

## An iPlant Grand Challenge Workshop Proposal:

### Evolution of multicellularity and sexuality in the life cycles of photosynthetic eukaryotes

#### Organizers

**Main contact person:** Elisabeth Gantt, Distinguished University Professor Emerita, Dept. Cell Biol. Mol. Genetics, University of Maryland, College Park, MD 20742 <[egantt@umd.edu](mailto:egantt@umd.edu)> 301-405-1649 FAX: 301-314-9081. Evolution of the photosynthetic apparatus and accessory pigments; carotenoids; genomics of multicellular and unicellular red algae.

Charles Delwiche, Associate Professor, Dept. Cell Biol. Mol. Genetics, Univ. Maryland, MD 20742 <[delwiche@umd.edu](mailto:delwiche@umd.edu)> 301-405-8286; FAX: 301-314-9081 Molecular systematics; origin of land plants: evolution of chloroplasts

Michael Lynch, Distinguished Professor, Dept. of Biology, Indiana University, Bloomington, IN, <[milynch@indiana.edu](mailto:milynch@indiana.edu)> 812-855-7384. FAX: 812-855-6705. Mechanisms of evolution at the gene, genomic, and phenotypic levels focusing on the roles of mutation, random genetic drift, and recombination in round worm, yeast, *Paramecium* and *Daphnia*.

Stephen Mount, Associate Professor, Dept. Cell Biol. Mol. Genetics, and Associate Director of Center for Bioinformatics and Computational Biology, Univ. Maryland, MD 20742 <[smount@umd.edu](mailto:smount@umd.edu)> 301-405-6934 FAX: 301-314-9081. Molecular genetics of splice site selection during pre-mRNA splicing in eukaryotes focusing on *Arabidopsis* and *Drosophila*.

#### Participants: (\*confirmed; all others invited)

E. Virginia Armbrust\* University of Washington. Leader of 2 diatom genome sequencing projects; molecular ecology

Jo Ann Banks Purdue University. Leader of lycophyte sequencing project; sexual differentiation in ferns

Susan Brawley\* University of Maine. Ecology of red and brown algae; leader of genome sequencing project for multicellular red alga *Porphyra*.

Rose Ann Cattolico. University of Washington. Marine algae; chloroplast evolution; carbon production in marine ecosystems

Todd Cooke\* University of Maryland. Developmental mechanisms in land plant evolution

Susan Dutcher\* Washington University School of Medicine. Molecular approaches to structure and function of *Chlamydomonas* flagella

Melanie Fields\* Sidwell Friends School. High school biology teacher

James Galagan\* Broad Institute of MIT. Genome sequencing and analysis concentrating on fungi and protozoa.

Ursula Goodenough\* Washington University. Molecular basis and evolution of life-cycle transitions in *Chlamydomonas*

Eric Haag\* University of Maryland, Reproductive adaptations and sexual differentiation in round worms.

Josephine Michael. Eleanor Roosevelt High School. High school biology teacher.

Kenneth Karol\* New York Botanical Garden. Molecular systematics of green algae and land plants.

John Logsdon\* University of Iowa. Genetic aspects of the origin and early evolution of eukaryotes and their genomes; evolution of sex.

Stephen Miller\* University of Maryland, Baltimore County. Genetics of multicellularity in green algae.

Cynthia Parr\* Smithsonian Institution. Ecological informatics and biodiversity. Encyclopedia of Life.

Simon Prochnik\* DOE Joint Genome Institute. *Chlamydomonas* sequencing project; large-scale trends in animal gene evolution; bioinformatics education

Ralph Quatrano\* Washington U. Leader of moss sequencing project; brown algae biology.

Daniel Rokhsar\* DOE Joint Genome Institute and University of California, Berkeley. Computational, comparative, and functional analysis of eukaryotic genomes.

Stephen Wolniak\* University of Maryland and NSF (as of 7/2008). Plant cell biology; differentiation of land plant sperm.

## An iPlant Grand Challenge Workshop Proposal:

### Evolution of multicellularity and sexuality in the life cycles of photosynthetic eukaryotes

#### Summary

**This workshop will articulate the cyberinfrastructure needed to use existing and forthcoming genomic data to explore the genomic basis of the evolution of alternating multicellular generations in the life cycles of photosynthetic organisms.**

#### Background

Plants are distinguished by two key features: photosynthesis and alternating generations of haploid gametophytes and diploid sporophytes. The different lineages of red, green, and brown plants exhibit parallel trends in life cycle evolution. Unicellular species in these lineages exhibit the basal eukaryotic life cycle in which haploid unicells dominate and the only diploid cell is the zygote. Related multicellular species undergo haploid gametophyte-dominant life cycles, isomorphic gametophyte and sporophyte life cycles, and diploid sporophyte-dominant life cycles. In fact, a dominant diploid (or dikaryotic) multicellular stage characterizes the life cycles of all of the largest eukaryotic lineages: eumetazoa (animals), basidiomycota (fungi), kelps (brown algae) and vascular plants (green land plants). The reproductive cells operating in these life cycles show parallel evolutionary trends, which range from ordinary haploid cells functioning as isogametes in the basal eukaryotic life cycle, to specialized gametes developing in specialized organs in complex multicellular life cycles. These parallels suggest that life cycle evolution across multiple plant lineages is strongly constrained by their common genetic and genomic heritage, similar developmental channeling, similar selection pressures, or some combination of these.

#### Grand Challenge

The tree of life project has generated an explicit phylogenetic framework for characterizing life cycle evolution in the major lineages of red, green, and brown plants. Completed genomic sequences are newly available (and more are rapidly becoming available) for representative unicellular and multicellular species from the major photosynthetic lineages. Therefore, it has now become possible to address the grand challenge of identifying **the genetic and genomic basis for the evolution of multicellularity and sexuality in the life cycles of these lineages**. This grand challenge will require three types of comparative genetic and genomic analyses: 1) the identification and characterization of **common genes and genomic structures** from multiple unicellular eukaryotic lineages in order to determine the genomic basis for the basal eukaryote life cycle; 2) the identification and characterization of the those genes and genomic structures involved in **the evolution of multicellularity and sexuality** in each major lineage of red, green, and brown plants in order to determine the genomic basis of life cycle evolution in each lineage; and 3) the global comparative analysis across all major plant lineages in order to resolve **the roles of genetic heritage, developmental mechanisms, and selection pressure** in plant life cycle evolution. Of special interest is an understanding of those genomic components (suites of genes required for specific processes) that may potentiate organismal complexity.

