Research Development Fund – Spring 2016 Cover Page

Application Title: Synthetic and Systems Biology Innovation Hub (SSBIH)

Lead contact for RDF application:

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Key Participating units:

At the department level: PLPM, BioBio, ChemE, Chem, ECE, P&P, VIBS, VTPB
At the institute level: Institute for Plant Genomics and Biotechnology, Office of the Texas State Chemist
At the college level: COALS, COE, COM, COS, and CVM
At the agency level: TAMHSC, Texas A&M AgriLife Research, TEES, TAMU

Anticipated Request Amount ($): 1.96 million

Executive summary:

The proposal is a re-submission with all the questions from the RDF committee for previous version well addressed in Page 8. With several recent major federal research grants on synthetic biology to TAMUS, we propose to build a Synthetic and Systems Biology Innovation Hub (SSBIH) to promote the integration of cutting-edge science, engineering, and industry development at this important emerging field. The emerging synthetic and systems biology is taking biological and engineering research into a new era. The funding of Synthetic and Systems Biology Innovation Hub (SSBIH) will not only provide the matching funds for the incoming and future federal grants, but also distinguish us from our peer institutes in our missions for feeding the world, protecting the environment, delivering health solutions, developing new energy resources, and enhancing our economy.

Benefits to TAMUS: It is so often neglected that a successful shared facility relies not only on the instruments, but on the extensive expertise and rigorous research program. SSBIH sets its mission in leveraging and integrating the existing strong expertise in bioinformatics, metabolic engineering, synthetic biology, systems biology, bioanalytical chemistry, and various biological and biomedical research disciplines to enable a world-class synthetic and systems biology research facility. Such research facility will further support, enable, and integrate the research from participating faculty members and entire campus to build stronger interdisciplinary and cutting-edge programs. Detailed management plan were laid out to ensure the broad usage of the facility by both participating faculty and scientists around the campus. With the extensive management experience and strong funding track record of the team, we expect SSBIH will become a sustainable and productive research facility to drive the research, development and commercialization at TAMUS.

Anticipated Outcome: The team has a strong record in leveraging state funding for federal grants. In particular, the PI has leveraged nearly $10 million funding from DOE using limited internal funding. We expect SSBIH will amplify the track record to both enable cutting-edge scientific research and leverage extensive federal funding as follows.

- Support the submission of >$8 million federal grants each fiscal year.
- Support the research for >10 publications each year.
- Enable the emerging multidisciplinary scientific research programs by service and collaboration, and promote the submission of major interdisciplinary proposals accordingly.
- Support research to disclose >5 new technologies each year.
- Engage industrial partners for rapid commercialization of technologies.

As one of the leading public research institutes in the nation, synthetic biology are noticeably absent from our programs and initiatives. The establishment of a cutting-edge synthetic and systems biology facility and the integration of faculty expertise in the area will both keep TAMU as a front-runner in life science and engineering research, and benefit the research and enterprise development in Brazos Valley significantly.

Section 1: Scope of request

Synthetic biology refers to the integration of molecular tools, engineering principles, and mathematical modeling to engineer organisms toward previously unattainable functions. The multidisciplinary discipline often requires a well integration of life sciences with engineering and modeling. Synthetic biology is still in its infancy of development, yet already bringing breakthroughs in therapeutics, energy production, environmental remediation, and crop improvement. The foundation of synthetic biology was built on several core research including organism engineering, high-throughput screening, synthetic genome construction, and synthetic pathway design. Synthetic biology design often depends on or integrates with the systems biology studies. Systems biology, on the other hand, brings various 'omics' tools to render a comprehensive view of biological processes, and has taken the synthetic biology research to a new level. For these reasons, many leading institutes around the nation are promoting synthetic and systems biology initiatives (Table 1). **However, as one of the leading public research institutes in the nation, synthetic biology is noticeably absent from our programs and initiatives. The establishment of a cutting-edge synthetic and systems biology facility and the integration of faculty expertise in the area will both keep TAMU a front-runner in life science and engineering research, and benefit the research and enterprise development in Brazos Valley.**

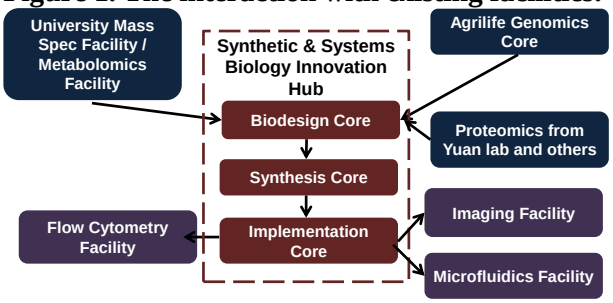
Table 1. Examples of Synthetic Biology Initiatives in Peer Institutes

Institutes	Initiatives
MIT	Center for Synthetic Biology as a leading initiative in the world.
UC Berkeley	Synthetic Biology Institute integrates research with industry.
UT Austin	Center for Systems and Synthetic Biology (CSSB) as a leading research enterprise.
NCSU	Recent cluster of senior and junior hires on systems and synthetic biology

Impact on the Texas A&M research enterprise

The SSBIH is designed to integrate our existing strength in pathway design, plant and microbial engineering, shot-gun proteomics, bioinformatics, and mathematical modeling into a global-leading research facility in synthetic and systems biology. The emphasis is on synthetic biology, where three functional cores will be integrated to enable a highly effective synthetic biology facility and enablement (Figure 1 and Figure 2). The first functional core is the Biodesign Core, where software, hardware, personnel, and expertise will be integrated to enable the design including optimization and control of gene/operon expression (e.g. promoter and rbs design, sequence optimization, codon usage, and genome engineering) and protein production and secretion (e.g. protein targeting and secretion signals) pathways. The output from the Design Core will be passed to Synthesis Core, where large components and even synthetic genome will be assembled. The fragment DNA synthesis will be outsourced. Bacteria and plants will be transformed with these constructs via working closely with the user labs. The output from the Synthesis Core will be implemented in the Implementation Core, which will work together with the user labs and other core facilities to perform the high-throughput functional characterization of the designed organisms. The high-throughput fermentation will be combined with customized detection system to monitor the cellular homeostasis, metabolic flux and target product yield. The detailed components for each functional core can be found in Section 3, Figure 2 and Appendix Table 1. The three functional cores will achieve a complete path for synthetic biology, where a synthetic pathway or functionality can be designed, synthesized, and implemented in plants, microbes, or other systems. SSBIH will promote collaborative state-of-the-art research, provide service and instrument usage, lead the development of major grants and contracts, and enhance corporate relationships to foster the industry-academia joint research initiatives in three very unique ways.

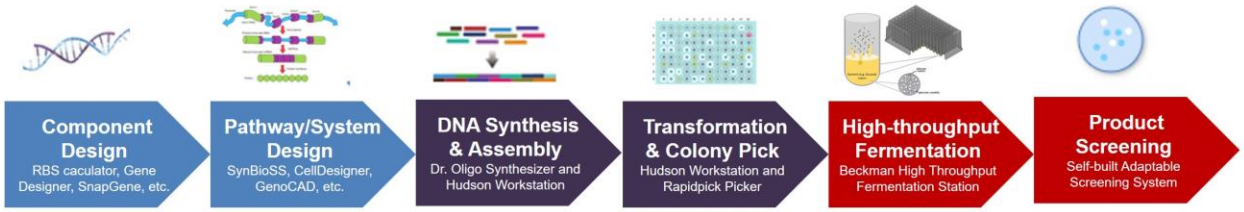
Figure 1. The interaction with existing facilities.



First, SSBIH will well integrate the current university resources and expertise to enable a cutting-edge and high impact research direction. TAMUS is lack of a research facility to compete in this important new direction. Even though SSBIH can function as an independent unit, the facility will complement and integrate with current

core facilities and research capacities to elevate the overall scientific excellence on campus (Figure 1 and 2). The genomics, transcriptomics, metabolomics, and proteomics information from current core facilities can be processed in the Biodesign Core to design efficient components, pathways, and systems. The engineered organisms can be screened in the microscopic and flow cytometry facilities existing on campus. As an enabling unit of university research network, SSBIH thus can integrate current resources to enable a new research direction and overall scientific excellence on campus. **Second, SSBIH will be the driving force for cutting-edge research and intellectual property development.** SSBIH will allow us to integrate our existing strength in both engineering and life sciences to advance multidisciplinary research. In particular, SSBIH will enable cutting-edge research by extensive collaborations, standard service, and instrument usage, all of which will benefit a broad range of researchers, programs, and university initiatives (Figure 1 and Appendix Table 2). Synthetic and systems biology will not only help us gain insights into fundamental principles of life, but also will deliver solutions for a vast range of applications including diagnostics, therapeutics, biosensors, environmental remediation, energy production, and so forth (Figure 1). **Third, SSBIH will become an essential resource for education of the state-of-the-art research integrating engineering and life sciences.** For example, the research facility can engage Aggie Research Leadership Program (ARLP) to help undergraduate and graduate students to develop research projects to compete in iGEM contest. **Fourth, SSBIH will promote the growth of the Texas economy by recruiting strong corporate engagement and support.** The resulting IP and scientific discoveries will offer enormous business opportunities. SSBIH will be integrated with recent initiatives in the Research Valley, TEES, AgriLife, and HSC.

Figure 2. The implementation of SSBIH. The integration of Biodesign, Synthesis and Implementation Cores will achieve a coherent synthetic biology capacity. The three cores are colored in light blue, dark blue, and maroon boxes. The different applications are shown in the boxes below the diagram, where the potential funding agencies for each application is itemized. The users for each discipline are listed.



Sustainable Bioproducts and Biofuels	Protein Therapeutics and Drug Production	Crop Protection and Improvement	Biodesign of New Pathways and Tools	Efficient Catalyst and Proteins	Development of New Therapy
DOE EERE, DOE ARPA E, DOE OS, DARPA, NIH, NSF	***NIH, DARPA, DOD other agencies, BARDA***	***USDA, DOE, NSF, Gates Foundation***	***NSF , NIH, DOE, DARPA, DOD other agencies***	***NSF , DOE EERE, DOE ARPA E, DARPA, NIH***	***NIH, Foundations, DARPA, DOD other agencies***
Joshua S. Yuan, Katy Gao, Susie Y. Dai, Tim Devarenne	Xiaoning Qian, Peter Rentzepis, Joshua Yuan, Katy Gao	Marty Dickman, Sandy Pierson, Besty Pierson, Mike Kolomiets, Ping He, Libo Shan, Xiuren Zhang	Xiaoning Qian, James Cai, Anne Shiu, Yang Shen, Joshua Yuan	Joe Zhou, Susie Dai, Wenshen Liu, Joshua Yuan	Paul de Figueiredo, Xiaoning Qian

Increased competitiveness for extramural funds related to this request

With the recent federal funding of major synthetic and systems biology research initiatives (Table 2), it is perfect timing for TAMU to establish the facility to enhance this multidisciplinary research area.

First, the funding will provide the matching funds for the current overall more than $15 million dollars in federal grants (Table 1). In particular, the matching fund will be crucial to leverage the current federal grants, as the allocation of funding to the state of Texas in these multi-state federal grants will depend on the level of matching funds provided by Texas. Moreover, the founding of this advanced research innovation hub will enhance research capacity to further obtain major supported initiatives.

Second, SSBIH will allow us to compete for more major federally funded research initiatives based on our strong track-record. The PI has a strong track record of leveraging major federally funded

programs at around ~$10 million as leading PI, often in collaboration with researchers on campus (Table 2). The strong track record will ensure the successful implementation of SSBIH toward competitive funding. Many federal agencies, including DARPA, DOE EREE, DOE ARPA E, NIH, and NSF are launching major initiatives in systems and synthetic biology (Figure 2). SSBIH will work closely with scientists on campus to assemble the research expertise from multiple investigators to develop major multidisciplinary research initiatives and grants.

Table 2. Examples Federal Funding Obtained for Synthetic and Systems Biology

Agency	Research Topics	Level	PI
DOE EERE	Upgrading Lignin Containing Biorefinery Waste for Bioplastics	$2.5million	Yuan
DOE ARPA E	Synthetic feedstock for hydrocarbon production	$1.87 million	Yuan
NSF	Visualizing evolution in real-time (VERT)	$0.51 million	Kao
DOE EREE	Synthetic biology for lignin fuel conversion	$2.4 million	Yuan
NSF	Argonaute-RNA interactome in Arabidopsis	$0.65 million	Zhang
NSF CAREER	Argonaute10-protein interactome in Arabidopsis	$1.28 million	Zhang
NIH	Phosphorylation and ubiquitination of immune sensory complexes in innate immune signaling	$1.2 million	Shan
USDA	Cotton functional genomics in biotic and abiotic stress responses	0.5 million	Shan
NIH	Differential regulation of plant innate immunity	$1.27 million	He
NSF	Orchestrating transcriptional reprogramming by combinatorial complexity of general transcriptional regulation and specific immune responses	$1.09 million	He
USDA	Cotton functional genomics in biotic and abiotic stress responses	0.5 million	Shan
DOE ARPA E	Synthetic feedstock for hydrocarbon production (P2)	$3 million	Yuan
Total		**>15 million**	

Major Users and Examples of Imminent Needs

SSBIH is an appealing core lab on campus serving a broad group of researchers with multi-department and college participation. The current users and their specific applications are as shown in Figure 2 and Appendix Table 2. The mechanisms to engage new users are in Section 2. SSBIH will bring scientific excellence in various fields including crop protection and improvement, plant immunity, therapeutics development, nutraceutical production, and sustainable fuels and chemical productions. We hereby focused on discussing a few key applications implementing synthetic biology. Synthetic biology has evolved from the original simple gene cloning to a much deeper understanding on life itself. It is already achievable to synthesize a whole bacterial genome and assemble it back to bacterial cytosol to create new hybrid cells. Various tools (e.g. MAGE, CRISPR-CAS system, TALEN) can also implement genome editing to change phenotypes in a system level. These knowledge and tools can be used by co-PIs in plant and microbial biology. The CRISPR-CAS system can be implemented into plant study to understand plant-microbe interaction (Key members include Co-PIs Dickman, Shan, Zhang etc.), enhance plant protection (Co-PIs He and Dickman), and improve crop yield. Genome editing could also bypass potential GMO regulations in plant study and accelerate the process of science to industry transition. In addition, biofuel research can be greatly advanced through implementing high-throughput phenotyping platform in the core lab. PI Yuan, coPI Devarenne and Dai are leading $10 million initiatives in synthetic design of plants and microorganisms for sustainable fuel and chemical production. CoPI Kao also focuses on microbial strain development for biofuels and bioproducts. Traditional metabolic engineering for biofuels and bioproducts has been hindered by low throughput, unpredictable outcomes, and challenges in identifying key metabolic bottlenecks. Synthetic biology has enabled us to overcome these bottlenecks with biodesign of efficient metabolic pathways as well as high throughput engineering and screening of efficient production strains. Implementing tools such as MAGE can systematically enhance pathway performance and produce strains of extraordinary capacities. This would be impossible without the core functions of Biodesign, Synthesis and Implementation. In conclusion, SSBIH will allow us to achieve scientific excellence and competitiveness for major plant, energy and environmental initiatives.

Similar Resources and Inadequacy

The facility can be located at a proper location as recommended by STAC (see Management) and no facility upgrade is expected. All of the instruments we proposed are cutting-edge and do not currently exist on campus.

Section 2: Management and Sustainability Plan

Prior experience in managing, supporting, and evaluating major equipment resources or facilities

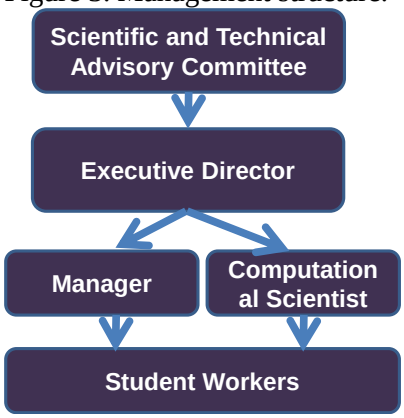
The team has rich experience to manage and support the SSBIH for several reasons. **First, the PI has a strong track record in managing similar facilities. Before coming to TAMU, Dr. Yuan served as the Genomics Hub Director at University of Tennessee and Microarray Core Manager at University of California, San Francisco.** He has extensive experience in managing a university-level research core in terms of cost structure, revenue generation, budget balancing, instrument maintenance, user recruitment and engagement, facility upgrades, and staff management. He successfully generated enough revenue as Director of the UTIA Genomics Hub to maintain the service contracts for the instrumentation and to expand the research support team. His expertise and experience will help to establish the guidelines to achieve the sustainability and productivity required for serving the broad scientific research community. **Second, the PI and the team have a strong track record of leveraging the university resources to develop rigorous and federally funded research program.** It is so often neglected that a successful core facility relies not on the instruments, but on the extensive expertise and rigorous research program. Such negligence often results in building university facilities with world-class instruments, yet no deliverables for university research enterprise. With a refurbished seven year old LC-LTQ instrument, the PI along with several coPIs established both shot-gun proteomics and protein structure dynamics platforms, and subsequently translate the research platforms into successfully funded and highly competitive projects (Table 1). Moreover, even though the facility is not a university facility, we managed to help multiple researchers to advance their research. The PI has the right expertise, experience, record and management skills to translate the state-of-the-art instruments and platforms into integrated scientific programs that can compete for federal funding. **Third, the team has the precise expertise needed for establish, manage, and expand SSBIH.** Besides the management and scientific record, our team has the expertise and track record for essentially all of the platforms proposed. The RDF grant will allow us to integrate the existing multidisciplinary expertise at TAMU community into a well-integrated state-of-the-art facility.

