

ERIC LYONS

CURRICULUM VITAE

School of Plant Sciences
Bio5 Institute
1657 E. Helen Street
Tucson, AZ 85721

Tel Work: 520-626-5070

E-mail: elyons.uoa@gmail.org
E-mail: ericlyons@email.arizona.edu

Education

BA	University of California, Berkeley	Molecular and Cell Biology	1997
MA	University of California, Berkeley	Microbial Biology	1999
	Thesis Advisor: Norman Pace (Microbial Diversity) Project: Human microbial diversity		
PhD	University of California, Berkeley	Plant Biology	2008
	Thesis Advisor: Michael Freeling (Maize Geneticist) Project: Comparative genomics of plants		
Postdoc	University of California, Berkeley	Plant Genome Evolution	2009
	Thesis Advisor: Michael Freeling (Maize Geneticist) Project: Comparative genomics of plants		

Citizenship

United States of America

Research Interests

Genome structure, evolution and dynamics
Computational systems for genomes
Advanced visualization of genomic data

Professional Experience

Assistant Professor	Plant Sciences, University of Arizona, Tucson	2012-present
Senior Scientific Developer	iPlant Collaborative, University of Arizona, Tucson	2010-2012
Postdoctoral Research	University of California, Berkeley	2009-2010
Graduate Student Research	University of California, Berkeley	2006-2008
Programmer/Analyst III	University of California, Berkeley	2005
Senior Scientific Developer	Biotique Systems, Inc.	2004
Computational Biologist	Berlex Biosciences (Bayer)	2002-03
Research Bioinformatics	Genencor International, Inc.	2001
Computational Biology Associate	The Molecular Sciences Institute	2000-2001
Graduate Student Research	University of California, Berkeley	1997-1999
Lab Assistant	University of California, Berkeley	1995-1997

Scientific Society Offices and Committees

MaizeGDB Working Group	2011-2013
Genomes2Germplasm (EU-US Working Group) Genomic Variation	2013
International Arabidopsis Information Consortium: Working group member	2012
Plant Science Research Summit: Paper writer on cyberinfrastructure	2011
Cyberinfrastructure for Collaborative Science Workshop, NESCENT	2011
RECOMB Satellite Workshop on Comparative Genomics Program Committee	2011-2012

University of Arizona Offices and Committees

ARS Genomic Analytical Services	2013-present
CALS Cyberinfrastructure Advisory Board	2012-present
SPLS Web/IT Committee	2012-present
SPLS Seminar Committee	2012-present

Non-profit Boards

Phoenix Bioinformatics	2013
------------------------	------

Web-Based Tools for Comparative Genomics

CoGe: A new kind of comparative genomics <http://genomeevolution.org/CoGe/>. CoGe contains 20,000 genomes from 15,000 organisms comprising 750,000,000,000 nucleotides (and growing). CoGe's suite of 30+ interconnected web-tools for open-ended analyses support whole genome comparisons to high-resolution comparative analyses.

Examples

Whole genome analysis of Maize and Sorghum:
Whole genome analysis of Arabidopsis thaliana and lyrata:
GC and amino acid content shifts in Plasmodia:

<http://genomeevolution.org/r/8li>
<http://genomeevolution.org/r/3rm>
<http://genomeevolution.org/r/8lm>

Whole genome of human and chip (video tutorial):
Identifying and characterizing genomic inversions in bacteria:

<http://genomeevolution.org/r/8lw>
<http://genomeevolution.org/r/8m8>

Public Outreach:

Panel Participant for AZPM, PBS “G-8 International Conference on Open Data for Agriculture”	2013
Invited Participant for the Institute on Science for Global Policy “Emerging Diseases”	2013
Tucson Festival of Books, “What You Can Learn from Your Genome”	2013
Special Speaker for middle school and high school students, Sonoran Science Academy	2013

Reviewer:

NSF; NIH, Nature, Nature Biotechnology, Molecular and Cellular Evolution; NSF Merit; Plant Physiology; Plant Cell; The Plant Journal; BMC Plant Biology; BMC Bioinformatics; Molecular Biology and Evolution; Systematic Botany; Bioinformatics; RECOMB Comparative Genomics

Teaching

Co-Instructor General Bio (MCB181)	University of Arizona	2012-2013
Co-Instructor CyberInfrastructure (ISTA420)	University of Arizona	2012-2013
Workshops on CyberInfrastructure (iPlant)	~6 per year	2011-2013
Workshops on Comparative Genomics	International; ~12 per year	2008-2013
Docent	University of California Botanical Garden	2008-2010
Undergraduate Research Advisor	University of California, Berkeley	2006-2009
TA General Ecology	University of California, Santa Cruz	2008
Scientific Reviewer	Lawrence Hall of Science	2007
Co-Instructor Medical Virology	Extension University of California, Berkeley	2004-2006
Advisor Masters Program In Bioinformatics	Amarita Vishwa Vidyapeetham, Kerala India School of Applied Science, Centre For Biotechnology	2005-2006
Mentor for High School Interns	The Molecular Sciences Institute	2002
TA Microbial Diversity	University of California, Berkeley	1999