#### Workshop Format and Agenda

We are seeking support for a workshop involving about 30 participants (22 are listed, not including any iPlant Collaborative representatives). For each of the three questions we will need to identify the appropriate genetic and genomic tools that would constitute the cyberinfrastructure necessary to support this grand challenge project. A two day meeting with the following sessions is envisioned: 1. Definition of the problem. 2. An overview of genomic resources. 3. Genomic components of interest. 4. Challenges and cyberinfrastructure needs. 5. Dissemination, outreach and education. 6. Future directions. The outcome of this meeting will be a clear articulation of the cyberinfrastructure needed to address the evolution of multicellularity and the alternation of generations among photosynthetic eukaryotes.

## Elisabeth GANTT

### Professional Preparation:

Blackburn College, Carlinville, IL, Biology, B.A. 1958  
Northwestern University, Evanston, IL, Biology, M.Sc. 1960  
Northwestern University, Evanston, IL, Biology, Ph.D. 1963  
USPHS Postdoc., Microbiol., Dartmouth Medical School, Hanover, NH, 1963-66

### Appointments:

Distinguished Professor Emerita, Cell Biol. & Molec. Genet., Univ. Maryland, 2007 -present  
Distinguished Professor, Cell Biol. & Molec. Genet., Univ. Maryland, 1997- 2007  
Member of the National Academy of Sciences, 1996 - present  
Professor, Plant Biology Dept., University of Maryland, College Park, MD, 1988-96  
Visiting Professor, Plant Biology, Cornell Univ., Ithaca, NY, Fall Semester, 1983  
Biologist, Radiation Biology Laboratory, Smithsonian Inst., Washington DC, 1966-88

### Most Relevant to Genomics:

Durnford, D.G., J.A. Deane, S. Tan, G.I. McFadden, **E. Gantt**, and B.R. Green. 1999. A phylogenetic assessment of the eukaryotic light-harvesting antenna proteins with implications for plastid evolution. *J. Molec. Evol.* 48: 59-68.

Grabowski, B., F.X. Cunningham, Jr., and **E. Gantt**. 2001. Chlorophyll and carotenoid binding in a simple red algal complex crosses phylogenetic lines. *Proc. Natl. Acad. Sci. (USA)*. 98: 2911-2916.

Cunningham, F.X. and **E. Gantt**. 2007. A portfolio of plasmids for identification and analysis of carotenoid pathway enzymes: *Adonis aestivalis* as a case study. *Photosynthesis Research*. 92: 245-259.

Cunningham, F.X., H. Lee and **E. Gantt**. 2007. Carotenoid biosynthesis in the primitive red alga *Cyanidioschyzon merolae*. *Eukaryotic Cell*. 6: 533-545.

### Selected Publications (other):

Wolfe, G.R., Cunningham, F.X. Jr., Durnford, D., Green, B.R., **Gantt, E.** 1994. Evidence for a common origin of chloroplasts with differently pigmented light-harvesting complexes. *Nature* **367**:566-568.

Cunningham, F.X., T. Lafond, and **E. Gantt**. 2000. A possible role for LYTB in the non-mevalonate pathway of isoprenoid biosynthesis. *J. Bacteriol.* 182: 5841-5848.

Cunningham, F.X., Jr. and **E. Gantt**. 2001. One ring or two? Determination of ring number in carotenoids by lycopene  $\epsilon$ -cyclase. *Proc. Natl. Acad. Sci. (USA)*. 98: 2905-2910.

Cunningham, F.X., and **E. Gantt**. 2005. A study in scarlet: enzymes of ketocarotenoid biosynthesis in the flowers of *Adonis aestivalis*. *Plant Journal*. 41: 478-492.

Ershov, Y., R.R. Gantt, F.X. Cunningham, Jr. and **E. Gantt**. 2002. Isoprenoid biosynthesis in *Synechocystis* PCC6803 is stimulated by compounds of the pentose phosphate cycle but not by pyruvate and deoxyxylulose-5-phosphate. *J. Bact.* 184: 5045-5051.

**Gantt, E.**, B. Grabowski, and F.X. Cunningham, Jr. 2003. Antenna systems of red algae: phycobilisomes with photosystem II and chlorophyll complexes with photosystem I. In: B. R. Green and W.W. Parson (eds.) *Light - Harvesting Antennas*, pp. 307-322. Kluwer Academic Publishers, The Netherlands.

Poliquin, K., Y. Ershov, F.X. Cunningham, Jr, T.T. Woreta, R.R. Gantt, and **E. Gantt**. 2004. Inactivation of *sll1556* in *Synechocystis* Strain PCC 6803 impairs isoprenoid biosynthesis from pentose phosphate cycle substrates in vitro. *J. Bact.* 186: 4685-4693.

Green, B.R. and **E. Gantt**. 2005. Distal and extrinsic photosystem II antennas. In: T. Wydryzynski and K. Satoh (eds.) *Photosystem II: The Light-Driven Water: Plastoquinone Oxidoreductase*. pp. 23-44. Springer Verlag. The Netherlands.

### **Synergistic Activities (5):**

1. National Lecturer of the Phycological Society of America, 1982-1983.
2. President - American Society of Plant Physiologists, 1988-89.
3. Program Manager - National Research Initiative Competitive Grants Program: Photosyn. & Respiration 1994-95.
4. Co-PI, JGI *Porphyra* genome project, 2007-09.
5. Plenary Lecture, "Chloroplast evolution: Past and present", & Organizer of Symposium on "Physiological and structural advantages of chloroplast evolution", Joint meeting of the Phycological Society of America and the International Society of Protistologists, 2007.

### **Collaborators (last 48 mo):**

F. X. Cunningham (Univ. Maryland)  
C. Delwiche (Univ. Maryland),  
Y. Ershov (Bakh Institute Plant Physiology, Moscow, Russia),  
R. R. Gantt (Univ. Maryland),  
B. Grabowski (Free lance editor including Amer. Soc. Plant Biologists, Rockville, MD),  
E. Hermann (Danforth Center, Plant Physiol., St. Louis, MO),  
K. Poliquin (Plant Biol. Washington State Univ.)

