

Dorith Rotenberg

co-Director of the Plant Virus-Vector Interactions (PVVI) Lab



Department of Affiliation: Entomology & Plant Pathology

Areas of Expertise:

Multi-omics of insect vector – plant virus – plant host interactions

Transmission biology of insect vectors of plant-pathogenic viruses (bunyavirus and rhabdovirus)

Applied plant virology

Current Research

- Molecular determinants of insect vector competence to transmit plant viruses
- Ecological genomics of plant virus-insect vector-plant host interactions
- Functional interrogation of insect vector proteins that interact with plant viruses and plants
- Ecology of recurring and emerging plant-pathogenic viruses that threaten food security
- Plant host genetic and transgenic resistance to plant viruses

Ideas

- **Development and maintenance of synchronized, immortal cell lines of non-model, important crop pests** (thysanopteran vectors) to open the door wide open to studying biological processes during orthospovirus viral entry, trafficking, replication, assembly and exit.
- **Investigating epigenetic regulation of insect vector (thrips and planthoppers) response to virus infection** – moving beyond the central dogma.
- **In situ tagging of insect saliva protein effectors** to visually track their fate in plant host tissues and subcellular compartments after feeding
- **Identify conserved core salivary proteins** associated with host range and host specificity of polyphagous vectors – evolution and host adaptation

Collaborations

Cytologist and cell line-cell culture specialist, epigeneticist, insect physiologist & biochemist, arthropod evolutionary biologist & phylogenomicist, genetic engineers

My hobbies: Gardening, cooking, novel-reading, playing with my dog Louie, wine-tasting and sampling all the cuisine Raleigh has to offer

My team is a hard- and smart-working, international, multi-cultural, diversity-embracing and very humorous group of individuals who share a common interest in bakery, warm beverages and comradery... AND Viruses, Insects and Plants, oh my!



Dorith and Louie



(back, from left) Marlonni Maurastoni, Cesar Xavier, Jinlong Han, (mid) Dorith Rotenberg, Anna Whitfield (Co-Director, PVVI Lab), S. Kanakala, (front) Swapna Priya Rajarapu, Kirsten Lahre (not pictured: Hao Wei Teh)



(left to right) Kirsten Lahre, Swapna Priya Rajarapu, Dorith Rotenberg, Joshua Yueh, Abby Vickery, and Lucas de Oliveira (GGG 2022)



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Adapted from "Disruption of insect transmission of plant viruses" by Whitfield and Rotenberg in Current Opinion in Insect Science, 2015 [https://doi.org/10.1016/j.cois.2015.01.009]



Marcé Lorenzen

Department of Entomology and Plant Pathology

Areas of Expertise:

Genetics, Genomics, Transgenics,
Functional Genomics (CRISPR etc)



Current Research

- Uncovering the Molecular Mechanisms of a Naturally Occurring Selfish Genetic Element
- CRISPR-based Sterile Insect Technique for Controlling a Hemipteran Pest of Corn
- Quest for the Maleness Gene in the Red Flour Beetle

Ideas

Gene drive and/or population suppression trials, and Genetic improvement of edible insects

Collaborations

Expertise in Measuring mitochondrial/cell respiration, ATP production/use, and Confocal microscopy would also be greatly appreciated



Evolutionary Systems Lab

Cast (in order of appearance)

- Gavin Conant (PI)
- Logan McRae
- Jaells Naranjo
- Abbey Coppage
- Mustafa Siddiqui



