K. G., H. M. Fourcade, R. G. Vanjani and J. L. Boore, 2004 The mitochondrial genome of *Paraspadella gotoi* is highly reduced and reveals that chaetognaths are a sister-

- group to protostomes. *Proceedings of the National Academy of Sciences USA* **101 (29)**: 10639-10643.
37. Ruiz-Trillo, I., M. Riutort, H. M. Fourcade, J. Baganà and J. L. Boore, 2004 Mitochondrial genome data support the basal position of Acoelomorpha and the polyphyly of the Platyhelminthes. *Molecular Phylogenetics and Evolution* **33 (2)**: 321-332.
 38. Macey, J. R., T. J. Papenfuss, J. V. Kuehl, H. M. Fourcade and J. L. Boore, 2004 Phylogenetic relationships among amphisbaenian reptiles based on complete mitochondrial genome sequences. *Molecular Phylogenetics and Evolution* **33(1)**: 22-31.
 39. Mueller, R. L., J. R. Macey, M. Jaekel, D. B. Wake and J. L. Boore, 2004 Morphological homoplasy, life history evolution, and historical biogeography of plethodontid salamanders: Novel insights from complete mitochondrial genome sequences. *Proceedings of the National Academy of Sciences USA* **101(38)**: 13820-13825.
 40. Boore, J. L., 2004 Complete mitochondrial genome sequence of *Urechis caupo*, a representative of the phylum Echiura. *BMC Genomics* **5**: 67.
 41. Wyman, S., R. K. Jansen and J. L. Boore, 2004 Automatic annotation of organellar genomes with DOGMA. *Bioinformatics* **20(17)**: 3252-3255.
 42. Carapelli, A., F. Nardi, R. Dallai, J. L. Boore, P. Lio and F. Frati, 2005 Relationships between hexapods and crustaceans based on mitochondrial genomics. In *Crustacean and Arthropod Relationships*. (Stefan Koenemann and Ronald A. Jenner, eds.). pp. 295-306.
 43. Wolf, P. G., K. G. Karol, D. F. Mandoli, J. Kuehl, K. Arumuganathan, M. W. Ellis, B. D. Mishler, D. Kelch, R. Olmstead, J. L. Boore, 2005 The first complete chloroplast genome sequence of a lycophyte, *Huperzia lucidula* (Lycopodiaceae): Implications for land plant phylogeny. *Gene* **350(2)**: 117-128.
 44. Place, A. R., X. Feng, C. R. Steve, H. M. Fourcade and J. L. Boore, 2005 Genetic markers in Blue Crabs (*Callinectes sapidus*) II: Complete mitochondrial genome sequence and characterization of genetic variation. *Journal of Experimental Marine Biology and Ecology* **319**: 15-27.
 45. Macey, J. R., J. J. Fong, J. V. Kuehl, S. Shafiei, N. B. Ananjeva, T. J. Papenfuss and J. L. Boore, 2005 The complete mitochondrial genome of a gecko and the phylogenetic position of the Middle Eastern *Teratoscincus keyserlingii*, *Molecular Phylogenetics and Evolution* **36**: 188-193.
 46. Boore, J. L., J. R. Macey and M. Medina, 2005 Sequencing and comparing whole mitochondrial genomes of animals. In *Molecular Evolution: Producing the Biochemical Data, Part B* (E. A. Zimmer and E. Roalson, eds.). Volume 395 of the *Methods in Enzymology* series, Elsevier, Burlington, Massachusetts, pp. 311-348.
 47. Jansen, R. K., L. A. Raubeson, J. L. Boore, C. W. dePamphilis, T. W. Chumley, R. C. Haberle, S. K. Wyman, A. Alverson, R. Peery, S. J. Herman, H. M. Fourcade, J. V. Kuehl, J. R. McNeal, J. Leebens-Mack and L. Cui, 2005 Methods for obtaining and analyzing whole chloroplast genome sequences. In *Molecular Evolution: Producing the Biochemical Data, Part B* (E. A. Zimmer and E. Roalson, eds.). Volume 395 of the *Methods in Enzymology* series, Elsevier, Burlington, Massachusetts, pp. 348-384.

48. Mueller, R. L., and J. L. Boore, 2005 Molecular mechanisms of extensive mitochondrial gene rearrangement in plethodontid salamanders. *Molecular Biology and Evolution* **22**: 2104-2112.
49. Leebens-Mack, J., L. A. Raubeson, L. Cui, J. V. Kuehl, H. M. Fourcade, T. W. Chumley, J. L. Boore, R. K. Jansen and C. W. dePamphilis, 2005 Identifying the basal angiosperm node in chloroplast genome phylogenies: Sampling one's way out of the Felsenstein zone. *Molecular Biology and Evolution* **22**: 1948-1963.
50. Dehal, P., and J. L. Boore, 2005 Two rounds of genome duplication in the ancestral vertebrate genome. *PLoS Biology* **3(10)**: e314.
51. Parham, J. F., J. R. Macey, T. J. Papenfuss, C. R. Feldman, O. Türkozan, R. Polymeni and J. L. Boore, 2006 The phylogeny of Mediterranean tortoises and their close relatives based on complete mitochondrial genome sequences from museum specimens. *Molecular Phylogenetics and Evolution* **38 (1)**: 50-64.
52. Parham, J. F., C. R. Feldman and J. L. Boore, 2006 The complete mitochondrial genome of the enigmatic bigheaded turtle (*Platysternon*): Description of unusual genomic features and the reconciliation of phylogenetic hypotheses based on mitochondrial and nuclear DNA. *BMC Evolutionary Biology* **6**: 11.
53. Dehal, P., and J. L. Boore, 2006 A phylogenomic gene cluster resource: The Phylogenetically Inferred Groups (PhIGs) database. *BMC Bioinformatics* **7**: 201.
54. Simison, W. B., D. R. Lindberg and J. L. Boore, 2006 Rolling circle amplification of metazoan mitochondrial genomes. *Molecular Phylogenetics and Evolution* **39(2)**: 562-567.
55. Medina, M., A. G. Collins, T. L. Takaoka, J. Kuehl and J. L. Boore, 2006 Naked stony corals: Skeleton loss in Scleractinia. *Proceedings of the National Academy of Sciences* **103(24)**: 9096-9100.
56. Boore, J. L., 2006 Requirements and standards for organelle genome databases. *OMICS* **10(2)**: 119-126.
57. Carapelli, A., L. Vannini, F. Nardi, J. L. Boore, L. Beani, R. Dallai and F. Frati, 2006 The mitochondrial genome of the entomophagous endoparasitoid *Xenos vesparum* (Insecta: Strepsiptera). *Gene* **376(2)**: 248-259.
58. Boore, J. L., 2006 The complete sequence of the mitochondrial genome of *Nautilus macromphalus* (Mollusca: Cephalopoda). *BMC Genomics* **7**: 182.
59. Boore, J. L., 2006 The use of genome-level characters for phylogenetic reconstruction. *Trends in Ecology and Evolution* **21(8)**: 439-446.
60. Chumley, T. W., J. D. Palmer, J. P. Mower, H. Matthew Fourcade, P. J. Calie, J. L. Boore and R. K. Jansen, 2006 The complete chloroplast genome sequence of *Pelargonium × hortorum*: Organization and evolution of the largest and most highly rearranged chloroplast genome of land plants. *Molecular Biology and Evolution* **23**: 2175-2190.
61. McNeal, J. R., J. H. Leebens-Mack, K. Arumuganathan, J. V. Kuehl, J. L. Boore and C. W. dePamphilis, 2006 Using partial genomic fosmid libraries for sequencing complete organellar genomes. *Biotechniques* **41(1)**: 69-73.

62. Tyler, B. M., S. Tripathi, X. Zhang, P. Dehal, R. Jiang, A. Aerts, F. D. Arredondo, L. Baxter, D. Bensasson, J. Beynon, J. Chapman, C. M. B. Damasceno, A. E. Dorrance, D. Dou, A. W. Dickerman, I. Dubchak, M. Garbelotto, M. Gijzen, S. G. Gordon, F. Govers, N. J. Grunwald, W. Huang, K. Ivors, R. W. Jones, S. Kamoun, K. Krampis, K. Lamour, M. –K. Lee, W. H. McDonald, M. Medina, H. J. G. Meijer, E. K. Nordberg, D. J. Maclean, M. D. Ospina-Giraldo, P. Morris, V. Phuntumart, N. Putnam, S. Rash, J. K. C. Rose, Y. Sakihama, A. Salamov, A. Savidor, C. F. Scheuring, B. M. Smith, B. W. S. Sobral, A. Terry, T. A. Torto-Alalibo, J. Win, Z. Xu, H. Zhang, I. Grigoriev, D. Rokhsar and J. L. Boore, 2006 *Phytophthora* genome sequences uncover evolutionary origins and mechanisms of pathogenesis. *Science* **313**: 1261-1266.
63. Podsiadlowski, L., A. Carapelli, F. Nardi, R. Dallai, M. Koch, J. L. Boore and F. Frati, 2006 The mitochondrial genomes of *Campodea fragilis* and *C. lubbocki* (Hexapoda: Diplura): high genetic divergence in a morphologically uniform taxon. *Gene* **381**: 49-61.
64. Cai, Z., C. Penaflor, J. V. Kuehl, J. Leebens-Mack, J. Carlson, C. W. dePamphilis, J. L. Boore and R. K. Jansen, 2006 Complete plastid genome sequences of *Drimys*, *Liriodendron*, and *Piper*: Implications for the phylogenetic relationships of magnoliids. *BMC Evolutionary Biology* **6**: 77.
65. Vallès, Y., and J. L. Boore, 2006 Lophotrochozoan mitochondrial genomes. *Integrative and Comparative Biology* **46 (4)**: 544-557.
66. Krampis, K., B. Tyler and J. L. Boore, 2006 Extensive variation in nuclear mitochondrial DNA content between the genomes of *Phytophthora sojae* and *Phytophthora ramorum*. *Molecular Plant-Microbial Interactions* **19(12)**: 1329-36.
67. Martin, F. N., D. Bensasson, B. M. Tyler and J. L. Boore, 2007 Mitochondrial genome sequences and comparative genomics of *Phytophthora ramorum* and *P. sojae*. *Current Genetics* **51**: 285-296.
68. Timme, R. E., J. V. Kuehl, J. L. Boore and R. K. Jansen, 2007 A comparative analysis of the *Lactuca* and *Helianthus* (Asteraceae) plastid genomes: Identification of divergent regions and categorization of shared repeats. *American Journal of Botany* **94**: 302-312.
69. Raubeson, L. A., R. Peery, T. W. Chumley, C. Dziubek, H. M. Fourcade, J. L. Boore and R. K. Jansen, 2007 Comparative chloroplast genomics: Analyses including new sequences from the angiosperms *Nuphar advena* and *Ranunculus macranthus*. *BMC Genomics* **8**: 174.
70. Roper, J., S. K. Hansen, P. G. Wolf, K. G. Karol, D. F. Mandoli, K. Everett, J. Kuehl and J. L. Boore, 2007 The complete plastid genome sequence of *Angiopteris evecta* (G. Forst.) Hoffm. (Marattiaceae). *American Fern Journal* **97(2)**: 95-106.
71. Hoegg, S., J. V. Kuehl, J. L. Boore and A. Meyer, 2007 Comparative phylogenomic analyses of teleost fish Hox gene clusters: lessons from the cichlid fish *Astatotilapia burtoni*. *BMC Genomics* **8**: 317.
72. Hansen, D. R., S. G. Dastidar, Z. Cai, C. Penaflor, J. V. Kuehl, J. L. Boore and R. K. Jansen, 2007 Phylogenetic and evolutionary implications of complete chloroplast genome sequences of four early diverging angiosperms: *Buxus* (Buxaceae), *Chloranthus* (Chloranthaceae), *Dioscorea* (Dioscoreaceae), and *Illicium* (Schisandraceae). *Molecular Phylogenetics and Evolution* **45**: 547-563.

