

## **Impacts of Climate Change on Plant Productivity World-Wide. Prediction of Phenotype from Genotype. Data Integration for Analysis and Prediction Across Process Scales**

### **Organizers**

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Ruth Grene. Professor. Plant Physiology, Virginia Tech. Blacksburg, VA 24061. Phone: (540) 231-6761. Fax: (540) 231-5755. E-Mail: [grene@vt.edu](mailto:grene@vt.edu) Functional genomics of abiotic stress responses in plants. Diversity of stress resistances within crop species. Teach Biological Paradigms for Bioinformatics (grad course for computational students). Faculty Liaison for Virginia Tech Alliance for Minority Participation ( part of VA-NCAMP) in STEM fields.

T.M. Murali, Assistant Professor, Computer Science, Virginia Tech, Blacksburg, VA 24061. Phone (540) 231- 8534. E-Mail: [tmurali@vt.edu](mailto:tmurali@vt.edu). Computational and systems biology. Cellular response networks and their building blocks. Design and analysis of algorithms. Teach Computational and Systems Biology

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Jeffrey W. White. Plant Physiologist. Arid Land Agriculture Research Center, USDA ARS, Maricopa, AZ. Tel: +1-520-316-6368. FAX: +1-520-316-6330. E-mail: [Jeffrey.White@ars.usda.gov](mailto:Jeffrey.White@ars.usda.gov) Using ecophysiological models and geo-spatial tools, studies plant response to global change factors in agroecosystems.

Pamela Ronald. Plant Pathologist. UC Davis Tel 1530 752-1654, email [Peronald@ucdavis.edu](mailto:Peronald@ucdavis.edu) UC Davis. Ronald studies the role that genes play in the rice plant's response to its environment, with a focus on disease resistance and flood tolerance. She leads a K-12 program for students about rice genetics and bioenergy and written about genetic engineered for the general public.

### **Research Teams Who have Agreed to Collaborate to date.**

**VirtualPlant Team:** [www.virtualplant.org](http://www.virtualplant.org)

Rodrigo Gutierrez ([rg98@nyu.edu](mailto:rg98@nyu.edu)), Manpreet Katari ([mkatari@nyu.edu](mailto:mkatari@nyu.edu)), and Dennis Shasha ([shasha@cs.nyu.edu](mailto:shasha@cs.nyu.edu)), & Gloria Coruzzi ([gloria.coruzzi@nyu.edu](mailto:gloria.coruzzi@nyu.edu))  
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**Sol Genomics Network** <http://www.sgn.cornell.edu/>

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### Possible participants (to be invited if proposal is selected)

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3. Bartels, Dorothea, Rheinische Friedrich-Wilhelms-Universität, Bonn, Desiccation tolerance. Extremophiles
4. Beavis, Bill. Professor. Iowa State Univ. Ames, IA. QTL analysis and quantitative genetics. Formerly chief scientific officer at the National Center for Genomics Research, where he worked on a data interchange system (ISYS) similar to what we propose.
5. Boerma, Roger. Professor. Univ. Georgia. Athens, GA. Email: [rboerma@uga.edu](mailto:rboerma@uga.edu). Phone: (706) 542-0927. Molecular breeding and genetics with emphasis on soybean.
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12. Dierig, Dave. Research Geneticist. Arid Land Agriculture Research Center, USDA ARS, Maricopa, AZ. Tel.: 520-316-6360 Fax.: 520-316-6330. Email: [David.Dierig@ars.usda.gov](mailto:David.Dierig@ars.usda.gov) Breeding new crops for novel oil characteristics.
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14. Dyer, John. Arid Land Agriculture Research Center, USDA ARS, Maricopa, AZ. Molecular biology of lipid synthesis in cotton and Lesquerella.
15. Gallo, Maria. Associate Professor in the Dept. of Agronomy , University of Florida, Co-director of Scientific Thinking and Educational Partnership (STEP) <http://step.ufl.edu/research.html>. E mail: [mgmea@ifas.ufl.edu](mailto:mgmea@ifas.ufl.edu)
16. Grant, Robert. Professor. Dept. Renewable Resources. Univ. Alberta, Edmonton, AB, Canada. Tel.: (780)4926609. Fax: (780)4924323. Email: [robert.grant@ualberta.ca](mailto:robert.grant@ualberta.ca) Plant to ecosystem scale modeling.
17. Heath, Lenwood. Virginia Tech (VT). Computer Science, Bioinformatics
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20. Jaiswal, Pankaj. Research Associate. Plant Breeding and Genetics. Cornell Univ., Ithaca, NY. Gramene database and the Plant Ontology Consortium.
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28. Mendes, Pedro. Associate Professor, Virginia Bioinformatics Institute. Modeling and simulation of biochemical systems. Global optimization and inverse problems. (540) 231-7411.
29. Mittler, Ron. Hebrew University and University of Nevada . Abiotic stress effects and modeling.
30. Pardo, Jose. Instituto de Recursos Naturales y Agrobiología, Consejo Superior de Investigaciones Científicas, Sevilla 41012, Spain Functional Genomics of abiotic stress tolerance in plants
31. Pereira, Andy, VBI. Stress tolerance in crop plants. Networks.
32. Rhee, Sue. Carnegie Institute of Sciences
33. Saghai Maroof, VT, Molecular genetics of stress tolerance in soybean
34. Schlapfleitner, Roland, Centro Internacional de La Papa (CIP), Lima, Peru. Drought tolerance traits in Andean potato populations.
35. Schmitt, Johanna, Stephen T. Olney Professor of Natural History and Professor of Biology and Environmental Studies. Dept Ecology & Evolutionary Biology, Brown University. Adaptive evolution of developmental, physiological, and life history traits in natural plant populations
36. Schwender, Jorg. Research Scientist, Brookhaven National Lab. Lipid metabolism.
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## Summary

Anticipated global climate change will require directed adaptations of crop species on an unprecedented magnitude in order to sustain agricultural production. Our Grand Challenge seeks to dramatically improve quantitative prediction of phenotypes by facilitating the characterization of “molecular pathways” of ecologically and agriculturally important traits affected by climate change. The project will create computational tools that enable the integration of phenotypes across diverse species. A key focus will be the development of infrastructure tools for the global integration of all available high throughput data for effects of abiotic stress factors, associated with climate change, that shape crop plant performance in natural environments. Such integration can greatly accelerate the generation and testing of new hypotheses. The most promising hypotheses can be implemented in process-based simulation tools for further testing and application to climate change research issues ranging from plant breeding strategies to regional impact and mitigation studies.

Within the next few years, enormous amounts of functional genomics, proteomics, metabolomics, and comparative genomics data will be acquired. Multidisciplinary approaches are needed that use current biological knowledge to relate genetic change to phenotypic outcome, as are young scientists that are trained in more than one discipline. The existing datasets are often incomplete, dated, difficult to access, lacking in quality control, and error-prone. Nevertheless, they contain valuable data that are under-utilized. Using statistical and computational methods developed within the iPlant context, these data will be integrated to generate more accurate views of gene function and to identify species- or genotype-specific deviations, alterations, and adaptations to abiotic stresses associated with climate change. Such networks can directly inform phenotypic predictions of developmental characteristics in varied tissues and environmental contexts, which can guide plant breeding. This level of modeling can also support how processes are represented in the more integrative crop simulators, which typically provide quantitative predictions of phenotypes at the tissue, organ, plant or community scales.

This workshop will generate new, and intensify existing, communications concerning form and content of available datasets across different crop communities, and then relating those, where possible and useful, to the model plants *Arabidopsis* and rice, as well as to other major crop species. Through the Grand Challenge proposal development process, we will identify existing data and software resources, computational and mathematical gaps, and relevant models toward the goal of predicting crop phenotypes from genotypes. Three major plant productivity traits affected by climate change will be discussed in detail: (i) ***temperature, atmospheric CO<sub>2</sub>, and ozone induced responses***; (ii) ***water deficit and flooding induced responses***; and (iii) ***phenology***. The proposed Grand Challenge Workshop (GCW) will include participants from the fields of plant biology, genomics, bioinformatics, crop breeding, crop physiology, plant simulation modeling, computer science, mathematics, and education. Expected workshop outcomes include an initial consensus on key limitations in cyberinfrastructure that limit current modeling approaches, a better understanding of how different quantitative models interconnect, prioritization among traits, and identification of working groups needed to finalize the Grand Challenge Proposal.

## Introduction

**Our Grand Challenge seeks to radically improve the characterization of the “molecular pathways” of selected ecologically and agriculturally important traits affected by climate change with the specific, testable goal of improving quantitative prediction of phenotypes.** We are guided by the call from the National Academy of Sciences for “a significant broadening of the National Plant Genome Initiative mission to include the basic biology of economically relevant traits in models and crop species, deeper investigations into plant diversity, and plant adaptation to various ecological niches, and continued expansion of translation to breeders and farmers”<sup>1</sup>.