Biological Sciences; Bioinformatics Research Center; GGA

- Bioinformatics
- Evolutionary Biology
- Polyploidy
- Metagenomics

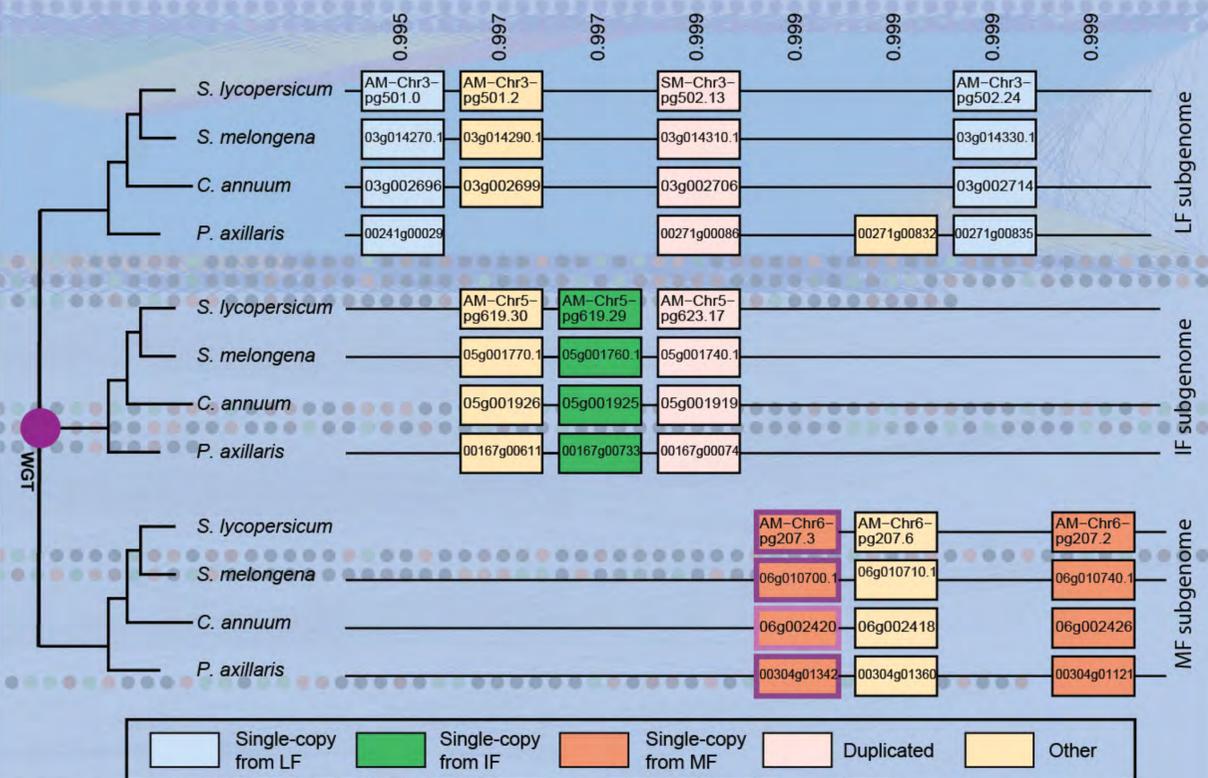
gconant@ncsu.edu



Lab website:
conantiab.org

Interests

- Evolution of polyploid genomes. Our lab distributes POInT: The Polyploidy Ortholog Inference Tool, which allows us to model gene losses after polyploidy events.
- Community metabolic networks of microbial communities. We also study how community metabolic networks can be inferred from shotgun metagenomic data.



Genomic regions from tomato and its relatives produced by a genome triplication



POInT_{browse}
wgd.statgen.ncsu.edu

Collaborations

- Modeling gene expression after hybridization
- Taxonomy and function in microbial communities
- Cool applications of networks to biology

Brian Wiegmann

Wiegmann Lab:
Insect Phylogenomics and Evolution

Lab Members:

Cristian Beza-Beza (postdoc)

Charles Sither (PhD grad student)

Ezra Bailey (PhD grad student)

Brian Cassel (Research Technician)



Department of Entomology & Plant Pathology/ CALS

Areas of Expertise: Phylogenomics, Genomics, Phylogenetics, Molecular Evolution, Population Genomics, Biodiversity Science, Macroevolution

Current Research

- **Phylogenomics and the fly tree of life** - We study the phylogeny flies (Diptera), primarily using evidence from gene sequences captured using anchored hybrid enrichment (AHE).
- **Culicitree – Mosquito phylogeny and macroevolution** - This is a collaborative project focused on providing a phylogenetic context for all world mosquito diversity.
- **NSF Dimensions of Biodiversity – The evolution of parasitism in blow flies** - An international team, including multiple laboratories at NCSU, Univ. Sao Paulo, U. Calgary, and Univ. of Technology, Sydney to investigate phylogenetic, functional, genomic, behavioral, and microbiome research to investigate the origin and key pathways leading to trophic specialization.
- **Diagnostic Identification Tools in the Neotropical fruit fly genus, *Anastrepha*** – A collaborative project funded by the USDA using phylogenomics to investigate genome-wide DNA markers for their diagnostic potential for these major fruit pests.
- **Evolution and diversification of leaf-mining flies (Agromyzidae)**

Ideas

We seek new collaborations to investigate evolutionary patterns, phylogenetic relationships, organismal interactions, and the evolution of behavioral and genetic adaptations

Collaborations

Evolutionary and comparative functional genomics, genome comparisons, gene family evolution, genome architecture and genomic interactions, bioinformatics, vector-borne diseases.



WHO WE ARE...

I am John Britt, from the Rao lab. We do a lot of work with early development in humans using different models. While my background is in genetics many of my labmates are engineers. This combination allows us to tackle these problems from a mutidiscipline angle.

CURRENT PROJECTS

- **Macaque models:** Modeling early embryonic development in humans using macaque derived trophoblast and iPSC lines.
- **Trophoblat Metabolic Engineering:** Designing conditions tha improve trophoblast stem cell "stemliness" through altering cell metabolism
- **Signaling Pathways in placental development:** Looking at how TGF-B and HIF signaling leads placental invasion after implantation
- **3D co-culture model:** Studying interaction between endometrial stromal cell and fetal cytotrophoblast

COLLABORATIONS

- **UNC Med School:** Metabolic differences between stromal cells from different populations (imortalized cell lines, patient health samples, and patients with diseased condition) and how decidualization of stromal cells affect cell metabolism
- **UNC:** Use of trophoblast stem cells in regenerative medicine

CONTACT

John Britt
 jwbritt@ncsu.edu
Mahe Jabeen
 mjabeen@ncsu.edu
Victoria Karakis
 vkaraki@ncsu.edu
Dr. Balaji Rao
 bmrao@ncsu.edu

FUTURE COLLAB

Anyone interested in what we do is more than happy to talk about collaboration. While this laboratory takes a look at stem cell biology from an engineering point of view, gaining insight from other fields I think could greatly benefit many of our projects.

John Joyce

Johnna Bingham

Chrisy Smith (Lab Manager)

Michael Hyman (PI)

Department of Biology - Microbiology



Hyman Lab Areas of Expertise:

- Bioremediation
- Activity-Based Labeling of Active Monooxygenases
- Microbial Hydrocarbon Utilization
- Compound Specific Isotope Analysis (CSIA)
- ^{13}C -DNA Stable Isotope Probing (SIP)

Current Research

- Activity Based Labeling of Alkene Monooxygenases
- Regulation of gaseous alkene sensing in *Mycobacterium* sp. ELW1
- *Mycobacterium* sp. ELW1 genetic manipulation and/or plasmid transfer

Ideas

- N-terminal protein sequencing of active monooxygenases in biologically relevant environments
- Plasmid/gene manipulation in non-model bacterial systems