73. McNeal, J. R., J. Kuehl, J. L. Boore and C. W. dePamphilis, 2007 Complete plastid genome sequences suggest strong selection for retention of photosynthetic genes in the parasitic plant genus *Cuscuta*. *BMC Plant Biology* **7**: 57.
74. Jansen, R. K., Z. Cai, L. A. Raubeson, H. Daniell, C. W. dePamphilis, J. Leebens-Mack, K. Müller, M. Guisinger-Bellian, R. C. Haberle, A. K. Hansen, T. W. Chumley, S.-B. Lee, R. Peery, J. McNeal, J. V. Kuehl and J. L. Boore, 2007 Analysis of 81 genes from 64 chloroplast genomes resolves relationships in angiosperms and identifies genome-scale evolutionary patterns. *Proceedings of the National Academy of Sciences USA* **104(49)**: 19369-19374.
75. McNeal, J. R., K. Arumugunathan, J. V. Kuehl, J. L. Boore and C. W. dePamphilis, 2007 Systematics and plastid genome evolution of the cryptically photosynthetic parasitic plant genus *Cuscuta* (Convolvulaceae). *BMC Biology* **5**: 55.
76. Fujita, M. K., J. L. Boore and C. Moritz, 2007 Multiple origins and rapid evolution of duplicated mitochondrial genes in parthenogenetic geckos (Heteronotial binoei; Squamata, Gekkonidae). *Molecular Biology and Evolution* **24(12)**: 2775-2786.
77. Field, D., G. Garrity, T. Gray, N. Morrison, J. Selengut, P. Sterk, T. Tatusova, N. Thomson, M. Allen, S. V. Angiuoli, M. Ashburner, N. Axelrod, S. Baldauf, S. Ballard, J. L. Boore, G. Cochrane, J. Cole, P. Dawyndt, P. de Vos, C. de Pamphilis, R. Edwards, N. Faruque, R. Feldman, J. Gilbert, P. Gilna, F. O. Glöckner, P. Goldstein, R. Guralnick, D. Haft, D. Hancock, H. Hermjakob, C. Hertz-Fowler, P. Hugenholtz, I. Joint, L. Kagan, M. Kane, J. Kennedy, G. Kowalchuk, R. Kottmann, E. Kolker, S. Kravitz, N. Kyripides, J. Leebens-Mack, S. Lewis, K. Li, A. Liste, P. Lord, N. Maltsev, V. Markowitz, J. Martiny, B. Methe, R. Moxon, K. Nelson, J. Parkhill, L. Proctor, S. Sansone, A. Spiers, R. Stevens, P. Swift, C. Taylor, Y. Tateno, A. Tett, S. Turner, D. Ussery, B. Vaughan, N. Ward, T. Whetzel, G. Wilson and A. Wipat, 2008 The minimum information about a genome sequence (MIGS) specification. *Nature Biotechnology* **26**: 541-547.
78. Rensing, S. A., D. Lang, A. Zimmer, A. Terry, A. Salamov, H. Shapiro, T. Nishiyama, P.-F. Perroud, E. Lindquist, Y. Kamisugi, T. Tanahashi, K. Sakakibara, T. Fujita, K. Oishi, T. Shin-I, Y. Kuroki, A. Toyoda, Y. Suzuki, S.-I. Hashimoto, K. Yamaguchi, S. Sugano, Y. Kohara, A. Fujiyama, N. Ashton, A. Anterola, S. Aoki, W. B. Barbazuk, E. Barker, J. Bennetzen, R. Blankenship, S. H. Cho, S. Dutcher, M. Estelle, J. A. Fawcett, H. Gundlach, K. Hanada, A. Heyl, K. A. Hicks, J. Hughes, M. Lohr, K. Mayer, A. Melkozernov, T. Murata, D. Nelson, B. Pils, M. Prigge, B. Reiss, T. Renner, S. Rombauts, P. Rushton, A. Sanderfoot, G. Schween, S.-H. Shiu, K. Stueber, F. L. Theodoulou, H. Tu, Y. Van de Peer, P. J. Verrier, E. Waters, A. Wood, L. Yang, D. Cove, A. C. Cuming, M. Hasebe, S. Lucas, B. D. Mishler, R. Reski, I. Grigoriev, R. S. Quatrano and J. L. Boore, 2008 The genome of the moss *Physcomitrella patens* reveals evolutionary insights into the conquest of land by plants. *Science* **319 (5859)**: 64-69.
79. Vallès, Y., K. Halanych and J. L. Boore, 2008 Group II introns break new boundaries: Presence in an animal genome. *PLoS One* **3(1)**: e1488.
80. Wickett, N. J., Y. Zhang, S. K. Hansen, J. M. Roper, J. V. Kuehl, S. A. Plock, P. G. Wolf, C. W. dePamphilis, J. L. Boore and B. Goffinet, 2008 Functional gene losses occur with

- minimal size reduction in the plastid genome of the parasitic liverwort *Aneura mirabilis* (Metzgeriales, Aneuraceae). *Molecular Biology and Evolution* **25(2)**: 393-401.
81. Boore, J. L. and S. I Fuerstenberg, 2008 Beyond linear sequence comparisons: The use of genome-level characters for phylogenetic reconstruction. *Philosophical Transactions of the Royal Society of London, B, Biological Sciences* **363**: 1445-1451.
 82. Masta, S. E, and J. L. Boore, 2008 Parallel evolution of truncated transfer RNA structure in arachnid mitochondrial genomes. *Molecular Biology and Evolution* **25(5)**: 949-959.
 83. Haberle, R. C., H. M. Fourcade, J. L. Boore and R. K. Jansen, 2008 Extensive rearrangements in the chloroplast genome of *Trachelium caeruleum* are associated with repeats and tRNA genes *Journal of Molecular Evolution* **66(4)**: 350-361.
 84. Mueller, R. L., T. R. Gregory, S. M. Gregory, A. Hsieh and J. L. Boore, 2008 Genome size, cell size, and the evolution of enucleated erythrocytes in attenuate salamanders. *Journal of Zoology* **111(3)**: 218-230.
 85. McCoy, S. K. R., J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2008 Complete plastid genome sequence of *Welwitschia mirabilis*: An usually compact plastome with accelerated divergence rates. *BMC Evolutionary Biology* **8**: 130.
 86. Simison, W. B., and J. L. Boore, 2008 Molluscan evolutionary genomics, in *Phylogeny and Evolution of the Mollusca* (W. Ponder and D. Lindberg, eds.) University of California Press, Berkeley, CA, pp. 447-461.
 87. Boore, J. L., 2008 Detecting evolutionary transfer of genes using PhIGs. *Journal of Phycology* **44(1)**: 19-22.
 88. Anderson, S. J., C. L. Stone, M. Lucia Posada-Buitrago, J. L. Boore, B. A. Neelam, R. M. Stephens, D. G. Luster, R. D. Frederick and K. F. Pedley, 2008 Development of simple sequence repeat markers for the soybean rust fungus, *Phakopsora pachyrhizi*. *Molecular Ecology Resources* **8**: 1310-1312.
 89. Guisinger, M. M., J. V. Kuehl, J. L. Boore and R. K. Jansen, 2008 Genome-wide analyses of Geraniaceae plastid DNA reveal unprecedented patterns of increased nucleotide substitutions. *Proceedings of the National Academy of Sciences USA* **105**: 18424-18429.
 90. Zhengqiu, C., H.-G. Kim, E. Ruck, M. Guisinger, V. McMurtry, J. V. Kuehl, J. L. Boore and R. K. Jansen, 2008 Extensive reorganization of the plastid genome of *Trifolium subterraneum* (Fabaceae) is associated with numerous repeated sequences and novel DNA insertions. *Journal of Molecular Evolution* **67(6)**: 696-704.
 91. Masta, S. E., S. J. Longhorn and J. L. Boore, 2009 Arachnid relationships based on mitochondrial genomes: Asymmetric nucleotide and amino acid bias affects phylogenetic analyses. *Molecular Phylogenetics and Evolution* **50**: 117-128.
 92. McNeal, J. R., J. Kuehl, J. L. Boore, J. Leebens-Mack and C. W. dePamphilis, 2009 Parallel loss of plastid introns and their maturase in the genus *Cuscuta*. *PLoS One* **4(6)**: e5982.
 93. Baker, R. H., J. Morgan, X. Wang, J. L. Boore and G. S. Wilkinson, 2009 Genomic analysis of a sexually-selected character: EST sequencing and microarray analysis of eye-antennal

- imaginal discs in the stalk-eyed fly *Teleopsis dalmanni* (Diopsidae). *BMC Genomics* **10**: 361.
94. Boore, J. L. and S. I Fuerstenberg, 2009 Beyond linear sequence comparisons: The use of genome-level characters for phylogenetic reconstruction. In *Animal Evolution: Genes, Fossils and Trees*. (Max Telford and Tim Littlewood, eds.). Oxford University Press, pp. 139-147.
 95. Torricelli, G., A. Carapelli, P. Convey, F. Nardi, J. L. Boore and F. Frati, 2009 High divergence across the whole mitochondrial genome in the “pan-Antarctic” springtail *Friesea grisea*: Evidence for cryptic species? *Gene* **449**: 30-40.
 96. Guisinger, M. M., T. W. Chumley, J. V. Kuehl, J. L. Boore and R. K. Jansen, 2010 Implications of the plastid genome sequence of *Typha* (Typhaceae, Poales) for understanding genome evolution in Poaceae. *Journal of Molecular Evolution*. **70(2)**: 149-166.
 97. Oliver, M. J., A. G. Murdock, B. D. Mishler, J. V. Kuehl, J. L. Boore, D. F. Mandoli, K. Everett, P. G. Wolf and K. G. Karol, 2010 Chloroplast genome sequence of the moss *Tortula ruralis*: Gene content, polymorphism, and structural arrangement relative to other green plant chloroplast genomes. *BMC Genomics* **11**: 143.
 98. Stone, C. L., M. L. Posada Buitrago, J. L. Boore and R. D. Frederick, 2010 Analysis of the complete mitochondrial genome sequences of the soybean rust pathogens *Phakopsora pachyrhizi* and *P. meibomia*. *Mycologia* **102(4)**: 887-897.
 99. Rawlings, T. A., M. J. MacInnis, R. Bieler, J. L. Boore and T. M. Collins, 2010 Sessile snails, dynamic genomes: Gene rearrangements within the mitochondrial genome of a family of caenogastropod molluscs. *BMC Genomics* **11**: 440.
 100. Lévesque, C. A., H. Brouwer, L. Cano, J. P. Hamilton, C. Holt, E. Huitema, S. Raffaele, G. P. Robideau, M. Thines, J. Win, M. M. Zerillo, G. W. Beakes, J. L. Boore, D. Busam, B. Dumas, S. Ferriera, S. I. Fuerstenberg, C. M. M. Gachon, E. Gaulin, F. Govers, L. Grenville-Briggs, N. Horner, J. Hostetler, R. H. Y. Jiang, J. Johnson, T. Krajaejun, H. Lin, H. J. G. Meijer, B. Moore, P. Morris, V. Phuntmart, D. Puiu, J. Shetty, J. E. Stajich, S. Tripathy, S. Wawra, P. van West, B. R. Whitty, P. M. Coutinho, B. Henrissat, F. Martin, P. D. Thomas, B. M. Tyler, R. P. De Vries, S. Kamoun, M. Yandell, N. Tisserat and C. R. Buell, 2010 Genome sequence of the necrotrophic plant pathogen, *Pythium ultimum*, reveals original pathogenicity mechanisms and effector repertoire. *Genome Biology* **11**: R73.
 101. Karol, K. G., K. Arumuganathan, J. L. Boore, A. M. Duffy, K. D. E. Everett, J. D. Hall, S. K. Hansen, J. V. Kuehl, D. F. Mandoli, B. D. Mishler, R. G. Olmstead, K. S. Renzaglia and P. G. Wolf, 2010 Complete plastome sequences of *Equisetum arvense* and *Isoetes flaccida*: Implications for phylogeny and plastid genome evolution of early land plant lineages. *BMC Evolutionary Biology* **10**: 321.
 102. Baxter, L., S. Tripathy, N. Ishaque, N. Boot, A. Cabral, E. Kemen, M. Thines, A. Ah-Fong, R. Anderson, W. Badejoko, P. Bittner-Eddy, J. L. Boore, M. C. Chibucos, M. Coates, P. Downton, P. Dehal, K. Delehaunty, S. Dong, B. Dumas, C. Fronick, S. I. Fuerstenberg, L. Fulton, E. Gaulin, F. Govers, L. Hughes, S. Humphrey, R. Jiang, H. Judelson, S. Kamoun, K. Kyung, H. Meijer, P. Minx, P. Morris, J. Nelson, V. Phuntumart, D. Qutob, A. Rehmany, P. Ryden, T. Torto-Alalibo, Y. Wang, J. Win, J. Wood, S. W. Clifton, J. Rogers, G. Van den

