CURRICULUM VITAE

Huansheng Cao, Ph.D.
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PROFESSIONAL EXPERIENCE

2020-present	Assistant Professor, Duke Kunshan University
2017-2020	Assistant Research Professor Biodesign Institute Center for Fundamental and Applied Microbiomics Arizona State University
2014–2017	*Bioinformatics Post-Doctorate Research Associate* Institute of Bioinformatics | Department of Biochemistry and Molecular Biology University of Georgia
2012–2014	*Bioinformatics Post-Doctorate Research Associate* Department of Biological Sciences Northern Illinois University

EDUCATION

Ph.D.	**Cell and Molecular Biology**, Fordham University *Dissertation: Effects of population size on fitness effects of mutations and long-term fitness trajectories in E. coli populations for 4,000 generations* Advisors: Professors James D Lewis and Gordon R Plague	2006-2012
Ph.D.	**Limnology**, Chinese Academy of Sciences *Dissertation: Development and formation of Microcystis aeruginosa blooms and major stage-specific driving factors* Advisor: Professor Fanxiang Kong	2003-2006
M.Eng.	**Environmental Science**, Jinan University, China *Thesis: Induction of hairy roots from hairy roots of pharmaceutical plant Trichosanthes bracteata Voigt for treatment of sewage* Advisor: Professor Mingfang Xu	2002-2003
B.S.	**Biochemistry**, Yantai University, China *Thesis: Extraction and analyses of asterosaponin from Yellow Sea starfish* *Advisor: Professor Chenghua Guo*	1996-2000

AWARDS AND HONORS

2014	Nomination for Northeastern Association of Graduate Schools Dissertation Award
2010	Kathleen O'Connell Tamburro, M.D. and Carlo H. Tamburro Memorial Scholarship, Fordham University
2010	Burroughs Wellcome Fund Travel Scholarship
2008	Award for the Advancement of Science and Technology (2nd place, Award no. 20080593, with Kong F, Ma R, Chen J, Gao G, Wu X, Zhang M, Yu Y, Ji J, **Cao H**, Yang Z, Xing P, and Tao Y), Jiangsu Province, China
2006	Schering-Plough Award, Fordham University
2006	Excellent Graduate Award, Nanjing Institute of Geography and Limnology, Chinese Academy of Sciences

2006 Chinese Academy of Sciences, Nanjing Academy Award
2006–2011 Graduate Teaching Assistantship, Fordham University

RESEARCH INTERESTS

Experimental and computational systems biology

Human and environmental microbiomics

Harmful algal blooms

RESEARCH EXPERIENCE

Bioinformatics Research Associate (with Prof. Ying Xu) 2014-2017
Department of Biochemistry and Molecular Biology, University of Georgia

- Systems-level elucidation of biofuel ethanol stress and adaptation in *E. coli* by integrating of phenotypic data (ethanol-tolerance genes, growth rate, stress response genes) with multi-omics data (transcriptomics, genomics, and proteomics) in non-evolved and evolved strains
- Flux balance analysis of metabolic networks and optimization across conditions
- Topological decomposition of bacterial genome-scale metabolic networks
- Integration of multi-omics data based on metabolic networks
- Development of next-generation pipeline for bioengineering by large-scale reconstruction of metabolic networks and flux optimization

Bioinformatics Research Associate (with Dr. Yanbin Yin) 2012-2014
Department of Biological Sciences, Northern Illinois University

- Functional genomics comparison between blooming and non-blooming cyanobacteria to identify major bloom-driving pathways
- Transcriptomic and phenotypic responses in the top water-bloom cyanobacterium *Microcystis aeruginosa* in extra-eutrophic conditions
- Molecular evolution of genes encoding cellulose-active enzymes and cellulosome genes in three domains of life and five species of *Clostridium* genus
- Whole-genome sequencing and annotation of water-bloom cyanobacterium *Aphanizomenon flos-aqua*e NIES-81 and plant pathogen *Penicillium expansum*

