

# Courtney M. Gardner

## Personal Statement

### Research

My research focuses on understanding the interactions and dynamics between crop systems and soil microbiomes in both natural and engineered systems. My overarching goal is to bridge the gap between biotechnology, agriculture, and engineering in order to understand how rhizospheres are affected by both soil chemistry and exposure to emerging contaminants of concern, with the ultimate goal of manipulating these communities to improve sustainability, resilience to environmental stressors, and phytoremediation potential. My multidisciplinary training in molecular biotechnology, microbiology and engineering has provided me with the necessary foundation to successfully perform this type of research.

At the beginning of my research career, I used ecology and molecular biology principles to examine the role of genomic factors in plant adaptations to environmental stressors. Specifically, I worked to understand how plant genomes are able to influence the overall health and fitness of a population using *Passiflora incarnata* as a model system. As an undergraduate student, I evaluated the fitness of individual *P. incarnata* vines exhibiting phenotypic plasticity in response to nutrient limiting conditions through the detection of unique microsatellite DNA sequences via capillary sequencing. As my research developed, I expanded the project by identifying additional putative microsatellite sequences from *P. incarnata* plants and coordinated with other research institutions to obtain additional plant samples from across the US.

This time spent as an undergraduate research assistant ignited my interests in applied agricultural and environmental research. This experience helped me recognize where new interdisciplinary research was needed to fill in knowledge gaps in emerging research areas concerning how genetic and environmental factors shape agroecology. As a graduate student, I became interested in investigating how antibiotic resistance genes (ARGs) contained within the transformation plasmids inserted into transgenic crops may persist in soils and impact soil microbial communities. To evaluate this risk, I began by quantifying the ability of environmentally relevant clays and soils to adsorb free ssDNA and dsDNA derived from transgenic BT maize using a series of adsorption isotherms. Because wastewater-derived biosolids are becoming an increasingly common agricultural fertilizer amendment, I also investigated the prevalence of multiple transgenes in wastewater treatment plants (WWTPs). I found novel evidence of four transgenes in wastewater activated and digester sludges obtained from WWTPs across the US (i.e., *p35* promoter, *nos* terminator, *bla* ARG, and *nptII* ARG). Based on this preliminary data, I led additional studies to assess the persistence and bacterial uptake of these transgenes in model anaerobic digesters.

Little -omic work has been applied to understanding how transgenic crops interact with agricultural microbiomes due to past limitations of applying expensive metagenomic sequencing to environmental studies. Because of this, the structures of key microbiomes associated with transgenic crops had not been fully characterized, making fundamental research extremely challenging. I recognized this knowledge gap and used it to inform the direction of my dissertation research. I characterized the bulk soil, rhizosphere soil, and stalk endophyte microbiomes of transgenic BT *Zea mays* and conventional maize using Illumina Miseq sequencing. During my analysis, I found that many of the endophyte *16S* sequences identified as *Cyanobacteria* genera were in fact maize chloroplast DNA. Based upon these preliminary results, I have led additional studies to design a series of blocking primers meant to prevent

the amplification of chloroplast DNA in *16S* rDNA metagenomic libraries created from plant endophyte samples. As the nitrogen cycle is one of the grand challenges facing engineers and agroecologists, I also recognized the importance of assessing how transgenic crops may be differentially affecting the nutrient cycles within these microbiomes. For example, the Cry toxin protein contained within BT crop tissues has been shown to negatively impact sensitive nutrient cycling bacteria. Using a quantitative ELISA assay and metagenomic data, I associated the levels of this protein with the abundance of soil and endophyte nitrogen cycling communities.

In addition to conducting research focused on agroecology, I also had key roles in research projects aimed at understanding how anthropogenic chemicals and remediation clean-up strategies impact soil microorganisms. Because regulations surrounding the pre-treatment of wastewater-generated biosolids are focused on reducing pathogens, I saw these agricultural amendments as a potentially unexplored reservoir of biocidal compounds. To explore this, I constructed a series of planter pots seeded with alfalfa cover crops to assess the vulnerability of sensitive nutrient cycling bacteria to a model biosolids contaminant, Triclosan. I amended these pots with lab-generated biosolids containing Triclosan and monitored the expression of nitrogen cycling genes within soil microbiomes using quantitative reverse-transcription PCR (RT-PCR). I also assessed changes in the structure of these soil microbiomes using T-RFLP.

