

## **XIAOPING LI, Ph.D.**

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### **SUMMARY OF QUALIFICATIONS**

*Microbiome - High throughput sequencing – Data analysis and programming - Team work*

Well experienced PhD in high-throughput sequencing data analyses and well trained in performing molecular biology research. Professional work ethic and scientific integrity. Highly motivated by challenge, solutions-oriented and a persistent truth seeker. Excellent interpersonal skills, a great team player with leadership potential. Dedicated and passionate teacher with four years of experience in college biology lab entry courses.

#### **Skills:**

- Microbiome and transcriptome data analyses
- Nanopore sequencing
- Well-trained in Molecular biology research: DNA extraction, PCR, qPCR, etc.
- Competent to apply a bundle of bioinformatics tools and UNIX system.
- Skilled in R, Python and Excel for data analyses and visualization.
- Experienced with igraph, Gephi and Cytoscape for network analysis and visualization.
- Ability to make web applications using R, Python, Node JS and Express.
- Familiar with SQL and MongoDB databases.
- Teaching in biology.

### **EDUCATION**

#### **Ph.D. in Biology, Minor in Applied Statistics**

August 2016

New Mexico State University, Las Cruces, NM, U.S.A.

*Dissertation Title: "Diverse Pathways to Control Programmed Cell Death during Vegetative Incompatibility in the Chestnut Blight Pathogen Cryphonectria parasitica"*

#### **B.S. in Biotechnology**

August 2008

Guangxi University, Nanning, Guangxi, China

*Undergraduate Thesis Title: "Preliminary Research on the Proteomics of the Wild-type Strain EP155 and Hypovirus-infected Strain EP713 using 2D Electrophoresis in Cryphonectria parasitica"*

## PROFESSIONAL EXPERIENCE

### **College of Agriculture and Life Sciences, Virginia Tech AREC, Virginia Beach, VA 2020 – Current** *Microbiome Scientist (Postdoctoral Researcher)*

- Investigating impacts of climate factors on boxwood phyllosphere microbiome
- Assessing fungicide effects on boxwood phyllosphere microbiome
- Evaluating anti-desiccant effects on boxwood phyllosphere microbiome
- Nanopore MinION sequencing
- Set up bioinformatics pipeline for analyzing Nanopore MinION sequencing data
- Analyzing soil microbiome in boxwood garden soils
- Design and set up irrigation and fertilization field trials
- Manuscript preparation
- Collaborating with growers and team members for sample collections

### **Department of Plant Pathology, Oregon State University HAREC, Hermiston, OR 2017 – 2020** *Postdoctoral Research Associate*

- Investigated soil fumigation impacts on soil microbiome using DNA metabarcoding
- Studied short term effects of pesticides on soil microbiota using DNA metabarcoding
- Constructed/curated DNA markers databases for research: *trnL*, ITS2, COX1, and *rbcL*
- Collaborated with other PIs and graduate students on projects:
  1. Testing DNA metabarcoding quantitative capabilities on artificial pollen mixture
  2. Using DNA metabarcoding in seed lot trials
  3. Diets of crayfish species in John Day rivers
  4. Investigated soil microbiome from soils collected from 3 states: OR, WA and SC
  5. Diets in Lygus
- Created and deployed web applications in cloud servers:
  1. R-shiny app for sequence blast
  2. Python Dash web app to forecast late blight disease using Johnson's model
  3. NodeJS web app to forecast late blight disease using Wallin's model
- Manuscripts writing
- Assisted in crops planting and harvesting
- Held bioinformatics workshop for lab members

### **Department of Biology, New Mexico State University, Las Cruces, New Mexico 2016 - 2017** *Research Associate*

- Applied multiple bioinformatics tools to analyze in *Shewanella oneidensis* and *Deinococcus radiodurans* transcriptome data
- Wrote python scripts to process data
- Manuscript preparation

### **Department of Biology, New Mexico State University, Las Cruces, New Mexico 2009-2016** *Research Assistant*

- Knockout a transcriptional regulator CpVIB-1 in two *C. parasitica* strains for vegetative incompatibility analysis
- Constructed overexpression vectors inserted with *sec9* and *patatin* genes for transcriptional analysis
- Collaborated with and assisted other lab members, trained rotating undergraduates, maintained the instruments and the lab duties

**State Key Laboratory for Conservation and Utilization of subtropical Agro-bioresources,**

Guangxi University, Nanning, Guangxi, China

Aug 2008 – July 2009

**Research Associate**

- Extracted mitochondria DNA in *C. parasitica* wildtype and virus-infected strains for proteomics research.
- Assisted with 2D electrophoresis in the *C. parasitica* comparative secretome analysis project.