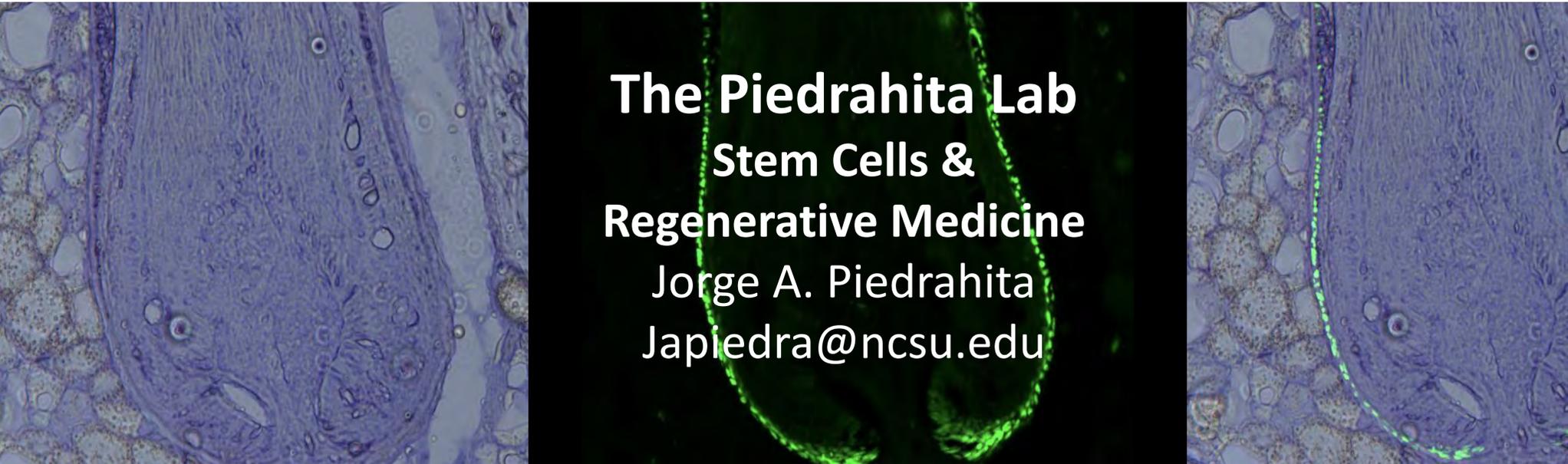
Collaborations

Interested in collaborating with someone:

- Experienced in proteomics/metaproteomics
- Experienced in large plasmid extraction

Hobbies:

Rock climbing, Dungeons and Dragons, Aquascaping/fish keeping



The Piedrahita Lab Stem Cells & Regenerative Medicine

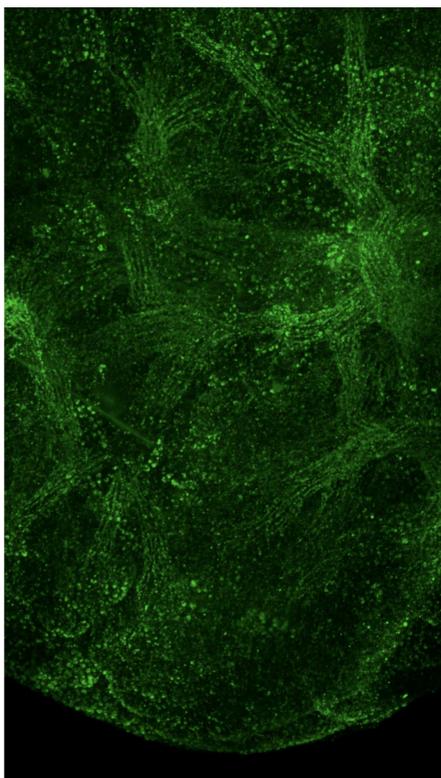
Jorge A. Piedrahita
Japiedra@ncsu.edu

1. Research Focus:

- Understanding the role of LGR5 stem cells in development, repair and regeneration.



2. Animal Model: Gene edited pig expressing an H2B-GFP tag in LGR5 cells



- LGR5 antibodies do not work. In mice, all findings have used transgenic mice.
- Our H2B-GFP tag allows identification of LGR5 cells at high spatial resolution, and their enrichment by flow sorting for transcriptome or organoids studies.
- More recently RNAscope and scRNAseq have allowed human studies. The emerging theme is that mice and humans differ with respect to LGR5 biology. So far, there is a high degree of concordance between pigs and humans with respect to LGR5 biology.
- Pigs have greater similarities to humans allowing more detailed studies on the role of LGR5 cells in a more relevant translational model.



3. Examples of ongoing work:

- Role of LGR5 cells in Lung (Piedrahita/Greenbaum/Mishra Lab)
- Role of LGR5 cells in Gastrointestinal track (Gonzalez lab)
- Role of LGR5 cells in Cochlea (Greenbaum's lab)



4. Interested in collaboration related to:

a. Developmental questions related to LGR5 in lung and peripheral nerves.

b. Organoid Biology/genetics.

- Predictive modelling using lung organoids and lung fetal explants.

Polyploid genome analysis

Bioinformatics Research Center
Department of Horticultural Science



Marcelo Mollinari mmollinari@ncsu.edu
Gabriel Gesteira gdesiqu@ncsu.edu
Zhao-Bang Zeng szeng@ncsu.edu

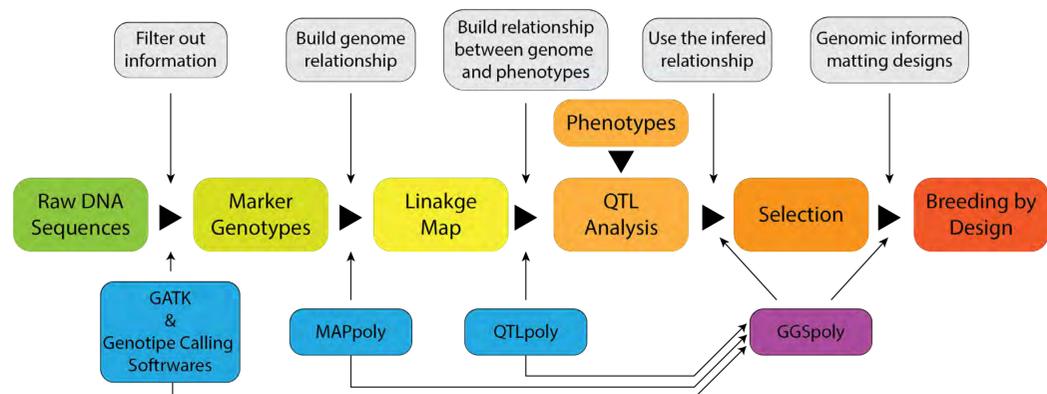
Multiple Genomes

Polyploids are organisms with multiple copies of the complete set of chromosomes. These multiple genome copies impose numerous challenges to polyploid genome analysis and its subsequent applications in practical breeding.