- Ackerveken, J. D. G. Jones, J. M. McDowell, J. Beynon and B. M. Tyler, 2010 Signatures of adaptation to obligate biotrophy in the *Hyaloperonospora arabidopsidis* genome. *Science* **330**: 1549-1551.
103. Rota-Stabelli, O., E. Kayal, D. Gleeson, J. Daub, J. L. Boore, M. Telford, D. Pisani, M. Blaxter and D. Lavrov, 2010 Ecdysozoan mitogenomics: Evidence for a common origin of the legged invertebrates, the Panarthropoda. *Genome Biology and Evolution* **2**: 425-440.
104. Nardi, F., A. Carapelli, J. L. Boore, G. Roderick, R. Dallai and F. Frati, 2010 Domestication of olive fly through a multi-regional host shift to cultivated olives: Comparative dating using complete mitochondrial genomes. *Molecular Phylogenetics and Evolution* **57**: 678-686.
105. Colbourne, J. K., M. E. Pfrender, D. Gilbert, W. K. Thomas, J.-H. Choi, A. Aerts, G. Arnold, M. K. Basu, D. Bauer, C. Caceres, L. Carmel, P. Dehal, C. Detter, Q. Dong, S. Dusheyko, T. Frohlich, P. Hatcher, S. Jogdeo, J. Krijgsveld, D. Kueltz, C. Laforsch, E. Lindquist, J. Lopez, J. Manak, J. Muller, T. Oakley, J. Pangilinan, R. Patwardhan, S. Pitluck, E. Pritham, A. Rechtsteiner, M. Rho, I. Rogozin, O. Sakarya, A. Salamov, S. Schaack, H. Shapiro, Y. Shiga, C. Skalitzy, Z. Smith, A. Souvorov, W. Sung, Z. Tang, S.-I. Tokishita, D. Tsuchiya, H. Tu, A. Tucker, M. Wang, U. Wolf, H. Yamagata, T. Yanada, Y. Ye, J. Shaw, J. Andrews, T. Crease, H. Tang, S. Lucas, H. Robertson, P. Bork, E. Koonin, E. Zdobnov, I. Grigoriev, M. Lynch and J. L. Boore, 2011 The ecoresponsive genome of *Daphnia pulex*. *Science* **331**: 555-561.
106. Medina, M., S. Lal, Y. Valles, T. Takaoka, B. Dayrat, J. L. Boore and T. Goslinger, 2011 Crawling through time: Transition of snails to slugs dating back to the Paleozoic based on mitochondrial phylogenomics. *Marine Genomics* **4(1)**: 51-59.
107. O'Quin, K. E., D. Smith, Z. Naseer, J. Schulte, S. D. Engel, Y.-H. E. Loh, J. T. Steelman, J. L. Boore and K. L. Carleton, 2011 Divergence in *cis*-regulatory sequences surrounding the opsin gene arrays of African cichlid fishes. *BMC Evolutionary Biology* **11**: 120.
108. Guisinger, M. M., J. V. Kuehl, J. L. Boore and R. K. Jansen, 2011 Extreme reconfiguration of plastid genomes in the angiosperm family Geraniaceae: Rearrangements, repeats, and codon usage. *Molecular Biology and Evolution* **28(1)**: 583-600.
109. Zhan, S., C. Merlin, J. L. Boore and S. M. Reppert, 2011 The monarch butterfly genome yields insights into long-distance migration. *Cell* **147**: 1171-1185.
110. Murtagh, V. J., D. O'meally, N. Sankovic, M. L. Delbridge, Y. Kuroki, J. L. Boore, A. Toyoda, K. S. Jordan, A. J. Pask, M. B. Renfree, A. Fujiyama, J. A. M. Graves and P. D. Waters, 2012 Evolutionary history of novel genes of the tammar wallaby Y chromosome: Implications for sex chromosome evolution. *Genome Research* **22(3)**: 498-507.
111. Radakovits, R., R. E. Jinkerson, S. I. Fuerstenberg, H. Tae, R. E. Settlege, J. L. Boore and M. C. Posewitz, 2012 Draft genome sequence and genetic transformation of the oleaginous alga *Nannochloropsis gaditana*. *Nature Communications* **3**: 686.
112. Price, D. C., C. X. Chan, H. S. Yoon, E. C. Yang, H. Qiu, A. P. M. Weber, R. Schwacke, J. Gross, N. Blouin, C. Lane, A. Reyes-Prieto, D. Dumford, J. Neilson, B. F. Lang, G. Burger, J. M. Steiner, W. Loffelhardt, J. E. Meuser, M. C. Posewitz, S. Ball, M. C. Arias, B. Henrissat, P. M. Coutinho, S. A. Rensing, A. Symeonidi, H. Doddapaneni, B. Green, V. D.

- Rajah, J. L. Boore and D. Bhattacharya, 2012 *Cyanophora paradoxa* genome elucidates origin of photosynthesis in algae and plants. *Science* **335 (6070)**: 843-847.
113. Simakov, O., F. Marletaz, S.-J. Cho, E. Edsinger-Gonzales, P. Havlak, U. Hellsten, D.-H. Kuo, T. Larsson, J. Lv, D. Arendt, R. Savage, K. Osoegawa, P. de Jong, J. Grimwood, J. A. Chapman, H. Shapiro, A. Aerts, R. P. Otiillar, A. Y. Terry, J. L. Boore, I. V. Grigoriev, D. R. Lindberg, E. C. Seaver, D. A. Weisblat, N. H. Putnam and D. S. Rokhsar, 2012 Insights into bilaterian evolution from three spiralian genomes. *Nature* **493(7433)**: 526-31.
114. Schartl, M., R. B. Walter, Y. Shen, T. Garcia, J. Catchen, A. Amores, I. Braasch, D. Chalopin, J.-N. Volff, K. -P. Lesch, A. Bisazza, P. Minx, L. Hillier, R. K. Wilson, S. Fuerstenberg, J. L. Boore, S. Searle, J. H. Postlethwait and W. C. Warren, 2013 The genome of the platyfish, *Xiphophorus maculatus*, provides insights into evolutionary adaptation and several complex traits. *Nature Genetics* **45(5)**: 567-572.
115. Rice, D. W., A. J. Alverson, A. O. Richardson, G. J. Young, M. V. Sanchez-Puerta, J. Munzinger, K. Barry, J. L. Boore, Y. Zhang, C. dePamphilis, E. B. Knox and J. D. Palmer, 2013 Horizontal transfer of entire genomes via mitochondrial fusion in the angiosperm *Amborella*. *Science* **342**: 1468-1473.
116. Bell, N. E., J. L. Boore, B. D. Mishler and Jaakko Hyvönen, 2014 Organellar genomes of the four-toothed moss, *Tetraphis pellucida*. *BMC Genomics* **15**: 383.
117. Bankers, L., P. Fields, K. McElroy, J. L. Boore, J. M. Logsdon, Jr. and M. Neiman, 2017 Genomic evidence for population-specific responses to co-evolving parasites in a New Zealand freshwater snail. *Molecular Ecology* **26(14)**: 3663–3675.
118. Guarnieri, M. T., J. Levering, C. A. Henard, J. L. Boore, M. J. Betenbaugh, K. Zengler and E. P. Knoshaug, 2018 Genome sequence of the oleaginous green alga, *Chlorella vulgaris* UTEX 395. *Frontiers in Bioengineering and Biotechnology*. **6**:37. doi: 10.3389/fbioe.2018.00037.
119. Sharbrough, J. T., M. Luse, J. L. Boore, J. M. Logsdon, Jr. and M. Neiman, 20xx Radical amino acid changes persist longer in the absence of sex. In press.
120. Price, N. D., J. L. Boore, G. Glusman and L. Hood, 20xx Systems Medicine. In preparation.

INVITED TALKS / PRESENTATIONS WITH PUBLISHED ABSTRACTS

(Primary presenter underlined)

1. Boore, J. L. and W. M. Brown, 1989 Mitochondrial Control Region Sequences and Hominoid Evolution. Keystone Symposium on Molecular Evolution, Lake Tahoe, CA – Poster Presentation.
2. Boore, J. L. and W. M. Brown, 1989 Comparisons of Mitochondrial Control Region Sequences and Implications for Hominoid Phylogeny. Annual meeting of the Society for the Study of Evolution, Pennsylvania State University, University Park, PA – Contributed Talk.

3. Boore, J. L. and W. M. Brown, 1992 Mitochondrial Genomes and the Evolution of Mollusks. International Congress of Malacology, Siena, Italy—Invited speaker.
4. Boore, J. L. and W. M. Brown, 1993 Mitochondrial Genomes and Metazoan Phylogeny. Annual meeting of the Society for Molecular Biology and Evolution, Irvine, CA – Contributed Talk.
5. Boore, J. L., 1995 Mitochondrial Genome Rearrangements and Metazoan Evolution. Annual meeting of the Society for Molecular Biology and Evolution, Mishima, Japan—Invited speaker.
6. Boore, J. L., 1995 Use of Shared-Derived Molecular Characters for Understanding Metazoan Evolution. US-Japan Workshop on Molecular Evolution, Hayama, Japan—Invited speaker.
7. Boore, J. L., 1995 The Pattern of Early Metazoan Diversification as Deduced From Mitochondrial Genome Rearrangements. Evolution of Development: Molecules, Mechanisms, Phylogenetics. Bodega Marine Laboratory (University of California, Davis), Bodega Bay, CA—Invited speaker.
8. Boore, J. L. and W. M. Brown, 1996 Mitochondrial Genomes and Metazoan Phylogeny. Annual meeting of the Society for Molecular Biology and Evolution, Tucson, AZ – Poster Presentation.
9. Boore, J. L., 1997 Mitochondrial Genomics: A Tool For Determining Ancient Evolutionary Relationships and a Model for Genome Evolution. Center for the Study of Evolution and the Origins of Life, University of California, Los Angeles, CA—Invited speaker.
10. Brown, W. M., J. L. Boore and D. V. Lavrov, 1997 Mitochondrial Gene Arrangements and Arthropod Phylogeny. Meeting on Molecules and Morphology in Systematics. Museum national d'Histoire naturelle, Paris, France – Contributed Talk.
11. Boore, J. L. and W. M. Brown, 1997 Gene Rearrangements Trace the Early Evolution of Animals. Meeting on Molecules and Morphology in Systematics. Museum national d'Histoire naturelle, Paris, France – Contributed Talk.
12. Boore, J. L. and W. M. Brown, 1997 Gene Rearrangements in Early Animal Evolution. Annual meeting of the Society for Molecular Biology and Evolution, Garmisch-Partenkirchen, Germany – Contributed Talk.
13. Brown, W. M., J. L. Boore and D. V. Lavrov, 1997 Gene Arrangements Prevail When Nucleotides Fail: The Use of Complex, Sequence-Derived Characters to Infer Phylogeny. Annual meeting of the Society for Molecular Biology and Evolution, Garmisch-Partenkirchen, Germany – Contributed Talk.
14. Boore, J. L., D. V. Lavrov and W. M. Brown, 1998 Mitochondrial Gene Rearrangements Trace Metazoan Phylogeny. Annual meeting of the Society for Integrative and Comparative Biology, Boston, MA—Invited speaker.
15. Boore, J. L., D. V. Lavrov and W. M. Brown, 1998 Deducing Metazoan Phylogeny by Gene Arrangement Comparisons. Annual meeting of the Society for Molecular Biology and Evolution and the Society for the Study of Evolution, Vancouver, British Columbia, Canada – Contributed Talk.

16. Lavrov, D. V., J. L. Boore and W. M. Brown, 1998 Mitochondrial Genomes and Arthropod Phylogeny. Annual meeting of the Society for Molecular Biology and Evolution and the Society for the Study of Evolution, Vancouver, British Columbia, Canada – Contributed Talk.
17. Helfenbein, K., J. L. Boore and W. M. Brown, 1998 The Mitochondrial Genome of the Brachiopod *Terebratella*. Annual meeting of the Society for Molecular Biology and Evolution and the Society for the Study of Evolution, Vancouver, British Columbia, Canada – Contributed Talk.
18. Boore, J. L., 1998 Beyond Linear Sequence Comparisons—The Use of Complex Genomic Features for Inferring Phylogeny. Institute for Advanced Studies, Kyoto, Japan — Invited speaker.
19. Boore, J. L., K. G. Helfenbein, D. V. Lavrov, L. A. Rosenberg and W. M. Brown, 1999 Mitochondrial Genomics. Annual meeting of the American Genetics Association, Pennsylvania State University, University Park, PA – Contributed Talk.
20. Boore, J. L., K. G. Helfenbein, D. V. Lavrov, L. A. Rosenberg and W. M. Brown, 1999 Mitochondrial Gene Rearrangements and Metazoan Phylogeny. Annual meeting of the Society for the Study of Evolution, University of Wisconsin, Madison, WI – Contributed Talk.
21. Lavrov, D. V., J. L. Boore and W. Brown, 1999 Arthropod Phylogeny Based on Gene Arrangement and other Characters from Mitochondrial DNA. Annual meeting of the Society for the Study of Evolution, University of Wisconsin, Madison, WI – Contributed Talk.
22. Helfenbein, K., J. L. Boore and W. Brown, 1999 Complete Mitochondrial Genome Sequence of the Brachiopod *Terebratalia transversa*. Annual meeting of the Society for the Study of Evolution, University of Wisconsin, Madison, WI – Contributed Talk.
23. Boore, J. L., K. G. Helfenbein, D. V. Lavrov, L. A. Rosenberg and W. M. Brown, 1999 Mitochondrial Genomics. Annual meeting of the Society for Molecular Biology and Evolution and the Genetics Society of Australia, Brisbane, Australia – Contributed Talk. Along with David Mindell, I hosted a symposium with the same name.
24. Lavrov, D. V., J. Boore and W. Brown, 1999 Arthropod Phylogeny Based on Gene Arrangement and other Characters from Mitochondrial DNA. Annual meeting of the Society for Molecular Biology and Evolution and the Genetics Society of Australia, Brisbane, Australia (contributed talk) (won the “Best Student Paper” award).
25. Boore, J. L., K. G. Helfenbein, D. V. Lavrov, L. A. Rosenberg, M. von Nickisch-Roseneck and W. M. Brown, 1999 Mitochondrial Genomics. Gordon Conference on Molecular Evolution, Graduate Institute for Advanced Studies, Mishima, Japan – Poster Presentation.
26. Boore, J. L., 1999 The Primordial Partnership that Produced the Eukarya— Endosymbiosis and the Evolution of Mitochondria. Joint Genome Institute, Walnut Creek, CA—Invited speaker.
27. Boore, J. L., 2000 Lessons for Genomics Learned from Mitochondrial Genome Comparisons. Department of Energy Genomics Meeting, Santa Fe, NM—Invited speaker.