Guest Lectures:

Life Science Data Management	UA, Tucson, Bryan Wang	2013
Comparative Genomics	UA, Tucson, Bryan Wang	2013
Comparative Genomics	U Indiana, Volker Brendel	2013
Big Data	UA, Tucson, KEYS program for High-school students	2013
Genomics	UA, Tucson, David Galbrith	2012
Computational Biology	UA, Tucson, Michael Barker	2012
Comparative Genomics	Iowa State, Volker Brendel	2012
Big Data	UA, Tucson, KEYS program for High-school students	2012
Introductory Biology I	UA, Tucson, Brian Larkins	2011
Introduction to Biotechnology	UA, Tucson, Ken Feldman	2011
Genetics and Society	UC Berkeley, Mike Freeling	2010
Plant Genome Evolution	UC Berkeley Mike Freeling	2006
Medical Virology	UC Berkeley Extension	2003

Development of High School Education Module for CoGe

Worked with an educator intern, Michael Nakashima, to develop a high school level web-based teaching module for using CoGe to learn comparative genomics: http://genomeevolution.org/wiki/index.php/Tutorial_for_High_School_Students

Tutorials for Comparative Genomics CoGePedia 2009-2013

Continually developing new web-based education modules using CoGe for comparative genomics. Currently there are 30 text-based how-to tutorials, 20 video tutorials, 3 complete workshops, and 5 high school modules. <http://genomeevolution.org/wiki/index.php/Tutorials>

Grants

EPIC-CoGe (\$273,169)	Gordon and Betty Moore Foundation	2012-2014
iAnimal (\$500,000)	USDA, AFRI	2013-2016

Awards

CITE award (Outstanding Employee of the Year)	Berlex Biosciences	2002
-----------------------------------------------	--------------------	------

Patents

Methods for modulating proteins not previously known as proteases.	Genencore Int.	2001
--------------------------------------------------------------------	----------------	------

Peer-reviewed Publications

1. ECH Chen, CFBA Najar, C Zheng, A Brandts, **E Lyons**, H Tang, L Carretero-Paulet, VA Albert, D Sankoff The dynamics of functional classes of plant genes in rediploidized ancient polyploids BMC Bioinformatics 14 (15), 1-10 (2013).
2. Ibarra-Laclette E, **Lyons E**, Hernández-Guzmán G, Pérez-Torres CA, Carretero-Paulet L, Chang T-H, Lan T, Welch AJ, Juárez MJA, Simpson J, Fernández-Cortés A, Arteaga-Vázquez M, Góngora-Castillo E, Acevedo-Hernández G, Schuster SC, Himmelbauer H, Minoche AE, Xu S, Lynch M, Oropeza-Aburto A, et al. Architecture and evolution of a