### **Ph.D. and Postdoctoral Advisors (and present locations):**

Howard J. Arnott, Ph.D. Advisor at Northwestern Univ., former faculty Univ. Texas, Arlington, TX. (retired).  
Samuel Conti, Postdoc. Advisor at Dartmouth Univ., NH, former faculty at Univ. Mass. Amherst, MA. (retired).

### **Graduate Student Advisees (last 5 years, of 9 career total):**

Kelly Poliquin, Ph.D. 2006 (Washington State Univ.)

### **Postdoctoral Advisees (last 5 years, of 18 career total)**

None

### **Grants:**

NSF RCN [0741907](#) The *Porphyra* Genome: Promoting Resource Development and Integrative Research in Algal Genomics. Co-PI with Susan Brawley, Arthur Grossman, and John Stiller. (2008-2013)

## Charles Delwiche

### a. Professional preparation:

University of California - Berkeley Botany	A.B.	1984
University of Wisconsin - Madison Botany	Ph.D.	1990
University of Wisconsin - Madison Plant Physiology & Evolution	PDF	1990-1992
Indiana University	Molecular Systematics	PDF 1992-1996

### b. Appointments

1996-2002	Assistant Professor	Dept. Cell Biol. Mol. Genetics, Univ. MD, College Park
2002-present	Associate Professor	Dept. Cell Biol. Mol. Genetics, Univ. MD, College Park
2002-present	Fellow	Canadian Institute for Advanced Research
2005-present	Research Associate	Smithsonian Institution National Museum of Natural History

### c. Publications

#### ***Five publications most closely related to project***

Bachvaroff, T. R., G. T. Concepcion, C. R. Rogers, E. M. Herman, and **C. F. Delwiche**. 2004. Dinoflagellate expressed sequence tag data indicate massive transfer of genes to the nuclear genome. *Protist* 155: 65-78. <http://dx.doi.org/10.1078/1434461000165>

**Delwiche, C. F.** 2004. The genomic palimpsest: genomics in evolution and ecology. *BioScience* 54:991-1001. [http://dx.doi.org/10.1641/0006-3568\(2004\)054\[0991:TGPGIE\]2.0.CO;2](http://dx.doi.org/10.1641/0006-3568(2004)054[0991:TGPGIE]2.0.CO;2)

Johnson, M. D., T. Tengs, **C. F. Delwiche**, D. Oldach, and D. K. Stoecker. 2004. Highly divergent SSU rRNA genes found in marine ciliates *Myrionecta rubra* and *Mesodinium pulex*. *Protist* 155:347-359. <http://dx.doi.org/10.1078/1434461041844222>

Bachvaroff, T.R., M.V. Sánchez Puerta & **C.F. Delwiche**. 2006. Evolutionary rates of dinoflagellate chloroplast genes: heterogeneous rates of evolution between plastid-encoded and plastid-targeted genes. *J. Mol. Evol.* 62:42-52. <http://dx.doi.org/10.1016/j.ympev.2007.03.003>

Johnson, M. D., Oldach, D., **Delwiche, C. F.**, and Stoecker, D. K. 2007. Retention of transcriptionally active cryptophyte nuclei by the ciliate *Myrionecta rubra*. *Nature* 445, 426-428. <http://www.nature.com/nature/journal/v445/n7126/full/nature05496.html>

#### ***Five other significant publications***

Karol, K. G., R. M. McCourt, M. T. Cimino, and **C. F. Delwiche**. 2001. The closest living relatives of land plants. *Science* 294:2351-2353. <http://dx.doi.org/10.1126/science.1065156>

**Delwiche, C. F.**, K. G. Karol, M. T. Cimino, and K. J. Sytsma. 2002. Phylogeny of the genus Coleochaete (Coleochaetales, Charophyta) and related taxa inferred by analysis of the chloroplast gene *rbcL*. *Journal of Phycology* 38: 394-403. <http://dx.doi.org/10.1046/j.1529-8817.2002.01174.x>

**Delwiche, C.F.**, Andersen, R.A., Bhattacharya, D., Mishler, B.D. and McCourt, R.M. 2004. Algal evolution and the early radiation of green plants. in Cracraft, J. and Donoghue, M. J. *Assembling the Tree of Life*. Oxford University Press, London. [http://books.google.com/books?id=\\_jLl8zIRzucC&pg=PA121&lpg=PA121&dq=algal+evolution+and](http://books.google.com/books?id=_jLl8zIRzucC&pg=PA121&lpg=PA121&dq=algal+evolution+and)

+the+early+radiation+of+green+plants&source=web&ots=MvDJqOgqcJ&sig=hjD3LoznprKDLnh7OtmStT4PpEQ

Sanchez Puerta, M. V., T. R. Bachvaroff, and **C. F. Delwiche**. 2005. The complete plastid genome sequence of the haptophyte *Emiliania huxleyi*: a comparison to other plastid genomes. *DNA research*. 12:151-156 <http://dx.doi.org/doi:10.1093/dnares/12.2.151>

Palenik, Brian, *et al.* 2007. Tiny eukaryotes provide genomic insights into the Paradox of the Plankton. *Proc. Natl. Acad. Sci. USA*. 7705-7710. <http://dx.doi.org/10.1073/pnas.0611046104>

#### **d. Synergistic Activities**

##### **Service to the Scientific Community**

2002-2005; 2007-present      Editorial Board, *Journal of Phycology*  
2002-present                      Associate Editor, *Molecular Biology and Evolution*  
2005-present                      Research Associate, Smithsonian Institution (Paleontology)

Was involved with the inception and development of the Green Plant Phylogeny Research Coordination group ("Deep Green").

Key role in development of bioinformatics education at the University of Maryland, including formal instruction, curriculum development, and community outreach.

Judge, Montgomery County Science Fair, Botany. 2004.

Participant in German/American Frontiers of Science organizing committee (including co-chairing the 2007 organizing committee), 2004-2007.

#### **e. Collaborators and other affiliations**

**Collaborators and co-editors (last 4 years):** Richard McCourt, National Science Foundation, Philadelphia. Kjetill Jakobsen, Torstein Tengs, Ole Dahlberg, Matthew Johnson, Kamran Sanchian-Tabrizi, Marianne Skaanseng, Fredrik Ronquist, Diane Stoecker, Dag Klaveness (University of Oslo, Norway). Torsten Eriksson (Stockholm); Anne D. Yoder, Michael J. Donoghue (Yale). Debashish Bhattacharya, U. Iowa; Robert Andersen, Bigelow Labs; Brent Mishler, UC Berkeley. Brian Palenik, (Scripps/UCSD). Thomas G. Doak, Princeton; Robert B. Moore, U. Sydney, AU; Ove Hoegh-Guldberg, U. Queensland, AU; Mary Alice Coffroth, SUNY Buffalo. Jonathan Eisen, U.C. Davis.