28. Boore, J. L., 2000 Lessons for Genomics Learned from Mitochondrial Genome Comparisons. Wayne State University, Detroit, MI—Invited speaker.
29. Boore, J. L., 2000 Mitochondrial Genomics. University of California, Riverside, CA—Invited speaker.
30. Boore, J. L., 2000 Mitochondrial Genomics. University of Wisconsin, Madison, WI—Invited speaker.
31. Boore, J. L., 2000 Metazoan Phylogeny and Genome Evolution. Texas A&M University, College Station, TX—Invited speaker.
32. Boore, J. L., 2000 Mitochondrial Genomics—A Model for Genome Evolution. Meeting on “Gene Order Dynamics, Comparative Mapping and Multigene Families” (DCAF), near Montreal, Canada—Invited speaker.
33. Boore, J. L., 2000 Beyond Linear Sequence Comparisons—Genome level characters for inferring metazoan phylogeny. Annual meeting of the Italian Society for Zoology, San Benedetto del Tronto, Italy—Invited speaker.
34. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute. Lawrence Livermore National Laboratory—Invited speaker.
35. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute. University of California, Berkeley—Invited speaker.
36. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute. University of California, Davis—Invited speaker.
37. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute. Iowa State University, Ames, IA—Invited speaker.
38. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute. Special meeting of the Bay Area Biosystematists—Invited speaker.
39. Boore, J. L., H. M. Fourcade, A. Haim, K. G. Helfenbein, J. R. Macey, S. Masta, M. Medina, M. Passamonti, D. Rokhsar, and I. Ruiz-Trillo, 2001 Sampling Animal Diversity with Mitochondrial Genomics. Cold Spring Harbor Laboratory meeting on “Genome Sequencing and Biology” – Poster Presentation.
40. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute—Molecular Evolution at 20 Million Nucleotides per day. Institute for Theoretical Physics, Santa Barbara, CA—Invited speaker.
41. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute—Molecular Evolution at 20 Million Nucleotides per day. Lawrence Livermore National Laboratory Program Series—Invited speaker.
42. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute—Molecular Evolution at 20 Million Nucleotides per day. Simon-Fraser University, Burnaby, Canada—Invited speaker.
43. Boore, J. L., 2001 Comparative Genomics at the Joint Genome Institute—Molecular Evolution at 20 Million Nucleotides per day. Annual meeting of the Society for the Study of Evolution, Knoxville, TN – Contributed Talk.

44. Boore, J. L., 2001 The Comparative Genomics Program at the Joint Genome Institute. Monterey Bay Aquarium Research Institute (MBARI), Moss Landing, CA—Invited speaker.
45. Boore, J. L., D. DeGusta, H. M. Fourcade, A. Haim, K. G. Helfenbein, K. Lindstrom, J. R. Macey, S. Masta, M. Medina, R. Mueller, M. Passamonti, R. Shao and Y. Vallès, 2001 Sampling Diversity with Mitochondrial Genomics. Genome Sequencing and Analysis Conference (GSAC), San Diego, CA – Poster Presentation.
46. Boore, J. L., 2001 Sampling Organismal Diversity with Organelle Genomics. Meeting on “Evolutionary Genomics—A New Paradigm for the 21st Century”. Atami, Japan – Contributed Talk.
47. Boore, J. L., N. Danos, D. DeGusta, H. M. Fourcade, L. Gershwin, A. Haim, K. G. Helfenbein, M. Jaekel, K. Lindstrom, J. R. Macey, S. Masta, M. Medina, R. Mueller, M. Passamonti, C. Saux, R. Shao and Y. Vallès, 2002 Sampling Diversity with Mitochondrial Genomics. Pacific Biocomputing Conference, Kauai, HI – Poster Presentation.
48. Boore, J. L., N. Danos, D. DeGusta, H. M. Fourcade, L. Gershwin, A. Haim, K. G. Helfenbein, M. Jaekel, K. Lindstrom, J. R. Macey, S. Masta, M. Medina, R. Mueller, M. Passamonti, C. Saux, R. Shao and Y. Vallès, 2002 Sampling Diversity with Mitochondrial Genomics. DOE Genome Contractors and Grantees Meeting, Oakland, CA – Poster Presentation.
49. Boore, J. L., 2002 The Comparative Genomics Program at the Joint Genome Institute. UC Berkeley Paleontology Group—Invited speaker.
50. Boore, J. L., 2002 The Comparative Genomics Program at the Joint Genome Institute. Utah State University, Logan, UT—Invited speaker.
51. Boore, J. L., 2002 PEET, Organismal Biology, and High-Throughput Genome Centers. PEET IV, Berkeley, CA—Invited speaker.
52. Boore, J. L., 2002 The Genome of *Ciona intestinalis*, an Outgroup to the Vertebrata. University of Chicago, IL—Invited speaker.
53. Boore, J. L., S. Lucas, D. Rokhsar and T. Hawkins 2002 The Genome Sequence of the Primitive Chordate *Ciona intestinalis*. Annual meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy – Contributed Talk.
54. Passamonti, M., J. L. Boore and V. Scali, 2002 Mitochondrial DNA Recombination in Doubly Uniparental Systems: New Insights from *Tapes philippinarum* (Mollusca, Bivalvia, Veneridae). Annual meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy – Poster Presentation.
55. Francino, M. P., S. Lucas, D. Rokhsar, S. Stilwagen, F. Larimer, J. Boore and T. Hawkins, 2002 Phylogenetic Placement of Environmentally Important Bacterial Species Sequenced at the Joint Genome Institute (JGI) Based on Translation-Related Proteins. Annual meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy – Poster Presentation.
56. Medina, M., Y. Vallès, H. M. Fourcade and J. L. Boore, 2002 Evolution of Crown Gastropods: Insight from Mitochondrial Gene Order Data. Annual meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy – Poster Presentation.

57. Helfenbein, K. G., and J. L. Boore, 2002 The Mitochondrial Genome of the Chaetognath *Paraspadella gotoi*: Phylogenetics and Molecular Evolution. Annual meeting of the Society for Molecular Biology and Evolution, Sorrento, Italy – Poster Presentation.
58. Haberle, R. C., S. K. Wyman, W. M. Eddie, J. L. Boore and R. Jansen 2002 Evolutionary Implications of the Complete Sequence of the *Trachelium caeruleum* (Campanulaceae) Chloroplast Genome. Botany 2002, Madison, WI – Poster Presentation.
59. Medina, M., Y. Vallès, T. Gosliner, H. M. Fourcade and J. L. Boore 2002 Mitochondrial Gene Order Versus Sequence Data in Heterobranch Gastropods. Annual Meeting of the American Malacological Society, Charleston, SC – Contributed Talk.
60. Boore, J. L., 2002 The Role of Genome Centers for the Future of Molecular Evolution. University of Siena—Invited speaker.
61. Boore, J. L., 2002 The Evolutionary Genomics Program at the JGI. Lawrence Berkeley Lab Science Seminar Series—Invited speaker.
62. Boore, J. L., S. Lucas, P. Richardson, D. Rokhsar and E. Rubin 2002 Genomic Approaches Soon to be Available for Understanding Sudden Oak Death, Meeting on Sudden Oak Death Syndrome, Monterey, CA – Poster Presentation.
63. Boore, J. L., 2003 The Phytophthora Genome Sequencing Project, Meeting on Molecular Genetics of Phytophthora, Asilomar, CA—Invited keynote speaker.
64. Boore, J. L., 2003 Data Gathering for New Research Initiatives. Natural Science Collections Alliance, Berkeley, CA—Invited speaker.
65. Bensasson, D., J. Chapman, S. Lucas, P. Richardson, D. Rokhsar, B. Tyler, J. L. Boore, 2003 Comparison of the Whole Genome Draft Sequences of Two Plant Blights. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
66. Bensasson, D., J. L. Boore and K. M. Nielsen, 2003 Genes Without Frontiers. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
67. Boore, J. L., and R. H. Baker, 2003 Molecular Evolution of the Wingless Gene in Stalk-eyed Flies. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
68. Boore, J. L., and S. K. Wyman, 2003 An Experimental Evaluation of Four Methods for Identifying Animal Mitochondrial tRNAs. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
69. Boore, J. L., and Y. Valles, 2003 Are All Annelids Polychaetes? Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
70. Boore, J. L., H. M. Fourcade, R. K. Jansen, R. Haberle and S. Wyman, 2003 Structure and Evolution of Two Highly Rearranged Chloroplast Genomes in the Campanulaceae. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
71. Boore, J. L., D. Bensasson, S. Lucas, P. Richardson, J. Chapman, D. Rokhsar, B. Tyler, 2003 Comparing the Whole Genome Sequences of Two Oomycetes - *Phytophthora sojae* and *P. ramorum*. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.

72. Boore, J. L., H. M. Fourcade, R. K. Jansen, T. W. Chumley, P. Caile, J. Mower and J. Palmer, 2003 Evolutionary Implications of the Highly Rearranged Chloroplast Genome of *Pelargonium* (Geraniaceae). Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
73. Engle, D. K., M. Medina and J. L. Boore, 2003 Evolution of scleractinian Corals by Analysis of Complete Mitochondrial Genomes. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
74. Fourcade, H. M., S. Bench, O. Ryder, R. Feldman and J. L. Boore, 2003 High Throughput Sequencing of Mammalian Mitochondrial Genomes. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
75. Francino, M. P., and J. L. Boore, 2003 Bacterial Phylogeny and Genome Evolution. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
76. Frati, F., F. Nardi, A. Carapelli, J. L. Boore, G. Spinsanti and R. Dallai, 2003 Mitochondrial Genomics: New Data for the Phylogeny of Hexapods. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
77. Helfenbein, K. G., R. G. Vanjani, H. M. Fourcade and J. L. Boore, 2003 The Mitochondrial Genome of the Chaetognath *Paraspadella gotoi*. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
78. Kuehl, J., H. M. Fourcade and J. L. Boore, 2003 Amplifying the Mitochondrial Genome using RCA. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
79. Macey, J. R., J. L. Boore, R. M. Bonett and P. T. Chippindale, 2003 Evolution of Complete Mitochondrial Genomes in Salamanders of the *Eurycea multiplicata* Complex. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
80. Masta, S. E., and J. L. Boore, 2003 Inferring Systematics and Molecular Evolution in Arachnids Using Mitochondrial Genomes. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
81. Medina, M., D. K. Engle, J. L. Boore, T. L. Takaoka, C. Marroquin, J. Kuehl, 2003 New Mitochondrial Genomes of Unrepresented Metazoan Phyla. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
82. Medina, M., J. L. Boore, H. M. Fourcade, T. L. Takaoka, Y. Valles, 2003 Evolution of Opisthobranch Gastropods Based on Complete Mitochondrial Genome Comparisons. Annual meeting of the Society for the Study of Evolution, Chico, CA – Poster Presentation.
83. Mueller, R., J. R. Macey, H. M. Fourcade, J. V. Kuehl, M. Jaekel, D. B. Wake and J. L. Boore, 2003 Phylogeny of Plethodontid Salamanders Inferred from Mitochondrial Genomes. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
84. Passamonti, M., J. L. Boore, V. Scali, 2003 How Old is Doubly Uniparental Inheritance: New Data from Veneridae and Mytilidae (Mollusca Bivalvia). Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.