PhD Student/Research Fellow (with Drs. Gordon Plague and James D Lewis) 2006-2012
Department of Biological Sciences, Fordham University

- Fitness effects of mutations at high and low population density in *E. coli* using genome resequencing and transcriptomics
- Evolutionary trajectories of *E. coli* populations in high and low density and rich and minimal medium for 4,000 generations
- Clonal interference of *E. coli* populations at high and medium populations in rich and minimal medium

MEng Student/Research Fellow (with Dr. Mingfang Xu) 2003-2006
Institute of Hydrobiology, Jinan University, China

- Induction hairy roots in medical Thesis: Induction of hairy roots from hairy roots of pharmaceutical plant *Trichosanthes bracteata* Voigt for treatment of sewage
- Preparation and application of nanocrystalline TiO2 photocatalysis for degradation of crude oil poIlutants

BS Biochemistry Student (with Dr. Chenghua Guo) 2003 Life
School of Life Sciences, Yantai University, China

- Extraction and analyses of asterosaponin from Yellow Sea starfish

RESEARCH FUNDING

Active grant

1. Duke Kunshan University PI NSFC RMB 590,000
   Jan 2023-Dec 2026 Systems biology mechanism of cyanobacterial blooms

Completed Grants

1. Arizona State University PI Startup grant
2. Arizona State University co-I SOLS/OKED Program $43,406
   Jan-Jun 2018 Engineering bacterial community for efficient biogas conversion. Grant No: ECRA548BC
3. Fordham University PI Graduate Research Program $2,000
   2011-2012 Long-term evolution of *E. coli* under nutrient-minimal and rich environment

PUBLICATIONS

(†: co-first; *****: corresponding)

Systems Biology and Bioinformatics

1. Du W, Li G, Ho N, Jenkins L,Hockaday D, Tan J and **Cao H***. CyanoPATH: a knowledgebase of genome-scale functional repertoire for toxic cyanobacterial blooms. **Briefings in Bioinformatics** (IF=9.0, 中科院一区、顶刊): bbaa375. DOI: 10.1093/bib/bbaa375.
2. **Cao H**, Shimura Y, Steffen MM, Yang Z, Lu J, Joel A, Jenkins L, Kawachi M, Yin Y, Garcia-Pichel F. 2020. The trait repertoire enabling cyanobacteria to bloom assessed through comparative genomic complexity and metatranscriptomics. **mBio** (IF=6.8, 中科院一区、顶刊) 11: e01155-20. https://doi.org/10.1128/mBio.01155-20
3. Zhou T, **Cao H***, Zheng J, Teng F, Wang X, Lou L, Zhang X, Tao Y*. Suppression of water-bloom cyanobacterium *Microcystis aeruginosa* by algaecide hydrogen peroxide maximized through programmed cell death. **Journal of Hazardous Materials** (IF=9.0)
4. Li G†, **Cao H†**, and Xu Y. Structural and functional analyses of microbial metabolic networks reveal novel insights into genome-scale metabolic fluxes. ***Briefings in Bioinformatics*** (IF=9.0), bby022. 2018
5. **Cao H**, Ma Q, X Chen, and Xu Y. DOOR: A microbial operon database for gene organization and function discovery. ***Briefings in Bioinformatics***

ACADEMIC PRESENTATIONS

Invited Talks

1. **Cao H**. *Within-genus diversity in the microbial communities associated with cyanobacterial blooms in Harsha Lake, Ohio, USA.* School of Life Sciences, Nanjing Normal University, China, May 29, 2019
2. **Cao H**. *Toward systems ecology of cyanobacterial blooms: integrating driving factors and ecophysiology at the systems level*. School of Biological Sciences, Nanjing Normal University, Nanjing, China, June 9, 2017