The overall management plan and structure

Based on the needs of scientific, technical and operational management, the management structure was set as shown in Figure 2, where a scientific and technical advisory committee (STAC) will be formed by five to seven co-PIs. These committee members will include representatives from COALS, COE, HSC, COS, and other potential entities in the university systems. **Dr. Huimin Zhao,** the theme leader of the Biosystems Design in the Carl R. Woese Institute for Genomic Biology at the University of Illinois at Urbana-Champaign, has agreed to serve on the committee (See supporting letter). He is an elite scientist in the field of synthetic biology, and has particularly established the Illinois Biological Foundry for Advanced Biomanufacturing (iBioFAB). With him serving on the advisory committee, we would get valuable input for the development of SSBIH. Moreover, **Dr. Martin Dickman** also agreed to serve as the chair of the advisory committee, and has offered space in Borlaug Center to set up necessary instruments. The STAC will evaluate the performance and needs of the facility on a quarterly basis to determine the productivity, user needs, scientific and technical excellence, and future direction of the facility. The STAC will formulate and provide recommendations for facility management guidelines, platform development, and funding engagement on a regular basis. The STAC members will serve three year terms, with a two term limitation. The PI will serve as the Executive Director for SSBIH. He will be responsible for coordinating the multidisciplinary expertise to establish cutting-edge technical platforms, leading efforts to develop follow on funding for instrument upgrades, promote scientific and technical interactions, establish guidelines for facility management, engage and initiate academic and industrial collaborations, and other duties are required. The manager of the facility will be responsible for developing new methods, maintaining quality control, running the instruments for service on a daily basis, providing training, and book keeping. Two more full-time employees will be in charge of biodesign core and will be responsible for maintaining the biodesign platforms, providing training for data analysis, and engaging research collaborations for various synthetic biology designs. Active faculty involvement is highly expected. A user group will be created and integrated through the use of an email cluster and

discussion board, which will promote interactions between experimental and computational faculty. Monthly "innovation club" meetings will be held to promote scientific exchange and interactions. Our vision is to leverage the SSBIH to promote interactions among computational and experimental faculty that will ultimately result in novel and exciting scientific advances. Finally, we will hold quarterly events to engage and inform industry about our latest platforms and scientific developments. The commercialization and sponsored research activities of the PI and co-PIs on this proposal will facilitate these industry interactions.

Figure 3. Management structure.



Scientific and technical management

As aforementioned, a successful university research facility relies on the integration of state-of-the-art instruments with matching scientific expertise. SSBIH will have an active management plan to help increase our research capacity and competitiveness for federal funding. First, we will actively upgrade and develop the latest platforms using the instruments. The team has the expertise and publication record to translate the instruments into new scientific programs and innovations. Second, as aforementioned, we will create opportunities to engage multidisciplinary researchers, including computational and experimental scientists, as well as physicists, chemists, engineers, biologists, and computer scientists. The engagement will promote multidisciplinary research.

Recruitment of users and engagement of scientific community

The research capacity and expertise will be accessible to the TAMUS community in five different ways. 1) Standard service will include high-throughput screening, microbial fermentation, and bioinformatics design to deliver solutions for researchers on campus. 2) Some instruments will be accessible to a broader research community through instrument usage to further improve our research capacities. 3) Collaborative research will be promoted with maximum flexibility to enhance access to resources and expertise that enable the most advanced research in engineering, energy, environment, and healthcare projects. 4) The facility will promote graduate student training in the state-of-the-art synthetic biology approaches. 5) As a special type of engagement, we will also actively lead the development of major federal, state and industry funding initiatives, where the users can participate to both obtain funding and services. The multiple approaches to engage the faculty will ensure maximized impact of SSBIH. We will also use the aforementioned activities to engage more users.

Allocation of usage, documentation of usage

Allocation and priority of usage is always a challenging task for a popular user facility, which the PI has experienced before. STAC will establish guidelines for user priorities. As always, TAMUS faculty will have the highest priority. The instrument usage log and the appointment-based research will be posted online and will be accessible for all users. This will promote communication to achieve high efficiency for instrument and service usage.

Sustainability of the operation and maintenance/service of the requested resource beyond RDF

Sustainability of a major user facility is another major challenge for the university research facilities. A financially sustainable user facility requires proper integration of expertise and instrumentation that achieves revenue generation, provides quality user services that allow cost recovery, and promotes scientific programs that attract major funding. Our sustainability plan includes four aspects. First, we will continue to develop funding to support the service contracts and additional personnel. We will encourage major users of the instruments to include service and personnel charges in their grants. Second, standard instrument usage and service fees will also recover part of the cost for service contracts and personnel. Third, we will continue to seek major research instrument grants from NSF, NIH, and DOD to expand future instrument capacity. Finally, SSBIH will lead major research grant applications, which will assist in covering costs of facility personnel and service contracts.

Section 3: Budget and Funding Usage

As aforementioned, the proposed instruments need to be well integrated with the scientific expertise to deliver the functional cutting-edge platforms, which in turn can be utilized by our faculty to translate into leading research programs. As shown in Figure 4, SSBIH will achieve a coherent synthetic biology capacity with three functional cores. The instrument, personnel, software, hardware and other resources were budgeted to achieve the overall function of the SSBIH

Itemized costs of equipment, instrumentation, or other items to be purchased

Based on the scientific needs, the following budget are requested for the instrument and relevant needs. The total requested budget is $1.96M (Appendix Table 1).

For Biodesign Core

- Most of the software is open source and minimal costs related to licensing some are budgeted.
- We will mainly use supercomputer center. Some local server and personal computers are budgeted for the users to carry out special functions that cannot be achieved by supercomputer.
- Key personnel are budgeted to carry out pathway and system design to support the campus. This is not a permanent position, and future funding will be recovered from research grant and fees.

For Synthesis Core

- The instrument purchase is the major cost. DNA synthesis can be outsourced to commercial companies.
- The automatic station is budgeted to carry out assembly of short DNA fragment to long fragment and eventually to clone. The transformation can be done synthetic biology work station.
- The population of bacteria, cells, or protoplast can be handled by a colony picker is budgeted to carry out initial screening and colony picking. This can be also coupled with the customized/self-built screening instrument.
- Small supporting laboratory equipment was budgeted to support the SBBIH pipeline including 96-well plate readers, microcentrifuges, water baths, heat blocks, incubators and/or -80C freezers.

The three equipment together will enable synthetic biology techniques like MAGE and MuGENT.

For Implementation Core

- Instrument purchase is again the major cost. A Beckman high-throughput fermentation system will be purchased. This well complements with the microfluidics, microscopic and flow cytometry based screening capacity already on campus. The instrument offers the new capacity of evaluating fermentation performance of many strains with different conditions, which cannot be achieved by the aforementioned platforms.
- We propose to design and construct a versatile HTS set up that will detect and record the fluorescence spectrum of molecules. We envision the set up to consist of small laser diode(s) that emit in the 250nm, 400nm, and 600nm region. The laser diodes will be easily interchangeable for other laser diodes that meet the specific excitation wavelength requirements of the particular molecular specie(s) being studied. A grating, lens system, CCD detector, and small display screen are the major components of the fluorimeter. Such an instrument can be integrated with the Beckman high throughput fermentation set up to achieve the monitoring of NADPH, ATP, key metabolites of the cell and in the medium. Computer servers and relevant software were budgeted for the computational needs of the project.

Initial service contracts

All instruments will be purchased with a three year service contact to allow SSBIH to achieve sustainability with future income from research grants and fees.

Additional anticipated costs and technical expertise requirements;

Two technical positions are budgeted, though it is expected the personnel cost will be somewhat higher than proposed. At the initial stage, we will subsidize the facility with the PI's funding. Future personnel cost and expansion will be recovered mainly from collaborative and major research grant.

Renovation or installation requirements

No significant renovation request and minimal installation cost are included.

Response to Previous Questions

Several questions have been raised by the committee regarding the management and sustainability from last round and we would like to address as follows.

1. Your application proposes 3 components of a synthetic biology resource - biodesign, synthesis, and implementation cores. Please provide additional justification, or pros/cons of a synthesis core being located onsite rather than negotiating with/utilizing commercial suppliers. Realistically, what frequency would synthesis be occurring?
   We agree with the committee that some part of the synthesis can be outsourced. We therefore removed the DNA oligo synthesis instrument and adjust the budget accordingly. The other two instruments of Synthesis Core are to set up a high-throughput station to efficiently build and screen desired phenotypes. It will be very costly and difficult to outsource these functions as they need heavy engagement with the researchers. An on-campus set-up is particularly important for both cost and user integration considerations.
2. How broad is usage across campus realistically anticipated for the entire resource in general, and in particular, for the implementation core?
   We expect the usage to be very broad on campus across different colleges. We will not just buy a set of instruments, but rather establish the platforms that can be broadly used by multiple faculties. There are researchers who will use all three cores, and some who will focus on one or two core capacities. The high-throughput screening capacity is particularly designed for researchers in biomedical, agriculture and engineering research. In addition, we also laid out several paths for user engagement, including taking leadership in developing major Synthetic Biology federal grants, which will certainly translate the facility into new research initiatives and further enlarge the user group.
3. Also note that Dr. Beiyan Zhou is no longer at TAMU.
   Dr. Zhou left TAMU after the grant submission to University of Connecticut. We have removed her from the user list.
4. What are anticipated maintenance costs?
   As stated in the proposal, we expected that maintenance cost include both the instrument maintenance and management. For the maintenance cost, the PI has previously evaluated different models to run a core facility. We will run a selective service contract model, basically, only the highly complicated instruments were covered consistently by service contract. We expect that most of the instruments in the SSBIH does need service contract beyond year 2 or 3. They are not as delicate as a high end mass spectrometer. The instrument maintenance cost will only need to cover the repair and routine maintenance at $50K to $100K per year. The major cost will be the personnel cost at about $200K per year. Texas A&M AgriLife Research has agreed to help with the long-term maintenance support during a Director's meeting. More importantly, we expect that we will lead the major grants to build in the maintenance cost and recover the cost with service charge, instrument charge, and other cost recovery strategies. Again, a successful research program is more important than anything in maintaining a sustainable facility, and we have strong record in developing vigorous federal programs using state-funded facilities. The PI's lab currently used a 10 year old LC-LTQ to build both shot-gun proteomics and structure dynamics platforms, and these platforms played essential role in building the nearly $10Million research program. The facility has been ran well and expanded.
5. Provide some information about how the proposed acquisitions will affect what this group of investigators is already doing.
   The information is available in Figure 2, Page 3, and Appendix Table 2.
6. Justify the need for an onsite synthesis core in more detail.
   See answers for question 1.
7. Describe the utility as a service beyond the investigators personal research in more detail, including potential breadth of utility.
   The management plan has listed it in details.

Appendix Table 1. The instrument, platforms, budget and justification

Facility Cores	Instrument	Platforms	Justification	Budget
Biodesign Core	Component Designing softwares including RBS calculator, SnapGene	Design of ribosome binding site (RBS) and RBS libraries, Gene Codon optimization, design proteins/enzymes	Optimize gene sequences to enhance protein expression significantly in target host. Tunable and controllable protein and pathway expression	$ 20,000
	Pathway and System Designing Software	Pathway modeling	Mathematical modeling study to identify pathway bottlenecks	$ 0
	Computer and local servers	Various usage	Modeling and user interactions	$ 30,000
	Personnel (One FTE plus some student workers for two years)	Component, pathway and system design	These include a manager to carry out daily operation, a computational biologist to support the imitative, and student workers	$120,000
Synthesis Core	Hudson synthetic biology workstation	Pipeline from DNA assembly to plasmid extraction to transformation and others	Screen target strains with exceptional phenotype; pipeline for high-throughput construct making, transformation, colony selection, and plasmid prep	$500,000
	RapidPick™ Complete fully automated high-throughput colony picker	High-throughput transformants selection in large libraries (MAGE, mutagenesis, etc.)	Very important tool for screening large library constructed in synthetic biology design	$120,000
	Small lab equipment and installation cost	Connect various functions of the SSBIH	Small supporting laboratory equipment was budgeted to support the SBBIH pipeline. Minimal installation costs are included.	$150,000
Implementa-tion Core	Automated high throughput fermentation system (Beckman-Coulter, Fullerton, CA)	Prepare, cultivate, and monitor up to 768 parallel experiments	Highly efficient in screening best phenotypes in the application of biofuel or chemical productions	$600,000
	Laser and detector to build the customized high throughput screening systems	Screening strains for metabolite, NADPH, and ATP pools	Identify the key flux and metabolite profile	$300,000
	Personnel (one FTE plus some student workers for two years)	SSBIH Management	These include a manager to carry out daily operation, a computational biologist to support the imitative, and student workers	$120,000
	Total			$1,960,000

Appendix Table 2. The table of current users and coPIs. SSBIH was enthusiastically supported by the faculty from multiple units, and the table contains a group of committed users and PIs who will actively involve in the design and implement of SSBIH.

Name	Department	College	Applications/Expertise
James Cai	Veterinary Integrative Biosciences	Veterinary Medicine	Biodesign – Pathway and system design
Susie Dai	Veterinary Pathobiology	Veterinary Medicine	Biodesign – Design efficient biocatalysts
Timothy Devarenne	Biochemistry and Biophysics	Agriculture	Plant/algae engineering – efficient biofuel synthesis
Marty Dickman*	Plant Pathology and Microbiology	Agriculture	Plant/microbial engineering – crop protection
Paul de Figueiredo*	Microbial and Molecular Pathogenesis	Medicine	Microbial/cell engineering --
Ping He	Biochemistry and Biophysics	Agriculture	Plant engineering – crop protection against pathogens
Michael Kolomiets	Plant Pathology and Microbiology	Agriculture	Plant engineering – crop protection against insects
Wenshe Liu	Chemistry	Science	Biodesign – Design new functions for proteins
Katy Gao	Chemical Engineering	Engineering	Microbial engineering – producing high value products
Elizabeth Pierson	Horticulture Sciences	Agriculture	Microbial engineering – New function of microbiota
Leland Pierson	Plant Pathology and Microbiology	Agriculture	Microbial engineering – biosensor design
Xiaoning Qian	Electrical and Computer Engineering	Engineering	Biodesign – Network modeling for therapy strategies
Peter Rentzepis*	Electrical and Computer Engineering	Egnineering	Screening design – Targeted screening of key metabolites
Yang Shen	Electrical and Computer Engineering	Engineering	Biodesign – Pathway modeling for efficient production
Xiuren Zhang	Biochemistry and Biophysics	Agriculture	Plant engineering – Crop improvement and protection
Joe (Hongcai) Zhou*	Chemistry	Science	Chemical design – Efficient MOF-biocatalyst

*Potential member of STAC. A STAC with excellent scientific background, strong funding record, and unique TAMU research strength will ensure the SSBIH facility not only has a coherent function, but also advances new areas of synthetic biology.

CURRICULUM VITA

JOSHUA S. YUAN
2123 TAMU
College Station, TX 77843
Phone: 979 845 3016
Email: syuan@tamu.edu

Professional Experience

2013 – now	Associate Professor Faculty of Department of Plant Pathology and Microbiology Institute for Plant Genomics and Biotechnology Graduate Program in Biotechnology Texas A&M University (TAMU), College Station, TX
2013 – now	Chief Scientific Advisor Synshark LLC
2014 – now	Chief Scientific Advisor Cleamol LLC
2008 – 2013	Assistant Professor Department of Plant Pathology and Microbiology Institute for Plant Genomics and Biotechnology Texas A&M University, College Station, TX
2004 – 2008	Director, Institute of Agriculture (UTIA) Genomics Hub Genomics Scientist, Department of Plant Sciences, University of Tennessee, Knoxville, TN
2001 – 2004:	Microarray Core Manager, Ernest Gallo Clinic & Research Center University of California, San Francisco, CA
2000 – 2001:	Senior Research Associate, BASF Plant Sciences LLC, RTP, NC

Education

Sungrant Fellow		National Renewable Energy Lab	2008
Ph.D.	Major: Plant Functional Genomics Minor: Statistics	University of Tennessee	Dec. 2007
M.S.	Plant Sciences	University of Arizona	Aug. 2001
B.S.	Major: Biology Minor: International Economics	Fudan University	Jul. 1997

Teaching

BESC357/PLPA657: Biotechnology for Biofuels and Bioproducts, Spring, 2009 – 2014; Evaluation: 4.34-4.90/5.00
BESC489/PLPA689: Genome Informatics, Fall, 2009 – 2013; Evaluation: 4.67/5.00

Honor and Recognition

Sigma Delta Gamma Outstanding Graduate Student, 2007
BMC Bioinformatics All Time Most Viewed Article 2012 – 2014, Second All Time Most Viewed Now:
http://www.biomedcentral.com/bmcbioinformatics/mostviewed/alltime
BMC Bioinformatics Most Viewed Article of the Year, in 2011 and 2012

Research Program (**10 Million** as the leading PI in past four years)

Project Name (for representative projects only)	***Agency***	***Amount***	***Role***
Upgrading Lignin-containing Biorefinery Waste for Bioplastics	DOE EERE	$2.6 Million	PI
Develop Synthetic Crop through Photorespiration Re-channeling and Terpenoid Biosynthesis Optimization, Phase 2	DOE ARPA E	$3 Million	PI
Synthetic Design of Microorganisms for Lignin Fuel	DOE EERE	$2.4 Million	PI
Develop Synthetic Crop through Photorespiration Re-channeling and Terpenoid Biosynthesis Optimization, Phase 1	DOE ARPA E	$1.9 Million	PI
Novel Strategy to Improve Plant Biomass by Manipulating PHB Gene Function	Sungrant	$69,985	PI
Biodesign of Lignin-Derived Terpene Biofuel	State of Texas	$150,000	PI
Structure Dynamics- Guided Enzyme Improvement	Sungrant	$34,966	Co-PI
National Alliance for Advanced Biofuels and Bioproducts	DOE EERE	$166,592	Co-I
Systems Biology Analysis NBUS for Biofuel	State of Texas	$200,000	PI

Editorial Positions & Synergistic Activities

2014	Session Chair	Special Session in Synthetic Biology, 36th Sym for Biotech for Fuels and Chemicals
2014 – now	Review Panel	NSF Sustainable Energy
2011 – now	Review Panel	US DOE JGI CSP and Synthetic Biology
2011 – 2013	Board of Director	MidSouth Comp Biol & Bioinformatics Society
2008 – now	BMC Research Notes	Associate Editor
2009	US-China Bioenergy Forum	Co-Chair
2010	Biofuels	Guest Editor for Special Issue

Peer-Reviewed Publications (Out of 52)

1. Cheng Zhao[$], Shangxian Xie[$], Yunqiao Pu, Rui Zhang, Fang Huang, Arthur J. Ragausaks, ***Joshua S. Yuan***, Synergistic enzymatic and microbial conversion of lignin for lipid, *Green Chemistry*, 2015, In press. DOI: 10.1039/C5GC01955A
2. Shangxian Xie, Xing Qin, Yanbing Cheng, Weichuan Qiao, Su Sun, Scott Sattler, Zhanguo Xin, Susie Y. Dai, Katy Gao, Bin Yang, Xiaoyu Zhang, and ***Joshua S. Yuan***, Simultaneous conversion of all cell wall components with oleaginous fungi without chemical pretreatment, *Green Chemistry*, 2015,17, 1657-1667.
3. Xin Wang, Don Ort, and ***Joshua S. Yuan***, Photosynthetic terpene hydrocarbon production for fuels and chemicals, *Plant Biotechnology Journal*, 2015,13:137-46.
4. Wusheng Liu, ***Joshua S. Yuan***, and C. Neal Stewart Jr., Advanced genetic tools for plant biotechnology, *Nature Review Genetics*, 2013, 14, 781–793
5. Weibing Shi, Shangxian Xie, Su Sun, Xueyan Chen, Xin Zhou, Lantao Liu, Peng Gao, Nikos C. Kyprides, En-Gyu No, ***Joshua S. Yuan,*** Comparative genomic analysis of the endosymbionts of herbivorous insects reveals eco-environmental adaptations: biotechnology applications. *PLoS Genetics*, 2013, 9(1): e1003131.