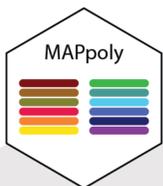


Our goal

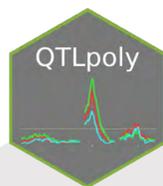
Our group focus on advancing the knowledge of polyploid genetics while developing computational tools to assist breeders in making strategic decisions in their breeding programs. We interact with a diverse group of breeders from several countries, especially in Africa.



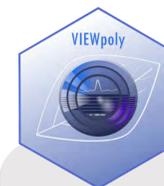
Our Computational Tools



MAPpoly:
R package to build genetic maps in polyploids.



QTLpoly:
R package to map quantitative trait loci (QTL) in polyploids.



VIEWpoly:
Interactively explore QTL regions connecting them to genome information



Current projects

SweetGAINS: a BMGF project to modernize Africa's current systems for sweetpotato breeding and early generation seed production.



TOOLS FOR POLYPL 

Tools for polyploids: NIFA/USDA project brings together breeders, geneticists, and computational scientists to develop computational tools and train breeders on genomic tools for polyploids

Genetics and Genomic Selection: NIFA/USDA project aims to provide a computational tool called **GGSpoly**, to assist breeders in making informed decisions based on the collected and learned information about their breeding populations for different breeding objectives.



Do you want to be part of the polyploid genetics group?

If you like genetics, genomics, statistics, software development (R and C++) and want to work with a challenging, and yet fascinating genetic system, **contact us!** We will be happy to talk more about our current efforts and assess potential mentorship and collaborations.

Adriana San Miguel

Department of Chemical &
Biomolecular Engineering



Areas of Expertise:

C. elegans, neurodegeneration, aging, high-content imaging, high-throughput microfluidics and automation

Current Research

- A new pipeline for quantitative analysis of neurodegeneration in *C. elegans*
- Intersection of neuronal activity, oxidative stress, and aging.
- Alzheimer's Disease model in *C. elegans*

Ideas

Use of *C. elegans* for drug or genetic screening, use of microfluidics and high-content screening for other model systems

Collaborations

Anybody with expertise in RNA structure and transport, aging, neurodegeneration, stress response, proteostasis

<https://sanmiguel.wordpress.ncsu.edu/>



Christina Zakas

Department of Biological Sciences



Areas of Expertise:

Evolutionary Genetics, Developmental Evolution, Maternal Genetic Effects, and Life-history evolution

Current Research

Current preprints:

- Maternal patterns of inheritance alter transcript expression in eggs;
- Assortative mating and mate-choice maintains a developmental dimorphism in *Streblospio benedicti*

Current Funding:

- NIH- Maternal Genetic Effects Shape Developmental Evolution;
- NSF: Finding the genetic basis of mate choice in *Streblospio benedicti*

Ideas

Our marine invertebrate model system is ideal for studies of environmental genetic effects, maternal provisioning, and developmental evolution.

Collaborations

We are interested in proteomics, metabolomics, ecological toxicology and high-throughput phenotyping of development.



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Open Scholarship

We can consult with you on open publishing platforms and ways to increase the impact of your scholarship in the public sphere.

Digital Media

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Heike Sederoff, PhD Megan Franklin, PhD cand.



Department of Plant & Microbial Biology

Areas of Expertise:

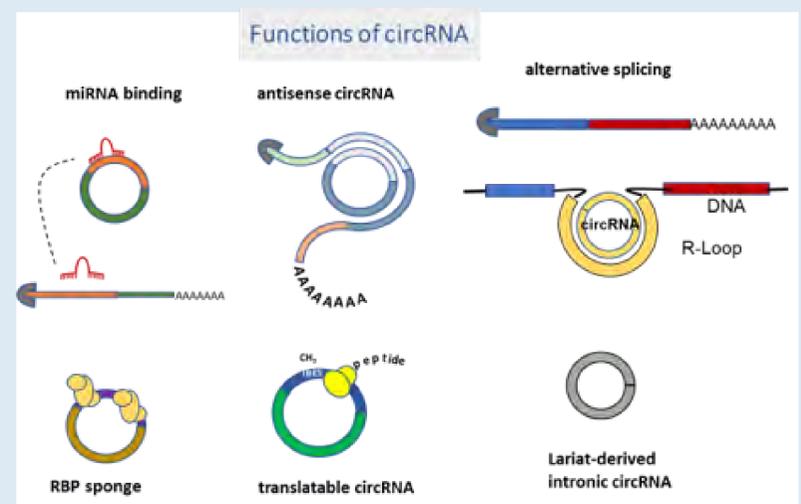
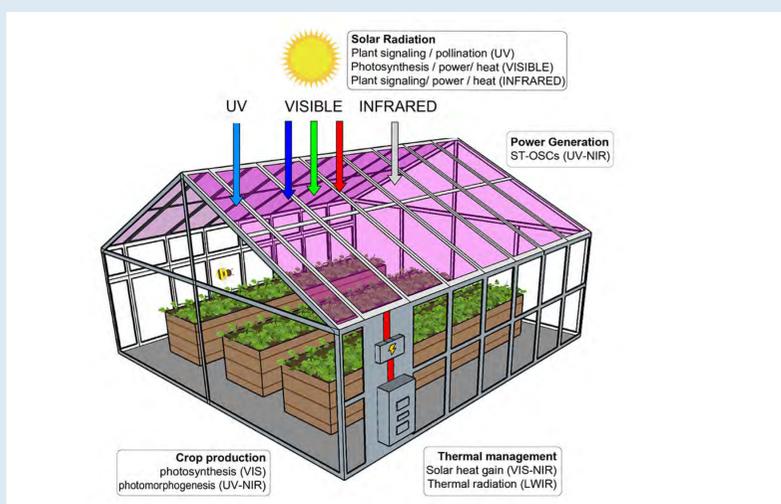
Plant Molecular Engineering, Systems and Synthetic Biology