3. **Cao H**. *Toward systems-level integration of multi-omics data: applications in ethanol stress/adaption and microbial metabolic structure*. Department of Science, John Jay College of Criminal Justice, City University of New York, NYC, March 10, 2017
4. **Cao H**. *Toward systems ecology of cyanobacterial blooms: integrating driving factors and ecophysiology at the systems level*. Department of Biological Sciences, University of Cincinnati, Cincinnati, March 5, 2017
5. **Cao H**. *Systems-level understanding of ethanol stresses and adaptation in E. coli by integrating genomic, transcriptomic, and protein data*. Department of Environmental Health Science, College of Public Health, University of South Carolina, Columbia, Feb 1, 2017
6. **Cao H**. *Systems-level understanding of ethanol stress and adaptation in E. coli and heterogeneous architecture of bacterial metabolic networks*. Biodesign Institute, Arizona State University, Tempe, Jan. 24, 2017
7. **Cao H**. *A primer to bioinformatics: learning by doing*. Department of Biology, Stonehill College, Boston, MA, Jan 20, 2017
8. **Cao H+**, Du W+, Yang Y, Shang Y, Li G, Zhou Y, Ma Q, and Xu Y. *Systems-Level Understanding of Ethanol-Induced Stresses and Adaptation in E. coli*. Integrative BioSystems Institute, Georgia Institute of Technology, Atlanta, GA, December 7, 2016
9. **Cao H**, Li G, and Xu Y. *Development of next-generation pipeline for biological engineering*. Dr. Yanjun Yan's lab in the College of Engineering at the University of Georgia, Athens, GA, September 10, 2016
10. **Cao H**. *Fitness effect of mutations and evolutionary trajectories of E. coli populations are high and low N_es*. Dr. Siobain Duffy lab, Rutgers, New Brunswick, NJ, April, 2012
11. **Cao H**. *Fitness effect of a crp mutation depends not only on environment, but also population size*. Fordham University GSAS Communitas, Bronx, NY, March 30, 2011
12. **Cao H**. *Variation of fitness effects of mutations and implications to cancer and pathogenesis*. Fordham University Summer Research Program, Armonk, NY, July 16, 2011
13. **Cao H**. *Evolutionary trajectories of pathogenic E. coli populations in rich and minimal medium for 4,000 generations*. Fordham University Summer Research Program, Armonk, NY, June 11, 2010

Talks

1. **Cao H**, Kong F, and Zhang X. *Seasonal variations of cyanobacteria recorded by phycocyanin and colony enlargement of* Microcystis aeruginosa *in Lake Taihu*. International Symposium on the Eutrophication Process and Control in Large Shallow Lakes (With special reference to Lake Taihu, a large shallow subtropical Chinese lake). Nanjing, China. 2005
2. **Cao H**, Kong F, and Zhang X. *Recruitment of phytoplankton and dominance establishment of Microcystis in Taihu*. The 12th International Symposium on River and Lake Environments-Freshwater Environment and Biodiversity. Wuhan, China. 2004

Posters

1. **Cao H**, Chen X, Li G, Zuo C, Ma Q, and Xu Y. *An integrated computational suite of webservers and tools developed by CSBL*. U.S. Department of Energy BioEnergy Science Center Retreat, Chattanooga, TN, June 12, 2016
2. **Cao H**, Li G, Ma Q, and Xu Y. *A new computational framework of metabolic network analysis*. U.S. Department of Energy BioEnergy Science Center Retreat, Chattanooga, TN, June 12, 2016