- minute plant genome. Nature advance online publication. (2013).
3. Ming R, VanBuren R, Liu Y, Yang M, Han Y, Li L-T, Zhang Q, Kim M-J, Schatz MC, Campbell M, Li J, Bowers JE, Tang H, **Lyons E**, Ferguson AA, Narzisi G, Nelson DR, Blaby-Haas CE, Gschwend AR, Jiao Y, et al. Genome of the long-living sacred lotus (*Nelumbo nucifera* Gaertn.). *Genome Biology* 14: R41. (2013).
 4. Zheng C, Chen E, Albert V, **Lyons E**, and Sankoff D. Ancient Eudicot Hexaploidy Meets Ancestral Eurosid Gene Order *BMC Genomics* Accepted (2013)
 5. McCarthy F, and **Lyons E**. From Data to Function: Functional Modeling of Poultry Genomics Data. *Poultry Science*, 92(9), 2519-2529 (2013).
 6. Tang B and **Lyons E**. Unleashing the genome of *Brassica rapa*. *Front. Plant Sci.* 3:172. doi: 10.3389/fpls.2012.00172 (2012)
 7. D'Hont A, et al. (**Lyons E**). The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature* doi:10.1038/nature11241 (2012)
 8. Tang H, **Lyons E**. The Evolution of Genome Structure. *International Journal of Evolution* doi: 10.4172/ievj.1000e105 (2012)
 9. Reneker J, **Lyons E**, Conant GC, Pires JC, Freeling M, Shyu CR, Korkin D. Long identical multispecies elements in plant and animal genomes. *PNAS* 109 (19), E1183-E1191 (2012)
 10. Schnable JC, Freeling M, **Lyons E**. Genome-wide analysis of syntenic gene deletion in the grasses. *Genome Biology and Evolution* doi:10.1093/gbe/evs009 (2012)
 11. Schnable JC, **Lyons E**. Comparative genomics with maize and other grasses: from genes to genomes!. *Maydica* 56, (2011)
 12. Zheng C, Swenson K, **Lyons E** & Sankoff D. OMG! Orthologs in Multiple Genomes – Competing Graph-Theoretical Formulations. *Algorithms in Bioinformatics* 6833, 364-375 (2011).
 13. Goff SA, et al. (**Lyons E**). The iPlant Collaborative: Cyberinfrastructure for Plant Biology. *Frontiers in Plant Science* 2 (2011)
 14. Tang H, **Lyons E**, Pedersen B, Schnable JC, Paterson AH, Freeling M. Screening Synteny Blocks in Pairwise Genome Comparisons Through Integer Programming *BMC Bioinformatics* 12:102 (2011)
 15. Banks, J. A. et al. (**Lyons E**) The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. *Science* 332, 960-963 (2011).
 16. **Lyons E**, Freeling M, Kustu S, Inwood W, Using Genomic Sequencing for Classical Genetics in *E. coli* K12. *PLoS ONE* 6(2): e16717. doi:10.1371/journal.pone.0016717 (2011)
 17. Woodhouse MR, Schnable JC, Pedersen BS, **Lyons E**, Lisch D, Subramaniam S, Freeling M. Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homeologs. *PLoS Biol* 8(6): e1000409. (2010)
 18. Kane J, Freeling M, **Lyons E**. The Evolution of a High Copy Gene Array in *Arabidopsis* J. Mol. Evo. 70(6): 531-544 (2010)
 19. Paterson AH, et al. (**Lyons E**) The Sorghum bicolor genome and the diversification of grasses. *Nature*. 457(7229): 551-556 (2009)
 21. **Lyons E**, Pedersen B, Kane J, Alam M, Ming R, Tang H, et al. Finding and Comparing Syntenic Regions among *Arabidopsis* and the Outgroups Papaya, Poplar, and Grape: CoGe with Rosids. *Plant Physiol.* 148(4): 1772-1781. (2008)
 22. **Lyons E**, Pedersen B, Kane J, Freeling M. The Value of Nonmodel Genomes and an Example Using SynMap Within CoGe to Dissect the Hexaploidy that Predates the Rosids. *Tropical Plant Biology*. 1(3): 181-190. (2008)
 23. **Lyons E**, Freeling M. How to usefully compare homologous plant genes and chromosomes as DNA sequences. *The Plant Journal* 53: 661-673 (2008)
 24. Ming, R, Shaobin H, Yun F, et al. (**Lyons E**). The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). *Nature* 45: 991-996. (2008)
 25. Freeling M, **Lyons E**, Pedersen B, Alam M, Ming R, Lisch D. Many or most genes in *Arabidopsis* transposed after the origin of the order Brassicales. *Genome Res.* 18: 1924-1937(2008)
 26. Freeling M, Rapaka L, **Lyons E**, Pedersen B, Thomas, BC. G-boxes, Bigfoot genes and environmental response: characterization of conserved noncoding sequences in *Arabidopsis*. *The Plant Cell Online* 19, no. 5: 1441. (2007)
 27. Thomas BC, Rapaka L, **Lyons E**, Pedersen B, Freeling M. *Arabidopsis* intragenomic conserved noncoding sequences. *Proc. Natl. Acad. Sci.*, 104, 3348. (2007)
 28. Leung S, et al. (**Lyons E**) Differential inhibition of inducible T cell cytokine secretion by potent iron chelators. *J. Biomol Screen* 10(2):157-67 (2005)
 29. Frank DN, Spiegelman GB, Davis W, Wagner E, **Lyons E**, Pace NR. Culture-independent molecular analysis of microbial constituents of the healthy human outer ear. *J Clin Microbiol.* 41(1):295-303. (2003)
 30. Washburn JO, **Lyons EH**, Haas-Stapleton EJ, Volkman LE. Multiple nucleocapsid packaging of *Autographa californica* nucleopolyhedrovirus accelerates the onset of systemic infection in *Trichoplusia ni*. *J Virol.* 73(1):411-6. (1999)

Book Chapters

- Lyons E**, Bomhoff MD, Oliver SL, Lenards AJ. Comparative Genomics of Grass Genomes using CoGe, *Handbook of Plant & Crop Physiology* (2014 -- accepted)
- Lyons E** and Tang H. Syntenic sequence conservation between and within papaya genes. *Genetics and Genomics of Papaya* (2014 -- accepted)
- Lyons E**. Comparing genomes: Syntenic dotplots and high-resolution sequence analysis. *Methods in Molecular Biology: Plant Functional Genomics Vol I* (2012)
- Lyons E**, Castelletti S, Pedersen B, Lisch D, Freeling M. Maize GEvo: A comparative sequence alignment, visualization

and research tool. *Handbook of Maize Genetics and Genomics* (2009)