The focus of this Grand Challenge is on documenting, modeling, and understanding the plant global change response syndrome. This will generate predictive tools to guide crop breeding toward assured future food security and knowledge-based ecosystem preservation<sup>2</sup>. Responses to current and future food shortages require accurate predictions of how individual genotypes within crop species respond to abiotic stresses induced by climate change. This challenge aligns with the “genotype to phenotype problem”<sup>3</sup>, which, in reality, includes the effects of **Genotype, Environment, and Management on Phenotype (GEMP)** and is highlighted as a core research priority for international agriculture (e.g., [www.irri.org/media/press/press.asp?id=126](http://www.irri.org/media/press/press.asp?id=126)).

In the last 40 years, the numerical prediction of plant traits in the field has advanced greatly through models that are important springboards for the GEMP problem. They are used in climate change impact assessment<sup>4</sup>, and efforts have begun to incorporate realistic genetic controls<sup>5, 6</sup>). Genome structure and gene function information in model dicots and monocots (*Arabidopsis*, rice, poplar, maize) provides a reference framework to compare biological processes across species. High-throughput technologies have uncovered a wealth of information on gene expression and regulation in various developmental stages, conditions, and biological processes. Genome-wide reverse genetics analyses of gene functions are being addressed by mutations and natural variants.

Furthering the quantitative fusion of ecophysiological and “omic” approaches requires a robust cyberinfrastructure, a discovery environment, to integrate and analyze information from gene to phenotype, across species, and from the laboratory to the field. Research tasks to be facilitated by this discovery environment include (1) using genomic and phenotype data to extract approximate network structures responsive to climate change induced stresses, to (2) suggesting critical experiments, to (3) the creation, modification, and testing of models. These activities are not a linear sequence but should fluidly branch and iterate in order to optimally exploit/drive insight creation. Because of the many ecosystem services that plants provide and the ubiquity of climate change, the methods and models to emerge from this discovery environment should find broader use within plant science.

Our Grand Challenge activities emphasize key traits affected by climate change and as expressed in species having large amounts of existing genetic, metabolic, and/or phenotypic data, and already being modeled for environmental responses, albeit with variable levels of skill. This existing knowledgebase will allow for rapid integration into the cyberinfrastructure that we will develop to meet our Grand Challenge. We will focus on three response types affected by climate change, described briefly below.

***Water deficit and flooding induced responses:*** The frequency and severity of droughts and flooding (e.g. Myanmar) are expected to increase in many regions, while decreased runoff impairs reservoir and ground water recharge. This creates a need for drought and submergence tolerant crops, especially those with high water requirements (e.g. [drought.irri.org](http://drought.irri.org)). Inter- and intra-specific gene expression studies have identified multiple pathways that are regulated in response to water stress<sup>7, 8, 9, 10, 11</sup>, where available sequence data often reveal similar promoter motifs in orthologous, water deficit-responsive genes<sup>12</sup>. In general, osmotic changes, “recorded” at the cell membrane, are transduced in the form of rapid metabolic changes involving generation of reactive oxygen species (ROS), ABA metabolism, phospholipid metabolism, the generation of secondary messengers, calcium sensing, antioxidant signaling and defense pathways, and the synthesis of protective molecules<sup>13, 14</sup>. Integration of high throughput datasets across species and stresses will allow us to enhance our understanding of these cellular responses to abiotic stresses across plant species.

Rice and maize have been genetically modified based on modern genetic information for drought tolerance, water use efficiency or flooding tolerance<sup>15,16,17,18</sup>, and some of these genotypes are already dramatically improving yields in farmers' fields<sup>16</sup>; (Mackill and Ronald, unpublished). Various crop improvement programs targeting drought-prone environments already use simulation models to interpret genotype and environment interactions

**Temperature, atmospheric CO<sub>2</sub>, and ozone induced responses:** Elevated carbon dioxide [CO<sub>2</sub>] and ozone [O<sub>3</sub>] are increasing worldwide due largely to human activities. Many plant species experience stress in this altered atmosphere, defined as the deviation from normal, evolutionarily shaped homeostatic conditions<sup>19,20,21,22</sup>. Increases of just 20% over the natural concentration of ozone, which are common, reduce yield in a number of crops<sup>23</sup>. The necessity to increase crop production worldwide will require enhanced efforts in breeding both ozone-resistant genotypes, and genotypes adapted to function in a different CO<sub>2</sub> atmosphere from the one in which central metabolism evolved over millions of years. Relevant mechanisms include, in addition to those mentioned above: altered signaling between carbon and nitrogen assimilation pathways, and multiple control points for the expression of photosynthetic genes and proteins, partially through sugar sensing (which is also linked to stress responses<sup>24</sup>). Greenhouse gasses and temperature can interact as stressors. Under high CO<sub>2</sub>, soybean plants in the field were warmer than controls (Bohnert, pers. comm.), and gene expression data from plants under elevated CO<sub>2</sub> showed induction of several heat shock proteins<sup>22</sup>. This temperature sensitivity adversely affects crop yield<sup>25</sup>. Mechanistic models of leaf photosynthetic metabolism will be critical tools for establishing direct impacts of climate change factors on plant productivity<sup>26,27,28,29,30,31</sup>. Extant data and modeling environments will facilitate quantitative lipid modeling<sup>32</sup>, and brassica oil seed crops like rape and Lesquerella<sup>33</sup> present opportunities for leveraging from Arabidopsis. Warming and elevated CO<sub>2</sub> impacts were estimated by ecophysiological models by the IPCC<sup>4</sup>, but the reliability of model assumptions remains controversial<sup>34</sup> since the models failed to consider stressors including O<sub>3</sub> and heat shock.

**Phenology:** The timing of key events such as anthesis and maturity is often a primary determinant of net productivity and also influences other responses to abiotic and biotic stresses. Warmer temperatures typically accelerate flowering and maturity, and productivity reductions related to global warming partially reflect this response. Over 100 loci influence flowering time in Arabidopsis, and many of their functions are conserved in monocots such as rice and wheat<sup>35</sup>. A large body of molecular information exists for these gene interactions, and responses to environmental factors are being dissected at the genome level. Molecular and genotypic data have been integrated into ecophysiological models. An NSF-funded FIBR project (co-PI Welch) models flowering behavior of diverse Arabidopsis ecotypes in natural environments using simplified genetic networks. Major loci affecting response to photoperiod and vernalization are known for many crop species, but there is less certainty about loci for traits such as earliness per se. Comparisons with Arabidopsis suggest there are cases both of homology and of independent evolution of mechanisms (e.g., for vernalization in wheat). Gene-based prediction of phenology in crop species shows promise, but the models are still rudimentary (e.g.,<sup>36, 37, 38</sup>).

### **Current state of resources and computational thinking in the field**

One approach to predicting phenotype from genotype is based on quantitative genetics<sup>39</sup>, which involves linear, algebraic, population-level theory that (1) deals with trait means and (co)variances and (2) tracks phenotypic changes across generations. The genetic factors can be resolved into quantitative trait loci, which can sometimes be identified at the gene level, such as tomato fruit size and shape<sup>(40,41)</sup>, rice heading date<sup>42</sup> and yield<sup>42</sup>. Ecophysiological models, pioneered by de Wit<sup>43</sup>, mimic how plants respond to temperature, solar radiation, water and nutrient levels. Response components include: (i) phenology; (ii) dry matter production and partitioning; and (iii) growth processes. These models are nonlinear differential equations whose solutions are time series of variables such as plant biomass. Morphological realism can be improved via L-systems, sets of rules describing organ differentiation ([algorithmicbotany.org/FSPM07](http://algorithmicbotany.org/FSPM07)) as influenced by time, genetic switches<sup>44</sup> and morphogenetic factors<sup>45</sup>. An L-system was used<sup>46</sup> to link Arabidopsis growth and development with genes.

A third approach for predicting phenotypes has emerged based on genetic, metabolic, and system-level networks<sup>47; 48, 49; 50; 51; 52; 53; 54; 55; 56</sup>. Arabidopsis gene network models exist for stress and for metabolic processes<sup>57,58,19</sup> (Lee and Marcotte, in prep.) and are being extended to other plants (Krishnan & Pereira, in prep.; Ronald and Marcotte, in prep.). Metabolic systems models can provide the nuclei of genomic level hypotheses: their outputs are time series of metabolite concentrations, which can be directly compared to measured data<sup>29</sup>. The inputs to kinetic models are enzyme activities or concentrations obtainable from proteomics data. These network models provide a framework to append functionalities from crop interaction models. However, existing cyberinfrastructure poorly supports comparing and integrating of large datasets across species and genotypes. The VirtualPlant software system is a notable exception ([www.virtualplant.org](http://www.virtualplant.org)) (Katari, Shasha, Coruzzi and Gutierrez, in prep.). We propose to further develop this capability to facilitate the discovery of stress responsive mechanisms that may, or may not, be specific to given genera, species, or genotypes.