Current Research

- Systemic signaling in plants in response to different microbes
- Function of circular RNA in plant symbiotic signaling
- Re-engineering lost symbiotic host trait genes into Brassicaceae
- GreenERhouses - crop production in net-zero energy greenhouses using semitransparent organic photovoltaics

Ideas and Collaborations

- Engineering circular RNA for protein engineering in plants
- High-throughput methods for (circ)RNA:protein interactions



Translational Orthopaedic Research Laboratory

Department of Biomedical Engineering

Matthew Fisher
mbfisher@ncsu.edu

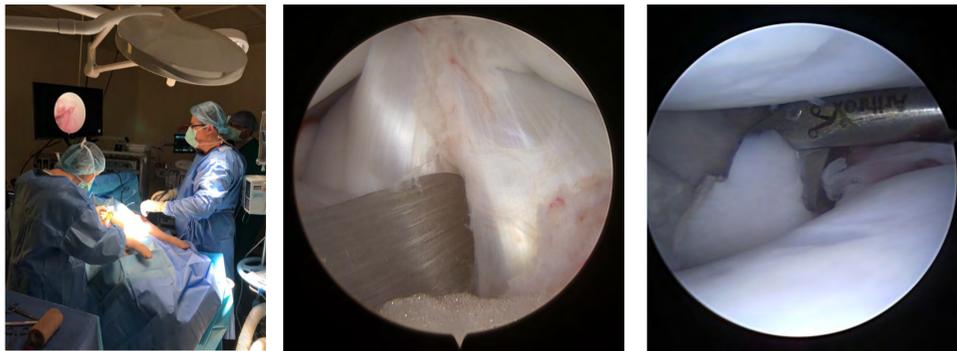
1. Musculoskeletal Biomechanics

robotic systems and materials testing



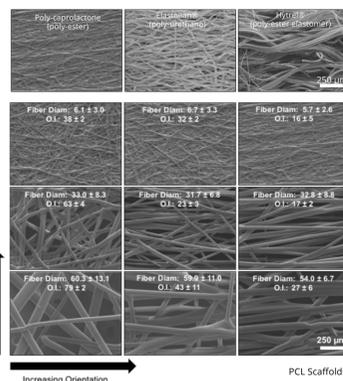
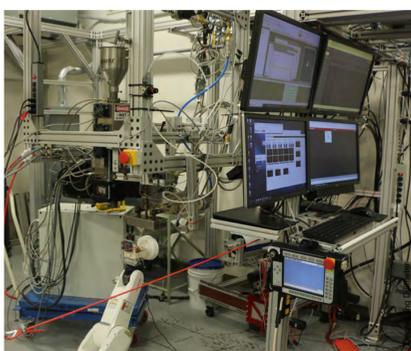
2. Large animal models of musculoskeletal injury

anterior cruciate ligament, meniscus, cartilage, etc.

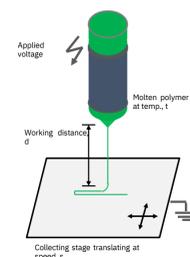


3. Tissue engineering

scaffold fabrication, tissue models, bioreactors



Stage Speed	Temperature	Working Dist.
1 mm/s	70 °C	1.5 mm
3 mm/s	80 °C	5 mm
5 mm/s	90 °C	10 mm



Our group is interested in collaborations in expanding our studies using genomics approaches. We can provide expertise in biomechanics, tissue engineering, and animal models in new collaborations.

Jason Delborne



Areas of Expertise:

- Professor, Dept. of Forestry and Environmental Resources [Environmental Policy]
- Director, Science, Technology, and Society Program [Governance of Emerging Technologies]
- Executive Committee, Genetic Engineering and Society Center [Social Dimensions of Biotechnology for Agriculture and Conservation]

Current Research

- Native American perspectives on the genetically engineered American chestnut tree.
- Social dimensions of genetic biocontrol of invasive aquatic species in the Great Lakes Region.
- Stakeholder engagement about genetic biocontrol of invasive carp in Minnesota.
- Stakeholder engagement to guide Real-time Analytics to Monitor and Predict Emerging Plant Disease

Ideas

- Governance and regulation of emerging biotechnologies
- Stakeholder collaborations to influence biotechnology design for agriculture or conservation

Collaborations

Genetic engineers, technology developers



Hobbies

- Tennis
- Biking
- Hiking
- Improvisational theater

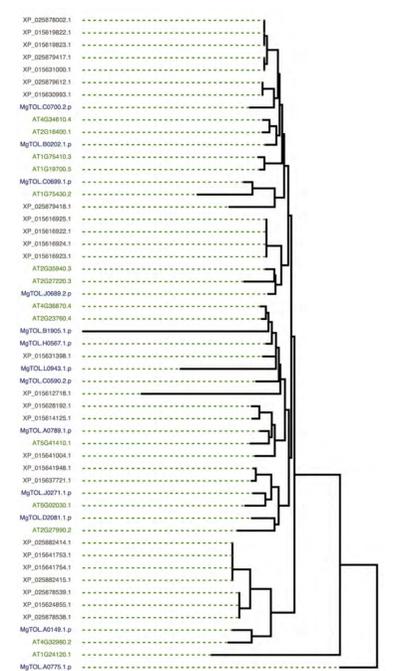
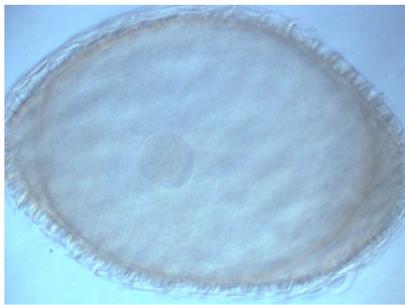
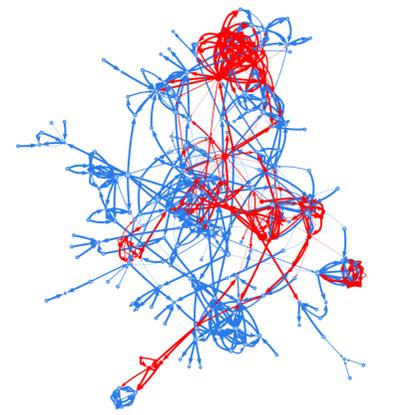
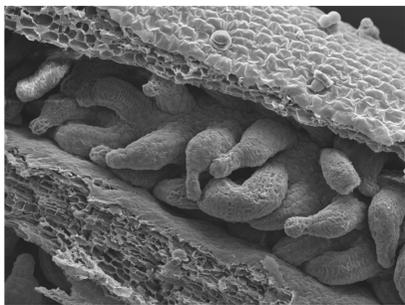
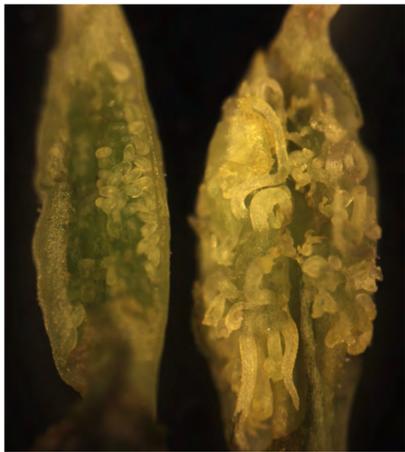