BIOGRAPHICAL SKETCH – KATY C. KAO

(a) Professional Preparation

University of California, Irvine	Chemical Engineering	B.S., 1997
University of California, Los Angeles	Chemical Engineering	Ph.D., 2005
Stanford University	Genetics	Postdoctoral 10/2005-7/2008

(b) Appointments

Associate Professor, Department of Chemical Engineering, Texas A&M University, College Station, TX – 9/2014 – present
Assistant Professor, Department of Chemical Engineering, Texas A&M University, College Station, TX – 8/2008 – 8/2014
Chemical Analysis Engineer, Western Digital Corporation, Lake Forest, CA – 9/1997 to 9/1999

(c) Products (* indicates publications with undergraduate student as co-author)

Publications most relevant to proposed work:

Winkler J, Garcia C*, Olson M, Callaway E*, Kao KC*. "Evolved *Escherichia coli* osmotolerant mutants frequently exhibit defective n-acetylglucosamine catabolism and point mutations in the cell-shape regulating protein MreB." Applied and Environmental Microbiology. 2014. Doi: 10.1128/AEM.00499-14.

Almario MP, Reyes LH, Kao KC. "Evolutionary engineering of *Saccharomyces cerevisiae* for enhanced tolerance to hydrolysates of lignocellulosic biomass." Biotechnology and Bioengineering. 2013. doi: 10.1002/bit.24938.

Winkler J, Kao KC. "Harnessing Recombination to Speed Adaptive Evolution in Escherichia coli." Metabolic Engineering. 2012. Sep;14(5):487-95.

Reyes LH, Almario MP*, Winkler J, Orozco MM*, Kao, KC. "Visualizing evolution in real time to determine the molecular mechanisms of n-butanol tolerance in Escherichia coli." Metabolic Engineering. Metabolic Engineering. 2012. Sep;14(5):487-95.

Kao, KC, Sherlock, G. "Molecular Characterization of Clonal Interference during Adaptive Evolution in Asexual Populations of *Saccharomyces cerevisiae*." Nature Genetics. 2008 Dec 40 (12): 1499-504.

Other significant publications:

Reyes LH, Gomez JM*, Kao KC. "Improving carotenoids production in yeast via adaptive laboratory evolution." Metabolic Engineering. 2014. Jan:21: 26-33.

Reyes LH, Abdelaal AS, Kao KC. " Genetic Determinants For N-Butanol Tolerance In Evolved E. Coli Mutants. Cross Adaptation And Antagonistic Pleiotropy Between N-Butanol And Other Stressors." Applied and Environmental Microbiology. 2013. Sept;79(17):5313-20.

Reyes LH, Winkler J, Kao KC. "Visualizing evolution in real-time method for strain engineering." Frontiers in Microbiotechnology, Ecotoxicology and Bioremediation. 2012. 3:198.

Huang M, McClellan M, Berman J, Kao KC. "Evolutionary dynamics of Candida albicans during in vitro evolution." Eukaryotic Cell. 2011. Sept 2. PMID: 21890821.

Kao KC, Sherlock G. "A Genome-Wide Analysis Reveals No Nuclear Dobzhansky-Muller Pairs of Speciation Genes Between *S. cerevisiae* and *S. paradoxus*, but Suggests More Complex Incompatibilities." PLoS Genetics. 2010 Jul 29;6(7):e1001038.

(d) Synergistic Activities

1. Hosted and mentored high school teachers from schools with high proportion of minority students as part of the Enrichment Experiences for Engineering (E3) co-sponsored by the NSF Research Experience for Teachers (RET) program and the College of Engineering at Texas A&M University.
2. Mentoring high school students from socioeconomically disadvantaged background to encourage them to pursue STEM-related area of studies in college.
3. International outreach – mentored 10 undergraduate student interns from Universidad de Los Andes and Industrial University of Santander in Colombia on their undergraduate research thesis as part of an international exchange program, and one Ph.D. visiting scholar from Agricultural Genetic Engineering Research Institute in Egypt.
4. Academic Editor for PLoS ONE (May 2010 – present).
5. Editorial board member for the Journal of Biological Engineering (January 2013 - present).

(e) Collaborators & Other Affiliations

Collaborators and Co-Editors within the last 48 months (outside of TAMU):
Judith Berman (Tel Aviv University, Israel), Juergen Hahn (RPI)

Graduate Advisor and Postdoctoral Sponsor:
James C. Liao (University of California, Los Angeles)
Gavin Sherlock (Stanford University School of Medicine)

Doctoral Students and Post-Doctoral Researchers Supervised:
Luis H. Reyes (NREL), James Winkler (University of Colorado, Boulder), Mian Huang (TAMU), Yuqi Guo (TAMU), George Peabody (TAMU), Michelle Olson (TAMU). Six Ph.D. students and four M.S. students advised since 2008.

Curriculum Vitae:

Huimin Zhao
University of Illinois at Urbana-Champaign (UIUC)
215 Roger Adams Laboratory, Box C-3
600 South Mathews Avenue
Urbana, Illinois 61801-3602
Voice: 217-333-2631, Fax: 217-333-5052
E-mail: zhao5@illinois.edu, http://scs.illinois.edu/~zhaogrp/
Date of Birth: April 5, 1969

I. PERSONAL HISTORY AND PROFESSIONAL EXPERIENCE

A. Educational Background

University of Science and Technology of China (USTC), B.S., Biology, June 1992
California Institute of Technology, Ph.D., Chemistry, June 1998

B. List of Academic Positions since Final Degree

Visiting Investigator, Agency for Science, Technology and Research (A*STAR), Singapore, 2012-date
Visiting Professor, Nanyang Technological University, 2011-date
Centennial Endowed Chair of Chemical and Biomolecular Engineering, UIUC, 2008-date
Professor, Chemical and Biomolecular Engineering, UIUC, August 2008-date
Associate Professor, Chemical and Biomolecular Engineering, UIUC, August 2006-date
Assistant Professor, Chemical and Biomolecular Engineering, UIUC, July 2000-August 2006
Faculty, Institute for Genomic Biology, UIUC, March 2004-date
Affiliate, Chemistry, UIUC, January 2004-date
Affiliate, Center for Biophysics and Computational Biology, UIUC, December 2000-date
Affiliate, Bioengineering, UIUC, December 2000-date
Affiliate, Biotechnology Center, UIUC, December 2000-date
Affiliate, Biochemistry, UIUC, August 2007-date

C. Other Professional Employment

Project Leader, Industrial Biotechnology, The Dow Chemical Company, San Diego, CA, April 1998 - May 2000

D. Honors, Recognitions, and Outstanding Achievements

Elmar Gaden Award, John Wiley & Sons and American Chemical Society Division of Biochemical Technology, 2014
Program Chair, ECI Biochemical Engineering Conference XVIV, 2013
Visiting Investigator, Agency for Science, Technology and Research (A*STAR), Singapore, 2012-date
John Simon Guggenheim Fellowship, 2012
Session Chair, NAE's Indo-American Frontiers of Engineering Symposium, 2012
National Academies Keck Futures Initiative Award, 2010
Merck Lecture, Department of Chemical Engineering, University of Virginia, 2010
Fellow of the American Association for the Advancement of Science, 2009

ELIZABETH ANN PIERSON

Education

Ph.D. Major: Botany (Ecology), Washington State University, Pullman, WA, 1987

BS, Honors Major: Biology, Indiana University, Bloomington, IN, 1982

Academic and Professional Experience

2009-present Associate Professor, Plant-microbe interactions, Department of Horticultural Sciences, Texas A&M University

1999-2009 Research Associate Professor, Division of Plant Pathology and Microbiology, Department of Plant Sciences, University of Arizona, Tucson, AZ

1990-1999 Research Assistant Professor, Department of Plant Pathology, University of Arizona

1989-1990 Research Associate, USDA-ARS Root Disease and Biological Control Research Unit, Pullman, WA

1987-1988 Statistical Consultant, Computer Information Center, Washington State University, Pullman, WA,

1982-1987 Teaching/Research Assistant, Dept. of Botany, Washington State University,

Current Research Funding

- Texas A&M AgriLife Research Zebra Chip Management Program 2014-2015. Title: Confirmation of 'ZC Tolerant' selections and development of molecular markers for the TAMU Potato Breeding and Variety Development Program. PIs JG Levy, EA Pierson, JC Miller.
- Texas A&M AgriLife Research Zebra Chip Management Program 2014-2015. Title: Development of Gene Silencing in Potato Varieties for Stable Resistance to Zebra Chip Disease". PIs: DC Gross, EA Pierson and H Lin.
- Texas A&M AgriLife Research Bioenergy Initiatives Program 2014-2015. Title: Development of efficient biocatalytic methods for lignin degradation in *Pseudomonas putida.* PI: EA Pierson, Collaborators: DC. Gross, JS Yuan.

Professional Memberships

American Society for Microbiology, American Phytopathological Society, American Society for Horticultural Science

Related Publications

Wang, DP, C Seeve, LS Pierson III *et al*. 2013. Transcriptome profiling reveals links between ParS/ParR, MexEF-OprN, and quorum sensing in the regulation of adaptation and virulence in *Pseudomonas aeruginosa*. BMC Genomics 14(1):618.

Wang, DP, SH Lee, C Seeve, *et al*. 2013. Roles of the Gac-Rsm pathway in the regulation of phenazine biosynthesis in *Pseudomonas chlororaphis* 30-84. MicrobiologyOpen, 2(3):505-24.

Loper, JE, KA Hassan, D Mavrodi, *et al*. 2012. Comparative genomics of plant-associated *Pseudomonas* spp.: Insights into diversity and inheritance of traits involved in multi-trophic interactions. PLoS Genetics. PLoS Genet 8(7): e1002784. doi:10.1371/journal.pgen.1002784

Wang D, JM YuG, LS Pierson III, and EA Pierson. 2012. Differential regulation of phenazine biosynthesis by RpeA and RpeB in *Pseudomonas chlororaphis* 30-84. Microbiol. 158(7): 1745-1757.

Marty Dickman, Professor

EDUCATION AND TRAINING

University of Hawaii, Hilo	Horticulture	B.S.	1979
University of Hawaii, Hilo	Plant Pathology	M.S.	1982
University of Hawaii, Hilo	Plant Pathology	Ph.D.	1987

PROFESSIONAL EXPERIENCE

2006-pres.	Director, Institute for Plant Genomics and Biotechnology, Texas A&M University
2006-pres.	Professor, Department of Plant Pathology and Microbiology, Texas A&M University
2006-pres.	Christine Richardson Professor of Agriculture, Texas A&M University
2003-2004	Charles Bessey Professor of Plant Pathology, University of Nebraska
1997-2003	Professor, Plant Pathology, University of Nebraska
1993-1997	Associate Professor, Plant Pathology, University of Nebraska
1987-1993	Assistant Professor, Plant Pathology, University of Nebraska
1987-1988	Post-doctoral Research Fellow, Institute of Biological Chemistry,Washington State U.

RESEARCH INTERESTS

The decision of whether a cell should live or die is fundamental to the wellbeing of all organisms. My lab investigates the molecular mechanisms underlying plant programmed cell death during fungal pathogen attack and environmentally induced stresses. Using a comparative pathobiology approach exploiting both plant and animal models, we have shown dissimilar fungi have strikingly similar needs and interests: nutrient acquisition, growth, niche establishment, and reproduction. To support these activities, fungi have evolved remarkably sophisticated mechanisms for interacting with host organisms particularly with respect to cell death regulation and metabolic reprogramming of the host cell. Our goal is to understand the mechanisms by which fungi modulate biological activities in plants, an area of significant research interest and practical importance

HONORS AND AWARDS

2014	Fellow-American Academy for Microbiology (ASM)
2011	Fellow-American Association for the Advancement of Science (AAAS)
2011	E.C. Stakman Award for Research Excellence in Plant Pathology
2006	Christine Richardson Professor of Agriculture-Texas A&M University
2003-2005	Charles Bessey Professor of Plant Pathology- University of Nebraska
2003	Fellow, American Phytopathological Society
2002	Distinguished Alumni Award- University of Hawaii-Hilo

PROFESSIONAL ACTIVITIES

2014	Bio-Protection Research Centre --International Science Advisory Board Panel Member Christchurch, New Zealand
2014	National Science Foundation (NSF) CDF/Signaling Panel
2012- 2014	Wolf Foundation Award-Panel
2012-2014	Technical Advisory Committee (TAC) Binational Agriculture Research and Development Fund (BARD) –Israel/United States
2013-	Academic Editor -Microbial Cell

2012-	Editor-in-Chief Molecular Plant Pathology
2011-	International Atomic Energy Agency IAEA-Panel Member-Mutation Breeding 2011- IITA Banana Improvement Program –Africa
2010-	Review Editor-Frontiers in Plant Biotechnology
2010-	Review Editor-Frontiers in Cellular and Infection Microbiology
2009-	Senior Editor-GM Crops
2007 -2008	National Science Foundation (NSF) Symbiosis, Defense and Self-Recognition
2007-2009	National Institute of Health (NIH) Development- Panel Member
2009	Bio-Protection Research Centre, External Advisory Committee-New Zealand
2007-2008	Oklahoma Center for the Advancement of Science and Technology (OCAST) Panel Member
2006	Department of Energy- Energy Biosciences Panel Member
2005	USDA-CSRS Comp Grants-PROGRAM MANAGER-Biology of Plant-Microbe
2001-2005	American Phytopathological Society-Senior Editor-APS Press
1996-1999	Senior Editor, Archives of Microbiology
1997-2013	Senior Editor, Physiological and Molecular Plant Pathology

SELECTED PEER REVIEWED PUBLICATIONS

Kabbage, M; Williams, B., Dickman, MB. 2013. Cell death control: The interplay of apoptosis and autophagy in the pathogenicity of *Sclerotinia sclerotiorum.* **PLoS Pathogens** 9: e1003287

Dickman, M.B. and Fluhr, R. 2013. Centrality of host cell death in plant-microbe interactions. **Annu. Rev. Phytopathol.** 51: 25.1-25.28.

O'Connell, R., et al., 2012. Life-style transitions in plant pathogenic *Colletotrichum* fungi deciphered by genome and transcriptome analyses. **Nature Genetics** 44, 1060-1065.

Bar-Dror, T., Dermastia, M., Kladnik, A., Znidaric., M.T., Novak, M.P., Meir, S., Burd,S., Philosoph-Hadas,S., Ori,N., Sonego,L., Dickman, M.B. and Lers, A. 2011. Programmed cell death occurs in an asymmetric manner during abscission. **Plant Cell** 23:4146-4163

Dickman, M.B. and de Figuerido, P. 2011. Comparative pathobiology of fungal pathogens of plants and animals. **PLoS Pathogens**. 7: e1002324

Williams, B., Kabbage, M., Kim, H-J., Britt, R. and Dickman, M.B. 2011. Tipping the balance: *Sclerotinia sclerotiorum* secreted oxalic acid suppresses host defenses by manipulating the host redox environment. **PLoS Pathogens** 7:1-10.

Amselem, J., Cuomo. C., van Kan Kan, J. and Dickman, M.B.2011. Genomic analysis of the necrotrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*. **PLoS Genetics** 7: e1002230.

Williams, B., Kabbage, M., Britt, R., and Dickman, M.B. 2010. AtBAG7, a unique endoplasmic reticulum-localized Bcl-2 associated athanogene is involved in stress responses in *Arabidopsis*. **Proc. Natl.Acad. Sci**. 107: 6088-6093.

Leland Stanley Pierson III
Department of Plant Pathology & Microbiology
Texas A&M University
College Station, TX 77843-2132

Professional Preparation

The University of California, Davis	Microbiology Faculty mentor: John L. Ingraham	B.A., 1979
Washington State University	Microbiology Major Advisor: Michael L. Kahn	Ph.D., 1986
USDA-ARS (Research Fellow)	Plant Pathology Post-doctoral advisor: Linda S. Thomashow	1986-1990

Appointments

2009-present	Professor and Head, Department of Plant Pathology & Microbiology, Texas A&M University, College Station, TX.
2011-2012	Interim Head, Department of Horticultural Sciences, Texas A&M University, College Station, TX.
2009	Associate Director, School of Plant Sciences, University of Arizona.
2003-2009	Division Chair, Division of Plant Pathology & Microbiology, Department of Plant Sciences, University of Arizona.
2002-2009	Professor, Division of Plant Pathology & Microbiology, Department of Plant Sciences, University of Arizona.
2000-2009	Chair, University of Arizona Institutional Biosafety Committee.
1996-2002	Associate Professor, Department of Plant Pathology, University of Arizona.
1990-1996	Assistant Professor, Department of Plant Pathology, University of Arizona.
1986-1990	Post-doctoral Research Microbiologist, USDA-Agricultural Research Service, Root Disease and Biological Control Research Unit, Pullman, WA.