## GRANTS

**2022-02** – Virginia Nursery and Landscape Horticulture Research Foundation (Proposal number: P3OQJNFS, \$4950). Title: *Evaluating biochar as a tool for control of boxwood blight*

- Experiment concept creation
- Proposal writing
- Proposal budgeting

## PUBLICATIONS

**Li, X.**, Kong, P., Daughtrey, M., Kosta, K., Schirmer, S., Howle, M., Likins, M., Hong, C. (2022) The Soil bacterial community in five boxwood gardens across the United States. *Microorganisms*. (Major revision)

**Li, X.**, Skillman, V., Dung, J., Frost, K. (2022) Soil microbial community diversity, structure, network association, and response to metam sodium application varies depending on previous fumigation exposure. *Environmental Microbiome*. (Submitted)

Kong, P., **Li, X.**, Sharifi, M., Bordas, A., Hong, C. (2022) Differential disease tolerance with phyllosphere endophytes abundance, microbiota core, and networks. *Phytobiomes*. (Submitted)

Delvental, K., Skillman, V., **Li, X.**, Busby, P., Frost, K. (2022) Characterizing variation in the bacterial and fungal tare soil microbiome of seed potato. *Phytobiomes*. (Major revision)

Arstingstall, K.A., DeBano, S.J., **Li, X.**, Wooster, D.E., Rowland, M.M., Burrows, S., Frost, K. (2022) Investigating the use of DNA metabarcoding to quantify bee foraging and effects of threshold selection. *PLoS One*. (Submitted)

Kong, P., Li, X., Gouker, K., Hong, C. (2022) cDNA transcriptome of *Arabidopsis* Reveals various defense priming induced by a broad-spectrum biocontrol agent *Burkholderia* sp. SSG. *International journal of molecular sciences* 23(6):3151. <https://doi.org/10.3390/ijms23063151>

Topolski, C., Divo, E., Li, X., Hicks, J., Chavez, A., Castillo, H. (2022) Phenotypic and transcriptional changes in *Escherichia coli* K12 in response to simulated microgravity on the EagleStat, a new 2D microgravity analog for bacterial studies. *Life Sciences in Space Research*, 34:1-8. <https://doi.org/10.1016/j.lssr.2022.04.003>

Arstingstall, K. A., DeBano, S. J., Li, X., Wooster, D. E., Rowland, M. M., Burrows, S., & Frost, K. (2021) Capabilities and limitations of using DNA metabarcoding to study plant–pollinator interactions. *Molecular Ecology*, 00, 1– 32. <https://doi.org/10.1111/mec.16112>

Castillo, H., Li, X., and Smith, GB. (2021) *Deinococcus radiodurans* UWO298 Dependence on Background Radiation for Optimal Growth. *Front. Genet.* 12:644292. doi: 10.3389/fgene.2021.644292

Castillo H., Li X., Schilkey F., Smith G.B. (2018) Transcriptome analysis reveals a stress response of *Shewanella oneidensis* deprived of background levels of ionizing radiation. *PLoS ONE* 13(5): e0196472. <https://doi.org/10.1371/journal.pone.0196472>

Wang, J., Shi, L., He, X., Lu, L., Li, X., & Chen, B. (2016) Comparative Secretome Analysis Reveals Perturbation of Host Secretion Pathways by a Hypovirus. *Scientific Reports*, 6, 34308. <http://doi.org/10.1038/srep34308>

## WEB APPLICATIONS AND PROGRAMMING

- Casting potato late blight in the Pacific Northwest region using Wallin’s forecast model: <https://wallin-blite-cast.herokuapp.com/>
- Casting potato late blight in Oregon using Johnson’s model: <https://johnson-lateblight-app.herokuapp.com/>
- R-shiny online blasting app: [https://xiaoping-shinyapps.shinyapps.io/Frost\\_Lab\\_Blast\\_APP/](https://xiaoping-shinyapps.shinyapps.io/Frost_Lab_Blast_APP/)
- Python package to interact with NCBI database and retrieve sequences [https://github.com/lixiaopi1985/NCBI\\_Companion](https://github.com/lixiaopi1985/NCBI_Companion)