Franks Lab

Plant and Microbial Biology, NC State University

Molecular Genetics of Plant Development, QTL Mapping, RNA-Seq, Genomic Imprinting, Bioinformatics

NC STATE UNIVERSITY



Lab Members



Robert Franks



Miguel Flores-Vergara



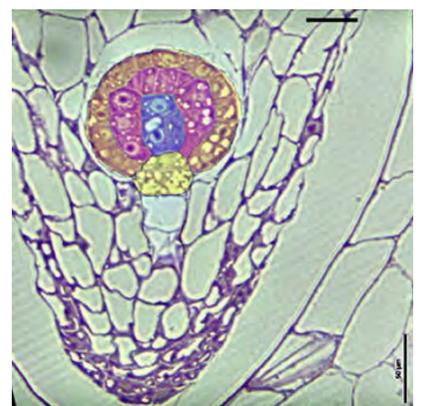
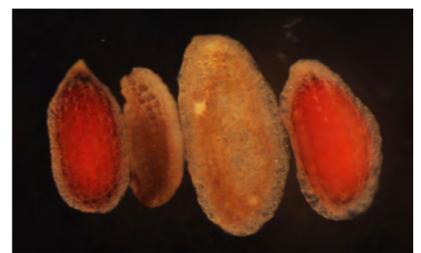
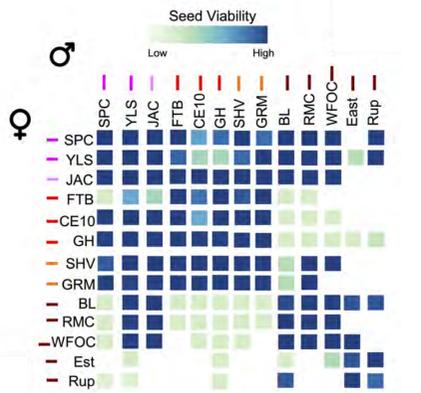
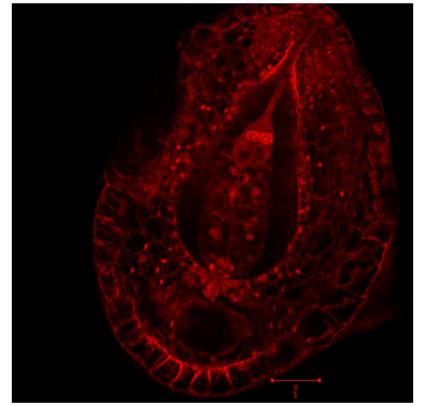
Albert Tucci



Elen Oneal



John Willis



Current Projects

Hybrid Seed Inviability and the Evolution of Endosperm Development in *Mimulus*

- Investigating hybrid seed failure via evaluation of seed development in crosses between species in *Mimulus* section *Erythranthe*.
- RNA sequencing analysis of endosperm tissue to isolate genes with imprinted expression that are critical for normal endosperm and seed development in *Mimulus*.
- QTL mapping with RADSeq data to identify genetic incompatibility loci from inter-species crosses of *Mimulus*.
- Utilizing gene regulatory network inference on time-course RNAseq data in order to highlight potential genes of biological importance in the developing endosperm.
- Identifying underlying genetic mechanisms responsible for a novel ovule mutation found in *Mimulus nudatus*.

Future Directions

Investigating Evolutionary Dynamics of Genomic Imprinting in *Mimulus*

- Leveraging phylogenetic, epigenetic, and bioinformatic approaches to elucidate the contexts under which genomic imprinting status is changed or conserved in *Mimulus*.

Development of Computer-Vision Tool for Automating the Count of Endosperm Nuclei

- Assessing the number and spacing of endosperm nuclei in a developing hybrid seed is an important step to determining potential causes of hybrid seed inviability.

Types of Collaborators Who Would be Helpful to Work With

Experts in AI and Computer Vision

Experts in Speciation

Experts in *In Situ* Hybridization and Microscopy

Experts in Bisulfite Sequencing

Dipali Srivastava
(Postdoctoral Scholar)
Terri A. Long
(Associate Professor)