Honors

Fellow	American Phytopathological Society	2015
Recipient	Outstanding Faculty Teaching Award, College of Ag & Life Sciences, University of Arizona (only one award given each year)	2007
Recipient	Student's Choice, The Microbiology Club Teaching Award	1999
Recipient	Creative Teaching Award. College of Agriculture, Arizona	1995

Selected Synergistic Activities

Vice-Chair	NCAC-14 Plant Pathology Department Heads Group	2014
Mediator	Texas A&M University Mediation Training	2013
Chair	Department Head Committee, American Phytopathological Society	2012
Member	Academic Program Review, UC Riverside Plant Pathology.	2011
Member	Microbial Community in Soils Panel, USDA-NIFA	2011
Invited	American SM BioQuest Institute	2007
Member	Academic Program Review, Dept of Plant Pathology at Iowa State University.	2005
Instructor	Microbial Genetics lecture/laboratory course Developed DNA sequence bioinformatic analysis exercises Developed Lab Ex for detection of cross-communication	1994-2009 2000
Member	*Colloquium on Microbial Communities: From Life Apart to Life Together. American Academy of Microbiology.*	*2002*
Organizer	Colloquium on Genomics of Plant-Associated Bacteria, ASM	2000
Member	CALS Curriculum Committee	2007-2009
Chair	CALS Curriculum Committee	2003-2004

Chair	Microbiology Curriculum Committee	2003-2005
Chair	CALS Promotion & Tenure Committee	2004-2005
Assoc. Ed.	Molecular Plant-Microbe Interactions	1998-2002
Assoc. Ed.	Applied & Environmental Microbiology	1997-2003
Member	Interdisciplinary Genetics Graduate Program	1995-2009
Member	W-147, 1147, 2147 Biological Control Working Group	1993-2010

Thesis Advisor & Postdoctoral Sponsor

Served as advisor or co-advisor for five post-doctoral, five PhD and five M.S. students. Service on >60 Graduate Student Committees and supervised >40 Undergraduate Research Projects

Areas of Interest

Gene regulation; microbial interactions; plant-microbe signaling; biofilms, biological control.

Selected Publications

Wang D, Dorosky RJ, Han CS, Lo CC, Dichosa AE, Chain PS, Yu JM, **Pierson LS 3rd**, Pierson EA. 2015. Adaptation genomics of a small-colony variant in a *Pseudomonas chlororaphis* 30-84 biofilm. Appl Environ Microbiol. 81:890-899.

Wang D, Han CS, Dichosa AE, Gleasner CD, Johnson SL, Daligault HE, Davenport KW, Li PE, Pierson EA, **Pierson LS 3rd**. 2014. Draft Genome Sequence of Enterobacter cloacae Strain S611. Genome Announc. 11;2. pii: e00710-14.

Wang D, Lee S-H, Seeve C, Yu J-M, **Pierson III LS**, Pierson EA. 2013. Roles of the Gac-Rsm pathway in the regulation of phenazine biosynthesis in *Pseudomonas chlororaphis* 30-84. Microbiology Open. doi: 10.1002/mbo3.90.

Wang D, Han C, Dichosa A, Gleasner C, Johnson S, Daligaulta H, Davenport K, Li P-E, Pierson E, and **Pierson LS III**. 2013. Draft Genome Sequence of *Pseudomonas putida* Strain S610, a Seedborne Bacterium of Wheat (genomeA01048-13). Genome Announc. 26;1(6). pii: e01048-13. doi: 10.1128/genomeA.01048-13.

Ortiz M, Neilson JW, Nelson WM, Legatzki A, Byrne A, Yu Y, Wing RA, Soderlund CA, Pryor BM, **Pierson LS 3rd**, Maier RM. 2013. Profiling bacterial diversity and taxonomic composition on speleothem surfaces in Kartchner Caverns, AZ. Microb Ecol. 65:371-383. doi: 10.1007/s00248-012-0143-6. Epub 2012 Dec 9.

Wang D, Seeve C, **Pierson LS 3rd**, Pierson EA. 2013. Transcriptome profiling reveals links between ParS/ParR, MexEF-OprN, and quorum sensing in the regulation of adaptation and virulence in Pseudomonas aeruginosa. BMC Genomics 13;14:618. doi: 10.1186/1471-2164-14-618.

Wang B, **Pierson III LS**, Rensing C, Gunatilaka MK, Kennedy C. 2012. NasT-mediated antitermination plays an essential role in the regulation of the assimilatory nitrate reductase operon in *Azotobacter vinelandii*. Appl Environ Microbiol. 2012 Jul 6. [Epub ahead of print].

Wang D, Yu JM, **Pierson III LS**, Pierson EA. 2012. Differential regulation of phenazine biosynthesis by RpeA and RpeB in *Pseudomonas chlororaphis* 30-84. Microbiology. 158:1745-57.

Loper JE, Hassan KA, Mavrodi D, Davis II EW, Lim CH, Shaffer BT, Elborne LDH, Stockwell VO, Hartney SL, Breakwell K, Henkels MD, Tetu SG, Rangel LI, Kidarsa TA, Wilson NL, van Mortel J, Song C, Blumhagen R, Radune D, Hostetler JB, Brinkac LM, Durkin AS, Kluepfel DA, Wechter WP, Anderson AJ, Kim YC, **Pierson III LS**, Pierson EA, Lindow SE, Raaijmakers JM, Weller DM, Thomashow LS, Allen AE, Paulsen IT. Comparative genomics of plant-associated *Pseudomonas* spp.: Insights into diversity and inheritance of traits involved in multitrophic interactions. PLoS Genet 8(7): e1002784. doi:10.1371/journal.pgen.10027.

Puopolo G, Raio A, **Pierson LS III**, Zoina A. 2011. Selection of a new *Pseudomonas chlororaphis* strain for the biological control of *Fusarium oxysporum* f. sp. *radicis-lycopersici*. Phytopathol. Mediterr. 50:228-235.

NAME	POSITION TITLE
Cai, James Jing	Assistant Professor of Systems Genomics Texas A&M Univ.
eRA COMMONS USER NAME (credential, e.g., agency login) JAMESCAI	

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Henan Medical Univ., China	B.S.	08/96	General Medicine
Univ. of New South Wales, Australia	M.S.	05/02	Biotechnology
Univ. of Hong Kong, Hong Kong	Ph.D.	08/06	Fungal Genomics
Stanford Univ., USA	Postdoctoral	08/10	Population Genomics

A. Positions and Experience

2010- Assistant Professor, Dept. of Veterinary Integrative Biosciences, Texas A&M Univ., TX
2011- Associate Editor, Frontiers in Genetics (ISSN 1664-8021)
2011- Editorial Board, Genomics, Proteomics & Bioinformatics (ISSN 1672-0229)
2013 NIH Genetic Variation and Evolution [GVE] Study Section, Reviewer
2015 European Research Council (ERC) Advanced Grant, Reviewer

B. Contributions to Science (*Corresponding author)

1. Regulation and evolution of gene expression. I have devoted much effort to the development of systemic approaches for assessing the impact of genetic variants on the gene expression variability at the population level.
    a. Zeng Y, Wang G, Yang E, Ji G, Brinkmeyer-Langford CL, **Cai JJ***. Aberrant gene expression in humans. ***PLoS Genet***. 2015 Jan;11(1):e1004942. PMID: 25617623.
    b. Hulse AM, **Cai JJ***. Genetic variants contribute to gene expression variability in humans. ***Genetics***. 2013 Jan;193(1):95-108. PMID: 23150607.
    c. Wang G, Yang E, Brinkmeyer-Langford CL, **Cai JJ***. Additive, epistatic, and environmental effects through the lens of expression variability QTL in a twin cohort. ***Genetics***. 2014 Feb;196(2):413-25. PMID: 24298061.
    d. Wang G, Yang E, Mandhan I, Brinkmeyer-Langford CL, **Cai JJ***. Population-level expression variability of mitochondrial DNA-encoded genes in humans. ***Eur J Hum Genet***. 2014 Sep;22(9):1093-9. PMID: 24398800.

2. Systems genomics approaches for human complex disease. A series of systems genomic analyses have been developed. These analyses use evolution and genetic network information to identify genes, mutations, and regulatory mechanisms that underlie human disease and complex traits of medical importance.
    a. **Cai JJ**, Borenstein E, Chen R, Petrov DA. Similarly strong purifying selection acts on human disease genes of all evolutionary ages. ***Genome Biol Evol***. 2009 May 27;1:131-44. PMID: 20333184.
    b. **Cai JJ***, Borenstein E, Petrov DA. Broker genes in human disease. ***Genome Biol Evol***. 2010;2:815-25. PMID: 20937604.
    c. Chang CL, **Cai JJ**, Cheng PJ, Chueh HY, Hsu SY. Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. ***Diabetes***. 2011 Mar;60(3):726-34. PMID: 21300845.
    d. Wang G, Yang E, Smith KJ, Zeng Y, Ji G, Connon R, Fangue NA*, **Cai JJ***. Gene expression responses of threespine stickleback to salinity: implications for salt-sensitive hypertension. ***Front Genet***. 2014;5:312. PMID: 25309574.

3. Genome scan for signals of positive selection and organismal adaptation. My research also involves the study of signatures of selection in the human genome and genetic variation under positive selection. For example, I identified widespread signals of genetic hitchhiking, driven by positive selection, at both coding and regulatory sites in the human genome (*PLoS Genet 5:1, 2009, >70 cit*). I showed that positive selection

has acted on a human incretin hormone gene, *GIP*, which plays critical roles in the regulation of insulin signaling and adipogenesis, and caused some most obvious differences between humans (*Genome Res 21:1, 2011*). I was among the first group of investigators who conceived the importance of the evolutionary age of protein-coding genes in relation to their functions (*J Mol Evol 63:1 2006*).

a. **Cai JJ**, Macpherson JM, Sella G, Petrov DA. Pervasive hitchhiking at coding and regulatory sites in humans. ***PLoS Genet***. 2009 Jan;5(1):e1000336. PMID: 19148272.
b. Chang CL, **Cai JJ**, Lo C, Amigo J, Park JI, Hsu SY. Adaptive selection of an incretin gene in Eurasian populations. ***Genome Res***. 2011 Jan;21(1):21-32. PMID: 20978139.
c. **Cai JJ**, Petrov DA. Relaxed purifying selection and possibly high rate of adaptation in primate lineage-specific genes. ***Genome Biol Evol***. 2010 Jul 12;2:393-409. PMID: 20624743.
d. **Cai JJ***, Woo PC, Lau SK, Smith DK, Yuen KY. Accelerated evolutionary rate may be responsible for the emergence of lineage-specific genes in ascomycota. ***J Mol Evol***. 2006 Jul;63(1):1-11. PMID: 16755356.

4. Scientific computation and software development. My research group has pioneered methods to develop high-level, high-performance scientific computing tools to deal with sequence, polymorphism, expression, and network data; these methods have been highly fruitful for studies of gene function, evolution, and complex traits. Over the years, several Matlab toolboxes for data analysis in molecular evolution, population genetics and biological networks have been developed (*BMC Bioinformatics 6:64, 2005; J Hered 99:4, 2008; Evol Bioinform 9:355, 2013*).
    a. **Cai JJ***, Smith DK, Xia X, Yuen KY. MBEToolbox: a MATLAB toolbox for sequence data analysis in molecular biology and evolution. ***BMC Bioinformatics***. 2005 Mar 22;6:64. PMID: 15780146.
    b. **Cai JJ***, Smith DK, Xia X, Yuen KY. MBEToolbox 20: an enhanced version of a MATLAB toolbox for molecular biology and evolution. ***Evol Bioinform Online***. 2007 Feb 6;2:179-82. PMID: 19455210.
    c. **Cai JJ***. PGEToolbox: A Matlab toolbox for population genetics and evolution. ***J Hered***. 2008 Jul-Aug;99(4):438-40. PMID: 18310616.
    d. Konganti K, Wang G, Yang E, **Cai JJ***. SBEToolbox: A Matlab Toolbox for Biological Network Analysis. ***Evol Bioinform Online***. 2013;9:355-62. PMID: 24027418.

5. Fungal genomics. I maintain a special interest in the molecular mechanisms underlying dimorphism in systemic fungi. For more than a decade, I have been studying *Penicillium marneffei* as a model organism to elucidate the genetic elements and pathways involved in regulating thermal dimorphism. My research group is one of few groups world-wide working on this fungus. To date, our research has been greatly facilitated by high-throughput sequencing technologies and comprehensive genomic tools, which allow unprecedented experimental designs for in-depth analyses of the genome and transcriptome of *P. marneffei* and other medically important fungal species.

    a. Yang E, Chow WN, Wang G, Woo PCY, Lau SKP, Yuen KY, Lin X, **Cai JJ*** (2014) Signature gene expression reveals novel clues to the molecular mechanisms of dimorphic transition in *Penicillium marneffei*. ***PLoS Genet***. 2014 Oct;10(10):e1004662. PMID: 25330172.
    b. Wang L, Tian X, Gyawali R, Upadhyay S, Foyle D, Wang G, **Cai JJ**, Lin X. Morphotype transition and sexual reproduction are genetically associated in a ubiquitous environmental pathogen. ***PLoS Pathog***. 2014 Jun;10(6):e1004185. PMID: 24901238.
    c. Yang E, Wang G, Woo PC, Lau SK, Chow WN, Chong KT, Tse H, Kao RY, Chan CM, Che X, Yuen KY, **Cai JJ***. Unraveling the molecular basis of temperature-dependent genetic regulation in *Penicillium marneffei*. ***Eukaryot Cell***. 2013 Sep;12(9):1214-24. PMID: 23851338.
    d. Woo PC, Lau SK, Liu B, **Cai JJ**, Chong KT, Tse H, Kao RY, Chan CM, Chow WN, Yuen KY. Draft genome sequence of *Penicillium marneffei* strain PM1. ***Eukaryot Cell***. 2011 Dec;10(12):1740-1. PMID: 22131218.

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/james.cai.1/bibliography/44335608/public/?sort=date&direction=descending

BIOGRAPHICAL SKETCH

NAME Paul de Figueiredo	POSITION TITLE Associate Professor
eRA COMMONS USER NAME (credential, e.g., agency login) PDEFIGUEIREDO	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Rice University, Houston TX	B.A.	1986	Mathematics & Political Science
Stanford, Palo Alto CA	M.A.	1989	Religious Studies
Cornell, Ithaca NY	Ph.D.	1997	Biochemistry, Molecular & Cell Biology
MIT, Cambridge MA	Postdoc	1998-1999	Vertebrate genetics
U. Washington, Seattle WA	Postdoc	2000-2005	Microbiology

A. POSITIONS AND HONORS

PROFESSIONAL EXPERIENCE

1986-1987 Consultant, Arthur Anderson & Co.
1989-1991 Biologist, Clinical Hematology, NHLBI NIH
1999 Consultant, Neural Computing Systems, Inc.
2005 Asst. Professor, Department of Plant Pathology and Microbiology, Texas A&M University
2006 Member, Faculty of Genetics, Texas A&M University
2006 Member, Program in Biotechnology, Texas A&M University
2006 Member, Faculty of Molecular and Environmental Plant Sciences, Texas A&M University
2007 Member, Center for Microencapsulation and Drug Delivery, Texas A&M System
2007 Member, Program in the Biology of Filamentous Fungi, Texas A&M University
2007 Adjunct faculty, Department of Veterinary Pathobiology, Texas A&M University
2010 Investigator, Borlaug Center, Texas A&M University
2011 Assoc. Professor, Dept. of Plant Pathology and Microbiology, Texas A&M University
2011 Joint faculty, Dept of Microbial and Molecular Pathogenesis, Texas A&M Health Science Center
2013 Member, Faculty of Evolutionary and Ecology, Texas A&M University
2013 Assoc. Professor, Dept. of Microbial Pathogenesis and Immunology, Texas A&M Health Science Center

OTHER EXPERIENCE AND PROFESSIONAL ACTIVITIES

2004 Founder, AvanViva, Inc., a biotechnology company
2008, 2010 Panel Member, NSF Integrated and Organismal systems (IOS)
2008-2012 Panel Member, NIH Special Emphasis Panel/Scientific Review Group ZRG1 IDM-A**,** Intracellular bacterial pathogenesis
2009-2012 Panel Member, NSF Chemical, Bioengineering, Environmental, and Transport Systems (CBET)
2011 Panel Member, CDC-NIH Family History and Diamond Blackfan Anemia
2005-present Member, American Association for the Advancement of Science
2010-present Associate Editor, Frontiers in Cellular and Infection Microbiology
2011-present Member, American Society for Microbiology (ASM)
2011-present Member, American Society for Cell Biology (ASCB)
2011-present Member, American Chemical Society (ACS)
2013-present Associate Editor, Frontiers in Cell and Developmental Biology

SELECTED HONORS

National Merit Scholar, Graduate Research Assistantship (Stanford), NIH Graduate Research Training Grant recipient (Cornell), Du Pont Teaching Prize (Cornell), Fuertes Writing Prize (Cornell), Biochemistry Teaching Prize (Cornell), The American Society for Cell Biology/Hybridon Predoctoral Travel Award (Cornell), Harvard

Biotechnology Business Plan Competition, Runner Up (Harvard Business School), MIT 50K Business Plan Competition. Semifinalist (MIT), Mexican American and Latino Research Center Fellow (Texas A&M), Alfred P. Sloan Foundation Minority Program Mentor (Texas A&M), Hispanic Leadership Program Mentor (Texas A&M), Oak Ridge Associated University Junior Faculty Award

B. SERVICE

TEXAS A&M UNIVERSITY

2006-2013	Co-Director, Research Experience for Undergraduates, Texas A&M Agrilife Research
2008-present	Faculty mentor, University Scholars Program
2009-2010	Chair, Seminar Committee, Plant Pathology and Microbiology
2009	Member, Biosafety Evaluation Sub-Committee, Council of Principal Investigators
2009-2012	Faculty Mentor, "Invisible Jungle", a weekly National Public Radio broadcast
2009-2012	Member, Graduate Student Recruiting Committee, Faculty of Genetics
2009-2012	Member, Curriculum Committee, Biotechnology Program
2010-2012	Member, Internal Advisory Board, Norman Borlaug Center
2012	Graduate Advisor, Department of Plant Pathology and Microbiology
2012	Chair, Graduate Program Committee, Department of Plant Pathology and Microbiology
2012-present	Member, Institutional Biosafety Committee