85. Warnow, T. J., J. L. Boore, H. M. Fourcade, R. K. Jansen, R. Haberle, T. W. Chumley, L. Raubeson, S. Wyman, C. dePamphilis, B. Moret, D. Bader and W. Miller, 2003 Comparative Chloroplast Genomics of Seed Plants: Integrating Computational Methods, Phylogeny, and Molecular Evolution. Annual meeting of the Society for the Study of Evolution, Chico, CA – Contributed Talk.
86. Bensasson, D., J. Chapman, S. Lucas, P. Richardson, D. Rokhsar, B. Tyler, J. L. Boore, 2003 Comparison of the Whole Genome Draft Sequences of Two Plant Blights. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
87. Dehal, P., and J. L. Boore, 2003 Dynamics of Gene Duplication Revealed by Comparing Complete Genomes of a Tunicate, Fish, Mouse, and Man. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Contributed Talk.
88. Engle, D., C. Marroquín, T. Takaoka, J. V. Kuehl, J. L. Boore and M. Medina, 2003 Evolution of Scleractinian Corals Based on Complete Mitochondrial Genomes. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
89. Francino, M. P., and J. L. Boore, 2003 Bacterial Phylogeny and Genome Evolution. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
90. Froula, J. L., J. R. Macey, C. Amemiya, S. Edwards, J. L. Boore, 2003 BAC Libraries for Five Reptilia: Genomic Resources for Comparative Biology of Amniotes. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
91. Froula, J. L., M. Medina, M. Passamonti, J. R. Macey, J. V. Kuehl, D. K. Engle, J. L. Boore, H. M. Fourcade, 2003 Amplifying Mitochondrial Genomes Using RCA. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
92. Macey, J. R., T. J. Papenfuss, J. Kuehl, H. M. Fourcade, J. L. Boore, 2003 Phylogenetic Relationships Among Amphisbaenian Reptiles Based on Complete Mitochondrial Genomic Sequences. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
93. Macey, J. R., T. J. Papenfuss, J. Kuehl, H. M. Fourcade, J. L. Boore, 2003 Socotra Island, the Forgotten Fragment of Gondwana: Evidence from Complete Mitochondrial Genomic Sequences of Chameleons and Amphisbaenian Reptiles. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
94. Masta, S. E., and J. L. Boore, 2003 The Mitochondrial Genome of a Spider: Evolution of tRNAs and Minimal Genome Size. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Contributed Talk.
95. Medina, M., D. K. Engle, J. L. Boore, T. L. Takaoka, C. Marroquin, J. Kuehl, 2003 New Mitochondrial Genomes of Unrepresented Metazoan Phyla. Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.

96. Mueller, R., J. R. Macey, M. Jaekel, M. H. Fourcade, J. V. Kuehl, D. B. Wake and J. L. Boore, 2003 Evolution of Salamander Mitochondrial Genomes: Duplication, Rearrangement, and Phylogenetic Implications. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Contributed Talk.
97. Passamonti, M., J. L. Boore, V. Scali, 2003 Doubly Uniparental Inheritance in the Manila Clam *Tapes Philippinarum*: Molecular Evolution and Recombination in Gender-Associated Mitochondrial DNAs. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Contributed Talk.
98. Takaoka, T. L., Y. Valles, H. M. Fourcade, J. L. Boore, M. Medina, 2003 Evolution of Opisthobranch Gastropods Based on Complete Mitochondrial Genome Comparisons. Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
99. Valles, Y., and J. L. Boore, 2003 Are All Annelids Polychaetes? Annual meeting of the Society for Molecular Biology and Evolution, Newport Beach, CA – Poster Presentation.
100. Boore, J. L., 2003 Sequencing and Bioinformatics for the *Daphnia Pulex* Genome. Daphnia Genome Consortium, Manchester, NH—Invited speaker.
101. Boore, J. L., 2003 Why Evolutionary Biology and Genome Sciences Need Each Other. Lawrence Livermore National Laboratory seminar series—Invited speaker.
102. Francino, M. P., and J. L. Boore 2003 Correlation of Genome Size, GC Content and Rate of Sequence Evolution Across Bacterial Phyla. International Conference on Microbial Genomes, Durham, NC – Poster Presentation.
103. Boore, J. L., 2004 Will Your Favorite Genome Be Sequenced? Plant and Animal Genomes Conference, San Diego, CA—Invited speaker.
104. Boore, J. L., 2004 Using Genome Level Features for Phylogenetic Inference. Gordon Conference on Structural, Functional, and Evolutionary Genomics, Ventura, CA—Invited speaker.
105. Boore, J. L., 2004 Using Genome Level Characters to Reconstruct Evolutionary Relationships. Neyman seminar, UC Berkeley—Invited speaker.
106. Boore, J. L., 2004 Comparing Complete Genomes for Understanding Evolutionary Pattern and Process. University of Idaho—Invited speaker.
107. Mandoli, D. F., R. Olmstead, B. Mishler, J. L. Boore, A. Smith, K. Renzaglia, P. Wolf, M. Donoghue and C. O'Kelley, 2004 Toward Resolution of the Fuzzy Nodes in Green Plant Phylogeny. Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
108. Mandoli, D. F., R. Olmstead, B. Mishler, J. L. Boore, A. Smith, K. Renzaglia, P. Wolf, M. Donoghue and C. O'Kelley, 2004 Toward Resolution of the Fuzzy Nodes in Green Plant Phylogeny. Annual meeting of the American Society for Plant Biology, Orlando, FL – Poster Presentation.
109. McNeal, J. R., R. K. Jansen, J. L. Boore, J. V. Kuehl and C. W. dePamphilis, 2004 Evidence for Photosynthetic Potential Across the Parasitic Plant Genus *Cuscuta* Using Complete Plastid Genome Sequences. Annual meeting of the Botanical Society of America, Snowbird, UT – Contributed Talk.

110. Raubeson, L. A., N. L. Y. Fine, R. Peery, H. M. Fourcade, J. V. Kuehl and J. L. Boore, 2004 A Comparison of Conifer Chloroplast Genomes Based on Complete Genome Sequences from Pinaceae, Podocarpaceae, and Cupressaceae. Annual meeting of the Botanical Society of America, Snowbird, UT – Contributed Talk.
111. Raubeson, L. A., P. M. Feysa IV, M. Phillips, N. L. Y. Fine, R. Peery, J. L. Boore, H. M. Fourcade and J. V. Kuehl, 2004 Loss of the Inverted Repeat from Conifer Chloroplast Genomes, A More Detailed Characterization. Annual meeting of the Botanical Society of America, Snowbird, UT – Contributed Talk.
112. Francino, M. P., and J. L. Boore 2003 Correlation of Genome Size, GC Content and Rate of Sequence Evolution Across Bacterial Phyla. Meeting on Evolutionary Genomics, Tucson, AZ – Poster Presentation.
113. Wolf, P. G., K. G. Karol, D. F. Mandoli, J. Kuehl, K. Arumuganathan, M. W. Ellis, J. M. Roper, B. D. Mishler, D. Kelch, R. Olmstead and J. L. Boore, 2004 The First Complete Chloroplast Genome Sequence of a Lycophyte, *Huperzia Lucidula* (Lycopodiaceae): Implications for Land Plant Phylogeny. Annual meeting of the Botanical Society of America, Snowbird, UT – Poster Presentation.
114. Jansen, R. K., C. dePamphilis, L. A. Raubeson, R. Haberle, T. W. Chumley, J. Leebens-Mack, S. Wyman, J. L. Boore and J. V. Kuehl, 2004 Comparative Chloroplast Genomics of Seed Plants - An Overview and Summary of Progress. Annual meeting of the Botanical Society of America, Snowbird, UT – Contributed Talk.
115. Leebens-Mack, J., C. dePamphilis, L. A. Raubeson, L. Cui, J. L. Boore, J. V. Kuehl, P. Piffanelli, T. Chumley and R. K. Jansen, 2004 Comparative Analysis of New Monocot Chloroplast Genome Sequences Improves Molecular Phylogeny of Angiosperms. Annual meeting of the Botanical Society of America, Snowbird, UT – Contributed Talk.
116. Posada-Buitrago, M. L., J. L. Boore and R. D. Frederick, 2004 Analysis of Expressed Sequence Tags in the Soybean Rust Pathogen *Phakopsora Pachyrhizi*. VII World Soybean Research Conference, Foz de Iguazu, Brazil – Poster Presentation.
117. Vallès, Y., K. Halanych and J. L. Boore, 2004 Annelids in the Light of Mitochondrial Genes. International meeting on the Annelida, Madrid, Spain – Contributed Talk.
118. Leebens-Mack, J., C. dePamphilis, L. A. Raubeson, L. Cui, Y. Zhang, J. McNeal, J. L. Boore and J. V. Kuehl, S. Wyman and R. K. Jansen, 2004 The Utility of Whole Chloroplast Genome Sequencing for Reconstructing Deep Nodes Within Basal Angiosperms. Annual meeting of the Society for Molecular Biology and Evolution, Pennsylvania State University, PA – Contributed Talk.
119. Dehal, P., and J. L. Boore, 2004 Insights Into the Evolution of Gene Structure Using Whole Genome Sequences. Annual meeting of the Society for Molecular Biology and Evolution, Pennsylvania State University, PA – Poster Presentation.
120. Francino, M. P., C. L. Li, A. Kobayashi and J. L. Boore, 2004 Applying The Comparative Method To Bacterial Genome Evolution. Annual meeting of the Society for Molecular Biology and Evolution, Pennsylvania State University, PA. – Poster Presentation.

121. Francino, M. P., C. L. Li, A. Kobayashi and J. L. Boore, 2004 Applying The Comparative Method To Bacterial Genome Evolution. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
122. Boore, J. L., J. Fong, K. Helfenbein, D. Lindberg, J. R. Macey, S. Masta, M. Medina, R. Mueller, T. Papenfuss, B. Simison, 2004 Bizarre Observations In Mitochondrial Genomics. Annual meeting of the Society for Molecular Biology and Evolution, Pennsylvania State University, PA – Contributed Talk.
123. Jansen, R. K., C. dePamphilis, L. A. Raubeson, R. Haberle, T. W. Chumley, J. Leebens-Mack, S. Wyman, J. L. Boore and J. V. Kuehl, 2004 Comparative Chloroplast Genomics of Seed Plants - An Overview and Summary of Progress. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
124. Boore, J. L., J. Fong, K. Helfenbein, D. Lindberg, J. R. Macey, S. Masta, M. Medina, R. Mueller, T. Papenfuss, B. Simison, 2004 Bizarre Observations In Mitochondrial Genomics. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
125. Leebens-Mack, J., C. dePamphilis, L. A. Raubeson, L. Cui, Y. Zhang, J. McNeal and J. L. Boore, 2004 Is *Amborella* a Basal Angiosperm? Evidence from Whole Chloroplast Genome Sequencing. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
126. Guisinger, M. M., R. K. Jansen, J. L. Boore, and J. V. Kuehl, 2004 The Highly Rearranged Chloroplast Genome of *Scaevola Aemula* in The Flowering Plant Family Goodeniaceae. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
127. Baker, R., G. Wilkenson, J. L. Boore, 2004 Transcript Profile of Eye-stalk Development in Stalk-eyed flies. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
128. Dehal, P., and J. L. Boore, 2004 Two Round of Genome Duplication in the Ancestral Vertebrate. Annual meeting of the Society for the Study of Evolution, Fort Collins, CO – Contributed Talk.
129. Boore, J. L., 2004 Reconstructing Animal Phylogeny by Comparing Complete Mitochondrial Genomes. Gordon Research Conference on Mitochondria and Chloroplasts, Meriden, NH—Invited speaker.
130. Carapelli, A., F. Nardi, J. L. Boore, P. Lio, R. Dallai and F. Frati, 2004 Mitochondrial Genomics and the Phylogeny of Basal Hexapods. 22nd International Conference of Entomology, Brisbane, Australia – Contributed Talk.
131. Carapelli, A., F. Nardi, J. L. Boore, P. Lio, R. Dallai and F. Frati, 2004 The Contribution of Mitochondrial Genomics to the Phylogeny of Basal Arthropods. International Conference of Zoology, Beijing, China – Contributed Talk.
132. Boore, J. L., 2004 Mitochondrial Genomics, a Dataset for Studying Arthropod Phylogeny and Molecular Evolution. International Conference of Zoology, Beijing, China—Invited speaker.