#### **Graduate and postdoctoral Advisors**

Ph.D.	Linda K. Graham	Univ. Wisconsin-Madison
Postdoctoral	Thomas D. Sharkey and Kenneth J. Sytsma	Univ. Wisconsin-Madison
Postdoctoral	Jeffrey D. Palmer	Indiana University

#### **Thesis Advisor and Postgraduate-Scholar Advisor**

Tsvetan Bachvaroff, Matthew Cimino, John Hall, Sara Handy, Malin Hibbs, Kenneth Karol, Jeff Lewandowski, Tanya Marushak, Gregg Mendez, John Miller, Virginia Sanchez-Puerta, Ruth Timme.

**Stephen M. Mount**

Dept. of Cell Biology and Molecular Genetics  
University of Maryland,  
College Park, MD 20742-5815

[www.stevemount.org](http://www.stevemount.org)

**Professional Preparation:**

Rice University	Biochemistry	BA., Magna cum laude	1978
Yale University	Molecular Biology	Ph.D.	1983
U.C. Berkeley	Molecular Genetics	Postdoctoral	1983-86

**Appointments:**

Associate Professor	<b>University of Maryland, College Park</b> Dept. of Cell Biology and Molecular Genetics	1997-
Associate Director	Bioinformatics and Computational Biology	2003-
Associate Professor	Dept. of Zoology	1995-

**Biological Sciences, Columbia University**

Associate Professor		1992-94
Assistant Professor		1986-92
Postdoctoral	Dept. of Biochemistry, U. C. Berkeley	1983-86
Graduate	Molecular Biophysics and Biochem., Yale	1978-83
Technician	Cell Biology, Baylor College of Medicine	1978

**Honors:**

<b>NSF pre-doctoral Fellowship</b>	1978
<b>NSF Presidential Young Investigator Award</b>	1987

**Five Publications Most Closely Related to the Proposed Project:**

Ming R, Hou S, Feng Y, Yu Q, Dionne-Laporte A, Saw JH, Senin P, Wang W, Ly BV, Lewis KL, Salzberg SL, *et al.* 2007. The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus) Nature 452:991-996.

Campbell MA, Haas BJ, Hamilton JP, Mount SM and Buell CR. 2006. Comprehensive analysis of alternative splicing in rice and comparative analyses with Arabidopsis. BMC Bioinformatics 7: 327.

Haas, BJ, Delcher, AL, Mount, SM, Wortman, JR, Smith, RK Jr, Hannick, LI, Maiti, R, Ronning, CM, Rusch, DB, Town, CD, Salzberg SL and O. White. 2003. Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. Nucleic Acid Res. 31: 5654-66.

Mount, S.M. "**On Genetics.**" A web log on genetics, genomics and gene expression.

<[ongenetics.blogspot.com/](http://ongenetics.blogspot.com/)> [July 29, 2007](#). "Plants, Animals and the ancient RNA toolkit" (not peer-reviewed)

Mount, S.M. and C. Chang. 2002. Evidence for a plastid origin of plant ethylene receptor genes. Plant Physiol. 130:10-14..

**Five Additional Significant Publications:**

Pertea M, Mount SM and Salzberg SL. 2007. A computational survey of candidate exonic splicing enhancer motifs in the model plant Arabidopsis thaliana. BMC Bioinformatics 8:159.

Dogan RI, Getoor L, Wilbur WJ and Mount SM. 2007. SplicePort -- an interactive splice site analysis tool. *Nucleic Acids Res.* 35:W285-91.

Dogan RI, Getoor L, Wilbur WJ and Mount SM. 2007. Features generated for computational splice-site prediction correspond to functional elements. *BMC Bioinformatics* 8:410.

Drosophila 12 Genomes Consortium 2007. Evolution of genes and genomes on the Drosophila phylogeny. *Nature* 450:203-218.

Mount SM, Gotea V, Lin CF and Makalowski W. 2007. Spliceosomal small nuclear RNA genes in 11 insect genomes. *RNA* 13: 5-14.

**Synergistic activities - involving undergraduates in research:**

The University of Maryland is a public University with a large and ethnically diverse student body. I have trained 15 undergraduates in research projects in my laboratory during the last five years. Several of these have been minority students. Three of them are now in graduate school in molecular biology or genetics programs (at Johns Hopkins, Stanford University and the University of California, San Francisco).

**Synergistic activities – general research tools:**

I have participated in the development of software (including SEE-ESE, Spliceport and software for analysis of low complexity protein domains) that is generally available.

**Collaborators**

U.C. Berkeley: S. Celniker, S. Lewis

Case Western Reserve University: H. Salz.

National Center for Biotechnology Information, W. John Wilbur

University of Maryland: S. Salzberg, E. Pertea, L. Getoor, C. Chang, J. Yorke, Z. Liu.

Penn State University and University of Muenster: W. Makalowski and C.F. Lin

**Advisors:**

Savio L. C. Woo. Employer (1978). currently at Mount Sinai School of Medicine

Joan Steitz. Ph.D. thesis advisor. Yale University and HHMI.

Gerald M. Rubin. Postdoctoral advisor. HHMI (Janelia Farm).

**Advisees (2 postdoctoral, 6 Ph.D. theses total):**

Atanu Duttaroy (Howard Univ.) Vinayaka Kotraiah (ExonHit therapeutics)

Jason Edmonds (Edgewood Chemical Biological Center, U.S. Army Research)

## **Michael Lynch**

### **Professional Preparation:**

**Undergraduate education:** St. Bonaventure University, Biology – B. S., 1973.

**Graduate education:** University of Minnesota, Ecology – Ph. D., 1977.

### **Appointments:**

Distinguished Professor; Biology, Indiana University, 2004 – present.

Professor; Biology, Indiana University, 2001 – 2003.

Professor; Biology, University of Oregon, 1989-2001.

Asst., Assoc., Full Professor; Ecology, Ethology, and Evolution, University of Illinois, 1977-1989.