C. SELECTED PUBLICATIONS (*30 total, 1 in press, 1 in review*)

1. Qin QM, Pei J, Ancona V, Shaw BD, Ficht TA, de Figueiredo P. RNAi screen of endoplasmic reticulum-associated host factors reveals a role for IRE1a in supporting Brucella replication. ***PLOS PATHOG.*** 2008 Jul 25;4(7):e1000110 PMID: 18654626
2. Jupiter D, Ficht TA, Samuel J, Qin Q, de Figueiredo P. DNA watermarking of infectious agents: progress and prospects. ***PLOS PATHOG.*** 2010 Jun 17;6(6):e1000950. PMID: 20585560
3. Qin, Q, Luo J, Lin X, Pei J, Ficht TA, de Figueiredo P. Functional analysis of host factors that mediate Cryptococcus neoformans intracellular trafficking. ***PLOS PATHOG.*** 2011. Jun;7(6):e1002078. Epub 2011 Jun 16. PMID: 21698225
4. Bechler M., de Figueiredo P, Brown WJ. A PLA1-2 punch regulates the Golgi complex. ***TRENDS CELL BIOL.*** 2011 Nov 28, PMID: 22130221
5. Dickman MB, de Figueiredo P. Comparative pathobiology of pathogenic fungi of plants and animals. ***PLOS PATHOG.*** 2011. December; 7(12): e1002324. PMID: 22194681
6. Criscitiello M, de Figueiredo P. Fifty shades of immune defense. ***PLOS PATHOG.*** 2013 9(2): e1003110. doi:10.1371/journal.ppat.1003110 PMID: 23408882
7. Han A, Hou H, Li L, Kim HS, de Figueiredo P. Microfabricated devices in microbial bioenergy sciences. ***TRENDS IN BIOTECHNOL.*** 2013. pii: S0167-7799(12)00221-1. PMID: 23453527
8. Criscitiello M, Dickman MB, Samuel JE and de Figueiredo P. Tripping on acid: trans-Kingdom perspectives on biological acids in immunity and pathogenesis ***PLOS PATHOG.*** 2013. 9(7): e1003402. doi:10.1371/journal.ppat.1003402. PMID: 23874196
9. Dickman and de Figueiredo. Death be not proud—cell death control in host fungal interactions ***PLOS PATHOG.*** 2013. 9(9): e1003542. doi:10.1371/journal.ppat.100354
10. Pandey, A., S. Li Deng, T.A. Ficht , de Figueiredo P. 2013. *Drosophila* S2 Cell Model of *Brucella* Infection: An Attractive Tool to Study Host-Pathogen Interactions. In **Methods in Molecular Biology**. Human Press (O'Callaghan, ed.) *In press*
11. Erbay C, Pu X, Choi W, Choi M-J, Ryu Y, Hou H, Lin F, de Figueiredo P, Yu C, and Han A. Control of geometrical properties of carbon nanotube electrodes: towards high-performance microbial fuel cells ***J. POWER SYSTEMS.*** 2015. *In press*
12. de Figueiredo P, Ficht TA, Rice-Ficht A, Rossetti CA, and Adams LG. Pathogenesis and immunobiology of Brucellosis: review of *Brucella*-host interactions. ***Am. J. OF PATHOL.*** 2015. *In press*
13. Ha, KD, de Figueiredo P, Hu F, and Brown WJ. Global human kinome analysis identifies novel regulators of retrograde Golgi trafficking and membrane tubule formation ***MOL BIOL CELL.*** 2015. *In review*

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Professional Preparation

Shanghai Jiaotong University, Shanghai, China	Electronic Engineering	B.S.E., 1997
Shanghai Jiaotong University, Shanghai, China	Electronic Engineering	M.S.E., 1999
Yale University, New Haven, CT	Electrical Engineering	M.S., M.Ph., 2003
Yale University, New Haven, CT	Electrical Engineering	Ph.D., 2005
Yale University, New Haven, CT	Medical Imaging	Postdoc, 2005 – 2007
Texas A&M University, College Station, TX	Bioinformatics	Postdoc, 2007 – 2009

Appointments

Assistant Professor, Department of Electrical & Computer Engineering, Texas A&M University, College Station, TX, 2013 – present.
Assistant Professor, Center for Bioinformatics & Genomic Systems Engineering, Texas A&M University, College Station, TX, 2013 – present.
Courtesy Assistant Professor, Departments of Computer Science & Engineering and Pediatrics, University of South Florida, Tampa, FL, 2013 – present.
Assistant Professor, Department of Computer Science & Engineering, University of South Florida, Tampa, FL, 2009 – 2013.
Research Assistant Professor, Associate Research Scientist, Departments of Statistics and Electrical Engineering, Texas A&M University, College Station, TX, 2007 – 2009.

Publications

Publications most closely related to the program:

1. **X Qian** and ER Dougherty, "Effect of function perturbation on the steady-state distribution of genetic regulatory networks: Optimal structural intervention," *IEEE Transactions on Signal Processing*, **56**(10):4966-4976, 2008.
2. BJ Yoon, **X Qian**, SME Sahraeian, "Comparative analysis of biological networks using Markov chains and hidden Markov models," *IEEE Signal Processing Magazine, Special Issue on Genomic and Proteomic Signal Processing in Biomolecular Pathways*, **29**(1):22-34, Jan 2012.
3. BJ Yoon, **X Qian**, ER Dougherty, "Quantifying the objective cost of uncertainty in complex dynamical systems", *IEEE Transactions on Signal Processing*, **61**(9): 2256-2266, 2013.
4. Y Wang and **X Qian**, "Functional module identification in protein interaction networks by interaction patterns," *Bioinformatics*, **30**(1):81-93, 2014.
5. S Ren, S Huang, J Onofery, X Papademetris, **X Qian**, "A scalable algorithm for structured kernel feature selection," *Proc. 18th International Conference on Artificial Intelligence and Statistics (AISTATS)*, 9 pages, 2015.

Other recent significant publications:

1. **X Qian**, MP Brennan, DP Dione, WL Dobrucki, MP Jackowski, CK Breuer, AJ Sinusas, X Papademetris, "A non-parametric vessel detection method for complex vascular structures," *Medical Image Analysis*, **13**(1):49-61, 2009.
2. **X Qian** and ER Dougherty, "On the long-run sensitivity of probabilistic Boolean networks," *Journal of Theoretical Biology*, **257**(4): 560-577, 2009.
3. **X Qian**, N Ghaffari, I Ivanov, ER Dougherty, "State reduction for network intervention in probabilistic Boolean networks," *Bioinformatics*, **26**(24): 3098-3104, 2010.

4. **X Qian** and ER Dougherty, "Validation of gene regulatory network inference based on controllability," *Frontiers in Genetics*, **4**(272):13 pages, 2013.
5. Y Wang and **X Qian**, "Joint clustering of protein interaction networks through Markov random walk," *BMC Systems Biology*, **8**(S1), S9: 13 pages, 2014.

Synergistic Activities

1. Curriculum Development:
Created new courses entitled "Computational Molecular Biology," "Data Mining in Bioinformatics," "Biological Network Analysis," and "Machine Learning with Networks" that encourage interdisciplinary research.

2. Software Development & Distribution:
Developed HMMPQ (HMM Pathway Query), a tool for identifying conserved pathways in biological networks using hidden Markov models (freely available at http://www.cse.usf.edu/∼xqian/hmmpq/). Visited the Lister Hill National Center at the National Library of Medicine (NLM) to install the developed shape-based medical image retrieval package (SBMIR) on the NHANES II database and give training to the staff, 2005.

3. Service to the Scientific Community:
(a) Editorial Services:
Journal Editorial Board Member: Pattern Recognition Letters; PLoS ONE; Journal of Biological systems; EURASIP Journal on Bioinformatics and Systems Biology.
Journal Guest Editor: IEEE/ACM Transactions on Computational Biology and Bioinformatics; EURASIP Journal on Bioinformatics and Systems Biology; BMC Genomics; Journal of Biological Systems, Special Issue on Genomic Signal Processing.

(b) Conference Organizing Services: Local Arrangement Co-Chair for the ACM International Conference on Bioinformatics, Computational Biology, and Biomedicine (2012); Student Award Co-Chair for the IEEE International Workshop on Genomic Signal Processing and Statistics (2012); Publication Co-Chair for the IEEE International Workshop on Genomic Signal Processing and Statistics (2013); Program Co-Chair for the International Workshop on Computational Network Biology: Modeling, Analysis, and Control (2014).

(c) Review Services:
Panel Reviewer: NSF Ad-hoc Reviewer (2011); NSF Review Panelist (2010); Research Grants Council (RGC) of Hong Kong (2009).
Reviewer for Journals and Conferences: IEEE Transactions on Signal Processing, IEEE Transactions on Medical Imaging, IEEE Transactions on Neural Networks, IEEE Transactions on Information Technology in BioMedicine, IEEE Transactions on Biomedical Circuits and Systems, IEEE Journal of Biomedical and Health Informatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Medical Image Analysis, Genome Biology, Bioinformatics, Journal of the American Chemical Society, PLoS ONE, BMC Bioinformatics, BMC Systems Biology, Infection, Genetics, and Evolution, Computers in Biology and Medicine, EURASIP Journal on Bioinformatics and Systems Biology, Statistics and its Interface, Journal of Biological Systems, Artificial Intelligence in Medicine; International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI), IEEE Computer Society Conference on Computer Vision and Pattern Recognition (CVPR), IEEE International Conference on Acoustics, Speech, and Signal Processing (ICASSP), IEEE International Conference on Bioinformatics & Biomedicine (BIBM), IEEE Statistical Signal Processing Workshop (SSP), International Workshop on Data Mining in Bioinformatics (BIOKDD), IEEE International Symposium on Information Theory (ISIT), European Signal Processing Conference (EUSIPCO).

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors. Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Zhang, Xiuren	POSITION TITLE Associate Professor of Genetics & Biochemistry
eRA COMMONS USER NAME XIURENZHANG	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing,*

INSTITUTION AND LOCATION	DEGREE	YEAR(s)	FIELD OF STUDY
Hefei College of Economy and Technology	B.S	1989	Botany
China Agricultural University	M.S.	1994	Fruit Tree/Horticulture
Cornell University	Ph.D.	2003	Plant Molecular Biology /Biochemistry
Rockefeller University	Postdoc	2008	Molecular Biology /RNA Biology

A. Positions and Honors.

Positions and Employment

1994-1997 Assistant to Director, Beijing Academy of Agriculture & Forestry, China
2008-2013 Assistant Professor, Institute for Plant Genomics & Biotechnology and Department of Biochemistry & Biophysics Texas A&M University
2014- Associate Professor, Institute for Plant Genomics & Biotechnology and Department of Biochemistry & Biophysics Texas A&M University

Other Experience and Professional Memberships

2005- Member for, American Society of Plant Physiologists / New York Academy of Sciences / American Association of Pharmaceutical Scientists
2009- *Ad hoc* members for NSF / NIH /USDA
2008- Reviewer for the following journals:
Cell/ Genes & Development / Molecular Cell / Genome Biology /Plant Cell / Plant Journal / Trends in Plant Biology / PLoS Pathogen / PLoS Genetics / Cell Research / Immunology / Vaccine / Nucleic Acid Research

Honors

1985-1989 Ranked 1st places for consecutive four years for undergraduate program in HCET, P.R.China.
1996 Distinguished young fellow in Municipality of Beijing, China.
2003 Graduate student with honor in Cornell University, NY.

B. Selected peer-reviewed publications (* equal contribution; ** corresponding author; authors in red are undergraduates trained in my lab; authors in green are CSC-supported visiting scholars.)

1. Zhonghui Zhang*, Fuqu Hu*, Min Woo Sung, Chang Shu, Chunxiao Ge, Claudia Castillo, Hisashi Koiwa, Martin Dickman, Pingwei Li, and **Xiuren Zhang**.** 2015. RICEs promote the maturation of miRNA-containing RISCs in Arabidopsis. Under review by ***Science***.
2. Claudia Castillo-González, Changjun Huang, Xiu-Ying Liu, Tao Hu, Feng Sun, Zeyang Ma, Yijun Zhou, Xiu-Jie Wang, Xueping Zhou, and **Xiuren Zhang****. 2015. Geminivirus-encoded TrAP suppressor inhibits SUVH4/KYP activity to counter host defense. ***eLife*** (in revision).

3. Yuyi Zhou, Minami Honda, Hongliang Zhu, Zhonghui Zhang, Xinwei Guo, Tianhong Li, Zhaohu Li, Xu Peng, Keiji Nakajima, Liusheng Duan**, and **Xiuren Zhang****.** 2015. Spatiotemporal sequestration of miR165/166 by Arabidopsis Argonaute10 promotes shoot apical meristem maintenance. **Cell Reports (on line on March 19)**
4. Hongliang Zhu, Yuyi Zhou, Claudia Castillo, Amber Lu, Yingtao Zhao, Liusheng Duan, Zhaohu Li, Xiujie Wang and **Xiuren Zhang****. 2013. Molecular mechanism for bi-directional processing of primary miRNAs with branched terminal loops by Dicer-like 1 in Arabidopsis. **Nature Structural and Molecular Biology.**
5. Zhonghui Zhang and **Xiuren Zhang****.** 2012. Argonautes fight for miRNAs to regulate stem cell activity in plants. **Current Opinion in Plant Biology.** 15:652-658.
6. Hongliang Zhu*, Fuqu Hu*, Ronghui Wang*, Xin Zhou, Sing-Hoi Sze, Lisa Wen Liou, Ashley Barefoot, Martin Dickman, **Xiuren Zhang****. 2011. The Arabidopsis Argonaute 10 specifically recruits miR166/165 to maintain shoot apical meristem. **Cell. 145:242-256.**

Please refer to " http://www.sciencedirect.com/science/article/pii/S0092867411003795 for perspective on this paper; PaperFlick http://www.youtube.com/watch?v=VuQvQCxHo-c from *Cell* (Top *5 Cell paperflick* in 2011)and http://f1000.com/search/all?query=Argonaute10&selectedDomain=all for comments by Faculty of 1000.

7. Huan Wang*, **Xiuren Zhang***, Jun Liu, Takatoshi Kiba, Tolulope Ojo, Markus Hafner, Thomas Tuschl, Nam-Hai Chua** and Xiu-Jie Wang**. 2011. Deep sequencing of small RNAs specifically associated with AGO1 and AGO4 uncovers new AGO functions. **The Plant J.** 67, 292–304. PMCID: PMC3135789

8. Rafael Catala, Jian Ouyang, Isabel A. Abreu, Yuxin Hu, Haksoo Seo, **Xiuren Zhang**, and Nam-Hai Chua. 2007. The Arabidopsis E3 SUMO ligase SIZ1 regulates plant development and drought responses. **Plant Cell.** 19:2952-2966. PMCID: PMC2048692

Please refer to http://www.f1000biology.com/article/id/1092259/evaluation for comments on this paper by Faculty of 1000.

9. **Xiuren Zhang**, Yu-Ren Yuan, Yi Pei, Shih-Shun Lin, Thomas Tuschl, Dinshaw J. Patel, and Nam-Hai Chua. 2006. *Cucumber mosaic virus*-encoded 2b suppressor inhibits Arabidopsis Argonaute1 cleavage activity to counter plant defense. **Genes & Development**. 20:3255-3268. PMCID: PMC1686603

Please refer to http://www3.interscience.wiley.com/cgi-bin/fulltext/114189947/PDFSTART; http://www.the-scientist.com/news/home/37060/; and http://www.f1000biology.com/article/id/1086111 for comments.

10. **Xiuren Zhang**, Rossana Henriques, Shih-Shun Lin, Qi-Wen Niu, and Nam-Hai Chua. 2006. *Agrobacterium*-mediated transformation of *Arabidopsis thaliana* using the floral dip method. **Nature Protocols** 1(2): 641-646.

11. **Xiuren Zhang**, Virginia Garreton and Nam-Hai Chua. 2005. The AIP2 E3 ligase acts as a novel negative regulator of ABA signaling by promoting ABI3 degradation. **Genes & Development**. 19: 1532-1543. PMCID: PMC1172060

Please refer to http://www.f1000biology.com/article/id/1026874/evaluation for comments on this paper by Faculty of 1000.

12. **Xiuren Zhang** and Hugh S. Mason. 2006. Bean Yellow Dwarf Virus Replicons for High-level Transgene Expression in Transgenic Plants and Cell Cultures. **Biotechnology and Bioengineering.** 93:271-279.

13. **Xiuren Zhang**, Norene Buehner, and Hugh S. Mason. 2006. Tomato is a highly effective vehicle for expression and oral immunization with Norwalk virus capsid protein. **Plant Biotechnology Journal**. 4 (4):419-432.

14. **Xiuren Zhang**, David G. Himelrick, Floyd M. Woods and Robert C. Ebel. 2005. Effect of Temperature, Photoperiod and Pretreatment Growing Condition on Floral Induction in Springbearing Strawberry. **Small Fruits Review**. 1(2): 113 – 123.
15. **Xiuren Zhang**, Guoguang Luo, Ronghui Wang Jin Wang and David G. Himelrick. 2003. Growth and developmental responses of seeded and seedless grape berries to shoot girdling. **Journal of the American Society for Horticultural Science.** 128(3): 316-323.

C. Patent

1) Nam-Hai Chua, Jose Reyes, **Xiuren Zhang**, Takashi Soyano. Artificial microRNAs (PCT/US2004/03379).