3. **Cao H**, Du W, and Xu Y. Ethanol toxicity and adaptation in E. coli revealed by transcriptomic, genomics and literature data. Department of Biochemistry and Molecular Biology Retreat, Helen, GA, May 16, 2016
4. **Cao H**, Xu Y. Dense modules in bacterial metabolic networks and network evolution. Department of Biochemistry and Molecular Biology Retreat, Athens, GA, March 16, 2015
5. **Cao H**, and Y Yin. Physiological modulations to extra eutrophication in *Microcystis aerugionsa* NIES-843 revealed by transcriptomics analyses (*being finalized*). Sigma conference, Northern Illinois University, April 12, 2014
6. **Cao H**, and Y Yin. Comparative genomics of water-bloom cyanobacterial for identification of important driver pathways. 19th Annual Phi Sigma Research Symposium, Northern Illinois University, April 12, 2013
7. **Cao H** and Yanbin Yin. *Sequence evolution and diversity of cellulosome modules in metagenomes*. Society for Molecular Biology and Evolution Conference. Chicago, IL, July 12, 2013
8. **Cao H**, Butler K, Housin M, and Lewis JD. *Effective population size-dependent mutational fitness effects in* Escherichia coli: *Common and gene function-related*. Society for Molecular Biology and Evolution Conference. Chicago, IL, July 12.
9. **Cao H**, Dougherty KM, and Plague GR. *Fitness evolution in experimental bacterial pathogens*. Ecology & Evolution of Infectious Diseases Conference. Atlantic City, NJ, March 22.

PROGRAMS AND DATABASES

1. WITOD: 16S/18S amplicon **WI**thin-**T**ax**O**n **D**iversity Tool (https://github.com/johncava/WITOD)
2. CyanoPATH: A database of metabolic pathways driving cyanobacterial blooms (http://47.92.225.177/CGDatabase)
3. *R package: ConstrictR* (R Package and Python Tool for Microbiome Analysis) (https://github.com/cnegrich/ConstrictR)
4. *Python tool:* ConstrictPy (R Package and Python Tool for Microbiome Analysis) (https://github.com/cnegrich/ConstrictPy)
5. *R* package: DDMAKER 2.0, for identification of clinical markers in extracellular circulation (https://github.com/yu-shang/DDMarker)
6. *R* package: Delta (DEep Learning biclusTer Algorithm based on gravitation field) (https://github.com/yu-shang/delta)

TEACHING/TRAINING EXPERIENCE

TEACHING EXPERIENCE

Instructor	Arizona State University, Biodesign Center for Applied and Fundamental Metabolomics	
	Microbiome Bioinformatics (MIC591)	Fall 2018
Guest Lecturer	Arizona State University, College of Health Solutions.	
	Nutrition and Food Metabolomics (NTR 598, Graduate class; instructor: Dr. Haiwei Gu)	Spring 2018
Guest Lecturer	Northern Illinois University, Department of Biological Sciences	
	Genetics (BIOS308, 5 credits, 60 students; five lectures)	Spring 2014

Teaching Fellow	Fordham University, Department of Biological Sciences	
	Human Physiology Lab (BISC3242, 3 credits, 24 students)	2009-2011
	Microbiology Lab (BISC3653, 3 credits, 24 students)	2008-2009
Teaching Fellow	Fordham University, Department of Biological Sciences	
	Introductory Biology Lab (BISC1413/1414, non-bio majors)	
	(3 credits, 24 students; team taught with two other peers)	2007-2008
Teaching Assistant	Fordham University, Department of Biological Sciences	
	Introductory Biology Lab (BISC 1413/1414, bio majors)	
	(3 credits, 24 students)	2006-2007

TRAINING EXPERIENCE

2015	Learn how to effectively apply for NSF funding, Spelman College, Atlanta, GA
2015	Teaching the STEM Undergraduates, Online CIRTL teaching course at the University of Georgia, Athens, GA
2014	The College Classroom, Online CIRTL teaching course at University of Georgia, Athens, GA
2014	Career Development Workshop: Getting a head start towards tenure: expectations and strategies for the first 3 years as a professor, University of Georgia, Athens, GA

STUDENT MENTORING

Ph.D. students

Beatriz R. Ramos	Microbial Ecology at ASU	co-mentor	2017-2018
Daniel Roush	Microbiology at ASU	Committee	2017-present
Julie B Rakes	Environmental Science at ASU	Committee	2017-present
Kassandra Dudek	Microbiology at ASU	Committee	2017-present
Yu Shang	Bioinformatics at UGA	Mentor	2014-2017
Gaoyang Li	Bioinformatics at UGA	Mentor	2014-2017
Chunman Zuo	Bioinformatics at UGA	Mentor	2014-2017
Sen Liang	Bioinformatics at UGA	Mentor	2014-2017
Rahil Taujale	Bioinformatics at NIU	Mentor	2013-2014