## PRESENTATIONS AND SCIENTIFIC MEETINGS

- (Zoom Talk) Boxwood Blight Insight Group, Feb 12, 2021  
“The plant microbiome and how to study it with high throughput sequencing”  
Video recording - <https://www.boxwoodhealth.org/knowledge-center#VIDEOGALLERY>
- (Poster) QIIME2 workshop. Bethesda MD, 2019  
“Impacts of soil fumigation on soil microbial community”
- (Poster) Arstingstall, K. A., DeBano, S. J., Frost, K., Wooster, D. E., Li, X., Rowland, M. M. (2019, August 11-16) Comparing behavioral observations with DNA metabarcoding techniques for identifying major food sources for native bees in eastern Oregon. ESA Annual Meeting 2019, Louisville, KY, United States. <https://eco.confex.com/eco/2019/meetingapp.cgi/Paper/80343>
- (Poster) Delventhal, K., Li, X., Skillman, V., Leopold, D., Busby, P., Frost, K. (2019, Aug 3-7) Tare soil microbiome of seed Potato (*Solanum tuberosum*) varies by geographic location and seed growing operation. APSNET Plant Health 2019. Cleveland, Ohio, United States. <https://apsnet.confex.com/apsnet/2019/meetingapp.cgi/Paper/14432>
- (Poster) Skillman, V., Li, X., Frost, K. (2019, Nov 17-20) Examining the diet of pest insects collected from potato crops using metabarcoding. ESA Entomology 2019, St. Louis, MO, United States. <https://esa.confex.com/esa/2019/meetingapp.cgi/Paper/148183>
- (Talk) Hermiston Farm Fair. Hermiston, OR 2019  
“Short term impacts of soil applied pesticides and fumigation on soil microbial communities”
- (Poster) Skillman, V., Li, X., Frost, K. (2018, Nov 11 - 14) Using metabarcoding to examine diet breadth of phytophagous insect pests of potato. ESA Entomology 2018, Vancouver, BC, Canada. <https://esa.confex.com/esa/2018/meetingapp.cgi/Paper/136233>
- (Poster) Arstingstall, K. A., DeBano, S. J., Frost, K., Wooster, D. E., Li, X., Rowland, M. M., Burrows, S. (2018, Aug 5-10) Enhancing native bee habitat in eastern Oregon: Identifying major food sources using DNA metabarcoding techniques. ESA Annual Meeting 2018, New Orleans, LA, United States. <https://eco.confex.com/eco/2018/meetingapp.cgi/Paper/74630>
- (Poster) Rio Grande Branch Annual Meeting of the American Society for Microbiology. El Paso, TX. April 2016

- (Talk) Biology Department Bio-symposium, spring 2014  
“Investigation of a putative transcription regulator CpVIB-1 in response to vegetative incompatibility in chestnut blight fungus *Cryphonectria parasitica*.”
- (Poster) Rio Grande Branch Annual Meeting of the American Society for Microbiology. El Paso, TX. February 2014  
“Investigation of a putative transcription regulator CpVIB-1 in response to vegetative incompatibility in chestnut blight fungus *Cryphonectria parasitica*.”

## TEACHING EXPERIENCE

**Department of Biology**, New Mexico State University, Las Cruces, New Mexico

*Microbiology Lab Teaching Assistant*

Aug 2013 – May 2016

- Lectured 2 lab sections of 40 undergraduates, demonstrated lab skills, monitored students’ techniques.
- Designed assessments, involved in protocol modification, and evaluated students’ performances.
- Facilitate learning by providing individual or group tutoring.
- Maintained bacteria culture viability for teaching, prepared reagents and media, organized the daily running of the labs.

*Natural History of Life Lab Teaching Assistant*

Jan 2011 – May 2011

- Lectured 2 lab sections, led the students in discussion and experiments.
- Designed quizzes, graded their weekly lab reports, and provided prompt feedbacks.
- Engaged in the discussions on effective teaching in the TA meetings.

*Cellular and Organismal Lab Teaching Assistant*

Aug 2009 – May 2010

- Lectured 2 lab sections, led the students in hypothesis formation and experimental design, motivated their developments in critical thinking and analytical skills.
- Designed quizzes, evaluated their lab reports, and provided prompt feedbacks.
- Assisted the students in their designs of the “diabetic research project”, encouraged their creativities, fostered their values on the importance of teamwork.