### **Identification and accessibility of available datasets**

Genomic data are well-curated through databases such as TAIR ([www.arabidopsis.org](http://www.arabidopsis.org)), which includes the complete Arabidopsis genome sequence along with data on gene structure, gene products, known metabolic pathways, gene expression (provided by Geneinvestigator), phenology of insertion mutants (in some cases), DNA and seed stocks, genome maps, and genetic and physical markers. However, TAIR has no repository of metabolomic data, nor are there records of physiological data that, in many cases, accompanied the expression and phenological data. Other plant genomic databases include GrainGenes ([wheat.pw.usda.gov/GG2](http://wheat.pw.usda.gov/GG2)), Gramene ([pathway.gamene.org](http://pathway.gamene.org)), TIGR Rice Genome Annotation ([www.tigr.org/tdb/e2k1/osa1](http://www.tigr.org/tdb/e2k1/osa1)), Soybase ([www.soybase.org](http://www.soybase.org)), PlantGDB ([www.plantgdb.org](http://www.plantgdb.org)), SGN ([sgn.cornell.edu](http://sgn.cornell.edu)) for Solanales including tomato, potato, and peppers, and several Medicago databases. SGN also provides SolCyc, and Gramene provides RiceCyc, which are biochemical pathway databases that have “Omics” Viewers allowing users to upload high throughput data and paint them onto a metabolic map. However, aside from Arabidopsis and rice, there is no public repository of high throughput gene expression data even for genera for whom genomic data are curated, nor is there one for metabolomics data for any species. A plant lipidomics database will come online during the iPlant project, adding another data type (Welti and Roth, pers. comm.). Further examples are the Arabidopsis Lipid Gene Database ([lipids.plantbiology.msu.edu/](http://lipids.plantbiology.msu.edu/)), the rice kinase database ([rkd.ucdavis.edu/](http://rkd.ucdavis.edu/)), the rice glycosyltransferase database (Cao and Ronald, submitted), and KEGG ([www.genome.ad.jp/kegg](http://www.genome.ad.jp/kegg)), which contains rice and Arabidopsis sites but lacks genes/enzymes, data that are needed, especially for rice.

The above databases have rudimentary quantitative data on phenotypes, environments, and plant management, having emphasized qualitative or semi-quantitative traits. Yet such data are essential to fully specify the dependent variable, “P”, in the GEMP problem. The International Crop Information System (ICIS) is the largest data repository for crop species and contains pedigree, phenotypic, genetic, management, and environmental data. The rice version, IRIS, contains over  $2 \times 10^6$  germplasm identifiers, representing landraces, crosses, breeding populations, selections, or lines evaluated in trials or nurseries. SGN contains about 7000 accessions and 15,000 images, links genomes to phenomes, currently mainly tomato, based on open plant and gene ontologies. Data types include images, literature associations, and free text descriptions. SGN will soon support data reanalysis via an in silico QTL functionality.

The Generation Challenge Program (GCP; [www.generationcp.org](http://www.generationcp.org)), an international consortium working on drought in major crops, also generates publicly available phenotypic, genotypic, and genomic data relevant to this proposal.

### **Computational models and cyberinfrastructure support for the GEMP problem is limited.**

Current approaches for reverse-engineering molecular interactions and modeling GEMP relationships<sup>59</sup> are limited; they (a) only mine potentially interesting data patterns in data, needing extensive manual review to translate results into hypotheses and experiments; (b) make simplifying assumptions to account for under-determined systems; (c) require detailed and large-scale knowledge about molecular interaction networks, information that is unavailable even for *Arabidopsis*; and (d) struggle with increasingly intractable data fusion issues for analytic software arising from ever newer data types. The

cyberinfrastructure for our Grand Challenge must overcome such limitations by being transparent (equations and assumptions not buried in code), breaking down scaling barriers, allowing high throughput computations, integrating diverse data sets, and facilitating model and algorithm specification and testing. The modeling and support systems should explicitly tackle four issues: (a) uncertainty representation at several biological interaction network levels when multiple models are consistent with experimental data; (b) needs analyses to identify levels of model uncertainty compatible with specific applications; (c) experiment suggestion so as to best reduce localized model uncertainties in a cost-effective way; and (d) model refinement by incorporating new experimental results.

### **Participation of both plant and computational researchers**

We seek to address the GEMP problem by interdisciplinary research and modeling using the three outlined quantitative approaches. As the proposed participant list shows, collaboration already exists between plant and computational researchers and will expand in the project. Genomics specialists will work with experts on systems biology, algorithms, distributed computing, and data mining to make sequence, gene expression, and metabolomic data available through (actually or virtually) unified, analytic tool, model, and user interfaces. Bioinformaticists will participate in efforts involving stochastic models, extracting models from data, and assessing model, data, and parameter uncertainty. Genetic regulatory networks associated with climate change factor responses, both those common across species, and those unique to species, or genotypes within species, identified by these computational tools can link to metabolic models. Joint work with ecologists, plant breeders, agronomists, and crop modelers will bridge to field scales. The latter disciplines will provide use cases, field expertise, and portions of required data, while using data and methods from other disciplines to produce genetically-aware ecophysiological models.

### **Education, Outreach and Training Opportunities**

The simulation models that will be developed in parallel with our Grand Challenge efforts can be built upon to address numerous issues in plant biology, genetics, evolution, and ecology. Therefore, education, outreach and training opportunities on our Grand Challenge topic, effects of global climate change abiotic stress factors on plant productivity and the GEMP problem, will need to reach a broad-range of disciplines and age groups. The common modeling framework to be developed would provide students from all age groups an *in silico* laboratory, allowing them to conduct virtual experiments in diverse environments, for example improving understanding of how water availability and greenhouse gasses affect productivity, and how genetic changes may affect these relations. As students gain experience and knowledge, they can progress to models of increasing complexity without having to learn new software interfaces or data formats.

Existing programs that can be leveraged for potential outreach activities for our Grand Challenge education and outreach efforts will be identified and selected for proposal development. A NSF-funded art-science K12 outreach program (developed by UC Davis) introduces the concept of protein networks to elementary school students and can be built upon to promote the tools and science of our Grand Challenge. This NSF project reaches approximately 60,000 visitors at a Picnic Day at UC Davis and visitors to the New York Museum of Modern Art. Options directed toward minorities and under represented groups in Science and Engineering will be highlighted during the workshop and included for proposal development. The Scientific Thinking and Educational Partnership (STEP) at the University of Florida partners with faculty and their graduate students to tailor multi-media outreach programs designed to effectively communicate their research to target audiences. These can be utilized for our Grand Challenge.

A primary test-bed for our iPlant effort will be crop improvement. Outputs relating to prediction of responses of phenology, plant architecture, and molecular and metabolic events related to climate change can readily be incorporated into plant breeding. Phenology also has direct application to decision support using crop models, assessment of climate change impacts. We thus anticipate that the project will provide test cases affecting decisions of plant breeders, agronomists or farmers within four years. Since the project involves plant breeding and climate change groups, initial transfer should be direct. We would

conduct additional workshops for interested breeders or other members of the plant science community, such as workshops prior to the annual meetings of the Crop Science Society of America and the American Society of Plant Biologists.

### **Goals for the Grand Challenge Workshop.**

The immediate goal of this workshop is to reach an initial consensus on the feasibility of different approaches for data and model integration across organizational levels, with emphasis on lessons from existing tools such as Virtual Plant, the Regulatory Network of Marcotte and Ronald, and ICIS. We expect to identify key limitations in cyberinfrastructure that limit current modeling approaches and to understand better how different quantitative modeling approaches interrelate (Appendix 1). The workshop will also allow further prioritization among traits and refinement of the strategy for outreach. We expect that the interchanges will allow us to produce a draft for the Grand Challenge Proposal by meeting's end.