### **Recent Professional Activities:**

President-elect, Society for Molecular Biology and Evolution, 2009.

President, American Genetics Association, 2007.

President, Society for the Study of Evolution, 2000.

Vice-president, Society for the Study of Evolution, 1994.

Council Member, Society of Molecular Biology and Evolution, 2005 – 2007.

Board of Scientific Counselors, National Center for Biotechnology Information (NCBI), 2008 – .

Associate Editor: Conservation Genetics, 1999 – present; Genetics, 1992 – 1996; Molecular Ecology, 1991– 1997; Evolution, 1988 – 1990.

Member of the Organizing Committee, FASEB Ciliate Molecular Genetics Meeting, 2009.

Member, NRC/NAS Ecosystems Panel, 1997 – 2000.

Member, NRC/NAS Committee on Scientific Issues in the Endangered Species Act, 1993 – 1995.

NIH Panel Member: Genomics, 1999; Quantitative Genetics, 1998; Genetics, 1997 – 2002; Genetic Variation and Evolution, 2004 – present.

Panel Member, NSF Sections: Eukaryotic Genetics, 2001– 2002; IGERT Program, 2000 – 2001; Population Biology, 1987 – 1988, 1998.

### **Recognition:**

Fellow, American Academy of Arts and Sciences – elected 2002.

Fellow, American Association for the Advancement of Science – elected 1998.

Beckman Fellow, Center for Advanced Study, Univ. of Illinois – 1981.

Fellow, Max Planck Institut fur Limnologie, Plön, West Germany – 1982, 1984, 1985.

### **Five Publications Related to the Proposed Project:**

Lynch, M. 2007. The evolution of genetic networks by nonadaptive processes. *Nature Reviews Genetics* 8: 803-813.

Lynch, M. 2006. The origins of eukaryotic gene structure. *Mol. Biol. Evol.* 23: 450-468.

Lynch, M., and J. S. Conery. 2003. The origins of genome complexity. *Science* 302: 1401-1404.

Lynch, M. 2002. Intron evolution as a population-genetic process. *Proc. Natl. Acad. Sci. USA* 99: 6118-6123.

Lynch, M., M. O'Hely, B. Walsh, and A. Force. 2001. The probability of fixation of a newly arisen gene duplicate. *Genetics* 159: 1789-1804.

### **Five Other Significant Publications:**

Lynch, M. 2007. The frailty of adaptive hypotheses for the origins of organismal complexity. *Proc. Natl. Acad. Sci. USA* 104 Suppl.: 8597-8604.

Lynch, M. 2006. Streamlining and simplification of microbial genome architecture. *Ann. Rev. Microbiol.* 60:327-349.

Lynch, M., B. Koskella, and S. Schaack. 2006. Mutation pressure and the evolution of organelle genome architecture. *Science* 311: 1727-1730.

Lynch, M., D. G. Scofield, and X. Hong. 2005. The evolution of transcription-initiation sites. *Mol. Biol. Evol.* 22: 1137-1146.

Lynch, M., and J. S. Conery. 2000. The evolutionary fate and consequences of duplicate genes. *Science* 290: 1151-1154.

**Books:**

Lynch, M., and B. Walsh. 1998. *Genetics and Analysis of Quantitative Traits*. Sinauer Assocs., Inc., Sunderland, MA.

Lynch, M. 2007. *The Origins of Genome Architecture*. Sinauer Assocs., Inc., Sunderland, MA.

**Other synergistic activities:** 1) Cofounder of the *Daphnia* Genomics Consortium, an interdisciplinary group involved in the development and promotion of this model system for ecological and evolutionary genomics; 2) past director of several graduate training grants, including an NSF IGERT in Evolution, Development, and Genomics; 3) currently writing a synthesis on *The Evolution of Quantitative Traits* (with Bruce Walsh); 4) give ~20 academic/public talks on various aspects of evolution per year.

**Graduate advisor:** Joseph Shapiro (U. Minnesota).

**Postdoctoral advisor:** none.

**Graduate students:** Deborah Allen (high school teacher, CA), Desiree Allen (U. Edinburgh, postdoc), Elizabeth Bohuski (Indiana U., School of Education), Jennifer Britt (Oregon State U., technician), David Butcher (computer programmer, CA), Hong-Wen Deng (U. Missouri – Kansas City, faculty), Suzanne Estes (Portland State U., faculty), Allan Force (Virginia Mason Res. Inst., postdoc), Xin Hong (current), Vaishali Katju (U. New Mexico, faculty), Travis Kibota (Clark College, faculty), Scott Kolpak (US Forest Service), Britt Koskella (current), Wenli Li (current), Casey McGrath (current), Kendall Morgan (Duke U., science publicist), Angela Omilian (U. Buffalo, postdoc), Susanne Paland (Indiana U., postdoc), Michael Pfrender (Utah State U., faculty), Aaron Richardson (U. Georgia, postdoc), Sarah Schaack (current), Kevin Simonelic (U. Miami Medical School), Margaret Smith (current), Barry Sullender (Rice U., instructor), Michael Vanni (Miami U. of Ohio, faculty), Lawrence Weider (U. Oklahoma, faculty).

**Post-doctoral associates:** Charles Baer (U. Florida, faculty), Jeffrey Blanchard (U. Massachusetts, faculty), Francesco Catania (current), John Colbourne (Indiana U., Center for Genomics and Bioinformatics, genomics director), Teri Crease (U. Guelph, faculty), Melania Cristescu (U. Windsor, faculty), Dee Denver (Oregon State U., faculty), Jeffrey Dudycha (U. South Carolina, faculty), Suzanne Edmands (U. Southern California, faculty), Xiang Gao (current), Kevin Higgins (U. South Carolina, faculty), Laura Higgins (NOAA, research scientist), David Houle (Florida State U., faculty), Niles Lehman (Portland State U., faculty), Ignasi Lucas (current), Emilia Martins (Indiana U., faculty and associate dean), Paul McElheny (National Marine Fisheries Service, research scientist), Phil Morin (Southwest Fisheries Science Center, research scientist), Martin O'Hely (U. Adelaide, faculty), Carolina Penalva-Arana (current), Susan Ratner (National Marine Fisheries Service, research scientist), Barrie Robison (U. Idaho, faculty), Douglas Scofield (UCLA, postdoc), Stewart Schultz (U. Croatia, faculty), Ken Spitze (U. Miami, retired faculty), Larissa Vassilieva (U. Utah, faculty), John Willis (Duke U., faculty).