My multidisciplinary work at Duke has also provided with a global and applied view of environmental microbiology research. To this end, I also pursued projects rooted in understanding how common chemical remediation strategies may be functionally impacting *in situ* microbial communities. To accomplish this, I constructed a series of lab-scale photocatalytic treatment reactors to remediate organophosphate-contaminated groundwater. Using these engineered systems, I examined the negative impacts of UV-generated reactive oxygen species on model aquatic bacteria *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Bacillus subtilis*. I continued this branch of research at the Holcomb Creosote Company Superfund site, characterizing the soil microbial communities associated with soils contaminated with polycyclic aromatic hydrocarbons (PAHs) using Illumina Miseq sequencing. I also helped to identify bacterial genera under selection within these soils that displayed the potential to increase the efficiency of microbial-based PAH bioremediation strategies using genetic bioaugmentation.

In addition, I led several long-term research projects aimed at identifying potential microbial degraders of recalcitrant flame retardant compounds within wastewater digester sludge. I performed this research in a collaborative team composed of analytical chemists, molecular biologists, and engineers under Duke's Superfund Research Program. I designed and maintained a series of anaerobic batch reactors containing wastewater digester sludge and added contaminants of concern, and monitored these reactors for evidence of biodegradation. I isolated potential degraders using a series of increasingly selective growth media and confirmed their phylogenetic identities using Sanger sequencing. Building upon this research area, I also led an interdisciplinary project to investigate the potential for biochar and activated carbon amendments to increase the efficiency of complete microbial debromination of tetrabromobisphenol A. Using Illumina Miseq sequencing, I was able to compare the impact of these carbon additions on the relative abundance of potential degraders within anaerobic digesters containing mixed microbial communities.

My diverse research background has provided me with the necessary knowledge and skills needed to bridge the gaps between applied biotechnology and agroecology. I have a demonstrated record of conducting collaborative and multidisciplinary research that draws upon biotechnology, agroecology,

and engineering to better understand the interactions among the environment, soil microbes, and plants. I plan to build on my current foundations in agriculture, engineering, and microbiology to develop a research program at a leading university using novel molecular biological methods and –omics approaches to microbial interactions in soil and agriculture environments. More specifically, I would like to harness rhizosphere-crop interactions to improve crop resilience and sustainability potential. I will then use this information to improve the bioremediation potential of soil microbiomes through plant-rhizosphere interactions and genetic bioaugmentation. I will also continue to focus on investigating the persistence and impacts of environmental contaminants, including free DNA and ARGs, in agricultural microbiomes.

This proposed work takes full advantage of the foundational knowledge and skills I acquired during the training years of my career. I look forward to performing research at a leading research institution like Colorado State University where I can pursue both individual and collaborative research. I believe my exposure to a wide array of molecular biological techniques and my foundations in agricultural systems and soil microbiomes provide me with a strong foundation to pursue cutting-edge research.

### **Teaching**

I have involved myself in a variety of teaching activities during my undergraduate and graduate education that have further encouraged me to pursue a career in the academic field. During this time, I have taught in one-on-one settings as well as in classrooms and large seminars. As an undergraduate, I sought out teaching opportunities in my university Honors Program. I taught multiple philosophy courses aimed at instilling critical thinking and rhetoric skills in new Honors students. As a graduate teaching assistant, I adapted my teaching styles towards more biological and engineering-based courses. I expanded my teaching experience to include courses in applied microbiology, environmental biotechnology, and bioinformatics. These diverse experiences have given me the confidence necessary to teach demanding material and insight into how to adapt my teaching methods to reach disparate audiences.

In my post-graduate career, I have taught many classes that draw upon my multidisciplinary background, including Environmental Microbiology, Molecular Biotechnology, Bioprocesses in Engineering, and Integrative Bioinformatics for Investigating and Engineering Microbiomes (IBIEM). For each class, I was responsible for preparing and delivering lectures and review sessions, holding office hours, and grading assignments and exams. In addition, many courses also contained a lab component that required careful planning, instruction, and supervision of technical exercises. When teaching in a traditional classroom environment, I believe the most effective way to connect students with the presented material is to provide context and tangible examples within lessons. For example, when lecturing on the impacts of contaminants and cleanup strategies on the environment, I have often described local Superfund sites and chemical spills as a means to provide an immediate connection with the material. I have also found that my most effective lectures do not rely on just one method of conveying information. Instead, they incorporate group work, guest speakers, and activities outside of the classroom—including day trips to wastewater treatment plants and local sustainable farms.

I have faced many challenges as a teaching assistant. As a teaching assistant in the IBIEM bioinformatics program at Duke, I gained invaluable experience teaching bioinformatic and –omics principles to audiences of mixed backgrounds and skill levels. This forced me to adapt my lessons to simultaneously address the learning needs of students with no bioinformatics experiences and students with advanced bioinformatics experience. To accomplish this, I used example data from my

dissertation and explicitly defined the sequencing platform and bioinformatics analysis steps needed to take metagenomic data from raw data to visualized data. For more advanced students, I also provided an overview of advanced coding techniques to apply to their data visualization. I have also found that many students are intimidated by math and engineering principles and do not find them applicable to their own fields. I saw this to be true not only as an undergraduate Honors program teacher, but also as a graduate teaching assistant within more advanced microbiology courses. However, I found incorporating these important concepts was more effective when providing discrete examples with a broader context.