**Proposed Agenda (speakers' names are just suggestions at this time). General discussions will be held at the end of each section, in addition to those formally scheduled below.**

#### **Day 1**

- I. Keynotes
  - A. Introduction to iPlant Collaborative: iPlant Staff
  - B. Climate Change and Agriculture. IRRI/CIMMYT; Bruce Kimball , Lew Ziska
  - C. Genotype to Phenotype: Case Studies and Prospects
    1. Tim Setter (Cassava and Maize Stress Tolerance, Cornell University)
    2. Steve Baenziger (Wheat Breeding; Univ. Nebraska)
  - D. Presentation and Discussion of this Grand Challenge (brief).
  - E. Computational Tools for Network Building: Simon Kasif, Boston University
- II. Modeling approaches
  - A. Modeling/Network Building and this GC. T.M.Murali, Computer Science, VT
  - B. Virtual Plant 1: The VirtualPlant development team, New York University
  - C. Virtual Plant 2: L-systems. Ted Dejong, UC Davis
  - D. Regulatory Networks for Plants: Marcotte (Texas); Ma (Yale)
  - E. Ecophysiological modeling. Jeff White
  - F. Merging Network and Ecophysiological Models: Steve Welch

#### **Day 2**

- III. WormBase Resources: Genotype to Phenotype: Suggestion from L.Stein.
- IV. Genomic Resources for Plants
  - A. Arabidopsis: TAIR. Sue Rhee, Carnegie
  - B. Grasses: The Gramene Databases. Rice genomic resources: Pam Ronald
  - C. Solanaceae: Sol Genomics. Lukas Mueller, Boyce Thompson
  - D. Medicago. M. Udvardi, Noble Foundation.
  - E. Conclusions: Infrastructure Gaps, Overlaps, and Needs, Group Discussion
- V. Metabolomics data - prospects for integration. Oliver Fiehn, UC Davis
- VI. Phenotypic, environmental, management data resources
  - A. Ontologies: Pankaj Jaiswal, Plant Ontology Consortium; Cornell.
  - B. ICIS: Graham McLaren, CGIAR GCP Bioinformatics subprogram.
- VII. Education and Outreach: Melanie Correll and Maria Gallo

#### **Day 3**

- VIII. Teams
  - A. Group Discussion of Organization
  - B. Come together in teams to formulate our GC for a formal proposal
  - C. First Reports from Teams to Workshop
  - D. Second round of team meetings
  - E. Final Reports from Teams
  - F. Conclusions- Organizers

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8. Watkinson, J.I., et al. (2008) *Tuber development phenotypes in adapted and acclimated, drought-stressed Solanum tuberosum ssp andigena have distinct expression profiles of genes associated with carbon metabolism*. *Plant Physiology and Biochemistry* 46, 34-45
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19. Grene, R., Li P, and Bohnert HJ. (2008) Elevated CO<sub>2</sub> and Ozone – Their Effects on Photosynthesis In Volume II: Stress, Genes, Genomes, Proteomes, Regulation, Transformation and Bioengineering of The Chloroplast: (C.Rebeiz, ed), in press, Springer
20. Miyazaki, S., et al. (2004) Transcript expression profiles of *Arabidopsis thaliana* grown under controlled conditions and open-air elevated concentrations of CO<sub>2</sub> and of O<sub>3</sub>. *Field Crops Research* 90, 47-59
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22. Li, P.H., et al. (2006) Response diversity of *Arabidopsis thaliana* ecotypes in elevated [CO<sub>2</sub>] in the field. *Plant Molecular Biology* 62, 593-609
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25. Prasad, P.V., K.J. Boote, and L.H. Allen. (2006) Adverse high temperature effects on pollen viability, seed-set, seed yield and harvest index of grain-sorghum [*Sorghum bicolor* (L.) Moench] are more severe at elevated carbon dioxide due to higher tissue temperatures. *Agr. For. Met.* 139, 237-251
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### Education:

Clemson University, B.S., Agricultural and Biological Engineering, 1994  
Worcester Polytechnic Institute, Ph.D., Interdisciplinary in Biochemical Engineering/Plant Science, 2001  
Miami University, Postdoctoral Associate, Plant Physiology, 2001–2004

### Appointments:

2004-present Assistant Professor, Agricultural and Biological Engineering Department, Univ. of Florida

### Publications (5 publications most closely related to proposed project):

- Molas, M.L., J.Z. Kiss, and M.J. Correll. 2006. Gene Profiling the Red-Light Signaling Pathways In Roots. *J Exp Bot.* 57: 3217-3229.
- Correll, M.J. and J.Z. Kiss. 2005. The roles of phytochromes in elongation and gravitropism of roots. *Plant Cell Physiol.* 46:317-323.
- Correll, M.J., K.M. Coveney, S.V. Raines, J.L. Mullen, R.P. Hangarter, and J.Z. Kiss. 2003. Phytochromes play a role in phototropism and gravitropism in Arabidopsis roots. *Adv. Space Res.* 31:2203-2210
- Kiss, J.Z., J.L. Mullen, M.J. Correll, and R.P. Hangarter. 2003. Phytochromes A and B mediate red-light-induced positive phototropism in roots. *Plant Physiol.* 131:1411-1417.
- Correll, M.J. and P.J. Weathers. 2001. Effects of light, CO<sub>2</sub>, and humidity on carnation growth, hyperhydration, and cuticular wax development in a mist reactor. *In Vitro Cell. Dev. Biol.-Plant.* 37(3):405-413.

### Publications (5 other publications):

- Lee, S.-C., W.-C. Hu, M.J. Correll, and J. Xin. 2006. Accessing genome databases from internet-enabled mobile handheld devices. *The Proceedings for the 4<sup>th</sup> World Congress on Computers in Agriculture.*
- Correll, M.J. and J.Z. Kiss. 2002. Interactions between gravitropism and phototropism in plants. *J. Plant Growth Reg.* 21:89-101.
- Kiss, J.Z., M.J. Correll, J.L. Mullen, R.P. Hangarter, and R.E. Edelman. 2003. Root phototropism: how light and gravity interact in shaping plant form. *Gravitational and Space Biology Bulletin* 17: 16:55-60.
- Correll, M.J., Y. Wu, and P.J. Weathers. 2001. Controlling hyperhydration of carnations (*Dianthus caryophyllus* L.) in a mist reactor. *Biotech. Bioeng.* 71(4):307-314.
- Correll, M.J. and P.J. Weathers. 2001. One step acclimatization of plantlets using a mist reactor. *Biotech. Bioeng.* 73(3):253-258.

### Awards and Honors

- 2007 Appreciation Award for Outstanding Participation on the TROPI experiment, from European Space Agency and National Aeronautics and Space Administration
- 2007 Young Research Award, Florida Section of the American Society of Agricultural and Biological Engineers

1990-1994 USDA National Needs Fellowship

### **Synergistic Activities**

(a) Editor, *Advances in Space Research* Volume 39, Issue 7, 2007, (b) Reviewer for scientific Journals (*Advances in Space Research*, *Journal of Biological Engineering*, *In Vitro-Plant*, *American Society of Space and Gravitational Biology Bulletin*) (c) Mentor for high school students in the Student Science Training Program (2006, 2007), (d) 4-H workshop development and presentation on Space Agriculture (2008), (e) Development of a new undergraduate course and labs entitled “Applications in Biological Engineering” (f) Session chair Congress on Space Research (COSPAR 2008), (g) Publications committee member (Institute of Biological Engineers) (h) Speaker and mentor for the Center for Precollegiate Education on Biological Engineering for recruitment of minorities (i) Science for Life mentor for undergraduate research.

### **Recent Collaborations:**

Melissa Towler (Worcester Polytechnic Institute), Richard Edelman (Miami Univ.), Roger P. Hangarter (Indiana Univ.), Jack L. Mullen (Colorado State), Quinn Li (Miami Univ.), Steven Raines (Wisconsin), Sudipta Seal (Univ. Central FL), Joe H. Cho (Univ. Central FL), Marianne Steele (NASA-Ames), Robert Bowmann (NASA-Ames), Robert Ferl (Univ. of FL), C. Eduardo Vallejos (Univ. of FL), Mike Eoidice (NASA-Ames), Ray Bucklin (Univ. of FL), M. Lia Molas (Argentina Dept. Agriculture), Barbara Wyslouzil (Ohio State), Alex DiIorio (Worcester Polytechnic Institute), Bin Gao (Univ. of FL), Khe Chau (Univ. of FL), Jim Jones (Univ. of FL).

### **Graduate and Post Doctoral Advisors:**

Pamela J. Weathers, Ph.D. Advisor, Worcester Polytechnic Institute, MA and postdoctoral advisor John Z. Kiss, Miami University, OH.

### **Graduate Students:**

Thesis advisor (Chair): Ph.D. Current: Richard (S.C.) Lee, Alexander Stimpson, Hemant Gohil, Former: M.S. student Yibing Fu. Undergraduates: Current (one); Former (eight).  
Thesis advisor (committee): Ph.D. Abbay Koppar, Sachin Gaddekar.