2) Hamilton, W., Hellendoorn, K., Jones, T., Dwayne Kirk, Hugh S. Mason, **Xiuren Zhang**, and Charlies Arthzen. 2003. Vectors and methods for immunization against Norwalk Virus using transgenic plants (Patent serial No: 10/895,791)

D. Selected invited talks

1) Genetic Program Seminar Series, Texas A&M University, USA. Dec. 2010.
2) Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China. July, 2011
3) College of Agriculture and Life Sciences, China Agricultural University, China. July, 2011
4) College of Life Sciences, Anhui University, China. July, 2011
5) College of Agriculture and Life Sciences, Zhejiang University, China. Aug. 2011
6) Department of Plant Pathology & Microbiology, Texas A&M University, USA. Aug. 2012
7) The Huck Institutes of the Life Sciences, Penn State University, USA. Feb. 2013
8) Boyce Thompson Institute for Plant Research, Cornell University, USA. Feb. 2013
9) Posttranscriptional Gene Regulation in Plants, Rhode Island, USA. July, 26, 2013
10) The 7th International Geminivirus Symposium, Hangzhou, China. Nov. 2013

E. Research Support

Funding Source: NSF (MCB-0951120; 2.1.2010 - 1.31.2014)
Project Title: "Argonuate-RNA interactome in Arabidopsis."
Total costs: $532,909 **Role**: PI (95%); Co-PI, Sing-Hoi Sze (5%)

Funding Source: American Heart Association
Funding Program: NCRP National Scientist Development Grant (10SDG2640139;1.1.2010 - 12.31.2013)
Project Title: "Stem cell development and organogenesis in Arabidopsis."
Total costs: $300,000 **Role:** PI

Funding Source: Welch Foundation (A-1777; 6.1.2011 - 5.31.2014)
Project Title: "**Biochemical features of Arabidopsis Argonaute 10**."
Total costs: $170,000 **Role**: PI

Funding Source: Texas AgriLife; Genomic center (7.1.2011 - 6.30.2012)
Project Title: "**Argonaute 10 homologs in crops.**"
Total costs: $ 50,357 **Role**: PI

Funding Source: NIH NIAID (R21 AI097570; 2.1.2012 - 1.31.2014)
Project Title: "**Pathogenesis mechanism of Geminivirus-encoded AL2 suppressor.**"
Total costs: $ 384,357 **Role**: PI

Funding Source: National Science Foundation of China-TAMU (10.1.2012 - 9.31.2013)
Project Title: "**Towards to genome-wide identification of competing endogenous RNAs in Arabidopsis.**"

Total costs: $ 35,000 **Role**: PI; Co-PI, Xiu-Jie Wang
Funding Source: NSFC

Funding Source: NSF (MCB-1253369; 6.15.2013-5.14.2018)
Project Title: "**CAREER: Arabidopsis Argonaute10-protein interactome**"
Total costs: $1,275,000. **Role**: PI

Funding Source: NIH, (R01 Pending)
Project Title: "**miRNA biogenesis in Arabidopsis**"
Role: PI

Funding Source: NIH, (R01 Pending)
Project Title: "**Epigenetic silencing and suppression by geminivirus**"
Role: PI

F. Teaching and Mentoring

The classroom teaching duties include:

Gene 302 Principles of Genetics (4-credit course for Biochemistry and Genetics major undergraduates)
BICH 683 Advanced Biochemical Genetics (3-credit course for graduate students, starting from 2015)

The non-classroom mentoring includes:

Former Postdoctoral researchers (2): Dr. Hongliang Zhu (now a faculty in China Agricultural University, China); Dr. Changjun Huang (Zhejiang University, China)

Current Postdoctoral researcher (3): Dr. Zhonghui Zhang; Dr. Ze-Yang Ma; Dr. Zhiye Wang

Ph.D. students (4): Claudia Castillo-Gonzalez; Fuqu Hu; Chunxiao Ge; Di Sun

Technician (1): Ronghui Wang

Visiting scholars/ students (7): Yuyi Zhou; Xiuying Liu; Tao Hu; Tong Zhou; Feng Sun; Xinwei Guo; Changjiang Zhao

Committee member for Doctoral candidates (16): Alfredo J Hernandez; Catherine Cifuentes Rojas; Chen Ru; Xi Chen; Hengyi Xu; Kyle Renfrew; Vikas Kumar; Aldrin Benzon Lugena; Jiaxin Lei; Juanita Marie McLachlan; Shane Aaron Guthrie, Jeremy Wood; Dongyin Su, Akihito Fukudome; Katerine Leehy

Rotation graduate students (15): Zhihobg Xue; Fuqu Hu; Huiyan Jin; Michael Zhou; Shanna Quinn Mayorov; Jaime Parra; Chenxi Wang; Claudia Castillo-Gonzalez; Shane Guthrie; Xiyu Ma; Jinggeng Zhou; Brati Das; Callie Kobayashi; Indranil Malik; Dongyin Su

Undergraduate students (36): Danielle Rekers; Katrina Trapp; Neeti Anjan Kothare; Ashley Barefoot; Lisa Wen Liou; Derian Lai; Amanda Vorpahl; Aninye Rashad; Amber Au; An Ho; Leah Barnett; Alan John; Tyler Martin; Nicole Elizabeth Schrock, Andre Nicolas Martinez, Kevin Wallace; Rachel Pacilio; Kevin Joseph Records; Chelsea Alexandra Hope; Shelley Vekasy; Chang Hwan Yi; Myrna Lilia Hurtado; Madelien Puig; Tess Pham; Khoi Ho Thi Mei; Umar Ahmed Tariq, etc.

Hongcai Joe Zhou

a. Education and Training

Institution	Major	Degree	Year
Beijing Normal University, China	Chemistry	B.S.	1984
Texas A&M University, TX	Chemistry	Ph.D.	2000

b. Professional Experience

2014-Present	Davidson Professor in Science, Texas A&M University, TX
2008-Present	Professor of Chemistry, Texas A&M University, TX
2002-2008	Associate/Assistant Professor of Chemistry, Miami University, OH
2000-2002	Postdoctoral Fellow, Harvard University, MA

c. Publications (190 total, H-index = 59) http://www.chem.tamu.edu/rgroup/zhou/

[1] "Direct Measurement of Adsorbed Gas Redistribution in Metal-Organic Frameworks", Chen, Y.-P.; Liu, Y.; Liu, D.; Bosch, M.; Zhou, H.-C., *J. Am. Chem. Soc.*, **2015**, *137*, 2919-2930.

[2] "Sequential Linker Installation: Precise Placement of Functional Groups in Multivariate Metal–Organic Frameworks", Yuan, S.; Lu, W.; Chen, Y.-P.; Zhang, Q.; Liu, T.-F.; Feng, D.; Wang, X.; Qin, J.; Zhou. H.-C., *J. Am. Chem. Soc.*, **2015**, *137 (9)*, 3177–3180.

[3] "Structure-Assisted Functional Anchor Implantation in Robust Metal–Organic Frameworks with Ultralarge Pores" Park, J.; Feng, D.; Zhou, H.-C., *J. Am. Chem. Soc*., **2015**, *137*, 1663-1672.

[4] "A Highly Stable Zeotype Mesoporous Zirconium Metal–Organic Framework with Ultralarge Pores", Feng, D.; Wang, K.; Su, J.; Liu, T.-F.; Park, J.; Wei, Z.; Bosch, M.; Yakovenko, A.; Zou, X.; Zhou, H.-C., *Angew. Chem. Int. Ed.*, **2015**, *54*, 149 –154.

[5] "Stable Metal-Organic Frameworks Containing Single-Molecule Traps for Enzyme Encapsulation", Feng, D.; Liu, T.-F.; Su, J.; Bosch, M.; Wei, Z.; Wan, W.; Chen, Y.-P.; Wang, X.; Wang, K.; Lian, X.; Gu, Z.-Y.; Park, J.; Yuan, D.; Zou, X.; Zhou, H.-C., *Nature Comm*, **2015**, 6, 5979. DOI: 10.1038/ncomms6979

[6] "Topology Guided Design and Syntheses of Highly Stable Mesoporous Porphyrinic Zirconium MOFs with High Surface Area", Liu, T.-F.; Feng, D.; Chen, Y.-P.; Zou, L.; Bosch, M.; Yuan, S.; Wei, Z.; Fordham, S.; Wang, K.; Zhou. H.-C., *J. Am. Chem. Soc.*, **2015**,*137 (1)*, 413–419.

[7] "Photochromic Metal–Organic Frameworks: Reversible Control of Singlet Oxygen Generation", Park, J.; Feng, D.; Yuan, S.; Zhou, H.-C., *Angew. Chem. Int. Ed.*, **2015**, *54*, 430 –435.

[8] "A Highly Stable Porphyrinic Zirconium Metal-Organic Framework with shp-a Topology", Feng, D.; Gu, Z.-Y. ; Chen, Y.-P.; Park, J.; Wei, Z.; Sun, Y.; Bosch, M.; Yuan, S.; Zhou, H.-C., *J. Am. Chem. Soc.*, ***2014, 136***, 17714–17717.

[9] "Kinetically tuned dimensional augmentation as a versatile synthetic route towards robust metal–organic frameworks", Feng, D.; Wang, K.; Wei, Z.;Chen, Y.-P.; Simon, C. M.; Arvapally, R. K.; Martin, R. L.; Bosch, M.; Liu, T.-F.; Fordham, S.; Yuan, D.; Omary, M. A.; Haranczyk, M.; Smit, B.; Zhou, H.-C., *Nature Comm*, **2014**, *5*, 5723. DOI: 10.1038/ncomms6723

[10] Liu, T.-F, Zou, L, Feng, D, Chen, Y.-P, Fordham, S, Wang, X, Liu, Y, Zhou, H.-C. Stepwise Synthesis of Robust Metal-Organic Frameworks via Post-Synthetic Metathesis and Oxidation of Metal Nodes in a Single-Crystal to Single-Crystal Transformation *J. Am. Chem. Soc.* **2014**, 136, 7813–7816.

d. Synergistic Activities.

1. Associate Editor, *Inorganic Chemistry*
2. Guest Editor (Co-Editor: Susumu Kitagawa) for *Chem. Soc. Rev.* Themed Issue on MOF (2014)
3. Guest Editor (Co-Editors: Jeff Long and Omar Yaghi) for *Chem. Rev.* Thematic Issue on MOF (2012)
4. Editorial board member: Inorganic Chemistry Frontier
5. Editorial board member: Comments on Inorganic Chemistry
6. Editorial board member for Frontiers: Energy Research

e. Collaborators & Other Affiliations

1. **Collaborators**

Perla Balbuena	Texas A&M
Stefan Bräse	Universität Karlsruhe, Germany
Mei Cai	GM
Jong-San Chang	KRICT, Korea
Juergen Eckert	LANL
Paul Forster	UNLV
Hae-Kwon Jeong	Texas A&M
Susumu Kitagawa	Kyoto University
Jeffrey Long	UC Berkeley
Armin de Meijere	Universität Göttingen, Germany
Berend Smit	LBNL
Omar Yaghi	UC Berkeley
Xiao-Zeng You	Nanjing University, China
Jing-Lin Zuo	Nanjing University, China

2. **Graduate Advisor**

Graduate:	Dr. F. Albert Cotton (Deceased)	Texas A&M University, College Station
Postdoctoral:	Dr. Richard H. Holm	Harvard University

3. **Thesis Advising**

Postdoctoral Fellows (24, 3 current): Mario Wriedt (Clarkson University), Jian-Rong Li (Beijing University of Technology), Zhi-Yong Wang (Troy State), Daofeng Sun (Chinese University of Petroleum), Hai-Long Jiang (USTC), and Daqiang Yuan (Chinese Academy of Sciences)

Graduate Students (39 total, 21 current): Shengqian Ma (USF), Dan Zhao (National University of Singapore), David Collins (SUNY Cortland), and Trevor Makal (UVA Wise)

Visiting Scholars (6, 2 current): Daren Timmons (VMI) and Jingbo Liu (TAMU Kingsville)

Undergraduate Students (32 total, 4 current)

Libo Shan

Education:

2003-2008 Harvard Medical School, Boston, MA	Molecular Biology	Postdoc
1998-2003 Kansas State University, Manhattan, KS	Plant Pathology	Ph.D.
1995-1998 Chinese Academy of Sciences, China	Genetics	M.S.
1991-1995 Beijing Normal University, China	Biochemistry	B.S**.**

Professional Positions and Appointments:

2009-present Assistant, Associate Professor
Department of Plant Pathology and Microbiology
Institute for Plant Genomics and Biotechnology
Faculty of Molecular & Environmental Plant Sciences (MEPS)
Texas A&M University, College Station, TX

Honors and Awards:

- Charles Albert Schull Award, American Society of Plant Biologists (ASPB), 2014
- Dean's Outstanding Achievement Award for Excellence in Early Career Research, College of Agriculture and Life Sciences, Texas A&M University, 2013
- American Society of Plant Biologists Women's Young Investigator Travel Award, 2010
- Don C. Warren Genetic Scholarship, Kansas State University, 2002-2003
- Di-Ao Scholarship, Chinese Academy of Sciences, 1998

Selected Publications:

- Zhou, J., Lu, D., Xu, G., He, P. and **Shan, L**. (2015) The dominant negative ARM domain uncovers multiple functions of plant U-box E3 ligase PUB13 in *Arabidopsis* immunity, flowering and senescence. ***Journal of Experimental Botany*** doi: 10.1093/jxb/erv148.
- Li, B., Jiang, S., Yu, X., Cheng, C., Chen, S., Cheng, Y., Yuan, J., Jiang, D., He, P**.,** and **Shan, L**. (2015) Phosphorylation of a trihelix transcription repressor ASR3 by MPK4 negatively regulates *Arabidopsis* immunity. ***The Plant Cell*****.** 27: 839-856.
- Feng, B., Liu, C., Oliveira, M.V.V., Intorne, A.C., Li, B., Babilonia, K., Filho, G.A.S., **Shan, L**., and He, P**.** (2015) Protein poly(ADP-ribosyl)ation regulates *Arabidopsis* immune gene expression and defense responses. ***PLoS Genetics*** 11(1): e1004936. doi:10.1371/journal.pgen.1004936.
- Manhães, A., de Oliveira, M., and **Shan, L**. (2015) Establishment of an efficient virus-induced gene silencing (VIGS) assay in *Arabidopsis* by *Agrobacterium*-mediated rubbing infection. ***Methods Mol. Biol.*** 1287:235-241.
- Li, F., Cheng, C., Cui, F., Oliveira, M.V.V., Intorne, A.C., Babilonia, K., Li, M., Chen, X., Ma, X., Xiao, S., Zeng, Y., Fei, Z., Metz, R., Johnson, C.D., Koiwa, H., Sun, W., Li, Z., Filho, G.A.S., **Shan, L.**, and He, P. (2014) Modulation of RNA polymerase II phosphorylation downstream of pathogen perception orchestrates plant immunity. ***Cell Host & Microbe***. 16: 748–758.
- Feng, B., and **Shan, L.** (2014) ROS open roads to roundworm infection. ***Science Signaling*** **7** (320), pe10.
- Lin, W., Li, B., Lu, D., Chen, S., Zhu, N., He, P., and **Shan, L.** (2014) Tyrosine phosphorylation of BAK1/BIK1 mediates *Arabidopsis* innate immunity. ***Proc Natl Acad Sci U S A***. 111: 3632-3637.
- Li, B., Lu, D., **Shan, L.** (2014) Ubiquitination of pattern recognition receptors in plant innate immunity. ***Mol. Plant Path.*** 15: 737-746.
- Manhães, A., de Oliveira, M., and **Shan, L**. (2014) Establishment of an efficient virus-induced gene silencing (VIGS) assay in *Arabidopsis* by *Agrobacterium*-mediated rubbing infection. ***Methods Mol. Biol.*** 1287: 235-241.
- Zhou, J., He, P., and **Shan, L**. Ubiquitination of plant immune receptors. (2014) ***Methods Mol. Biol*****.** 1209: 219-231.

- Zhou, J., Wu, S., Chen, X., Liu, C., Sheen, J., **Shan, L.,** and He, P. (2013) Pseudomonas syringae Effector HopF2 Suppresses Arabidopsis Immunity by Targeting BAK1. ***The Plant Journal.*** 77: 235–245.
- Cheng C., Gao X., Feng B., Sheen J., **Shan L.**, He P. (2013) Plant immune response to pathogens differs with changing temperatures. ***Nat Commun.*** 4:2530. doi: 10.1038/ncomms3530.
- Lin, W., Lu, D., Gao, X., Jian, S., Ma, X., Wang, Z., Mengiste, T., He, P., and **Shan L.** (2013) Inverse modulation of plant immunity and plant development by a receptor-like cytoplasmic kinase BIK1. ***Proc Natl Acad Sci U S A***. 110: 12114-12119.
- Cui, F., Wu, S., Sun, W., Coaker, G., Kunkel, B. N, **Shan, L**. (2013) The *Pseudomonas syringae* type III effector AvrRpt2 promotes pathogen virulence via stimulating Arabidopsis Auxin/Indole Acetic Acid protein turnover. ***Plant Physiology*** 162: 1018-1029.
- Gao, X., Chen, X., Lin, W., Lu, D., Niu, Y., Li, L., Cheng, C., McCormack, M., Sheen, J., **Shan, L**., and He, P. (2013) Bifurcation of *Arabidopsis* NLR Immune Signaling via Ca^{2+}-Sensor Protein Kinases. ***PLoS Pathog*** *9*, e1003127.
- Gao, X., Li, F., Li, M., Kianinejad, A., Dever, J., Wheeler, T., Li, Z., He, P., and **Shan, L.** (2013) Cotton *GhBAK1* mediates Verticillium wilt resistance and cell death. ***Journal of Integrative Plant Biology***. 55: 586-96.
- Gao X, **Shan L.** (2013) Functional genomic analysis of cotton genes with agrobacterium-mediated virus-induced gene silencing. ***Methods Mol Biol.*** 975: 157-165.
- Lu, D., Lin, W., Gao, X., Wu, S., Cheng, C., Avila, J., Heese, A., Devarenne, T., He, P., and **Shan, L**. (2011) Direct ubiquitination of pattern recognition receptor FLS2 attenuates plant innate immunity. ***Science***. 332: 1439-1442.
- Gao, X., Wheeler, T., Li, Z., Kenerley, C., He, P**.,** and **Shan, L.** (2011) Silencing GhNDR1 and GhMKK2 compromised cotton resistance to *Verticillium wilt*. ***The Plant Journal.*** 66: 293-305.
- Wu, S., Lu, D., Kabbage, M., Wei, H., Swingle, B., Dickman, M., He, P., and **Shan, L.** (2011) Bacterial effector HopF2 suppresses *Arabidopsis* innate immunity at the plasma membrane. ***Mol. Plant Microbe Interact.*** 24: 585-93.
- Lu, D., Wu, S., Gao, X., Zhang, Y., **Shan, L.** and He, P. (2010) A receptor-like cytoplasmic kinase BIK1 associates with flagellin receptor complex to initiate plant innate immunity. ***Proc Natl Acad Sci U S A.*** 107: 496-501.
- Boudsocq, M., Willmann M. R., McCormack, M., Lee, H., **Shan L**., He P., Bush, J., Cheng, S., and Sheen J., (2010) Differential innate immune signalling via Ca^{2+} sensor protein kinases. ***Nature.*** 464: 418-422.
- Chinchilla, D., **Shan, L**., He, P., de Vries, S. and Kemmerling, B. (2009) One for all-the receptor-associated kinase BAK1. ***Trend in Plant Science***. 14: 535-541.
- **Shan, L**, He, P., Li, J., Heese, A., Peck, S. C., Nurnberger, T., Martin, G. B., and Sheen, J. (2008). Bacterial effectors target the common signaling partner BAK1 to disrupt multiple MAMP receptor-signaling complexes and impede plant immunity. ***Cell Host & Microbe*** 4: 17-27.
- Chen, Z., Agnew, J., Cohen, J., He, P., **Shan, L**., Sheen, J., and Kunkel, K. (2007). The Pseudomonas syringae type III effector AvrRpt2 alters Arabidopsis thaliana auxin physiology. ***Proc. Natl. Acad. Sci. U. S. A*** 104: 20131-20136.
- **Shan, L**., He, P., and Sheen, J. (2007). Intercepting host MAPK signaling cascades by bacterial type III effectors. ***Cell Host & Microbe*** 1: 167-174.
- He, P., **Shan, L**., Lin, N.-C., Martin, G., Kemmerling, B., Nurnberger, T., and Sheen, J. (2006). Specific bacterial suppressors of MAMP signaling upstream of MAPKKK in *Arabidopsis* innate immunity. ***Cell*** 125: 563-575.
- **Shan, L**., Thara, V.K., Martin, G.B., Zhou, J.-M., and Tang, X. (2000). The Pseudomonas AvrPto protein is differentially recognized by tomato and tobacco and is localized to the plant plasma membrane. ***The Plant Cell.*** 12: 2323-2338.