133. Boore, J. L., 2004 Comparing Genomes for Understanding of Evolutionary Pattern and Process. University of Toronto—Invited speaker.
134. Boore, J. L., 2004 Comparing Genomes for Understanding of Evolutionary Pattern and Process. Dalhousie University—Invited speaker.
135. Boore, J. L., 2004 Comparing Genomes for Understanding of Evolutionary Pattern and Process. University of New Brunswick—Invited speaker.
136. Dehal, P. S., and J. L. Boore, 2004 PhIGs: Phylogenetically Inferred Groups, a Resource for Comparative Genomics. Genome Informatics, Sanger Centre, Hinxton, UK – Contributed Talk.
137. Tyler, B., S. Tripathi, N. Grunwald, K. Lamour, K. Ivors, M. Garbelotto, N. Putnam, I. Grigoriev, D. Rokhsar and J. L. Boore, 2005 Genome sequence of *Phytophthora ramorum*: Implications for management. Sudden Oak Death Science Symposium II, Monterey, CA – Contributed Talk.
138. Boore, J. L., 2004 Why Evolutionary Biology and Genome Sciences Need Each Other. Sonoma State University—Invited speaker.
139. Boore, J. L. 2004 Will Your Favorite Genome Be Sequenced? Nicholas Environmental Leadership Forum: Landscapes Genomics & Transgenic Conifer Forests, Duke University, Raleigh-Durham, NC—Invited speaker.
140. Halanych, K., M. Martindale, E. Seaver, D. McHugh, J. L. Boore and D. Rokhsar, 2004 Reconstructing the Early Evolution of Segmented Worms. NSF Workshop on Assembling the Tree of Life, Arlington, VA. – Poster Presentation.
141. Mandoli, D. F., J. L. Boore, M. Donoghue, R. Olmstead, K. Renzaglia, A. Smith, P. Wolf, B. Mishler, C. J. O’Kelly, A. Arumuganathan, J. F. Brown, A. Driscoll, M. W. Ellis, K. Everett, K. Karol, D. Kelsh, J. Kuehl, J. M. Roper and S. Schuette, 2004 Toward Resolution of Green Plant Phylogeny. NSF Workshop on Assembling the Tree of Life, Arlington, VA. – Poster Presentation.
142. Jansen, R. K., L. A. Raubeson, R. Haberle, T. W. Chumley, M. Guisinger, H.-G. Kim, R. Peery, S. K. Wyman, L.-S. Wang, T. J. Warnow, C. DePamphilis, J. Leebens-Mack, L. Cui, J. McNeal, Y. Zhang, D. Bader, B. Moret, J. Tang, H. M. Fourcade, J. Kuehl and J. L. Boore, 2004 Comparative Chloroplast Genomics of Seed Plants: Integrating Computational Methods, Phylogeny, and Molecular Evolution. NSF Workshop on Assembling the Tree of Life, Arlington, VA. – Poster Presentation.
143. Valles, Y., K. Halanych and J. L. Boore, 2005 Annelids in the Mist: The Influence of a New Marker. Annual Meeting of the Society for Integrative and Comparative Biology (SICB), San Diego, CA—Invited speaker.
144. Tyler, B. M., S. Tripathy, I. Grigoriev, D. Rokhsar, J. L. Boore et al., 2005 Genome Sequences of *Phytophthora sojae* and *P. ramorum* Shed New Light on their Evolution and Pathogenicity. Fungal Genetics Conference, Asilomar, CA – Contributed Talk.
145. Tyler, B. M., S. Tripathy, I. Grigoriev, D. Rokhsar, J. L. Boore et al., 2005 Genome Sequences of the Stramenopile Pathogens *Phytophthora sojae* and *P. ramorum* Shed New

- Light on their Evolution and Pathogenicity. TIGR Microbial Genomes Meeting, Halifax, Canada – Contributed Talk.
146. Posada-Buitrago, M. L., J. L. Boore and R. D. Frederick, 2005 Complete Sequences of the Mitochondrial Genomes of the Plant Pathogens *Phakopsora pachyrhizi* and *P. meibomia*. Fungal Genetics Conference, Asilomar, CA – Contributed Talk.
 147. Guisinger-Bellian, M. M., J. L. Boore, J. V. Kuehl and R. K. Jansen, 2005 Organization and Evolution of the Chloroplast Genome of *Erodium texanum* (Geraniaceae). Botanical Society of America, Austin, TX – Contributed Talk.
 148. Leebens-Mack, J., C. dePamphilis, L. A. Raubeson, J. L. Boore and R. K. Jansen, 2005 The Use of Whole Chloroplast Genome Sequences for Phylogeny Reconstruction in Angiosperms. Botanical Society of America, Austin, TX – Contributed Talk.
 149. Raubeson, L. A., J. D. Leigh, R. K. Jansen and J. L. Boore, 2005 Insights into Seed Plant Phylogeny from Comparative Chloroplast Genomics. Botanical Society of America, Austin, TX – Contributed Talk.
 150. Jansen, R. K., L. A. Raubeson, C. de Pamphilis, S. Wyman, J. L. Boore, T. Warnow, B. Moret, 2005 Comparative Chloroplast Genomics of Seed Plants - An Overview and Summary of Progress. Botanical Society of America, Austin, TX – Poster Presentation.
 151. Dehal, P., and J. L. Boore, 2005 PhIGs: A Tool for Whole Genome Evolutionary Analysis. Annual meeting of the Society for the Study of Evolution, Fairbanks, Alaska – Poster Presentation.
 152. Takaoka, T. L., K. G. Helfenbein, J. L. Boore and M. Medina, 2005 Complete Mitochondrial Genome Sequences for Four Bryozoan Species. Annual meeting of the Society for the Study of Evolution, Fairbanks, Alaska – Contributed Talk.
 153. Roper, J. M., S. K. Hansen, J. L. Boore, J. V. Kuehl, D. F. Mandoli, K. G. Karol, R. Olmstead and P. G. Wolf, 2005 The Chloroplast Genome Sequence of the Marattioid Fern *Angiopteris*. Botanical Society of America, Austin, TX – Contributed Talk.
 154. Haberle, R. C., R. K. Jansen, J. L. Boore and J. V. Kuehl, 2005 Comparative chloroplast genomics of Campanulales s.l.: phylogenomic implications and chloroplast genome evolution. Botanical Society of America, Austin, TX – Contributed Talk.
 155. dePamphilis, C., J. McNeal, Y. Zhang, L. Cui, J. V. Kuehl and J. L. Boore, 2005 Plastid Genomes of Parasitic Plants: Distinct Paths of Evolution in Independent Heterotrophic Lineages. Botanical Society of America, Austin, TX (symposium talk).
 156. Timme, R., J. V. Kuehl, J. L. Boore and R. K. Jansen, 2005 The First Sequenced Chloroplast Genomes in the Asteraceae: A Comparison of Sunflower and Lettuce. Botanical Society of America, Austin, TX – Poster Presentation.
 157. Mandoli, D., J. L. Boore, K. Everett, M. J. Donoghue, K. G. Karol, B. Mishler, C. O’Kelley, R. Olmstead, A. R. Smith, K. Renzaglia, P. Wolf, 2005 Toward Resolution of the Fuzzy Nodes in Green Plant Phylogeny. Annual meeting of the American Society of Plant Biologists, Seattle, WA – Poster Presentation.
 158. Boore, J. L., 2005 Why Evolutionary Biology and Genome Sciences Need Each Other. Palo Alto Research Center public seminar program, Palo Alto, CA – Invited speaker.

159. Leigh, J., J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2005 The Complete Chloroplast Genome Sequence of *Ginkgo biloba* and its Comparison with Other Seed Plant Plastid Genomes. Annual meeting of the Society for the Study of Evolution, Fairbanks, Alaska – Poster Presentation.
160. Dehal, P., and J. L. Boore, 2005 PhIGs: A Tool for Whole Genome Evolutionary Analysis. Cold Spring Harbor Laboratory “Biology of Genomes”, CSHL, NY – Poster Presentation.
161. Dehal, P., and J. L. Boore, 2005 Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate. Cold Spring Harbor Laboratory “Biology of Genomes”, CSHL, NY – Poster Presentation.
162. Boore, J. L., 2005 Organelle Genomics: A Model for Molecular Evolution and a Tool for Phylogenetics. University of California Riverside – Invited speaker.
163. Peñaflor, C., J. L. Boore, J. V. Kuehl and R. K. Jansen, 2005 Chloroplast Genome Sequences of Chloranthus and Piper: Implications for the Phylogeny of Angiosperms. Botanical Society of America, Austin, TX – Poster Presentation.
164. Posada-Buitrago, M. L., J. L. Boore and R. D. Frederick, 2005 Analysis of the Complete Mitochondrial Genomes from *Phakopsora pachyrhizi* and *Phakopsora meibomia*e. 23rd Fungal Genetics Conference, Pacific Grove, California – Poster Presentation.
165. Posada-Buitrago M. L., J. L. Boore and R. D. Frederick, 2005 Soybean Rust, a Rising Star in Phytopathology. 6th Congress on Genetics and Cellular Biology of Basidiomycetes, Pamplona, Spain – Poster Presentation.
166. Posada-Buitrago M. L., and J. L. Boore 2005 Genómica y Expresión Génica en la Roya de la Soja. Department of Genetics. Universidad Complutense de Madrid, Madrid, Spain – Invited speaker.
167. Posada-Buitrago M. L., and J. L. Boore 2005 Soybean Rust: A Rising Star in Phytopathology. 6th Congress on Genetics and Cellular Biology of Basidiomycetes. Pamplona, Spain – Invited speaker.
168. Posada-Buitrago M. L., and J. L. Boore 2005 Genomics, Gene Expression and Other Studies in Soybean Rust. CSIC-Centro de Investigaciones Biológicas (CSIC-Centre for Biological Research). Madrid, Spain – Invited speaker.
169. Posada-Buitrago M. L., and J. L. Boore 2005 Roya de la Soja: Una Nueva Amenaza Department of Microbiology, Faculty of Biology. Universidad Complutense de Madrid. Madrid, Spain – Invited speaker.
170. Boore, J. L. 2005 Using PhIGs to Detect Two Rounds of Whole Genome Duplication at the Base of Vertebrates. Meeting of the European Society for Evolutionary Biology, Krakow, Poland – Invited speaker.
171. Boore, J. L., 2005 Will Your Favorite Genome Be Sequenced? Retreat of the Integrated Center for Structure and Function Innovation, Los Alamos, NM – Invited speaker.
172. Boore, J. L., 2005 Whole Genome Analysis and the Origin of the Vertebrates. Virginia Bioinformatics Institute (Virginia Tech), Blacksburg, VA – Invited speaker.

173. Leebens-Mack, J. H., C. W. dePamphilis, L. A. Raubeson, J. L. Boore and R. K. Jansen, 2005 Taxon-specific Codon Usage Biases and Substitution Rate Variation in the Chloroplast Genomes of Flowering Plants. Plant and Animal Genomes Conference, San Diego, CA – Contributed Talk.
174. Dehal, P., and J. L. Boore, 2005 Using ESTs in Phylogenomic Analysis: Timing Vertebrate Genome Duplications. Meeting on “Genome Informatics”, Cold Spring Harbor Laboratory, NY – Contributed Talk.
175. Boore, J. L., 2005 Organelle Genomics and Using PhIGs for Phylogenomics. Workshop on “eGenomics”, European Bioinformatics Institute (EBI), Hinxton, United Kingdom – Invited speaker.
176. Posada-Buitrago, M. L., J. L. Boore and R. D. Frederick, 2005 Soybean Rust Genome Sequencing Project. Fungal Genetics Conference, Nashville, Tennessee – Poster Presentation.
177. Boore, J. L., 2005 Evolutionary Genomics of Life in (and from) the Sea. Dynamics of Ocean Biosystems, Tokyo, Japan – Invited speaker.
178. Boore, J. L., 2006 The Sequence of the Daphnia Genome. Meeting of the Daphnia Genome Consortium, Bloomington, Indiana – Invited keynote speaker.
179. Boore, J. L., 2006 Whole Genome Evolutionary Analysis and the Origin of the Vertebrates. Moss Landing Marine Laboratories, Moss Landing, CA – Invited speaker.
180. Longhorn, S., J. L. Boore and S. Masta, 2006 Ameliorating the Effects of Mutational Biases in Phylogenetic Analyses of Arachnid Mitochondrial Genomes. Annual Meeting of the Society for Molecular Biology and Evolution, Tempe, AZ – Contributed Talk.
181. Masta, S., S. Longhorn and J. L. Boore, 2006 RNA Evolution in Mitochondrial Genomes in Arachnids. Annual Meeting of the Society for Molecular Biology and Evolution, Tempe, AZ – Contributed Talk.
182. Dehal, P. S., and J. L. Boore, 2006 Two Rounds of Whole Genome Duplication in the Ancestral Vertebrate Genome. JGI Users’ Meeting, Walnut Creek, CA – Poster Presentation.
183. Dehal, P. S., and J. L. Boore, 2006 “PhIGs” (Phylogenetically Inferred Groups): A Tool for Whole Genome Phylogenetic Analysis. JGI Users’ Meeting, Walnut Creek, CA – Poster Presentation.
184. Hoegg, S., J. L. Boore and A. Meyer, 2006 Fish *Hox* Cluster and the Evolution of Regulatory Elements. JGI Users’ Meeting, Walnut Creek, CA – Poster Presentation.
185. Kozik, A., D. G. Caldwell, M. J. Truco, D. O. Lavelle, L. K. McHale, J. M. Argyris, M. Matvienko, O. E. Ochoa, F. Chen, S. Mathrakott, K. J. Still, J. L. Boore, A. V. Deynze and R. W. Michelmore, 2006 The Compositae Genome Project and Development of a Genechip for Massively Parallel Genotyping and Gene Expression Analysis in Lettuce. JGI Users’ Meeting, Walnut Creek, CA – Poster Presentation.
186. Mandoli, D. F., J. L. Boore, K. Everett, M. J. Donohue, K. G. Karol, J. Kuehl, B. Mishler, C. O’Kelly, R. Olmstead, A. R. Smith, K. Renzaglia and P. Wolf, 2006 Toward Resolution of Green Plant Phylogeny. JGI Users’ Meeting, Walnut Creek, CA – Poster Presentation.