**Other recent collaborators:** Thomas Berendonk (U. Leipzig); Carla Caceres (U. Illinois); John Conery (U. Oregon); William Cresko (U. Oregon); Elizabeth Housworth (Indiana U.); Sun Kim (Indiana U.); Thomas Little (U. Edinburgh); Lynn Maquat (U. Rochester); Patrick Phillips (U. Oregon); Brian Pickett (Loyola U.); Haixu Tang (Indiana U.); Kelley Thomas (U. New Hampshire); Bruce Walsh (U. Arizona).

## **Grand Challenge Workshop Description**

### **Multicellularity in the life cycles of photosynthetic eukaryotes**

Plants (i.e., embryophytes) are a monophyletic lineage distinguished by two key features. The first is photosynthesis via the activity of endosymbiotic organelles called plastids. The second is alternating multicellular generations of haploid gametophytes (gamete-producing plants) and diploid sporophytes (spore-producing plants). Over the last century, plant biologists have made enormous progress in characterizing the underlying biophysical and biochemical processes involved in plastid-based photosynthesis. Moreover, recent comparative genomic studies have elucidated the major events in the lateral transmission of plastids among eukaryotic lineages. By contrast, research on plant life cycles has been largely descriptive in nature. The life cycle of plants is of both theoretical and practical significance. Control of the plant life cycle is a key component of agricultural systems worldwide, and many of the most important properties that distinguish domesticated crops from their wild ancestors involve life cycle genes. The advent of genomic sequences from representative unicellular and multicellular species in the major plant lineages now makes possible systematic genome-based investigation of the plant life cycle.

**Overall Grand Challenge Workshop goal: to articulate the cyberinfrastructure needed to use existing and forthcoming genomic data to elucidate the genetic and genomic basis for the evolution of alternating multicellular generations in the life cycles of photosynthetic eukaryotes.**

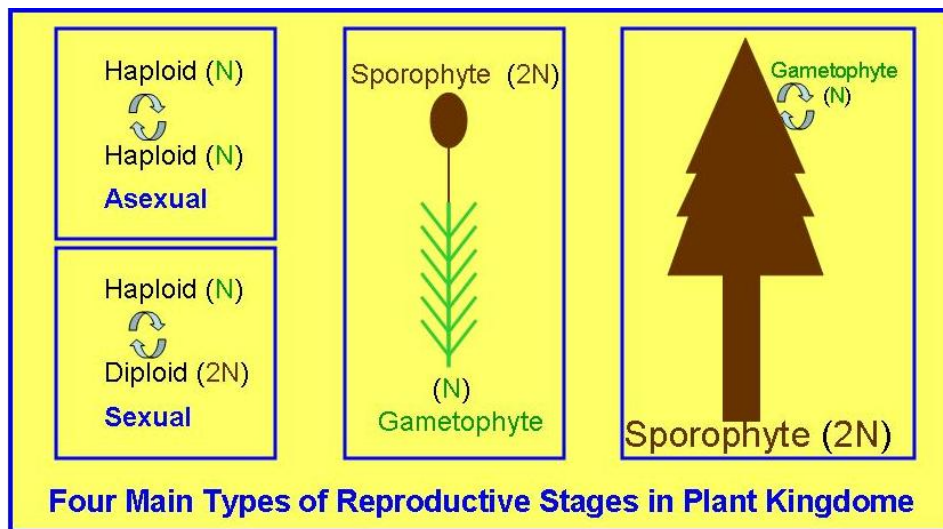
**Stem eukaryote life cycle:** To realize the potential of genomic information to address this grand challenge question it will be necessary to construct a conceptual framework for describing the evolution of plant life cycles, which should be based on contemporary research in eukaryotic phylogenetics (e.g., **Baldauf SL**, 2003). Of special interest is the life cycle of the stem eukaryote. The evidence available to date suggests that the stem eukaryote was a complex unicellular organism (**Cavalier-Smith T**, 2002) exhibiting a life cycle composed of four stages: 1) vegetative haploid unicells undergoing repeated mitoses, 2) gametogenesis, or the activation of certain haploid cells for functioning as isogametes, 3) fertilization, or the fusion of two isogametes forming diploid zygotes, and 4) zygotic meiosis resulting in haploid vegetative cells that repeat the life cycle. This hypothesis regarding the life cycle of the stem eukaryote is based on several arguments, viz., the persistence of this life cycle in the parabasalid group (**Ramesh et al.** 2005) that belongs to the excavates, a candidate for the most basal extant eukaryotic lineage; the widespread occurrence of this life cycle among unicellular eukaryotic lineages; and the likelihood that the complex sequential process of gametogenesis-fertilization-meiosis has only arisen once in the eukaryotes. Indeed, most unicellular species of red, green, and brown plants exhibit this life cycle, although as noted above, few formal analyses have been performed.

**1) What is the common genetic and genomic toolkit operating to control the stem eukaryote life cycle.**

**Phylogenetic relationships among plant lineages:** The tree of life project is generating an explicit phylogenetic framework that can be used to characterize life cycle evolution in plant lineages. Red plants (Rhodophyta) and green plants (Chlorophyta) are believed to be sister groups, which along with the glaucocystophytes derived from a common heterotrophic ancestor that underwent a primary endosymbiotic fusion with a cyanobacterium (Delwiche et al . 2004). All other photosynthetic eukaryotes have an additional level of genomic complexity in that their heterotrophic ancestor acquired its plastids via secondary endosymbiotic fusions with another eukaryote following the endosymbiotic origin of plastids. The conversions of engulfed photosynthetic organisms into plastid organelles were accompanied by the transfer of most endosymbiont genes to the host nucleus. Thus, the genes involved in the evolution of multicellular stages could ultimately be derived from both stem eukaryote and cyanobacterium genomes in the case of red and green plants or both stem eukaryote and endosymbiotic eukaryote genomes in the case of brown plants.