Department of Plant & Microbial Biology

Areas of Expertise:
Plant Molecular biology

Current Research

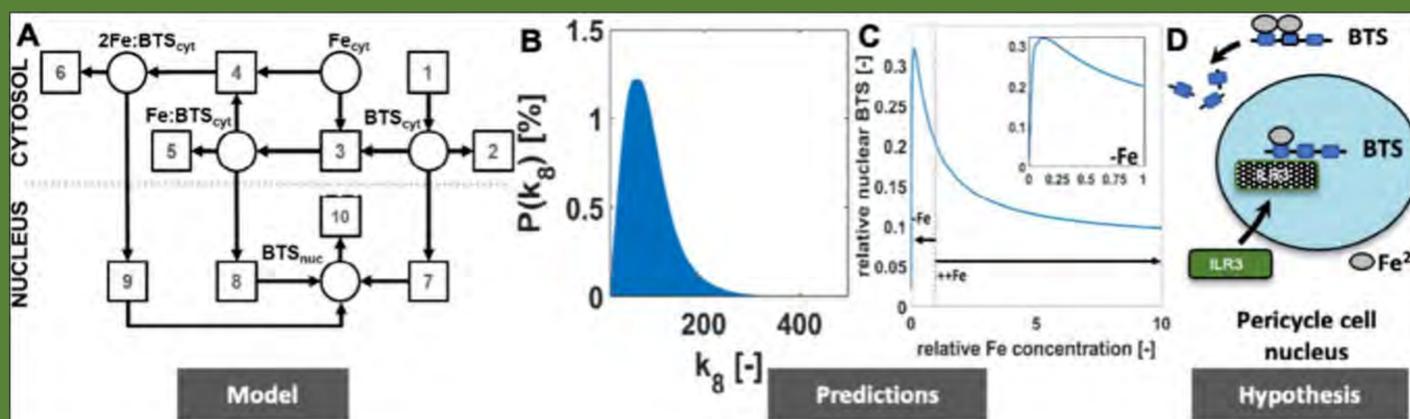
The project aims to explore the impact of iron in BRUTUS (BTS) protein stability, localization, and regulatory function through point mutations in BTS iron binding HHE domains.

Ideas

BTS and BTS homologs are E3 ligases that sense iron status via their iron-binding domains. They, subsequently, regulate levels of the transcriptional regulators, such as ILR3 that are responsible for iron redox, transport, and storage by facilitating their degradation. Using mathematical modeling (Figure 1) we propose to gain insight into molecular mechanism by which iron binding regulate the BTS function and how BTS nuclear localization impacts on ILR3 accumulation.

Collaborations

Our lab seeks to make fundamental discoveries in iron signaling in plants and develop enhanced strategies and methods for optimizing iron homeostasis in crops. We are looking for collaborators interested in expanding this study through multidisciplinary approaches like protein structural analysis, automated or semi-automated image analysis and computational biology. We are highly excited to explore the iron homeostasis in other plant species like soybean, maize etc.



Email: terri_long@ncsu.edu



Hobbies

Hand craft and painting, cooking, travelling, photography



Jeff Yoder

Department of Molecular
Biomedical Sciences, CVM



Areas of Expertise:

Comparative Immunology, Immunogenetics, Immunotoxicology

Current Research

- Impact of PFAS exposure on vertebrate immune function
- Molecular and functional evolution of innate immune receptor gene families

Ideas

- Immunotoxicology of chemical exposure
- Investigating the mechanisms of gene cluster evolution
- Comparative studies of new immune gene families
- Strategies to identify immune receptor ligands

Collaborations

Immunologists, Evolutionary geneticists, Biochemists



Martha Burford Reiskind

Burford Reiskind Lab

Department of Biological Sciences



Areas of Expertise:

Population genetics; Rapid evolution (abiotic & biotic drivers); Interactions between genes and environment; Invasive species; Conservation Science

Current Research

- Evolutionary of female choosiness induced by interspecific mating between naturalized and invasive *Aedes* mosquitoes
- Evidence of evolution in spreading populations of the invasive red lionfish

Ideas

- Evolutionary mechanism of invasion (introduction, establishment, and spread), connecting genotype to phenotype, modeling the future trajectory of spread, forecasting evolution
 - Figure 1
- Selection experiment and QTL analysis of female choosiness in *Aedes aegypti*, the yellow fever mosquitoes– how might we capitalize on female choosiness in management of arbovirus vector
 - Figure 2

Fig. 1

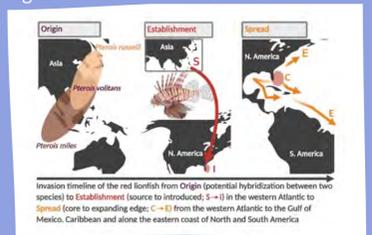
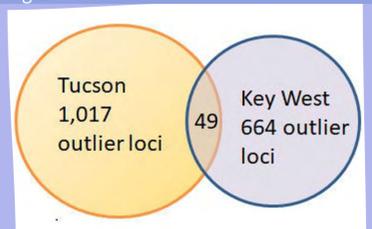


Fig. 2



Collaborations

- Population and climate modeler
- Molecular geneticists who specialize in gene expression, transcriptomics, immune gene evolution, microbiome,
- Protein biochemist
- Social scientists specializing in conservation questions that involve community stakeholders and managers of invasive species



Joe Gage

Department of Crop and Soil Sciences



Areas of Expertise:

Crop Genomics, High throughput phenotyping

Current Research

- Natural variation for ethylene sensitivity across diverse maize and sorghum
- Genomewide patterns of translation regulation by upstream open reading frames (uORFs)
- Characterizing and modeling the transcriptional basis of gene-environment interactions
- High throughput phenotyping using UAVs

Ideas

- Cross-species modeling of GxE based on conserved patterns of gene regulation
- Variation in temporal patterns of phenotypic variation across diverse germplasm
- Engineering gene regulation (transcriptional or translational) to produce more resilient and productive crops

Collaborations

- Computer scientists
- Computational biologists
- Plant physiologists

Twitter @JoeGage10

<https://gagelab.wordpress.ncsu.edu/>



We are a new lab – started in January 2021!



**NC STATE
UNIVERSITY**

Anna Stepanova & Jose Alonso



Department of Plant &
Microbial Biology

Areas of Expertise:

Plant hormones, Synthetic biology, Gene-specific translation regulation, and Genetic engineering/recombineering.

Current Research

- **Plant hormometer:** The goal is to use synthetic biology to generate sensors to monitor multiple plant hormones with cellular resolution.
- **Synthetic biology:** The goal is to generate CRISPR-based logic gates to develop complex decision-making genetic circuits.
- **Gene-specific translation regulation:** The goal is to identify DNA sequences (cis-elements) and proteins (trans-factors) involved in gene-specific translation regulation for biotechnological applications.
- **Genetic engineering:** The goal is to develop recombination-based technologies to facilitate genome editing and gene stacking.