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## Biographical Sketch

Greene, Ruth

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### Education

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INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Trinity College, Dublin, Ireland	BA Honors)	1961-5	Biochemistry
Washington University, St. Louis	MA	1966-8	Botany
University of California, Davis	PhD	1968-72	Plant Physiology
University of California, Berkeley	Post-Doc	1973-75	Ken Sauer Lab
Cornell University	Post-doc	1975-77	Andre Jagendorf Lab

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### Professional Experience

Professor of Plant Physiology, Virginia Tech, 1998-present  
Associate Professor of Plant Physiology, Virginia Tech, 1988-1998  
Adjunct Assistant Professor of Plant Biology, Cornell, 1985-1988  
Research Associate, Boyce Thompson Institute, Environmental Biology, Ithaca, NY.  
1979-1988

### Honors and Awards

National Science Foundation Career Advancement Award, 1992-94  
National Research Service Award (NIH), 1975-77  
National Institute of Health Postdoctoral Fellowship, 1973-74

### Five Relevant Peer-Reviewed Publications (all NSF-sponsored)

1. Watkinson JI, Sioson AA, Vasquez-Robinet C, Stromberg V, Heath LS, Bohnert HJ, and **Greene R** (2008) Tuber development phenotypes in adapted and acclimated, drought-stressed *Solanum tuberosum* ssp. *andigena* have distinct expression profiles of genes associated with carbon metabolism. *Plant Physiology and Biochemistry*. 46:34-45
2. Vasquez-Robinet C, Mane SP, Ulanov AV, Watkinson JI, Stromberg VK, De Koeeyer D, Schafleitner R, Willmot DB, Bonierbale M, Bohnert HJ, and Greene R (2008) Physiological and molecular adaptations to drought in Andean potato genotypes *J. Exp. Bot.*, 59: 2109 - 2123.
3. Mane SP, Vasquez-Robinet C, Sioson AA, Heath LS, **Greene R** (2007) Early PLD{alpha}-mediated events in response to progressive drought stress in Arabidopsis: a transcriptome analysis. *Journal of Experimental Botany* 2007 58:241-252.
4. Li P, Sioson A, Mane SP, Ulanov A, Grothaus G, Heath LS, Murali TM, Bohnert HJ, **Greene R**. (2006) Response diversity of Arabidopsis thaliana ecotypes in elevated [CO<sub>2</sub>] in the field. *Plant Mol Biol*. 62: 593-609
5. Li, P., Mane, S.P. Sioson, A., Vasquez Robinet, C. Heath, L.S. Bohnert, H.J., and **Greene, R** (2006). Effects of Chronic Ozone Exposure on Gene Expression in *Arabidopsis thaliana* Ecotypes and in *Thellungiella halophila*, *Plant Cell and Environment*, 29: 854-869

### Five Other Peer-Reviewed Publications:

6. Li P, Bohnert HJ, **Greene R** (2007) All about FACE--plants in a high-[CO<sub>2</sub>] world. *Trends Plant Sci*. 2007 12:87-9.

7. Sioson AA, Mane SP, Li P, Sha W, Heath LS, Bohnert HJ, **Greene R.** (2006) The statistics of identifying differentially expressed genes in Expresso and TM4: a comparison. *BMC Bioinformatics*; 7:215.
8. Pati A, Vasquez-Robinet C, Heath LS, **Greene R,** Murali TM (2006). XcisClique: analysis of regulatory bicliques. *BMC Bioinformatics.* 7: 218.
9. Watkinson JI, Hendricks L, Sioson AA, Vasquez-Robinet C, Stromberg V, Heath LS, Schuler, Bohnert HJ, Bonierbale M, and **Greene R,** (2006) Accessions of *Solanum tuberosum* ssp. andigena show differences in photosynthetic recovery after drought stress as reflected in gene expression profiles *Plant Science*, 171: 745–758
10. Watkinson, J.I. Sioson, A., Vasquez-Robinet, C. Shukla, M. Ellis, M. Heath, L.S., Ramakrishnan, N. Chevone, B., I., Watson, L.T., van Zyl, L., Sederoff, R.R. and **Greene, R.** (2003) Photosynthetic acclimation is reflected in specific patterns of gene expression in drought-stressed loblolly pine. *Plant Physiol*, 133: 1494-1503

#### Collaborators and Co-Editors

Bohnert, HJ, University of Illinois	Ramakrishnan, N, Virginia Tech
Bonierbale, M, Centro Internacional de la Papa	Sederoff, RR, North Carolina State University
Chevone, BI, Virginia Tech, retired	Sha, W, Virginia Tech
Grothaus, G, Google	Shukla, M, VBI
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Heath, LS, Virginia Tech	Sioson, AA, Ateneo de Naga University
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Pati, A, Virginia Tech	Watson, LW, Virginia Tech
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#### Graduate and Postdoctoral Advisors

Paul Castelfranco, University of California, Davis, retired, Daniel Kohl, Washington University, St. Louis, retired, Andre Jagendorf, Cornell University, retired, Richard Criddle, University of California, Davis, Ken Sauer, University of California, Berkeley

**Thesis Advisor and Postdoctoral Scholar Sponsor,** (6 graduate students, 4 post-doctoral), Alfred Hausladen, Duke University: Andreas Doulis, Mediterreanan Agronomic Institute: Neval Erturk, Converse College: Camellia Moses Okpodu, Norfolk State University: Cecilia Vasquez Robinet, Ludwigs Maximillian Universitat: Shrinivasrao Mane, Virginia Bioinformatics Institute: James V. Anderson, USDA: Ashima Sen Gupta, USDA: NR Madamanchi, University of North Carolina; Hiromi Tasaki, current

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### Professional Preparation

#### Education

Indian Institute of Technology, Madras, India	Computer Science	B. Tech	1991
Brown University, Providence, Rhode Island	Computer Science	Sc. M.	1993
Brown University, Providence, Rhode Island	Computer Science	Ph. D.	1999

#### Postdoctoral Research Appointment

Stanford University, Palo Alto, California    Computer Science    1998-1999

### Appointments

2003–present Assistant Professor, Department of Computer Science, Virginia Polytechnic Institute and State University  
2004–present Assistant Professor, Genetics, Bioinformatics, and Computational Biology Program, Virginia Polytechnic Institute and State University  
2003–2006 Adjunct Assistant Professor, Bioinformatics Program, Boston University  
2001–2003 Senior Research Associate, Bioinformatics Program, Boston University  
1999–2001 Member of Research Staff, Cambridge Research Lab, Compaq Computer Corp.

### Five Most Relevant Publications

- “Network Legos: Building Blocks of Cellular Wiring Diagrams,” T. M. Murali and Corban Rivera, *Journal of Computational Biology*, to appear, 2008. <http://bioinformatics.cs.vt.edu/~murali/papers/network-lego.pdf>
- “Compositional Mining of Multi-relational Biological Datasets,” Ying Jin, T. M. Murali, and Naren Ramakrishnan, *ACM Transactions on Knowledge Discovery from Data*, volume 2, number 1, pp. 1–35, 2008. <http://doi.acm.org/10.1145/1342320.1342322>
- “The Landscape of Human Proteins Interacting with Viruses and Other Pathogens,” Matthew D. Dyer, T. M. Murali, and Bruno W. Sobral, *PLoS Pathogens*, vol. 4, pp. e32, 2008. <http://dx.doi.org/10.1371/journal.ppat.0040032>
- “Whole Genome Annotation using Functional Linkage Networks,” Ulas Karaoz, T. M. Murali, Stan Letovsky, Yu Zheng, Chunming Ding, Charles R. Cantor, and Simon Kasif, *Proc. National Academy of Sciences*, vol 101, pp. 2888–2893, 2004. <http://www.pnas.org/cgi/content/full/101/9/2888>
- “Extracting Conserved Gene Motifs from Gene Expression Data,” T. M. Murali and Simon Kasif, in *Proceedings of the Seventh Pacific Symposium on Biocomputing*, 2003, pp. 77–88. <http://psb.stanford.edu/psb-online/proceedings/psb03/murali.pdf>

### Five Other Significant Publications

- “Atomic Level Computational Identification of Ligand Migration Pathways between Solvent and Heme Iron in Myoglobin,” Jory Z. Ruscio, Deept Kumar, Maulik Shukla, Michael G. Prisant, T. M. Murali and Alexey Onufriev, *Proceedings of the National Academy of Sciences*, to appear, 2008.
- “Computational Prediction of Host-Pathogen Protein Interactions,” Matthew D. Dyer, T. M. Murali, and Bruno Sobral, *Bioinformatics*, 13, 2007, pp. i159–i166, issue on the *15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2007. [http://bioinformatics.cs.vt.edu/~murali/papers/Predicting\\_HP\\_PPis.pdf](http://bioinformatics.cs.vt.edu/~murali/papers/Predicting_HP_PPis.pdf)