187. Posada-Buitrago, M. L., J. L. Boore and R. D. Frederick, 2006 Soybean Rust Genome Project. JGI Users' Meeting, Walnut Creek, CA – Poster Presentation.
188. Thomas, R. H., J. A. Mackenzie-Dodds, H. M. Fourcade and J. L. Boore, 2006 The *Hox* Cluster of a Model Chelicerate Arthropod – The Oribatid Mite *Archezogozetes longisetosus*. JGI Users' Meeting, Walnut Creek, CA – Poster Presentation.
189. Jansen, R. K., C. Zhengqiu, D. hansen, S. Dastidar, C. Peñafior, R. Timme, K. Hansen, T. W. Chumley, M. M. Guisinger-Bellian, H. Daniell, S. –B. Lee, L. A. Raubeson, R. Peery, C. W. dePamphilis, J. Leebens-Mack, J. R. McNeal, J. L. Boore and J. V. Kuehl, 2006 Phylogeny of Angiosperms Based on Whole Chloroplast Genome Sequences. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
190. Dastidar, S., C. Zhengqiu, C. Peñafior, J. V. Kuehl, J. L. Boore and R. K. Jansen, 2006 Phylogenetic Analysis of Chloranthus and Dioscorea Based on Whole Chloroplast Genome Sequences. Annual meeting of the Botanical Society of America, Chico, California – Poster Presentation.
191. Wickett, N. J., Zhang, Y., Hansen, S. K., J. V. Kuehl, S. A. Plock, B. Goffinet, C. W. dePamphilis, P. G. Wolf and J. L. Boore, 2006 Towards a Complete Chloroplast Genome Sequence of the Non-Photosynthetic Liverwort *Cryptothallus mirabilis* (Metzgeriales, Marchantiophyta). Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
192. Zhang, Y., J. R. McNeal, A. Smith, J. V. Kuehl, J. L. Boore and C. W. dePamphilis, 2006 Striking Convergence of Plastid Genomes in Independent Nonphotosynthetic Lineages. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
193. Raubeson, L. A., S. K. R. McCoy, K. Müller, P. K. Wall, J. Leebens-Mack, J. L. Boore, R. K. Jansen and C. W. dePamphilis, 2006 Seed Plant Phylogeny Based on Sequences from 61 (Mostly) Shared Plastid Genes. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
194. McCoy, S. K. R., J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2006 The Complete Plastid Genome Sequence of *Welwitschia mirabilis*. Annual meeting of the Botanical Society of America, Chico, California – Poster Presentation.
195. McNeal, J., J.V. Kuehl, J. L. Boore and C. W. dePamphilis, 2006 Evolution of matK, a Conserved Plastid Intron Matruase, in the Parasitic Plant Genus *Cuscuta*. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
196. Peery, R., J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2006 Comparisons of Three Apiaceae Chloroplast Genomes – Coriander, Dill and Fennel. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
197. Hansen, D., C. Zhengqiu, J. L. Boore, J. V. Kuehl and R. K. Jansen, 2006 Complete Chloroplast Genome Sequences of *Illicium* (Schisandraceae) and *Buxus* (Buxaceae): Genome Organization and Implications for Phylogeny of Angiosperms. Annual meeting of the Botanical Society of America, Chico, California – Poster Presentation.
198. Zhengqiu, C., C. Peñafior, J. V. Kuehl, J. Leebens-Mack, J. Carlson, C. W. dePamphilis, J. L. Boore and R. K. Jansen, 2006 Complete Chloroplast Genome Sequences of *Drimys*, *Liriodendron*, and *Piper*: Implications for the Phylogeny of Magnoliids and Evolution of

- GC Content. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
199. Karol, K. G., J. A. Banks, J. M. Roper, S. K. Hanson, P. G. Wolf, J. V. Kuehl, J. L. Boore, K. Everett, D. F. Mandoli and R. G. Olmstead, 2006 Plastid Genome Evolution in Lycophytes. Annual meeting of the Botanical Society of America, Chico, California – Contributed Talk.
 200. Murdock, A. G., B. D. Mishler, M. J. Oliver, J. V. Kuehl, J. L. Boore, K. G. Karol, D. F. Mandoli and K. Everett, 2006 Complete Chloroplast Genome Sequence of the Moss *Tortula Ruralis* and Structural Arrangement Relative to other Green Plant Chloroplast Genomes. Annual meeting of the Botanical Society of America, Chico, California – Poster Presentation.
 201. Hoegg, S., J. L. Boore and A. Meyer, 2006 *Hox* Clusters of a Haplochromine Cichlid, *Astatotilapia buroni*. European Society for Evolutionary Developmental Biology, Prague, Czech Republic – Contributed Talk.
 202. Boore, J. L., 2006 PhIGs: Phylogenetically Inferred Groups, Phylogenetic Analysis of All Gene Families of All Sequenced Genomes. Workshop on “Developing a Phylogenetic Ontology”, St. Louis, Missouri – Invited speaker.
 203. Boore, J. L., 2006 Using PhIGs to Detect Two Rounds of Whole Genome Duplication at the Base of Vertebrates. Genome Informatics, a meeting jointly sponsored by Cold Spring Harbor Laboratory and the Wellcome Trust, Hinxton, UK – Invited speaker (and session chair).
 204. Boore, J. L., 2006 Whole Genome Evolutionary Analysis, Mitochondrial Genomics, and the Use of Genome-Level Characters for Phylogeny. Genome Evolution Summer School, Bertinoro, Italy – Invited Speaker.
 205. Anderson, S. J., C. L. Stone, M. L. Posada-Buitrago, J. L. Boore, B. A. Neelam, R. M. Stephens, D. G. Luster, K. F. Pedley and R. D. Frederick, 2006 Assessment of Genetic Variation Among Asian soybean rust isolates using microsatellites. National Soybean Rust Symposium, St. Louis, MO – Poster Presentation.
 206. Tang, S., C. Saski, M. Munoz-Torres, M. Atkins, J. Tomkins, J. Kuehl, J. L. Boore and S. J. Knapp, 2007 A Large-Insert Bacterial Artificial Chromosome Library for Sunflower. Plant and Animal Genomes Conference, San Diego, CA – Contributed Talk.
 207. Boore, J. L., D. Degusta, H. Matthew Fourcade, D. Engle, J. Morgan and C. Gignoux, 2007 Primate Phylogeny and Divergence Dates Based on Complete Mitochondrial Genomes. Annual Meeting of the Physical Anthropology Society, Philadelphia, PA – Contributed Talk.
 208. Boore, J. L., 2006 Opportunities Within the Department of Energy. Annual Meeting of the American Society for Phytopathology, Quebec, Canada (within the session on “Navigating Funding Agencies and Updates from the Public Policy Board”) – Invited Speaker.
 209. Bhattacharya, D., and J. L. Boore, 2007 The Complete Genome Sequence of the Glaucophyte Alga *Cyanophora paradoxa*. Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.

210. Anderson, S. J., C. L. Stone, M. L. Pasado-Buitrago, J. L. Boore, B. A. Neelam, R. M. Stephens, D. G. Luster, R. D. Frederick and K. F. Pedley, 2007 Phenotypic and Genetic Variation Among Soybean Rust Isolates. Annual Meeting of the American Phytopathology Society, San Diego, CA – Contributed Talk.
211. Boore, J. L., 2007 The New Modern Synthesis: Evolutionary Biology Meets Genome Sciences. University of Georgia Annual Symposium on Computational and Systems Biology – Invited Speaker.
212. Boore, J. L., 2007 Detecting Evolutionary Transfer of Genes Using PhIGs. Annual meeting of the Botanical Society of America, Chicago, IL – Invited Speaker.
213. Zhengqiu, C., H.-G. Kim, E. Ruck, M Guisinger-Bellian, V. McMurtry, J. L. Boore and R. K. Jansen, 2007 Extensive rearrangements in the plastid genome of *Trifolium subterraneum* are associated with numerous repeated sequences and novel DNA insertions. Annual meeting of the Botanical Society of America, Chicago, IL – Contributed Talk.
214. Peery, R., S. R. Downie, J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2007 Chloroplast genome evolution in Apiaceae. Annual meeting of the Botanical Society of America, Chicago, IL – Contributed Talk.
215. Hansen, K., C. Blazier, S. Rehman, J. V. Kuehl, J. L. Boore and R. K. Jansen, 2007 Comparative Chloroplast Genomics in Passiflora. Annual meeting of the Botanical Society of America, Chicago, IL – Contributed Talk.
216. Halanych, K. M., Y. Valles, T. H. Struck, N. Schult, C. Bleidom, J. L. Boore and D. McHugh, 2007 Advances in our Understanding of Annelid Phylogeny. Meeting on Polychaete Biology, Portland, ME – Contributed Talk.
217. Boore, J. L., 2007 Beyond Linear Sequence Comparisons: Using Genome-Level Characters for Phylogeny. Meeting to celebrate the tercentenary of the birth of Linnaeus at the Royal Society, London – Invited Speaker.
218. McCoy, S. K. R., R. Peery, J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2007 Ephedra and Welwitschia: Divergence and Loss in Two Rapidly Evolving Gnetalean Plastid Genomes. Annual meeting of the Botanical Society of America, Chicago, IL – Poster Presentation.
219. Margheim, S. R., R. Peery, J. V. Kuehl, J. L. Boore and L. A. Raubeson, 2007 Mutation Patterns of Highly Similar Chloroplast Genomes. Annual meeting of the Botanical Society of America, Chicago, IL – Poster Presentation.
220. Guisinger-Bellian, M. M., J. L. Boore, J. V. Kuehl, R. K. Jansen, 2008 Genome-wide analyses reveal patterns of increased nonsynonymous substitutions in the flowering plant family Geraniaceae. Annual meeting of the Botanical Society of America, Vancouver, British Columbia, Canada – Poster Presentation.
221. Boore, J. L., 2008 Why Arthropod Genomics Needs Evolutionary Analysis. Meeting on Arthropod Genomics, Kansas City, MO – Contributed Talk.
222. Masta, S. E., and J. L. Boore, 2008 Parallel Evolution of Truncated Transfer RNA Genes in Arachnid Mitochondrial Genomes. Evolutionary Biology in the Pacific Northwest, Port Townsend, WA – Poster Presentation.

223. Masta, S. E., and J. L. Boore, 2008 Parallel Evolution of Truncated Transfer RNA Genes in Arachnid Mitochondrial Genomes. Annual meeting of the Society for the Study of Evolution, Minneapolis, MN – Contributed Talk.
224. Boore, J. L. and S. I. Fuerstenberg, 2008 Will Your Favorite Genome Be Sequenced? Annual meeting of the Society for the Study of Evolution, Minneapolis, MN – Poster Presentation.
225. Boore, J. L., 2008 The Daphnia Genome and You: Will Your Favorite Genome Be Sequenced? International Congress of Copepodology, Pattaya, Thailand – Invited Plenary Speaker.
226. Boore, J. L., and S. I. Fuerstenberg, 2009 Better Tools for Interpreting and Presenting Genomes. Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
227. Jansen, R. K., M. Guisinger, T. W. Chumley, J. V. Kuehl and J. L. Boore, 2009 Rates and Patterns of Plastid Genome Evolution in the Grasses. American Society for Plant Biology Annual Meeting, Honolulu, HI – Contributed Talk.
228. Boore, J. L., B. M. Tyler, S. Tripathy, R. Stiles and S. I. Fuerstenberg, 2009 Using PHRINGE for Understanding Oomycete Genomes. Oomycete Molecular Genetics Meeting, Pacific Grove, CA – Poster Presentation.
229. Tyler, B. M., S. Tripathy, F. Arredondo, J. L. Boore, R. Stiles, S. I. Fuerstenberg, H. Zhang, I. Grigoriev, C. Evans, R. Myers, J. Grimwood and J. Schmutz, 2009 Finishing and Resequencing of the *Phytophthora sojae* Genome. Oomycete Molecular Genetics Meeting, Pacific Grove, CA – Poster Presentation.
230. Boore, J. L., and S. Fuerstenberg, 2009 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The GATOR and PHRINGE System. Annual meeting of the Society for Molecular Biology and Evolution, Iowa City, IA – Poster Presentation.
231. Fuerstenberg, S., and J. L. Boore, 2009 Will Your Favorite Genome be Sequenced? Annual meeting of the Society for Molecular Biology and Evolution, Iowa City, IA – Poster Presentation.
232. Boore, J. L., and S. Fuerstenberg, 2009 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The GATOR and PHRINGE System. Meeting on Arthropod Genomics, Kansas City, MO – Poster Presentation.
233. Fuerstenberg, S., and J. L. Boore, 2009 Will Your Favorite Genome be Sequenced? Meeting on Arthropod Genomics, Kansas City, MO – Poster Presentation.
234. Boore, J. L., and S. Fuerstenberg, 2009 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The GATOR and PHRINGE System. Meeting on “CIPRES”, Berkeley, CA – Poster Presentation.
235. Fuerstenberg, S., and J. L. Boore, 2009 Will Your Favorite Genome be Sequenced? Meeting on “CIPRES”, Berkeley, CA – Poster Presentation.
236. Boore, J. L., 2009 Genomics: Where Have We Come and Where are We Going? California Academy of Sciences Annual “BioForum” for high school teachers, this year on the theme “Genomics: Insights and Impacts” – Invited Speaker.