**2) What critical genes are involved in the evolution of multicellular generations in plant life cycles?**

**Parallel evolutionary trends in plant life cycles:** Multicellular plant species exhibit three fundamental types of life cycles (See Figure): 1) gametophyte-dominant (or gametophyte-only) cycles, 2) isomorphic gametophyte and sporophyte cycles and 3) sporophyte-dominant (or sporophyte-only) cycles. Characterization of the stem eukaryote life cycle may allow us to identify the underlying mechanisms responsible for the evolution of multicellular generations in plant life cycles. In particular, our iPlant collaboration can now ask how subtle changes in the life cycles of ancestral unicellular plants could have resulted in the evolution of modern plant life cycles consisting of alternating multicellular stages. In general, the overall evolutionary tendency in most plant lineages seems to proceed from **gametophyte-dominant to sporophyte-dominant life cycle**. This is the same general pattern may be present across the entire eukaryotic lineage. In particular, a dominant diploid (or dikaryotic) multicellular stage characterizes the life cycles of all of the largest eukaryotic organisms: eumetazoa (animals), basidiomycota (fungi), kelps (brown algae) and vascular plants (green land plants). The precise relationship between the derived life cycle and large size remains poorly understood, but it is an intriguing observation, and one that warrants objective study.



**3) What critical genes distinguish the life cycles and account for key differences among representative unicellular and multicellular species within each major red, green, and brown plant lineage?**

**Recent advances in the molecular cell biology of life cycles:** The likely mechanisms for the evolution of multicellular plant structures suggest that we should focus on those genes responsible for regulating life cycles, patterns of mitosis and cytokinesis, gametogenesis, and cell wall biosynthesis in our comparative genomic investigations of unicellular vs. multicellular plants. Implicitly, the regulation of progression through a multifaceted life cycle involves the passage through multiple transition points, or checkpoints, where the biochemical conditions in a cell are altered irreversibly so that the cell is committed to develop in a different way. Many of these transitions through checkpoints involve the proteolytic degradation of effector molecules that allowed the cells to progress up to the commitment threshold, while others occur when previously segregated effector proteins interact in a cell. Well-characterized effectors include protein kinases and phosphatases, as well as transcriptional regulators.

A key challenge in understanding how multicellularity is linked to the alternation of generations is the identification of the regulatory components that mediate the transition into sustained vegetative sporophyte growth in the zygote and sustained vegetative growth in the spores for the production of the gametophyte. Of particular interest are those factors that control the cellular commitment to initiate differentiation of sporangia in specific sporophytic cells and gametangia in specific gametophytic cells. An important clue to one such developmental mechanism has emerged from recent work in *Chlamydomonas*, where it has recently been shown that mating factor proteins in the zygote function in a combinatorial fashion to regulate transcription in a manner that is clearly distinct from the function of these same factors in the gametes that produced that zygote (Lee *et al.* 2008). This observation describes an elegant evolutionary solution to a regulatory conundrum in development, and it sets the stage for the study of other major transitions that define growth and differentiation

in sporophytes and gametophytes in a variety of organisms. The finding also paves the way for the identification of the newly transcribed genes that facilitate an altered pattern of development.

Another key transformation necessary for evolution of a multicellular gametophyte involves delay the onset of gametogenesis in the cells that are produced by meiosis. The patterns of transcription and translation that control gamete formation are largely unknown, though similarities in developmental patterns suggest that the regulatory pathways may be conserved across broad reaches of these plant groups. Though the controlling factors may be similar, gametogenesis takes on an entirely different level of complexity when the gametes differ structurally from the cells that gave rise to them. Remarkably, a broad array of nonmotile plants retain rather expansive cassettes of genes that are expressed exclusively in spermatids to facilitate ciliary motility in the male gametes that are produced in the antheridia. As we look for a cohesive understanding of patterns of differentiation linked to ciliary motility in these gametes, we can incorporate our emerging understanding of the genes necessary to construct a ciliary axoneme, and utilize the *Chlamydomonas ciliome* as a gene set that can serve as a framework onto which additional data may be placed. A most important part of deciphering this biological process is to focus on mechanisms that control cell fate, allowing some cells in the gametophyte to differentiate into spermatids, while others do not (**van der Weele et al., 2007**). Here, post-transcriptional regulators may play key roles in cellular morphogenesis.

### **Genomic considerations: possible exaptations for multicellularity**

Of special interest is an understanding of those genomic components that may contribute to organismal complexity. In the example cited above, **Lee et al. (2008)** found that combinatorial transcriptional control mediated by homeodomain protein dimerization facilitates the haploid-diploid transition in *Chlamydomonas*. Thus, homeodomain protein-based transcriptional control of cell type, a common feature of the opisthokont (animal/fungal) cell type-specification, may have originated in a sexual context and enabled the evolution of land-plant body plans. Other suites of genes required for specific processes may play similar roles in favoring multicellularity. Candidates include the genes required for complex alternative splicing, regulatory microRNAs, nonsense-mediated decay, transposable elements, the minor (U12) spliceosome, etc. It is important to bear in mind that the roots of organismal complexity may reside in nonadaptive processes (**Lynch, 2007**).

### **Datasets and cyberinfrastructure**

The premise of the proposed workshop is that currently available and forthcoming genomic sequence information has the potential to provide answers to the grand challenge questions posed here. Several resources already exist that provide related sets of tools (notably [NCBI](#), [TAIR](#), [gramene](#) and [phytome](#)). However, a single integrated data structure into which all new genomes would be readily assimilated is still lacking. We view such a comparative genomics tool to be central to a fully developed plant cyberinfrastructure and suggest that it will be useful for other grand challenge questions.

**Data structures.** An important item for discussion at the workshop would be what data structure would be most amenable to the open and automated (or semi-automated) assimilation of new data. We envision two intersecting and fully integrated coordinate systems. One would be based on the taxonomic relationships among species (data would be assigned to species or to nodes on the “tree of life”). The other would be based on sets of orthologous groups (similar to NIH unigenes). Such clusters will represent not only protein-coding genes, but also miRNA genes, snRNA genes and other entities. Genomic information could be attached to locations on these two coordinate systems. The extent to which non-homologous functional replacement can be recognized and described within this data structure will be an item for discussion.

**Improved Gene Ontologies.** Another desirable feature in the cyberinfrastructure is an improved gene ontology for plants, ideally one that would allow immediate application of the numerous tools developed for operating on gene ontology data (see <http://www.geneontology.org/GO.tools.shtml>).