Invited Talks

Fujian Agriculture and Forestry University, Fuzho, China “Evolution of plant genomes”	2013
University of Georgia, Genomics Conference “Genomic Data Management and Analysis”	2013
University of Arizona, Vet and Animal Science “Insights into the evolution of genomes”	2013
Plant and Animal Genome Conference “Illumina, iPlant, and CoGe: Powering Comparative Genomics”	2013
Plant and Animal Genome Conference “EPIC-CoGe: Integration of epigenetics data with comparative genomics”	2013
Plant and Animal Genome Conference “Recent Developments at COGE and EPIC: quantitative function”	2013
Plant and Animal Genome Conference “Avian Comparative Genomics”	2013
Institute on Science for Global Policy “Cyberinfrastructure in the Life Sciences”	2013
University and Industrial Consortium “Cyberinfrastructure in the Life Sciences”	2012
University of Arizona CALS Bi-Annual Meeting “Comparative Genomics and You”	2012
Avian Phylogenomics Community “Avian Comparative Genomics”	2012
University of Florida, “Insights in the evolution of plant genomes”	2012
Bio5 Institute, KEYS program lecture “Big Data”	2012
University of Arizona, Consortium for Machine Computing “Big Data and Comparative Genomics	2012
I5K Consortium “iPlant Cyberinfrastructure and Comparative Genomics”	2012
University of Arizona, Evolution and Ecology “Comparative Genomics with CoGe”	2012
U. of Florida, “Insights in the evolution of plant genomes”	2012
Shennong Bilateral Center Symposium, “The iPlant Collaborative”	2011
National Science Board, “The iPlant Collaborative”	2011
JCVI, “The iPlant Collaborative”	2011
JCVI, “Comparative Genomics”	2011
U. of Missouri, “Comparative Genomics Made Easy!”	2011
RECOMB, Comparative Genomics “Comparative Genomic Resources	2010
Arizona Genomics Institute “Plant comparative genomics”	2010
Society of Invertebrate Pathology “Comparative genomics with 9,000 genomes.”	2010
UC Davis, Microbiology “Using genomic sequencing for classical genetics in <i>E. coli</i> K12”	2010
U of Arizona, iPlant Tech Talk “CoGe: The need for extensible multi-genome comparative genomics platforms”	2009
U of Texas, Advanced Computing Center “Identifying true homologous genes using whole genome analyses”	2009
Stanford University, Carnegie Institute “Syntenic Analysis of Fabaceae Genomes”	2009
U of Missouri, St. Louis, iPlant Genomics in Education “Genomic Tools for Hypothesis Testing.”	2009
Iowa State University, Computational and Systems Biology Summer Institute “Plant Comparative Genomics”	2009
Plant and Animal Genome Conference “Dissecting the Eurosid Paleoheptaploidy”	2009
Iowa State University, “Plant Whole Genome Analyses”	2008
Iowa State University, Department of Genetics, Development and Cell Biology	2008
Specht Laboratory, University of California, Berkeley	2008
USDA Western Regional Research Center, Albany 2008 The Molecular Sciences Institute	2008
Department of Biological Sciences, California State University, Long Beach	2008
Hebei Academy of Agricultural and Forestry Sciences, China	2005
Amrita Vishwa Vidyapeetham Center for Biotechnology Kerala, India	2005

Accepted Talks

Plant and Animal Genome Conference “Architecture and Evolution of a Minimal Plant Genome”	2013
Plant and Animal Genome Conference “The iPlant Collaborative”	2012
Plant and Animal Genome Conference “2nd order genome assembly: Syntenic Path Assembly”	2012
Plant and Animal Genome Conference “Whole Genome Comparisons with <i>Oryza</i> and <i>Brachypodium</i> ”	2012
Plant and Animal Genome Conference “iPlant Community Resources”	2011
Plant and Animal Genome Conference “Comparative Genomics Made Easy”	2011
Plant and Animal Genome Conference “10,000 Genomes at Your Fingertips”	2011
Society of Invertebrate Pathology “Identification of spontaneous mutations by genome sequencing”	2010
West Coast Bacteria Physiologist Conference “Genome analysis of 8 strains of <i>E. coli</i> ”	2009
UC Berkeley, Plant and Microbial Biology “Plasmodia Genome Evolution”	2009
UC, Berkeley Ph.D Finishing Talk “CoGe: Insights into the Evolution of Plant genomes	2008
International Maize Meeting, “Gene Loss Following Whole Genome Duplication Events”	2008

Additional Training

Docent training course (40 weeks)	University of California Botanical Garden	2008
-----------------------------------	-------------------------------------------	------