Biographical Sketch: **Michael V. Kolomiets**	Professor, Department of Plant Pathology and Microbiology, Texas A&M University

Professional Preparation

Kiev State University, Kiev, Ukraine	Genetics	B.S. and M.S.	1986
Institute of Plant Sciences, St. Petersburg,	Biochemistry	Ph. D. equivalent	1991
Iowa State University, Ames, Iowa	Horticulture	Ph.D.	1998

Appointments:

Professor, Department of Plant Pathology, Texas A&M University, 2014-current
Associate Professor, Department of Plant Pathology, Texas A&M University, 2008-2014
Assistant Professor, Department of Plant Pathology, Texas A&M University, 2002 –August 2008
Post Doctoral Research Fellow, Disease Resistance Group, Pioneer Hi-Bred Intl., Inc., 1999-2001
Post Doctoral Research Associate, Department of Agronomy, University of Missouri-Columbia, 1998-99
Graduate Research Assistant, Horticulture Department, Iowa State University, 1993-1998

Research Publications (last 5 years):

Brown S, Iberkleid I, Buki P, Kolomiets MV (2015) The Role of Lipid Signalling in Regulating Plant–Nematode Interactions. In book: Advances in Botanical Research, Publisher: ElSevier, Editors: C. Escobar, C. Fenoll, pp.139-166

Barrero Farfan ID, De La Fuente G, Murray SC, Isakeit T, Huang P-C, Warburton M, Williams P, Windham G, Kolomiets M. (2015) Whole genome association study for drought, aflatoxin resistance, and important agronomic traits in maize in a subtropical environment. *PLOS ONE*. DOI:10.1371/journal.pone.0117737

Starr J, Yang W, Yan Y, Crutcher F, Kolomiets MV (2014) Expression of Phenylalanine Ammonia Lyase Genes in Maize Lines Differing in Susceptibility to Meloidogyne incognita. *Journal of Nematology* 46(4):360–364

Christensen S, Nemchenko A, Park Y-S, Borrego E, Huang P-C, Schmelz EA, Kunze S, Feussner I, Nasser Yalpani N, Meeley R, Kolomiets MV (2014) The novel monocot-specific 9-lipoxygenase, ZmLOX12, is required to mount jasmonate-dependent defense against Fusarium verticillioides in maize. *Molecular Plant Pathogen Interactions* 27: 1263–1276

Yan Y, Huang PC, Borrego E, Kolomiets M. (2014) New Perspectives into Jasmonate Roles in Maize. *Plant Signal Behavior*. DOI**:**10.4161/15592316.2014.970442

Christensen S, Nemchenko A, Borrego E, Murray I, Sobhy I, Bosak L, DeBlasio S, Erb M, Robert CAM, Vaughn K, Göbel C, Tumlinson J, Feussner I, Jackson D, Turlings TCJ, Engelberth J, Nansen C, Meeley R, Kolomiets MV (2013). The maize lipoxygenase, ZmLOX10, mediates green leaf volatile, jasmonate, and herbivore-induced plant volatile production for defense against insect attack. *Plant Journal* 74, 59–73.

Constantino N, Mastouri F, Damarwinasis R, Kenerley C, Gao X, Kolomiets MV. (2013) Root Expressed Maize Lipoxygenase 3 Negatively Regulates Induced Systemic Resistance to Colletotrichum graminicola in Shoots. *Frontiers in Plant Sciences*. 4:510. doi: 10.3389/fpls.2013.00510.

De La Fuente GN, Murray SC, Isakeit T, Park Y-S, Yan Y, Warburton ML, Kolomiets MV (2013) Characterization of Genetic Diversity and Linkage Disequilibrium of ZmLOX4 and ZmLOX5 Loci in Maize. *PLOS ONE* 8(1): e53973. doi:10.1371/journal.pone.0053973

Yan Y, Christensen S, Isakeit T, Engelberth J, Meeley R, , Hayward, Emery N, Kolomiets M (2012) Disruption of OPR7 and OPR8 Reveals the Versatile Functions of JA in Maize Development and Defense. *Plant Cell* 24:1420-1436.

Yan Y, Borrego E, Kolomiets MV (2012) Jasmonate Biosynthesis, Perception and Function in Plant Development and Stress Responses. ***Lipid Metabolism***. Publisher, Intech.

http://dx.doi.org/10.5772/52675
Christensen S, Kolomiets M (2011) The lipid language of plant-fungal interactions. *Fungal Genetics and Biology*. 48:4-14
Park Y-S, Kunze S, Ni X, ·Feussner I, Kolomiets MV. (2010) Comparative molecular and biochemical characterization of segmentally duplicated 9-lipoxygenase genes ZmLOX4 and ZmLOX5 of maize. *Planta*. 231:1425–1437
Gao X, Brodhagen M, Isakeit T, Horowitz-Brown S, Göbel C, Betran J, Feussner I, Keller N, Kolomiets M (2009) Inactivation of the lipoxygenase *ZmLOX3* increases susceptibility of maize to *Aspergillus* spp. *Mol Plant Microbe Inter.* 22: 222-231.

Synergistic Activities:

- Editor, *Molecular Plant Pathology* (2015-2018), *Frontiers in Plant Sciences* (2013-present)
- NSF Panel Member, 2012, 2011, 2010.
- Developed and teaches a new graduate level course on molecular biology of plant-pathogen interactions PLPA 609 "Defense Hormone Signaling".
- Teaches an undergraduate/graduate class PLPA 301/601 "Plant Pathology".
- Member of the Advisory Committee for the Institute of Plant Genomics and Biotechnology, Texas A&M University.
- Member of Council of Principal Investigators (2009-2011), Texas A&M University
- Member of Executive and Symposium Committees, Molecular and Environmental Plant Sciences Interdepartmental Program (2004-13)
- Member of Graduate Program Committees (2008-13).
- Ad hoc reviewer for *Plant Cell*, *Plant Journal*, *Phytochemistry*, *Molecular Plant-Microbe Interactions, Physiological and Molecular Plant Pathology*, *Phytopathology, Plant Physiology, Plant Molecular Biology, Planta, Molecular Plant Pathololgy, Journal of Experimental Botany, PLOS One, Open Biology, Molecular and General Genetics*, etc.

Awards

2013, Best Research Faculty of 2012-2013 academic year, Department of Plant Pathology, Texas A&M University
2011, Outstanding Young Faculty Award, Faculty of Molecular and Environmental Plant Sciences, TAMU
2005, Outstanding Professor Award, Department of Plant Pathology and Microbiology, TAMU
1998, Graduate Research Excellence Award, Iowa State University

Short Description of Research Program

Dr. Kolomiets' research program is currently funded by NSF and USDA NIFA. The major focus is on lipid-mediated signal communication between plants and pathogens, plants and herbivorous insects, nematodes and insect parasitoids. More recently, his interests also include understanding the physiological functions of volatile and non-volatile oxidized lipids (oxylipins) including jasmonates, green leaf volatiles in maize interaction with rhizosphere microbiome, and tolerance to drought and heat. To understand biological relevance of diverse oxylipins in plant adaptation to adverse environmental conditions, *Mutator*-transposon insertional mutants were generated in most members of the lipoxygenase and oxo-phytodienoate reductase gene families as well as in other enzymes of the lipoxygenase pathway. Results of phenotypic, molecular and metabolomic analyses of the mutants indicate that many novel maize oxylipins play hormone-like signaling roles in diverse physiological processes of maize including defense against insects and pathogens, growth and development, mineral nutrition, water stress and interactions with biotic stressors as well as volatile mediated plant-to-plant signal communication.

PETER M. RENTZEPIS
Ph.D. University of Cambridge (UK)
Present Position:
Professor Electrical and Computer Engineering
Distinguished Professor TEES
Texas A&M University
College Station, Texas 77843
Awards **-** Over twenty five major awards and prizes
Honorary D. Sc. - four
Name Lectureships - over 35
Professorships - 10
Publications over 480
Patents - 89
Books - 5

Employment
Member of Technical Staff, Research Laboratories, General Electric Co., Schenectady, NY.
Member of Technical Staff, AT&T Bell Laboratories, Murray Hill, NJ 07974
Head, Physical and Inorganic Chemistry Research Department, AT&T Bell Laboratories, Murray Hill, NJ 07974 1964-1984
Presidential Chair and Professor Chemistry, Electrical Engineering and Material Sciences and Engineering University of California, Irvine, CA 92717 1974-2014
Professor, Electrical and Computer Engineering and Distinguished Professor TEES. Texas A&M University, College Station TX, 77843 2014-

Professorships (partial list)
Visiting Professor, Rockefeller University, N.Y.
Visiting Professor of Chemistry, Massachusetts Institute of Technology, Cambridge, MA
Visiting Professor of Chemistry, University of Tel-Aviv, Tel-Aviv, Israel
Adjunct Professor of Chemistry, University of Pennsylvania, Philadelphia, PA
Center for Biological Studies, State University of New York, Albany, New York
Adjunct Professor of Chemistry and Biophysics, Yale University, New Haven, CT.
Honorary Professor National Technical University of Greece.

Awards (Partial list)
The Irving Langmuir Award in Chemical Physics, Awarded by The American Physical Society
Scientist of the Year Award. Research and Development
Member of National Academy of Sciences,
The A. Cressy Morrison Award in Natural Sciences-awarded by the N.Y Academy of Sciences
ISCO Award, for Biological Sciences Research
Scientist of the year,1974
AHEPA Award-for Leadership in Science and Education
Honorary Doctor of Philosophy, Syracuse University
Honorary Doctor of Science, Denison University
The Peter Debye Award in Physical Chemistry-Awarded by The American Chemical Society.
Fellow-New York Academy of Sciences

Fellow-American Physical Society
Regent's Professor, University of California, at Los Angeles
Camille and Henry Dreyfus-Distinguished Scholar
Distinguished Alumni, SUNY
US Honorary Research Society, Sigma Xi
Honorary Doctor of Science, Carnegie-Mellon University
The H.S. Ganning Award, University of Alberta, Canada
Regent's Lecturer, University of California at Irvine
AAAS Fellow
Member, Athenian Academy, (National Academy of Greece)
Int. Quantum and Laser Society Award
Honorary Doctor of Science, National Technical University of Greece
Distinguished Faculty Research Award, University of California, Irvine
Honorary Professor, Academy of Sciences of The Peoples Republic of China
The American Chemical Society Tolman Medal

Name Lectureships (Partial list)
Robert A. Welch Foundation-Lecturer
Faculty Lecturer-Rensselaer Polytechnic Institute, Troy, New York
Alumni Scholar, Denison University
IBM Lecturer-Williams College
Distinguished Lecture Series-University of Utah
Regents Lecturer, University of California, Los Angeles
Xerox Lecturer-North Carolina State University
Frank C. Whitmore Lectures in Chemistry-Pennsylvania State University
Dreyfus Distinguished Scholar Lectures
Regent's lecturer, University of California, Irvine
The Harry S. Gannig Distinguished Lectures, University of Alberta, Canada
University of Crete, Greece, Distinguished Lecturer
York University, Canada, Distinguished Lecturer
Yale University, New Haven, CT., Distinguished Lecturer
University of Leuven, Belgium, Distinguished Lecturer

Advisory Boards (Partial list)
State University of New York, at Buffalo, Evaluation Panel, Physical Chemistry Division,
National Institute of Science and Technology, Bureau of Standards, Washington DC.
Evaluation Board for Center for Thermodynamics and Molecular Science
U.S.A., Foreign Applied Science Assessment, US. AmCCOM Advisory Committee
US. Army ARRACOM Executive Science Advisory Committee
Board of Army Science and Technology, International Science foundation

CURRICULUM VITAE

Ping He

EDUCATION

2003-2008	Harvard Medical School, Boston, MA	Molecular Biology	Postdoc
1998-2003	Kansas State University, Manhattan, KS	Plant Pathology	Ph.D.
1995-1998	Chinese Academy of Sciences, China	Genetics	M.S.
1989-1993	China Agricultural University, Beijing, China	Plant Breeding & Genetics	B.S.

PROFESSIONAL EXPERIENCE

2009-present Associate, Assistant Professor, Department of Biochemistry and Biophysics
Institute for Plant Genomics and Biotechnology
Faculty of Molecular & Environmental Plant Sciences (MEPS)
Texas A&M University, College Station, TX

HONORS

2008	American Society of Plant Biologists Early Career Award
2002-2003	Don C. Warren Genetic Scholarship, Kansas State University
1998	Second Prize of Natural Science Award, Chinese Academy of Sciences
1998	Special Prize of the President Scholarship, Chinese Academy of Sciences

PUBLICATIONS

- Zhou, J., Lu, D., Xu, G., **He, P.** and Shan, L., (2015) The dominant negative ARM domain uncovers multiple functions of plant U-box E3 ligase PUB13 in *Arabidopsis* immunity, flowering and senescence. ***Journal of Experimental Botany*** doi: 10.1093/jxb/erv148.
- Li, B., Jiang, S., Yu, X., Cheng, C., Chen, S., Cheng, Y., Yuan, J., Jiang, D., **He, P.,** and Shan, L. (2015) Phosphorylation of a trihelix transcription repressor ASR3 by MPK4 negatively regulates *Arabidopsis* immunity. ***The Plant Cell.*** 27: 839-856.
- Feng, B., Liu, C., Oliveira, M.V.V., Intorne, A.C., Li, B., Babilonia, K., Filho, G.A.S., Shan, L., and **He, P.** (2015) Protein poly(ADP-ribosyl)ation regulates *Arabidopsis* immune gene expression and defense responses. ***PLoS Genetics*** 11(1): e1004936. doi:10.1371/journal.pgen.1004936.
- Li, M., Li, F., and **He P.** (2015) Construction of a cotton VIGS library for functional genomic study. ***Methods Mol Biol.*** 1287: 267-279.
- Li, F., Cheng, C., Cui, F., Oliveira, M.V.V., Yu, X., Meng, X., Intorne, A.C., Babilonia, K., Li, M., Chen, X., Ma, X., Xiao, S., Zeng, Y., Fei, Z., Metz, R., Johnson, C.D., Koiwa, H., Sun, W., Li, Z., Filho, G.A.S., Shan, L., and **He, P.** (2014) Modulation of RNA polymerase II phosphorylation downstream of pathogen perception orchestrates plant immunity. ***Cell Host & Microbe*** 16: 748-758.
- Gao, X., Cox Jr., K.L., and **He, P**. (2014) Functions of calcium-dependent protein kinases in plant innate immunity. ***Plants*** 3: 160-176.
- Wu, S., Shan, L., and **He, P.** (2014) Microbial signature-triggered plant defense responses and early signaling mechanisms. ***Plant Science*** 228: 118-126.
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- Shan, L., **He, P.,** and Sheen, J. (2007) Intercepting host MAPK signaling cascades by bacterial type III effectors. ***Cell Host Microbe*** 1: 167-174.
- **He, P.,** Shan, L., and Sheen, J. (2007) Elicitation and suppression of MAMP-triggered immunity in plant-microbe interactions. ***Cell Microbiol*** 9: 1385-1396.
- Sheen, J., and **He, P.** (2007) Nuclear actions in innate immune signaling. ***Cell*** 128: 821-823.
- **He, P.,** Shan, L., Lin, N.-C., Martin, G., Kemmerling, B., Nurnberger, T., and Sheen, J. (2006). Specific bacterial suppressors of MAMP signaling upstream of MAPKKK in Arabidopsis innate immunity. ***Cell*** 125: 563-575.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Shen, Yang	Assistant Professor
eRA COMMONS USER NAME (credential, e.g., agency login) shenyang	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
University of Science and Technology of China	B.E.	06/2002	Automatic Control
Boston University	Ph.D.	01/2008	Systems Engineering
Boston University	Postdoctoral	08/2008	Biomedical Engineering
Massachusetts Institute of Technology	Postdoctoral	12/2011	Biological Engineering and Computer Science

A. Personal Statement

The goal of proposed Synthetic and Systems Biology Innovation Hub (SSBIH) is to leverage and integrate existing resources (facilities, expertise, and research programs here at TAMU) and build a cutting-edge interdisciplinary platform. I have the expertise and motivation necessary to successfully contribute to the proposed work, especially in computational protein and small-molecule design as well as systems modeling and control for medicine, agriculture, and energy.

I am driven by the curiosity to unravel molecular mechanisms of biomolecular interactions and biological systems and the desire to engineer biomolecules and their networks for better therapeutic, food, and energy solutions. To that end, my research focuses on modeling, predicting, and designing biomolecular interactions and biomolecular networks. And my computational research has been closely interacting with experimental and clinical scientists to address challenges at multiple scales ranging from molecules, systems, to big data.

At the molecular level, I have extensive experience in modeling protein interactions, including structural prediction and structure-based design. Our protein-docking methods have achieved considerable success in CAPRI (a community-wide critical assessment). Our computational study has also contributed to deciphering resistance mutations and developing drug design strategies for the treatment of advanced prostate and breast cancers. With a background in systems engineering and experiences in computational metabolic engineering, I have also been developing systems modeling, simulation, and control techniques in tandem with molecular modeling and design for systems and synthetic biology. Therefore, I have a demonstrated track record of achievements in modeling and designing biomolecules and systems; my experiences and expertise make me ready to contribute to the proposed project substantially.