“XcisClique: Analysis of Regulatory Bicliques,” Amrita Pati, Cecilia Vasquez-Robinet, Lenwood S Heath, Ruth Grene and T. M. Murali, *BMC Bioinformatics*, vol 7, 218, 2006. <http://www.biomedcentral.com/1471-2105/7/218/abstract>

“The Art of Gene Function Prediction,” T. M. Murali, Chiang-Jiun Wu, and Simon Kasif, *Nature Biotechnology*, vol 12, pp. 1474–1475, 2006. <http://www.nature.com/nbt/journal/v24/n12/full/nbt1206-1474.html>

“A Monte-Carlo Algorithm for Fast Projective Clustering,” Magda Procopiuc, Michael Jones, Pankaj K. Agarwal, and T. M. Murali, *Proceedings of the 2002 International Conference on Management of Data*, 2002. <http://bioinformatics.cs.vt.edu/~murali/papers/projective.ps.gz>

## Awards and Honours

**2005** Outstanding New Assistant Professor, Dean’s Award, Virginia Polytechnic Institute and State University.

**2004–2006** Faculty Fellowship, Virginia Bioinformatics Institute and College of Engineering, Virginia Polytechnic Institute and State University.

**1987** The first Indian participant in the International Summer Students Program conducted by the National Aeronautics and Space Administration, Washington, D.C.

**1986–1991** Scholarship from the National Council for Education, Research and Training, India.

## Synergistic Activities

(a) Programme committee or Session/Area chair: Gene expression and microarray analysis, 26th Annual International Conference, IEEE Engineering in Medicine and Biology Society, 2004; First IEEE workshop on Computer Vision Methods for Bioinformatics, 2005; 2007 IEEE International Conference on Data Mining; Algorithms and Bioinformatics track, 6th ACS/IEEE International Conference on Computer Systems and Applications, 2008; International Symposium on Information Visualization in Biomedical Informatics (2008); Microarray data analysis, 2008 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). (b) C-Tech<sup>2</sup> camp for high school girls, Virginia Tech, 2005–2007. (c) Graduate course on *Computational Systems Biology*, 2003–2007. (d) Co-organiser, special session on “Challenges and Opportunities in Host-Pathogen Systems Biology” at *16th Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB), 2008. (e) Tutorial on “Host-Pathogen Protein Interaction Networks,” 9th International Conference on Systems Biology, 2008.

## Collaborators and other Affiliations

**Current/Recent Collaborators** Srinivas Aluru (Iowa State), Mikael Benson (Gothenburg), Hans Bohnert (UIUC), Elizabeth Boone (Stony Brook Univ.), Charles R. Cantor (Boston Univ and Sequenom Inc.), Bruce Conklin (UCSF), Jacquelyn Fetrow (Wake Forest Univ), Ruth Grene (Virginia Tech), Lenwood Heath (Virginia Tech), Richard Helm (Virginia Tech), Simon Kasif (Boston Univ), Michael Katze (Univ. of Washington), Stanley Letovsky (Boston Univ), Madhav Marathe (Virginia Tech), Jean Peccoud (Virginia Tech), Vladimir Pavlovic (Rutgers Univ), Malcolm Potts (Virginia Tech), Michael Prisant (Duke Univ), Alexey Onufriev (Virginia Tech), Jean Peccoud (Virginia Tech), Andy Pereira (Virginia Tech), Naren Ramakrishnan (Virginia Tech), Padmavathy Rajagopalan (Virginia Tech), Vladimir Shulaev (Virginia Tech), Bruno Sobral (Virginia Tech), Beverly Snively (Wake Forest Univ), Brett Tyler (Virginia Tech), Peter Uetz (JCVI), (Joseph) Yue Wang (Virginia Tech), Jason Xuan (Virginia Tech), Jory Zmuda (Univ. of California, Berkeley)

**Graduate Advisor and Postdoctoral Sponsors** **Graduate** Jeffrey S. Vitter (Duke University). **Postdoctoral** Leonidas J. Guibas and Jean-Claude Latombe (Stanford University).

**Thesis Advisor** **Ph.D students** Current: Matthew D. Dyer and Corban Rivera. **Masters students** Current: David Badger, Naveed Massjouni, Clifford Conley Owens; Former: Greg Grothaus, Shivaram Narayanan, Corban Rivera, Srinivas Venkatraghavan. **Undergraduate students** One (current); Eight (former), of whom six are pursuing graduate studies.

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**Education:**

University of Strasbourg, France, French Language Studies, Diploma 1981.  
Reed College, Portland, Oregon, Biology, B.A. 1982.  
Stanford University, Biology, M.A. 1984.  
University of Uppsala, Uppsala, Sweden, Plant Physiology, M.S. 1985.  
UC Berkeley, Molecular and Physiological Plant Biology, Ph.D. 1990.

**Appointments:**

2007-present Biologist Scientist Faculty, Physical Biosciences Division at Lawrence Berkeley National Laboratory  
2004-2007 Faculty Assistant to the Provost  
2004-present Chair, Plant Genomics Program  
2002-present Professor, Department of Plant Pathology, UC Davis  
1997-2002 Associate Professor, Department of Plant Pathology, UC Davis  
1992-1997 Assistant Professor, Department of Plant Pathology, UC Davis  
1990-1992 Postdoctoral Fellow, Department of Plant Breeding, Cornell University  
1984-1985 Fulbright Fellow, Inst. Phys. Botany, University of Uppsala, Sweden  
1983-1984 Research Assistant, Department of Biology, Stanford University, CA

**Other experience and professional service:**

2007-present Director Grass Genetics, Joint Bioenergy Institute  
2006-present Faculty co-Director of UC Davis/Chevron \$25 M research program  
2004-present Chair, UCD Plant Genomics Program  
2006-present Associate Director, Davis Bioenergy Group  
2006-2007 Chair, Gardens, Art and the Environment Task Force  
2005-present Member, Genome Center Campus Advisory Committee  
2004-2007 Chair, American Society of Plant Biology Public Affairs Committee  
2003-2007 Advisor to NSF MPSS project, Blake Meyers, PI  
2005-present External advisor Zhejiang University Agricultural Institute  
2005-present Senior Editor, Plant Physiology  
2003 National Science Foundation panel review: Integrative Plant Biology  
2003-present International Rice Functional Genomics Consortium Steering Committee  
2002-present Scientific advisor for the UCD ArrayCore facility  
2001-present External Scientific Advisory Committee member for the NIH Minority program  
2001-present UC working group Linking Research and Education in Agricultural Biotechnology  
1999-present Scientific advisory board member of UC Davis CONNECT  
1995,96 USDA Plant Pathology Review Panels.

**Honors:**

2008-2009 Fulbright Distinguished Chair in the Natural Sciences and Engineering at the Hebrew University of Jerusalem  
2007 Consultative Group on International Agricultural Research Science Award for Outstanding Scientific Article  
2007-2008 Fellow, Japan Society for the Promotion of Science  
2006 Fellow, American Association for the Advancement of Science  
2006-2007 Fellow, Davis Humanities Institute  
2004 Gamma Sigma Delta  
2004 Davis Aquatic Masters Swimmer of the month  
2002-2005 Honorary Scientist at the National Institute of Ag Biotechnology, Korea  
1999-2000 John Simon Guggenheim Fellow

1990-1992 National Institute of Health Postdoctoral Fellowship, Cornell University.  
1988-1990 California Biotechnology Fellowship, University of California, Berkeley.  
1985-1986 McKnight Training Grant Fellowship in Plant Biology, UC Berkeley.  
1984-1985 Fulbright Fellow, Inst. Physiological Botany, University of Uppsala, Sweden.  
1982 Exxon Student Scholarship, Bermuda Biological Station.

***Publications most closely related to proposed project:***

Ronald P, An G and Jung K. 2008. Towards A Better Bowl of Rice: Assigning biological function to 60,000 rice genes. *Nature Review Genetics*. 9:91-101.  
Dardick C, Johann Chen, Todd Richter, Ouyang Shu, and Pamela Ronald. 2006. The Rice Kinase Database (RKD): a phylogenomic database for the rice kinome. *Plant Physiology*. 143: 579-586.  
Kenong Xu, Xia Xu, Takeshi Fukao, Patrick Canlas, Sigrid Heuer, Julia Bailey-Serres, Abdel Ismail, Ronald, PC, David J. Mackill. 2006. *Sub1A* encodes an ethylene responsive-like factor that confers submergence tolerance to rice. *Nature*. 442. 705-708. Selected by Faculty of 1000 Biology as one of the most important advances in the field. Awarded CGIAR prize for outstanding scientific article  
Dardick C and Ronald PC. Plant and Animal Pathogen Recognition Receptors Signal through Non-RD Kinases. 2005. *PLoS Pathogens*. *PLoS Pathog*. 2. (1):e2.  
Fukao T, Kenong X, Ronald P and Bailey-Serres J. 2006. A variable cluster of ethylene responsive-like factors regulates metabolic and developmental acclimation responses to submergence in rice. *Plant Cell*. 18: 1791-1802.