Master students

John Cava	Biostatistics at ASU	Mentor	2017-present
Qingqing Wu	Biostatistics at ASU	Mentor	2018-present

Undergraduate students

Elizabeth Thorley	Statistics/Microbiology at ASU	Mentor	2018-present
Christopher Negrich	Honors thesis at ASU	Mentor	2017-2018
Quinn Fischer	Barrett Honors College at ASU	Mentor	2017-2018
Abigail Pezelj	School of Life Sciences at ASU	Mentor	2018-2018
Marija Shhid	Genetics at ASU	Mentor	2018-2018
Yanire Vega	Microbiology at ASU	Mentor	2017-2018
Gabriela Rosas	Genetics at ASU	Mentor	2017-2018
Julia King	Microbiology at ASU	Mentor	2017-2018
Delaney Billig	Genetics at ASU	Mentor	2017-2018
Arnold So	Microbiology at ASU	Mentor	Spring 2018
Jack Meersman	Molecular Biology at UGA	Mentor	Fall 2016
Sean Alexander	Biochemistry at UGA	Mentor	Fall 2016
Alex Ekstrom	Bioinformatics at NIU	Mentor	2013-2014
Joel Dennison	Biochemistry at NIU	Mentor	Summer 2013

Mithi Hossain	General Biology at Fordham	Mentor	Summer 2012
Kevin Butler	General Biology at Fordham	Mentor	Summer 2012

PROFESSIONAL SERVICE

Program Installation for DOE KBase Website

March 2016 MayIntegration of DBCAN into KBase, DOE BioEnergy Science Center (BESC), Oak Ridge National Laboratory, Oak Ridge, TN

Computing Committee

2018-present Biodesign Institute of Arizona State University

2019-present University Computing Cluster of Arizona State University

Seminar Organizing

2015-2017 Ying Xu's lab bi-weekly seminar series at the University of Georgia

2009 Fordham University, Department of Biological Sciences, hosting student-selected speaker Dr. Paul Turner from Yale University

Editorial Service

2015 Guest Editor for the Scientific World Journal

Grant Review

2014 Earth and Life Sciences Division of the Netherlands Organisation for Scientific Research (NWO), The Netherlands (*1*)

2015-2017 Research Grants Council of Hong Kong, Hong Kong, China (*3*)

Journal Peer Review

Bioinformatics Journals

Bioinformatics (*3*), Briefings in Bioinformatics (15), BMC Genomics (*2*5), BMC Research Notes (*2*), IEEE/ACM Transactions on Computational Biology and Bioinformatics (*1*), Journal of Bioinformatics and Computational Biology (*12*), Mathematical Biosciences (*5*), Nucleic Acids Research (*2*), PLoS ONE (*1*), Scientific Reports *(9)*

Experimentation journals

Algal Research (*3*), Aquatic Toxicology (*3*), Biochemical Systematics and Ecology (*12*), Bulletin of Environmental Contamination and Toxicology (*2*), Chemosphere (*6*), Ecological Indicators (*6*), Environmental Pollution (*3*), Environmental Science and Technology (*2*), Environmental Science and Pollution Research (*2*), Energy, Ecology and Environment (*2*), Fundamental and Applied Limnology (*3*), Harmful Algae (*3*), ISME Journal (*1*), Journal of Freshwater Ecology (*1*) Limnology and Oceanography (*2*), Marine Biology Research (*1*), Marine Biotechnology (*1*), Phycological Research (*2*), Science of Total Environment (*3*), Water Research (*4*), Energy, Ecology and Environment (*3*), Journal of Hazardous Materials (*2*)

SOCIETY MEMBERSHIP

2013-present Society of Molecular Biology and Evolution
2014-present American Society of Microbiology
2011-2012 Sigma Xi, the Scientific Research Society