237. Boore, J. L., 2009 The GATOR and PHRINGE Systems for Reconstructing the Evolutionary History of Genes and Genomes. 100th Boehringer Ingelheim Fonds International Titisee Conference, Titisee, Germany – Invited Speaker.
238. Boore, J. L., and S. I. Fuerstenberg, 2010 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
239. Fuerstenberg, S. I., and J. L. Boore, 2010 Will Your Favorite Genome Be Sequenced? Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
240. Boore, J. L., and S. I. Fuerstenberg, 2010 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. JGI Users' Meeting, Walnut Creek, CA – Poster Presentation.
241. Boore, J. L., 2010 Thinking Big in Genomics. Ontario Genome Institute Workshop on the Evolution of Genome Size, Guelph, Ontario – Invited Speaker.
242. Fuerstenberg, S. I., and J. L. Boore, 2010 Will Your Favorite Genome Be Sequenced? Annual meeting of the Willi Hennig Society, Honolulu, HI – Poster Presentation.
243. Boore, J. L., and S. I. Fuerstenberg, 2010 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Annual meeting of the Willi Hennig Society, Honolulu, HI – Poster Presentation.
244. Boore, J. L., S. I. Fuerstenberg, C. Merlin and S. M. Reppert, 2010 Progress on the Whole Genome Sequencing of the Monarch Butterfly, *Danaus plexippus*. Arthropod Genomics, Kansas City, MO – Poster Presentation.
245. Fuerstenberg, S. I., and J. L. Boore, 2010 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Arthropod Genomics, Kansas City, MO – Poster Presentation.
246. Guisinger, M. M., J. V. Kuehl, J. L. Boore and R. K. Jansen, 2010 Genomes Gone Wild: Plastid Genomes in the Angiosperm Family Geraniaceae. Annual meeting of the Society for the Study of Evolution, Portland, OR – Contributed Talk.
247. Boore, J. L., and S. I. Fuerstenberg, 2010 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Annual meeting of the Society for the Study of Evolution, Portland, OR – Poster Presentation.
248. Fuerstenberg, S. I., and J. L. Boore, 2010 Will Your Favorite Genome Be Sequenced? Annual meeting of the Society for the Study of Evolution, Portland, OR – Poster Presentation.
249. Boore, J. L., 2010 Evolution and the Organizing Principle for Genomic Data. National Center for Research Resources (NIH) hosted meeting on “Realizing the Scientific Potential of Transcriptomics in Aquatic Models”, Portland, OR – Invited Speaker.
250. Boore, J. L., 2010 Bioinformatics Tools for Interpreting the Cyanophora Genome. Cyanophora Genome Jamboree, Rutgers University, NJ – Invited Speaker.

251. Boore, J. L., and S. I. Fuerstenberg, 2011 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
252. Fuerstenberg, S. I., and J. L. Boore, 2011 Will Your Favorite Genome Be Sequenced? Plant and Animal Genomes Conference, San Diego, CA – Poster Presentation.
253. Boore, J. L., 2011 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. University of Minnesota Departmental Seminar series, St. Paul, MN – Invited Speaker.
254. Boore, J. L., and S. I. Fuerstenberg, 2011 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The PHRINGE and GATOR System. Arthropod Genomics, Kansas City, MO – Poster Presentation.
255. Fuerstenberg, S. I., and J. L. Boore, 2011 Will Your Favorite Genome Be Sequenced? Arthropod Genomics, Kansas City, MO – Poster Presentation.
256. Boore, J. L., 2011 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The GATOR and PHRINGE System. Regular meeting of the Bay Area Bioinformatics Group, Berkeley, CA – Invited Speaker.
257. Boore, J. L., 2011 Evolutionary Analysis as the Basis for Interpreting, Comparing, and Presenting Genomes: The GATOR and PHRINGE System. Workshop on Tropical Biodiversity and Genomics, Xishuangbanna Tropical Botanical Gardens, Minglun, China – Invited Speaker.
258. Boore, J. L., 2012 Whole Genome Evolutionary Analysis of the Monarch Butterfly (*Danaus plexippus*). Genetics, Development, and Evolution Conference, Berkeley, CA – Poster Presentation.
259. Boore, J. L., 2012 Why the Scientific and Evolutionary Worldview Matters: Considering our Place in the Tree of Life and Biosphere, part of the Sawyer Symposium Series entitled, “The Future of Humanity: Biology, Culture, and Sociopolitics.” Berkeley, CA – Invited Speaker.
260. Boore, J. L., and S. I. Fuerstenberg, 2012 Whole Genome Evolutionary Analysis of the Monarch Butterfly (*Danaus plexippus*). Arthropod Genomics Conference, Kansas City, MO – Poster Presentation.
261. Boore, J. L., 2012 The Future of Evolutionary Genomics. Science and Skeptics Meeting, Ann Arbor, MI – Invited Speaker.
262. Boore, J. L., 2013 What if We Could Sequence Everything? University of California Museum of Paleontology Symposium entitled “Unraveling the Genome: What we’ve learned and why it matters.” Berkeley, CA – Invited Speaker.
263. Boore, J. L., 2013 Why Evolutionary Biology and Genome Sciences Need Each Other. University of Iowa, Iowa City, IA – Invited Speaker.
264. Phillips, N., J. L. Boore and E. L. Braun, 2013 Comparative Genomics of Heterokont Organelles. Annual Meeting of the Society for the Study of Evolution, Snowbird, UT – Poster Presentation.

265. Rice, C. S., C. Toll, J. Boore, M. Neiman and J. Logsdon, 2013 Evolution of Meiotic Genes under Reduced Functional Constraint. Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, IL – Poster Presentation.
266. Rice, C. S., C. Toll, J. Boore, M. Neiman and J. Logsdon, 2013 Fate of Meiotic Genes Under Relaxed Selection? Lessons from Sexual and Asexual Snails. Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, IL – Poster Presentation.
267. Rice, L., J. Logsdon, J. L. Boore and M. Neiman, 2013 The Effects of Polyploidy and Sex on Molecular Evolution at Positively Selected Genes. Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, IL – Poster Presentation.
268. Sullivan, M. K., J. Sharbrough, M. Neiman, J. L. Boore and J. Logsdon, 2013 Comparing Patterns of Molecular Evolution in Nuclear-Encoded Mitochondrial Genes in Sexual and Asexual Lineages of a New Zealand Freshwater Snail. Annual Meeting of the Society for Molecular Biology and Evolution, Chicago, IL – Poster Presentation.
269. Boore, J. L., 2013 Mitochondrial Genomics. University of California Berkeley Computational Biology Supergroup, Berkeley, CA – Invited Speaker.
270. Boore, J. L., 2014 Whole Eukaryotic Genomes, *de novo*, in the CLC Genomics Workbench. Plant and Animal Genomes Conference, San Diego, CA – Invited Speaker.
271. Boore, J. L., 2014 Why Evolutionary Biology and Genome Sciences Need Each Other. Rutgers University, NJ – Invited Speaker.
272. Sullivan, M. K., J. Sharbrough, J. L. Boore, J. Logsdon and M. Neiman, 2014 Comparing Patterns of Molecular Evolution in Nuclear-Encoded Mitochondrial Genes in Sexual and Asexual Lineages of a New Zealand Freshwater Snail. Annual Meeting of the Society for the Study of Evolution, Raleigh, NC – Contributed Talk.
273. McElroy, K., D. Soper, L. Bankers, J. L. Boore, J. Logsdon and M. Neiman, 2014 Differential Gene Expression in Ovarian Tissue of Sexual vs. Asexual Freshwater Snails, Annual Meeting of the Society for the Study of Evolution. Raleigh, NC – Contributed Talk.
274. Bankers, L., K. McElroy, J. Logsdon, J. L. Boore and M. Neiman, 2014 Differential Gene Expression in Freshwater Snails Infected and Uninfected with a Coevolving Trematode Parasite. Annual Meeting of the Society for the Study of Evolution, Raleigh, NC – Contributed Talk.
275. Sharbrough, J., M. Luse, J. L. Boore, J. Logsdon and M. Neiman, 2014 Patterns of Amino Acid Sequence Evolution Across Various Time Scales in the Mitochondrial Genomes of Sexual and Asexual Snails. Annual Meeting of the Society for the Study of Evolution, Raleigh, NC – Contributed Talk.
276. Rice, C., C. Toll, J. L. Boore, M. Neiman and J. Logsdon, 2014 Using a New Zealand Freshwater Snail to Evaluate the Fate of Genes Under Relaxed Selective Constraints. Annual Meeting of the Society for the Study of Evolution, Raleigh, NC – Poster Presentation.
277. Logsdon, J., E. Savelkoul, C. Toll, C. Rice, L. Bankers, J. Sharbrough, J. L. Boore and M. Neiman, 2014 Sexy genomes in asexual species. Annual Meeting of the Society for Molecular Biology and Evolution, Puerto Rico – Contributed Talk.

278. Phillips, N., M. Salomon, J. L. Boore and E. L. Braun, 2014 Comparative Genomics of Heterokont Organelles. Phycological Society of America, Orlando, FL – Poster Presentation.
279. Boore, J. L., 2014 Comparative Genomic Framework for Predictive Toxicology. European Joint Research Commission, Ispra, Italy – Invited Speaker.
280. Boore, J. L., 2014 What Can We Do With the Genomics Data Deluge? University of Birmingham Institute for Advanced Studies, Birmingham, United Kingdom – Invited Speaker, Public Lecture.
281. Boore, J.L., 2014 Evolutionary Biology and the Genomics Data Deluge. Uppsala University, Sweden – Invited Speaker.
282. Phillips, N., J.L. Boore and E. Braun, 2015 Brown Algal Organellar genomes: Overall Patterns and Insights from Heterokonts. Phycological Society of America, Philadelphia, PA – Contributed talk.
283. Boore, J.L., 2015 What If We Could Sequence Everything? Institute for Systems Biology, Seattle, WA – Invited Speaker.
284. Boore, J.L., 2016 What If We Could Sequence Everything? Evolutionary Biology and the Genomics Data Deluge. University of Washington, Bothell, WA – Invited Speaker.
285. Bankers, L., J.L. Boore, J.M. Logsdon and M. Neiman, 2016 Influences of Ploidy Level and Reproductive Mode on Patterns of Adaptive Molecular Evolution in a New Zealand Freshwater Snail. Annual Meeting of the Society for Evolution, Austin, Texas – Contributed Talk.
286. Sharbrough, J., M. Luse, J.L. Boore, J.M. Logsdon, Jr., and M. Neiman, 2016 Inefficient Purifying Selection and Variation in Functional Constraint Drive Accelerated but Heterogeneous Accumulation of Harmful Mutations in Asexual Lineages of a Freshwater Snail. Annual Meeting of the Society for Evolution, Austin, Texas – Contributed Talk.
287. Jalinsky, J., L. Bankers, P. Fields, K. Larkin, K. McElroy, J. Sharbrough, P. Wilton, J. L. Boore, J. Logsdon and M. Neiman, 2017 The Genomic Consequences of Asexuality. BioGenomics: Global Biodiversity Genomics Conference, Washington, D.C. – Poster Presentation.
288. Bankers, L., J.L. Boore, J.M. Logsdon and M. Neiman, 2017 Genome-wide Patterns of Adaptive Molecular Evolution in a New Zealand Freshwater Snail. Annual Meeting of the Society for the Study of Evolution, Portland, Oregon – Contributed Talk.
289. Neiman, M., J. Logsdon, J. Sharbrough, L.A. Bankers, J.L. Boore, K.E. McElroy, J. Jalinsky, P. Fields, P. Wilton, 2017 Genomic Consequences of Asexuality. Annual Meeting of the Society for the Study of Evolution, Portland, Oregon – Contributed Talk.
290. Bankers, L., J.L. Boore, J.M. Logsdon and M. Neiman, 2017 Influences of Polyploidy and Asexuality on Patterns of Adaptive Molecular Evolution in *Potamopyrgus antipodarum*. Congress of the European Society for Evolutionary Biology, Groningen, the Netherlands – Contributed Talk.
291. Logsdon, J., M. Neiman, J.L. Boore, J. Sharbrough, L. Bankers, K. McElroy, J. Jalinsky, P. Fields, P. Wilton, 2017 A Very Recent Whole Genome Duplication in *Potamopyrgus*

Jeffrey L. Boore

antipodarum Predates Multiple Origins of Asexuality and Associated Polyploidy. Annual Meeting of the Society for Molecular Biology and Evolution, Austin, Texas – Contributed Talk.