***Other significant publications:***

Chern, M.-S., Canlas, P.E., Fitzgerald, H.A., Ronald, PC. 2005. NRR, a Negative Regulator of Disease Resistance in Rice that Interacts with Arabidopsis NPR1 & Rice NH1. *TPJ*. 43. (5) : 623-635.  
Song W-Y, Wang G-L, Chen L, Kim H-S, Pi Li-Ya, Gardner J, Wang B, Holsten T, Zhai W-X, Zhu L-H, Fauquet C, Ronald PC. 1995. A receptor kinase-like protein encoded by the rice disease resistance gene *Xa21*. *Science*, 270:1804-1806.  
Lee SW, Han SW, Bartely L, Ronald P. 2006. The unique characteristics of *Xanthomonas oryzae* pv. *oryzae* AvrXa21 and implications for plant innate immunity. *PNAS* 103:44.  
Li L, Wang X, Sasidharan R, Stolc V, Deng W, He H, Korbel J, Chen X, Tongprasit W, Ronald P, Chen R, Gerstein M and Deng X-W. 2007. Global Identification and Characterization of Novel Transcriptionally Active Regions in the Rice Genome. *PLoS One*. 2(3): e294  
Yong-Sheng Wang, Li-Ya Pi, Xiuhua Chen, Pranjib K. Chakrabarty, Junda Jiang, Alfred Lopez De Leon, Guo-Zhen Liu, Liangcai Li, Ulla Benny, James Oard, Pamela C. Ronald, and Wen-Yuan Song. 2006. Rice XA21 Binding Protein 3 Is a Ubiquitin Ligase Required for Full Xa21-Mediated Disease Resistance. *The Plant Cell*. 18. 3635-3646

***Synergistic activities:***

1. Benefit Sharing: Established the UCD Genetic Resources Recognition Fund to equitably share benefits derived from developing nation germplasm
2. Transfer of knowledge: Organizer of symposia on Plant Microbe interactions (2001); Leader of multi-institutional Rice oligoarray consortium (2003), established Cesar Chavez Elementary Art and Science Program (2004-5).
3. Public Education: Speaker (10 presentations/yr) to public and industry audiences on agricultural biotechnology and intellectual property. Examples include: State of California (2004); UCD IGERT (2004), Monsanto Japan (2004), Copia Museum (2004). K-12 science through art program in Davis elementary schools (2003-present)
4. Professional service: History of professional service to USDA, NSF and NIH peer review panels, service on 3 major editorial boards. Chair of ASPB Public Affairs committee.



**NAME:** Stephen M. Welch

**PROFESSIONAL PREPARATION:**

B.S., Computer Science, Michigan State University	Dec. 1971
Ph.D., Zoology, Michigan State University	Feb. 1977
Postdoctoral Fellow, Entomology, Michigan State University	Feb.-Oct. 1977

**APPOINTMENTS:**

1990-present	Full Professor, Department of Agronomy. Theoretical plant modeling. Acting State Climatologist (1989-92).
1993 (6 mo.)	Assistant to the Vice Provost for Academic Services. Assisted in general technology-related issues and activities as directed by the VPAS.
1992 (5 mo.)	Interim Director, KSU Computing and Network Services. Overall administration of networking, mainframe computing, public computing laboratories, and support activities for Kansas State University.
1987-1989	Computer Systems Coordinator, Kansas Cooperative Extension Service. Overall administration of the Computer Systems Office (which included the KSU Weather Data Library). Policy, planning, personnel, and budgetary management.
1985-1986	Technical Development Coordinator, Kansas Cooperative Extension Service. Needs assessment, financing, and administration of electronic technology development programs for information delivery.
1981-1984	Associate Professor, Department of Entomology, Kansas State University. Design of decision support systems for selected agricultural commodities.
1982 (3 mo.)	Visiting Professor, North Central Computer Institute, Madison, Wisconsin. Computerized teleconferencing applications in multi-state cooperative projects.
1977-1981	Assistant Professor, Department of Entomology, Kansas State University. Pest management modeling of economic insects.

**PUBLICATIONS:**

Related to proposal:

Koduru, P. Dong, Z. Das, S. Welch, S. M. Roe, J. L., Charbit, E. 2008. A multi-objective evolutionary-simplex hybrid approach for the optimization of differential equation models of gene networks. *IEEE Transactions on Evolutionary Computation*. (*in press*)

Cai, X., P. Koduru, Welch, SM, Das, S. 2007. Simultaneous structure discovery and parameter estimation in gene networks. *Proceedings of the 4th Biotechnology and Bioinformatics Symposium*, pg. 79-82. Colorado Springs, CO.

Hammer G, Cooper M, Tardieu F, Welch S, Walsh B, van Eeuwijk F, Chapman S, Podlich D. 2006. Models for navigating biological complexity in breeding improved crop plants. *Trends in Plant Science* 11:587-593.

Welch, S.M., J.L. Roe, S. Das, Z. Dong, R. He, M.B. Kirkham. 2005. Merging genomic control networks with soil-plant-atmosphere-continuum (SPAC) models. *Agricultural Sys.* 86:243-74.

Welch, S.M., Roe, J.L., Dong, Z. 2003. A genetic neural network model of flowering time control in *Arabidopsis thaliana*. *Agronomy Journal*, 95:71-81.

Other related publications:

Bulatewicz, T., Andresen, D., Welch, S.M., Jin, W., Das, S., Miller, M., 2007. A software system for scalable parameter estimation on clusters. In: *Proc. of 8th LCI Int. Conf. on High-Performance Clustered Computing*.  
<http://www.linuxclustersinstitute.org/conferences/archive/2007/technicalpapers.html>

Weinig C, Brock MT, Dechaine JA, Welch SM. 2006. Resolving the genetic basis of invasiveness and predicting invasions. *Genetica*. DOI 10.1007/s10709-006-9015-7.

Welch, S. M., G. Wilkerson, K. Whiting, N. Sun, T. Vagts, G. Buol, and T. Mavromatis. 2002. Estimating soybean model genetic coefficients from private sector variety performance trial data. *Transactions ASAE*, 45(4):1163-75.

Chen, X., S. M. Welch, N. Zhang, D. Armbrust. 2002. Measurement of change in soybean plant cross-sectional area under wind conditions via image processing. *Trans. ASAE*, 44(6):1923-29.  
Roman-Paoli, E., S.M. Welch, and R.L. Vanderlip. 2000. Comparing genetic coefficient estimation methods using the CERES-Maize model. *Agricultural Systems*, 65:29-41.

#### **SYNERGISTIC ACTIVITIES:**

- Dr. Welch is KSU co-PI in an NSF Frontiers of Integrative Biological Research (FIBR) project. The project involves four US institutions with unfunded collaborators at six European plant molecular genetics labs. Its goal is to study the molecular evolutionary ecology of developmental signaling pathways of *Arabidopsis thaliana* in complex environments from the DNA sequence to continental scales. The five-year project combines approaches from molecular biology, molecular evolutionary genetics, quantitative genetics, evolutionary ecology, gene network modeling, and biogeography. The KSU team is responsible for the mathematical modeling of genet networks and the micro-meteorological monitoring at all field sites.
- Dr. Welch is a member of the Steering Committee for the Ecological Genomics Institute (EGI) in Kansas. EGI links responses of living systems to environmental change at the genetic level. Most environmental change studies span only one or two levels in the biological hierarchy, but biological responses depend on both genotype and gene-by-environment interactions, the relationships studied here. The EGI integrates the activities of 35 faculty and postdocs.
- Dr. Welch is a member of the Executive Committee of the Consortium for Global Research on Water-based Economies. GRoWE is developing coupled geo-spatial models for groundwater systems that include hydrological, plant, economic, and demographic components. It interacts closely with RIZA, the Dutch research and advisory body for inland waters management, renowned for its broad expertise in water issues world-wide. GRoWE also uses constructivist methods in educational experiments on teaching interdisciplinary topics in Water & Society.