B. Positions and Honors

Positions and Employment

2012-present Research Affiliate, Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, Cambridge, MA
06-07/2012 Visiting Assistant Professor, Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, Cambridge, MA
2012-2014 Research Assistant Professor, Toyota Technological Institute at Chicago, Chicago, IL
2015-present Assistant Professor, Department of Electrical and Computer Engineering, TEES-AgriLife Center for Bioinformatics and Genomic Systems Engineering, Texas A&M University, College Station, TX

Honors

2005 First prize in the 3rd CAPRI (Critical Assessment of PRedicted Interactions) evaluation, a community-wide comparative evaluation of protein docking methods, Toronto, Canada
2009 Member of the team with the best performance in the 4th CAPRI evaluation, Barcelona, Spain
2013 Fifth place among 63 international teams in the 5th CAPRI evaluation, Utrecht, the Netherlands
2015 4th place among 29 groups for performances predicting 25 oligomeric protein structures in the first joint CASP–CAPRI experiment

Other Experience and Professional Memberships

2005- Member, American Chemical Society
2006- Member, Institute of Electrical and Electronics Engineers
2007- Member, International Society of Computational Biology

C. Selected Peer-reviewed Publications (Selected from 19)

1. Y Shen, ICh Paschalidis, P Vakili, and S Vajda (2008) Protein Docking by the Underestimation of Free Energy Funnels in the Space of Encounter Complexes. PLoS Computational Biology 4(10), e1000191. PMC2538569
2. Y Shen, MK Gilson, and B Tidor (2012) Charge Optimization Theory for Induced-Fit Ligands. Journal of Chemical Theory and Computation 8(11), 4580–4592. PMC3496346
3. Y Shen, MD Altman, A Ali, MNL Nalam, H Cao, TM Rana, CA Schiffer, and B Tidor (2013) Testing the Substrate-Envelope Hypothesis with Designed Pairs of Compounds. American Chemical Society (ACS) Chemical Biology 8(11), 2433–2441. PMC3833293
4. MD Balbas, MJ Evans, DJ Hosfield, J Wongvipat, V Arora, PA Watson, Y Chen, GL Greene, Y Shen*, and CL Sawyers* (2013) Overcoming Mutation-Based Resistance to Antiandrogens with Rational Drug Design. eLife 2, e00499. (* Co-corresponding) PMC3622181
5. Y Shen (2013) Improved Flexible Refinement of Protein Docking in CAPRI Rounds 22-27. Proteins: Structure, Function and Bioinformatics 81(12), 2129–2136. PMC23996302
6. W Toy, Y Shen, H Won, B Green, RA Sakr, M Will, Z Li, K Gala, S Fanning, TA King, C Hudis, D Chen, T Taran, G Hortobagyi, GL Greene, M Berger, J Baselga, and S Chandarlapaty (2013) ESR1 Ligand-Binding Domain Mutations in Hormone-Resistant Breast Cancer, Nature Genetics 45(12), 1439–1445. PMC 24185512
7. Y Shen, ML Radhakrishnan, and B Tidor (2015) Molecular Mechanisms and Design Principles for Promiscuous Inhibitors to Avoid Drug Resistance: Lessons Learned from HIV-1 Protease Inhibition, Proteins: Structure, Function and Bioinformatics 83(2), 351–372. PMC25410041
8. Tomasz Oliwa and Y Shen (2015) cNMA: A Framework of Encounter Complex-based Normal Mode Analysis to Model Conformational Changes in Protein Interactions, Bioinformatics, 31(12), i151–i160. PMC 26072477
9. CR Drake, L Estévez-Salmerón, P Gascard, Y Shen, TD Tlsty, EF Jones (2015) Towards Aspirin-Inspired Self-Immolating Molecules which Target the Cyclooxygenases, Organic & Biomolecular Chemistry (Royal Society of Chemistry), epub ahead of print. PMC26400105

D. Research Support

Ongoing Research Support

CCF-1347865/1546278 (NSF) Shen (PI) 10/01/2013-09/30/2016
Dimension reduction and optimization methods for flexible refinement of protein docking
The goal of this study is to reduce the number of conformational variables to describe conformational changes of proteins during interactions and to implement efficient optimization methods in the reduced conformational space to predict the complex structures formed by protein interactions.
Role: Sole PI

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.
Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME	POSITION TITLE
Wenshe R. Liu	Emile & Marta Schweikert Associate Professor of Chemistry
eRA COMMONS USER NAME (credential, e.g., agency login)	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Beijing University, China	B.S.	2000	Chemistry
University of California, Davis, CA	Ph.D.	2005	Biological Chemistry
The Scripps Research Institute, La Jolla, CA	Postdoc	2007	Chemical Biology

A. Personal Statements

The PI has about ten years of experience in developing the genetic noncanonical amino acid incorporation and click reaction techniques and has published more than thirty papers in this field. Using engineered pyrrolysine incorporation systems, his group has demonstrated the genetic incorporation of a large number of noncanonical amino acids into proteins in *E. coli*. These noncanonical amino acids include lysine, tyrosine, phenylalanine, and histidine derivatives. Based on the genetically incorporated non-canonical amino acids in proteins, the PI's group has demonstrated a variety of click reaction types such as CuAAC, tetrazine-alkene, and nitrilimine-alkene reactions can be used to selectively and site-specifically conjugate and immobilize proteins. The PI's group is comprised of an organic chemistry section and a molecular biology section that guarantees the proposed evolution work can be independently carried out in his group.

B. Positions and Honors

Positions

2007-2013	Assistant Professor of Chemistry, Texas A&M University
2013-2014	Associate Professor of Chemistry, Texas A&M University
2014-	Emile & Marta Schweikert Associate Professor of Chemistry, Texas A&M University

Honors

G. Zen Scholarship (1996-2000), Huikai Scholarship (1997), Canon Scholarship (1998), Outstanding Student Leader Award (1999), UC Systemwide Biotechnology Research Training Fellowship (2000-2004), UC-Davis Travel Award (2003), UC-Davis Summer Research Award (2004), NSF Career Award (2012)

C. Research Support

Current Support

1. Welch Research Grant A-1715 06/01/2015-05/30/2018 Total direct cost: $240,000
   Title: Novel chemical biology tools for investigating the protein ubiquitination system
   Principle investigator: Wenshe Liu, Ph.D.
   The major goal of this project is to develop chemical biology tools to synthesis polyubiquitination systems for understanding deubiquitinase functions. There is no overlap with the current application.

2. NIH-1R01CA161158 07/01/2011-04/30/2016 Total direct cost: $1,050,000
   Title: Phage display with two genetically incorporated noncanonical amino acids
   Principle investigator: Wenshe Liu, Ph.D.
   The major goal of this project is to combine the rapid-screening feature of phage display and the diversity-generating power of synthetic chemistry to assemble approaches for high throughput identification of small-molecule antiangiogenic agents and apply these molecules to cancer diagnosis, profiling, imaging, and therapy. There is no overlap with the current application.

3. NSF CAREER Award CHE-1148684 04/01/2012-03/31/2017 Total direct cost: $380,000

Title: CAREER: Site-specific dual-labeling of a protein through two genetically incorporated noncanonical amino acids
Principle investigator: Wenshe Liu, Ph.D.
The goal of this application is to develop simple and reliable methods for site-specific dual labeling of a protein with a FRET pair for protein folding/dynamic analysis. There is no overlap with the current application.

4. NIH-1R01GM085092 07/01/2014-06/30/2018
Title: Develop and application of bioorthogonal chemistry
Principle Investigator: Qing Lin, University at Buffalo; Collaborator: Wenshe Liu
The major focus of this subcontracted grant is to support the identification of pyrrolysyl-tRNA synthetase mutants that can directly charge $\mathrm{tRNA}_{\mathrm{CUA}}^{\mathrm{Pyl}}$ with non-canonical amino acids composed of tetrazole and alkene functional groups. There is no overlap with the current application.

D. Publications (Selected from 44 peer-reviewed publications)

1. Bindman N.A., Bobeica S.C., **Liu W.R.*** & van der Donk W.A.*, "Facile removal of leader peptides from lanthipeptides by incorporation of a hydroxy acid", *J. Am. Chem. Soc.* **2015**, 137:6975-6978.
2. Guan D., Kurra Y., **Liu W.R.*** & Chen Z.*, "A Click Chemistry Approach to Site-specific Immobilization of a Small Laccase Enables Efficient Direct Electron Transfer in a Biocathode", *Chem. Commun.*, **2015**, 51: 2522-2525.
3. Piscotta F., Tharp J.M., **Liu W.R.*** & Link J.A.*, "Expanding the Chemical Diversity of Lasso Peptide MccJ25 with Genetically Encoded Noncanonical Amino Acids", *Chem. Commun.,* **2015**, 51:409-412.
4. Lee Y.-J., Kurra Y., Yang Y., Torres-Kolbus J., Deiters A. & **Liu W.R.***, "Genetically Encoded Terminal Olefins for Live Cell Labeling with Tetrazine Dyes", *Chem. Commun.*, **2014**, 50: 13085-13088.
5. Kurra Y., Odoi K.A., Lee Y.-J., Lu T., Wheeler S.E., Torres-Kolbus J., Deiters A. & **Liu W.R.***, "Two Rapid Catalyst-free Click Reactions for *In Vivo* Protein Labeling of Genetically Encoded Strained Alkene/alkyne Functionalities", *Bioconjug. Chem.* **2014**, 25: 1730-1738.
6. Zeng Y., Wang W. & **Liu W.R.***, "Toward Reassigning the Rare AGG Codon in *Escherichia coli*", *ChemBioChem*, **2014**, 15:1750-1754.
7. Tuley A., Lee Y.-J., Wu B., Wang Z.U. & **Liu W.R.***, "A Genetically Encoded Aldehyde for Rapid Protein Labeling", *Chem. Commun.*, **2014**, 50:7424-7426.
8. Wan W., Tharp M.J. & **Liu W.R.***, "Pyrrolysyl-tRNA synthetase: an ordinary enzyme but an outstanding genetic code expansion tool", *Biochem. Biophys. Acta*, **2014**, 1844:1059-1070.
9. Tharp J.M., Wang Y.-S., Lee Y.-J. & **Liu W.R.***, "The Genetic Incorporation of Seven *Ortho*-substituted Phenylalanine Derivatives", *ACS Chem. Biol.*, **2014**, 9:884-890.
10. Wang X.S., Lee Y.-J., & **Liu W.R.***, "The Nitrilimine-Alkene Cycloaddition is an Ultra Rapid Click Reaction", *Chem. Commun.* **2014**, 50: 3176-3179.
11. Tuley A., Wang Y.-S., Fang X., Kurra Y., Reznom Y.H. & **Liu W.R.***, "The Genetic Incorporation of Thirteen Novel Non-canonical Amino Acids", *Chem. Commun.* **2014***,* 50: 2673-2675.
12. Lee Y.-J., Wu B., Raymond J.E., Zeng Y., Fang X., Wooley K.L. & **Liu W.R.**, "A Genetically Encoded Acrylamide Functionality", *ACS Chem. Biol.* **2013**, 8:1664-1670 .
13. Odoi K.A., Huang Y., Rezenom Y.H. & **Liu W.R.***, "Nonsense and Sense Suppression Abilities of Original and Derivative *Methanosarcina mazei* Pyrrolysyl-tRNA Synthetase-$\mathrm{tRNA}^{\mathrm{Pyl}}$ Pairs in the *Escherichia coli* BL21(DE3) Cell Strain ", *PLOS One*, **2013**, 8:e57035.

Joshua Yuan

From: Xin Wang
Sent: Thursday, October 22, 2015 12:12 PM
To: Joshua Yuan
Subject: FW: Hudson Robotics

From: Joe Matthews [mailto:JMatthews@hudsonrobotics.com]
Sent: Thursday, October 22, 2015 11:43 AM
To: Xin Wang
Subject: RE: Hudson Robotics

Good morning Xin,
What is your time frame? Our quotes are good for 30 days, and some purchasing departments balk at processing an expired quote. We do this to protect against spikes in materials costs, but the prices haven't changed since I started a few years ago. When the time comes, I'm happy to send a proper quote.

Meanwhile, the single-pin RapidPick sells for ~$60,000, and the 20-pin RapidPick sells for ~$100,000. The only functional difference from the user perspective is thruput. Again, the single-pin picker will do 300 in an hour, and the 20-pin does 3,000. Controls are intuitive and powerful. There are many references around the world.

They are both fully automatable, and they both work free-standing. The 20-pin version requires a compressor.
I recommend checking out the Micro10x dispenser for media filling. That's a tedious operation, and the u10x does it in seconds. That costs $14,000.

A Plate Crane would give you walkway processing of a stack of culture plates- or more. Each plate may produce many inoculation plates, so we can include up to 10 stacks, holding 25 standard-height plates or dishes. We have four Plate Cranes. The basic, the standard Plate Crane EX comes in a little under $40,000.
Do you use deepwell plates for growth? In that case, maybe ten output plates per stack. How much volume are you expecting?

The synthetic biology workstation is the full set: Gene Assembly, Transformation, Plating, Plasmid Prep. NGS prep methods can be performed using this workcell, DNA/RNA purifications (and protein- with vacuum, positive pressure, or magnetic beads), normalization, PCR prep. The SynBio workstation starts as a standard system, and ultimately gets customized.

I'd like to know what you'll do upstream and downstream. In one of my customers' systems, we have a Q-PCR station. Nanodispensers prepare 1536-well Q-PCR plates, and we run them through the LightCycler. He will eventually pick colonies, prep the plasmids, and shuttle them directly into Q-PCR, all barcode-indexed. He gets his DNA from a 3rd party vendor and carries out transformations offline.

They aren't using our plating kit, and incubators are also offline. He's actually got a big custom system, not a SynBio Workcell. These workcells start around $65K. Gene Assembly, for example, includes a thermal cycler, a cold station and the Solo robotic pipettor.

I hope I've responded to your questions. When an email gets this long, it can wander.

Joy,
Joe

From: Xin Wang [mailto:Xin.Wang@ag.tamu.edu]
Sent: Thursday, October 22, 2015 10:44 AM
To: Joe Matthews <JMatthews@hudsonrobotics.com>
Subject: RE: Hudson Robotics

Thank you for your reply, Joe.

We will be working on all three systems, E. coli, yeast and cyanobacteria. We would need to screen large libraries so the 20 pin picking platform might just work. But could you give me a quote for both system? We are still looking into the budget for this.

Also, what does the synthetic biology workstation include? Is it standard package or just something we need set up our own? The website info provided what we want to do, starting from building large numbers of construct to plasmid prep. Would you kindly provide a quote for this too?

Best,
Xin

From: Joe Matthews [mailto:JMatthews@hudsonrobotics.com]
Sent: Thursday, October 22, 2015 9:06 AM
To: xwang@tamu.edu
Subject: Hudson Robotics

Good morning Xin,
Thank you for inquiring about our colony pickers and synthetic biology workstations.

Hudson Robotics' RapidPick colony picking platform is the solution to everyone's problems. I'd like to let you know all about it, but I should ask what you're doing. The RapidPick will work with bacteria, yeast, and customers are using it for algae.

The standard model is a 20-pin picker capable of 3,000 colony picks per hour. The new one is the Single-Pin RapidPick, which can pick 300 colonies per hour. Both are fully automatable, and both will fit into anaerobic chambers.

I can be reached at 201-240-1579 (cell). Email is good for sharing details. I have to clock out early today. My wife runs the offices of a nonprofit clinic, and tonight is the big annual dinner.

Joy,
Joe

Joe Matthews
ジョーサフ・マスユーズ
Hudson ROBOTICS, INC.
MidAtlantic Account Manager
Applications Specialist
201-240-1579
www.hudsonrobotics.com

Dr. Marty Dickman, Director
Institute for Plant Genomics and Biotechnology

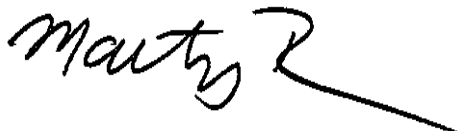
AgriLIFE RESEARCH
Texas A&M System

March 9, 2016

Dear Joshua:

I strongly support you for the RDF application to build a Synthetic and Systems Biology Innovation Hub. Synthetic biology is an emerging field with great potential. Unfortunately, an integrated facility and program in such an important area is not in place at TAMU/AgriLife. The Borlaug Center (Institute of Plant Genomics and Biotechnology) is an interdisciplinary center aiming for scientific excellence and cutting-edge technologies. SSBiH well aligns with our vision and mission. I am happy to provide sufficient space to host the facility. In addition, I am happy to serve as the chair of advisory committee for this facility. I will work with you and the team to build a strong nationally recognized scientific program in synthetic and systems biology.

Sincerely



Martin B. Dickman, Ph.D.
University Distinguished Professor
Christine Richardson Professor of Agriculture
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Huimin Zhao
Steven L. Miller Chair Professor
Tel: (217)333-2631
Fax: (217)333-5052
E-mail: zhao5@illinois.edu

March 10, 2016

Professor Joshua Yuan
Texas A&M University

Dear Joshua,

I am writing to support your initiative to apply for internal funding to build a synthetic and systems biology facility in your university. As the theme leader of the Biosystems Design in the Carl R. Woese Institute for Genomic Biology at the University of Illinois at Urbana-Champaign, my group has developed many synthetic biology tools for applications in biotechnology and bioengineering, and particularly established the Illinois Biological Foundry for Advanced Biomanufacturing (iBioFAB) (http://youtu.be/Hwb735qZ-IQ). I would be happy to serve as an advisory committee member and help you establish this facility to support synthetic biology research on your campus.

I wish you very best luck with you application.

Best regards,

Huimin Zhao
Steven L. Miller Chair Professor
Departments of Chemical and Biomolecular Engineering,
Chemistry, Biochemistry, and Bioengineering,
Biosystems Design (BSD) Theme Leader
Carl R. Woese Institute for Genomic Biology,
215 Roger Adams Laboratory, Box C3,
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E-mail: zhao5@illinois.edu, Web: scs.illinois.edu/~zhaogrp/
Lab in Singapore: www.merl.a-star.edu.sg