Literature Cited (in order of appearance):

**Baldauf SL, 2003.** The deep roots of eukaryotes. *Science* **300**: 1703-1706.

**Cavalier-Smith T 2002.** The phagotrophic origin of eukaryotes and phylogenetic classification of protozoa. *International Journal of Systematic and Evolutionary Microbiology* **52**: 297-354.

- Ramesh MA**, Malik SB and Logsdon JM Jr. 2005. A phylogenomic inventory of meiotic genes; evidence for sex in *Giardia* and an early eukaryotic origin of meiosis. *Curr Biol.* **15**:185-91.
- Delwiche CF**, Andersen RA, Bhattacharya D, Mishler B, McCourt Richard M 2004. Algal evolution and the early radiation of green plants. In J Cracraft, MJ Donoghue, eds, *Assembling the Tree of Life*. Oxford University Press, London, pp 121-137.
- Lee JH**, Lin H, Joo S, Goodenough U. 2008. Early sexual origins of homeoprotein heterodimerization and evolution of the plant KNOX/BELL family. *Cell* **133**:829-40.
- van der Weele CM**, Tsai CW and Wolniak SM. 2007. Mago nashi is essential for spermatogenesis in *Marsilea*. *Mol Biol Cell.* **18**:3711-22.
- Lynch M 2007. "The Origins of Genome Architecture." Sinauer Assocs., Inc., Sunderland, MA.

### **Table: Available genomes relevant to this proposal**

#### GREEN PLANT LINEAGE

- Arabidopsis thaliana* – angiosperm dicot - TIGR (TAIR)
- Carica papaya* – multicellular (draft sequence) (Nature 2008, 452:991)
- \**Ceratopteris richardii* fern - JGI
- Chlamydomonas reinhardtii* - unicellular chlorophyte - JGI
- \**Marchantia polymorpha* - liverwort -JGI
- Micromonas pusilla* CCMP1545 - unicellular prasinophyte (green alga) - JGI *Micromonas* strain RCC299 - unicellular prasinophyte (green alga) - JGI
- Oryza sativa* – (Japonica) angiosperm monocot - TIGR
- Ostreococcus lucimarinus* - unicellular prasinophyte (green alga) - JGI
- Ostreococcus tauri* - unicellular prasinophyte (green alga) - JGI
- Physcomitrella patens* ssp *patens* – bryophyte - JGI *Populus trichocarpa* – angiosperm dicot - JGI *Selaginella moellendorffii* – lycophyte - JGI
- Sorghum bicolor* – angiosperm monocot - JGI
- Vitis vinifera* – angiosperm dicot - Genoscope
- Volvox carteri* – multicellular green alga - JGI

#### BROWN PLANT LINEAGE

- Aureococcus anophagefferens* - unicellular chrysophyte - JGI
- \**Ectocarpus siliculosus* (multicellular brown) – Genoscope
- Emiliana huxleyi* - JGI
- \**Fragilariopsis cylindrus* - diatom -
- Phaeodactylum tricornutum* – diatom - JGI
- Thalassiosira pseudonana* – diatom - JGI
- EUKARYOTIC OUTGROUPS Many fungal (e.g. *Sporobolomyces*, *Saccharomyces cerevisiae*) and animal (*Monosigma brevicollis*, *Homo sapiens*, *Mus musculus*, *Caenorhabditis elegans*) species.

#### RED PLANTS

- Cyanidioschyzon merolae* – unicellular (Japan)
- \**Chondrus crispus* - multicellular - MGE
- \**Galdieria* – unicellular (Weber, MSU)
- \**Porphyra purpurea* – multicellular - JGI
- Also in Progress: at least 20 angiosperms, plus 7 basal angiosperms; 5 gymnosperms and numerous EST projects, including EST projects at Maryland for *Nitella*, *Coleochaete*, *Chaetosphaeridium*, *Spirogyra*, and *Klebsormidium* that we anticipate will be available well before the proposed workshop. (Zahn et al. 2008, *Science* 320:465).

## **Preliminary Agenda for the Grand Challenge Workshop**

### **I. Grand challenge problem: the evolution of multicellularity and sexuality in plants – Gantt, convener**

1. Welcoming remarks – Gantt
2. Multicellular generations in the life cycles of photosynthetic eukaryotes – Cooke
3. Phylogenetic relationships of photosynthetic eukaryotes – Delwiche
4. Discussion - focus on major themes in GC problem

### **II. Genomic resources for investigating the GC problem – Delwiche, convener**

1. Brief overview of genetic resources for addressing the GC problem – Delwiche
2. Red plants – Brawley and Gantt
3. Green plants – Karol, Miller, Banks and Quatrano
4. Brown plants – Armbrust and Cattolico
5. Potential outgroups – Galagan and Haag
6. Inferring metabolism from the genome - Galagan
7. Discussion - evaluate the suitability of available and forthcoming genetic resources for addressing GC problem

### **III. Important genes and genomic structures regulating the life cycles and sexuality of multicellular plants – Wolniak, convener**

1. Phylogenetic inventory of meiotic genes - Logsdon
2. Mating type genes in *Chlamydomonas* - Goodenough
3. Flagellum genes in *Chlamydomonas* - Dutcher
4. Flagellum structure in land plants – Wolniak
5. Genomic structures in eukaryotes - Lynch
6. Transcription factors and multicellularity - Miller
7. RNA processing genes - Mount
8. Discussion - identify major genes and genomic structures for eukaryotic life cycle regulation and the evolution of plant multicellularity

### **IV. Genomic challenges and cyberinfrastructural needs for addressing the GC problem – Mount, convener**

1. An assessment of current and forthcoming state of computational resources – Prochnik, Rokhsar and Galagan
2. An overview of new cyberinfrastructural needs for this GC project – Mount
3. The resources of iPlant Collaborative, and its plans to design, implement, and support new cyberinfrastructure - iPlant Collaborative representative
4. Discussion: evaluate the suitability of existing and proposed new cyberinfrastructure for performing GC project. – Everyone.

### **V. Panel discussion on potential education, outreach, and training opportunities – Cooke, moderator**

Panel participants – high school teachers (Fields and Michael), a K-12 educational software specialist (as identified by iPlant Collaborative), and iPlant Collaborative representative in charge of outreach activities.

### **VI. Future directions – GCW organizers**

1. The next steps in the GC process and the different roles of iPlant Collaborative and GC group - iPlant Collaborative representative
2. Discussion - how to achieve the future objectives of the Grand Challenge group. Everyone.