#### **COLLABORATORS & OTHER AFFILIATIONS:**

**Collaborators and Co-Editors:** Richard Amasino, UW; Dean Armbrust, KSU; Kenneth Boote, UFL; Bruce Bugbee, USU; Scott Chapman, CSIRO; Xingwen Chen, Tetra-Tech, Inc. (Fairfax VA); Mark Cooper, PIO; Sanjoy Das, KSU; Jenny Dechaine, UMN; Andre de Roos, UAM; Zhanshan Dong, PIO; Kathleen Donohue, HU; Graeme Hammer, UQ; William Hsu, KSU; Ayse Irmak, UFL; Mary Beth Kirkham, KSU; Praveen Koduru, KSU; Jan Leach, CSU; James Jones, UFL; Tin Yu Mak, Alltel, Inc (Overland Park, KS); Theo Mavromatis, UFL; Jack Oviatt, KSU; Jeffrey Peterson, KSU; Dean Podlich, PIO; Michael Purugganan, NYU; Judith Roe, KSU; Elvin Roman-Paoli, UPR; Ruiqing He, UU; William Schapaugh, KSU; Johanna Schmitt, BU; David Steward, KSU; Naijian Sun, Microsoft Corp, (Seattle, WA); Francois Tardieu, IE; Harold Trick, KSU; Fred van Eeuwijk, WU; Richard Vanderlip, KSU; Bruce Walsh, UA, Virgil Valentine, KSU; Cynthia Weinig, UMN; Gail Wilkerson, NCSU; Naiqian Zhang, KSU.

**Graduate Advisor:** William Cooper, MISU      **Postdoctoral Advisor:** Brian Croft, ORSU

**Thesis Advisor to:** M.S – Xingwen Chen, Tetra-Tech, Inc. (Fairfax VA); PhD – Zhanshan Dong, PIO, Praveen Koduru, KSU; Five-year total advisory committee participation – MS 2, Ph D 7.

**Affiliation codes:** BU Brown University, CSIRO Commonwealth Scientific and Industrial Research Organisation, CSU Colorado St Univ, HU Harvard, IE INRA-ENSAM, KSU Kansas St Univ, NCSU North Carolina St Univ; NYU, New York, University; OHSU Ohio St Univ, ORSU Oregon St Univ, PIO Pioneer Hi-Bred International, SIS Space Imaging Services, UFL Univ of Florida, UGA Univ of Georgia, UA Univ Arizona, UAM Univ Amsterdam, UQ Univ Queensland, USU Utah St Univ, UU Univ Utah, UW Univ Wisconsin, WU Wageningen Univ.

## Biographical Sketch: Jeffrey W. White

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### Professional Preparation

#### Education

B.A., Biology, 1975, Harvard College, Cambridge, MA  
Ph.D., Botany, 1981, Univ. Calif., Berkeley, CA. Supervisor, Don Kaplan

#### Postdoctoral Research Appointment

1981-1983: Agronomy & Phys. Dept. International Potato Center (CIP), Lima, Peru. Supervisor,  
Sidki Sadik.

### Appointments

2003-present: Plant Physiologist; GS-15; U.S. Arid-Lands Agric. Res. Center  
1995-2002: Head, GIS and Crop Modeling Laboratory; CIMMYT, Mexico  
1983-1995: Bean Physiologist; Int. Center for Tropical Agriculture (CIAT), Cali, Colombia

### Five Most Relevant Publications

- White, J.W., Herndl, M., Hunt, L.A., Payne, T.S. and Hoogenboom, G. 2008. Analyzing genotypic and environmental effects on flowering in bread wheat by integrating effects of *Ppd* and *Vrn* loci through ecophysiological modeling. *Crop Sci.* 48: 678-687.  
<http://agron.scijournals.org/cgi/reprint/95/1/82>
- White, J.W., K.J. Boote, G. Hoogenboom, and P.G. Jones. 2007. Regression-based evaluation of ecophysiological models. *Agron. J.* 99:419-427. <http://agron.scijournals.org/cgi/reprint/99/2/419>
- White, J.W. 2006. From genome to wheat: Emerging opportunities for modelling wheat growth and development. *Eur. J. Agron.* 25:79-88.  
<http://linkinghub.elsevier.com/retrieve/pii/S1161030106000396>
- White, J.W. and G. Hoogenboom. 2003. Gene-based approaches to crop simulation: past experiences and future opportunities. *Agron. J.* 95:52-64. <http://agron.scijournals.org/cgi/reprint/95/1/52>
- White, J.W., Hoogenboom, G., 1996. Simulating effects of genes for physiological traits in a process-oriented crop model. *Agron. J.* 88, 416-422. <http://agron.scijournals.org/cgi/reprint/88/3/416>

### Five Other Significant Publications

- Kornegay, J., White, J.W., Dominguez, J.R., Tejada, G., Cajiao, C., 1993. Inheritance of photoperiod response in Andean and Mesoamerican common bean. *Crop Sci.* 33, 977-984.  
<http://crop.scijournals.org/cgi/reprint/33/5/977>
- White, J.W., Castillo, J.A., Ehleringer, J., 1990. Associations between productivity, root growth and carbon isotope discrimination in *Phaseolus vulgaris* under water deficit. *Aust. J. Plant Physiol.* 17, 189-198. <http://www.publish.csiro.au/paper/PP9900189.htm>
- Hoogenboom, G., and J. W. White. 2003. Improving physiological assumptions of simulation models by using gene-based approaches. *Agron. J.* 95:82-89. <http://agron.scijournals.org/cgi/reprint/95/1/82>
- White, J.W., J.D. Corbett and A. Dobermann. 2002. Insufficient use of meso-resolution spatial analysis in the planning, execution and dissemination of agronomic research? *Field Crops Research* 76:45-54.  
[linkinghub.elsevier.com/retrieve/pii/S0378429002000412](http://linkinghub.elsevier.com/retrieve/pii/S0378429002000412)

Hunt L.A., J.W. White and G. Hoogenboom. 2001. Agronomic data: advances in documentation and protocols for exchange and use. *Agricultural Systems* 70: 477-492.

### **Awards and Honors**

2005 – Certificate of Merit. US Water Conservation Laboratory. USDA ARS

1979-1981 – Rockefeller Foundation Graduate Research Fellowship

1976-1979 –NSF Graduate Research Fellowship

1974 – Maria Cabot Moore Foundation Research Fellowship

### **Synergistic Activities**

- (a) 2008 Nominated as lead scientist for USDA ARS NP 212 activity Research Problems 1.4.1, “Evaluate and extend the capacity and robustness of crop models and ecophysiological models for higher CO<sub>2</sub> and altered temperature, water and nutrient availability” and 1.4.3 “Develop regional, national and global datasets to assess impacts of global change.”
- (b) 2008 Invited lecturer for training workshop “Assessing Crop Production, Nutrient Management, Climatic Risk and Environmental Sustainability with Simulation Models” at Univ. Georgia, Griffin, GA. May 12-21.
- (c) 2006-2009 Co-chair International Consortium for Agricultural Systems Applications (ICASA; <http://www.icasa.net>)
- (d) 2005 Chaired the 35<sup>th</sup> Biological Systems Simulation Conference. April 19-21, 2005, Phoenix, Arizona
- (e) 2003 Co-chaired Crop Science Society of America Div. C-3 Symposium “Opportunities for linking functional genomics with physiology for global change research” during the CSSA National meetings in Denver, CO.
- (f) Co-organized and -chaired with Gerrit Hoogenboom (Univ. Georgia) the “ICASA Open Forum” at the past ten Annual Meetings of the American Society of Agronomy.

### **Collaborators and other Affiliations**

#### **Current/Recent Collaborators**

Ken Boote (Univ. Florida); Steve DelGrosso (Soil Plant Nutrient Research, USDA ARS); Dave Dierig (ALARC, USDA ARS); Nick Galwey (GSK, UK); David Hodson (CIMMYT); Jim Hoell (NASA Langley); Gerrit Hoogenboom (Univ. Georgia); Tony Hunt (Univ. Guelph); Jim Jones (Univ. Florida); Peter Jones (CIAT); Bruce Kimball (ALARC, USDA ARS); Greg McMaster (Agricultural Systems Research Unit); Tom Payne (CIMMYT); Cheryl Porter (Univ. Florida); Paul Stackhouse (NASA Langley); Frits van Evert (Wageningen Agric. Univ., The Netherlands); Martin van Ittersum (Wageningen Agric. Univ., The Netherlands); Gary Wall (ALARC, USDA ARS); Paul Wilkens (IFDC)

**Thesis Advisor (past 5 years) Ph.D students** Former: Markus Herndl (U. Hohenheim). **Masters students:** former Alisha Rosssi (ASU); Diganta Nath (ASU).

**Suggested Reviewers: iPlant Workshop Proposal, Grene et al.**

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