I have also enjoyed taking on teaching responsibilities outside of a traditional classroom. I have acted as a lab mentor for both undergraduate and graduate students on many projects during my undergraduate and post-graduate years. I have taught students at multiple levels how to perform basic techniques such as DNA extraction and cell culturing as well as more advanced techniques such as RNA isolation and qRT-PCR. During these teaching events, I believe it is important to instill confidence and independence within the students I mentor. For complicated molecular techniques like qPCR or high throughput sequencing, I will often break up lessons into digestible smaller activities. I will start by describing to students the purpose, strengths, and caveats of a given technology. Then, I will discuss the relevant chemical or biological principles underlying a particular technology before addressing how to perform the protocol and optimize it for specific environmental samples. In addition to helping students learn technical skills, this method of teaching provides a theoretical understanding of how and why technical methods function. This provides students with the skills and agency needed to conduct independent research. I have found that this method of teaching technical procedures is more effective than simply teaching a specific protocol step by step. Finally, I enjoy providing career advice to students interested in both academic and industrial careers. I strongly believe that as an academic figure, my job extends beyond providing only technical and theoretical training. As a professor at Colorado State, I plan to continue helping to prepare my students to thrive at the university level and beyond.

My technical background in molecular biology and agroecology has provided me with the theoretical and applied skills required to courses in Soil Microbiology and Microbiomes at the undergraduate and graduate level. I would use my technical background to incorporate soil ecology, biochemistry, and current challenges in agriculture into a Soil Microbiomes course. In addition, I would focus Microbiomes on -omics approaches to environmental research as well as in depth descriptions of traditional and novel technologies applicable to soil and crop sciences. I would also like to develop a course covering the biodegradation of various environmental pollutants by soil microbiomes and plant systems and incorporate this knowledge into a course concerning practical remediation system designs.

### Outreach

Throughout my post-graduate career, I have pursued many opportunities to act as a research translator for my community. I believe that making direct personal connections with community members outside of my university is an extension of my job as an academic researcher. It is also an integral part of establishing and maintaining healthy community-university relationships. I have been involved in many outreach efforts targeted at multiple audiences in both formal and informal settings.

As an early career researcher, I sought out ways to become involved in research translation for the Superfund research program (SRP) at Duke. I communicated with several disparate audiences from middle schoolers to religious community leaders regarding the role of Duke and the SRP in conducting

valuable research for the community. In addition, I led a multidisciplinary team to conduct research that directly addressed the local community's concerns about PAH and heavy metal contamination in soils used for public food gardens. During this study, I oversaw the collection of garden samples, mediated between the objectives of the SRP and Durham communities, and kept community leaders informed of study progress. I was also involved in research translation events aimed at children for the Center for the Implications of NanoTechnology (CEINT) at local science museums. During these outreach events, I constructed and implemented activities designed to teach children about the unique properties of nanoparticles as well as their interactions with microorganisms. I believe this type of outreach helped the average Durham community member understand the importance of research conducted at local universities.

I am also passionate about acting as an advocate for STEM education in my community. I have acted as a research translator to middle and high school students with little to no STEM background. I have also helped to educate these students about possible STEM careers beyond high school and college education. As a lead counselor for a bioscience and engineering summer camp, I interacted with students from across the country with varying interests in STEM fields. I engaged in lectures and activities designed to attract students to environmental microbiology, biochemistry, and engineering fields. I have also spoken at science seminars for Duke's Talent Identification Program (TIP) and the North Carolina School for Science and Math regarding current research being conducted within my lab, the engineering department, and across Duke University. In addition, I have served as an appointed member of the first Diversity and Inclusion committee at Duke. I worked with multiple teams of students, staff, and faculty to educate local underrepresented communities about STEM fields. I also assisted in organizing events that would increase awareness of diversity issues on and off Duke's campus.

At Colorado State University, I will continue to engage the local community with my research efforts. I will perform collaborative research that focuses on pressing issues on the minds of the local community. To accomplish this, I will pursue the research interests outlined by the CSU agriculture extension program. Because of the multidisciplinary and applied focus of my research, I feel that collaboration with the CSU extension is a natural fit. In addition to incorporating an outreach component into my research program, I will continue acting as a teacher and mentor to students in local and state-wide communities. I will incorporate STEM outreach events that focus on educating local communities about current research efforts and increasing the presence of underrepresented demographics within STEM fields.

In conclusion, I look forward to the opportunity to become a member of the community in and around Colorado State. I believe my research qualifications, teaching expertise, and outreach history complement the trajectory of the Soil and Crop Sciences department.