Ideas

- To adapt our gene-stacking system for organisms other than plants
- To develop bioinformatic tools to analyze new types of RNA-seq data (e.g., Ribo-seq)

Collaborations

- Teams interested in testing/utilizing in their favorite experimental system any of the tools we are developing (plant hormometer, gene stacking, etc.)
- Volunteers joining our outreach program for museum and classroom demos and teacher training workshops.

<https://alonsostepanova.wordpress.ncsu.edu/>



Hobbies

Anna: Gardening (amateur tomato breeder)

Jose: Tinkering with 3D printers, Arduinos, Raspberry Pis, etc., to build DIY lab instruments

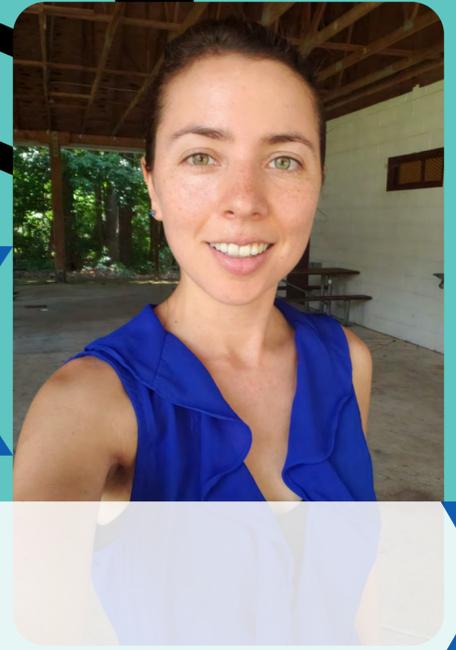
Nohelia Mora Ugalde

B.Sc.

Biomedical Science Master Program

School of Medicine, University of Costa Rica

Visiting Alonso Ramirez Lab, Dept. of Biological Sciences



Areas of Expertise: Cell culture and laboratory animal research

Interest in: Genetics, Immunology and Conservation

Current Research

- In CENIBiot, Costa Rica in collaboration with the researchers from the National Laboratory of Nanotechnology (LANOTEC), **We were interested in knowing the effect on cell viability on the NIH/3T3 ATCC® CRL-1658 cell line and any changes determined by a dermal test of irritability on New Zealand rabbits by exposing both to different concentrations of novel aqueous nanoparticles of *Tinospora cordifolia* extract.**
- We also tested scaffolds of type I collagen impregnated with nanoparticles of naturally extracted Propolis on NIH/3T3 ATCC® CRL-1658 cell line due to their potential in regenerative medicine and simple production.
- We published three papers as a result of these research projects
 - Orcid 0000-0003-2549-6471

Ideas

I'm interested in genetic projects that require techniques like qPCR, sequencing, gene editing and animal models (conventional or non-conventional models) with medical (chronic diseases, neglected tropical diseases or rare disorders) or conservation relevance.

Collaborations

I'm applying to the Genetic and Genomics Scholar Program and the Genetic Graduate Program at NCSU this year. Help me join the pack by introducing me to teams with projects where I could be useful.

Email: nohelia.mora@ucr.ac.cr

Hobbies and Fun Facts

- Former rhythmic gymnast medallist, current roller skater
- Avid reader, I was raised by a librarian
- Last position: Research Technician at the Health Unit, CENIBiot, Costa Rica.
- Moved to Cary, NC in December 2021.



Max Scott Lab

Lab members in the Departments of Entomology & Plant Pathology and Genetics

Areas of Expertise:

Insect molecular genetics, genome engineering, and genetic pest management.



Current Research

- **Genetic biocontrol of the New World screwworm and spotted wing *Drosophila* using:** Tetracycline-repressible female lethal genes, CRISPR/Cas9 homing gene drive targeting essential genes, Y chromosome-linked Cas9 targeting X-linked genes
- **Functional analysis of genes that mediate the attraction of blowfly larvae and adults to rotting meat**

Ideas

- Novel CRISPR-based systems for genetic biocontrol
- Genetic basis of the attraction of blowflies to rotting meat
- X chromosome dosage compensation and potential imprinting in blowflies
- Next-generation maggot debridement wound therapy using engineered maggots (patent awarded 2022)

Collaborations

We welcome any collaborators who are knowledgeable about insect behavior (particularly olfaction), genetic engineering, gene drives, microbiome analysis, CRISPR and wound healing.

Twitter @Max_Scott_Lab



© MATT BERTONE 2015



© MATT BERTONE 2021



Scott Lab Member
Alexis Kriete



The Scott Lab goes out for Howling Cow ice cream! (Winter 2021)



Ross Sozzani

**Plant & Microbiology Department
N.C. PSI, STEPS Center**



Areas of Expertise:

Plant Sciences, Plant Development, Root Biology, Computational Biology

Current Research

Our goal is to leverage the emergent system-level characteristics involved in cell-to-cell communication, patterning formation, and robustness that instruct stemness, differentiation, and growth of an organism. To this end, we have used 3D bioprinting platforms to arrange, at high-resolution, plant cells in predetermined architectures (e.g., placement of cell types for the generation of plant calli and plant organoids with precision only available with 3D bioprinting) amenable to manipulation to systematically quantify, explore, and predict the rules that drive efficient plant regeneration. By doing so, we continuously apply advanced deep-learning approaches.

Ideas

As the interface with soil, and the conduit for all water and nutrient resources, root systems are the foundation of plant health and productivity. Yet due to their complexity and difficulty of observation, roots have been largely ignored and arguably compromised during plant domestication and improvement, especially during and since the Green Revolution. New breeding and biotechnology-enabled breeding strategies that incorporate whole-plant structure and physiology are warranted across the spectrum of agricultural crops to simultaneously maximize resource use efficiency and yield.

Collaborations

STEAM

<https://steps-center.org/about/>
<https://cals.ncsu.edu/plant-and-microbial-biology/people/rsozzan/>

Hobbies and Fun Facts

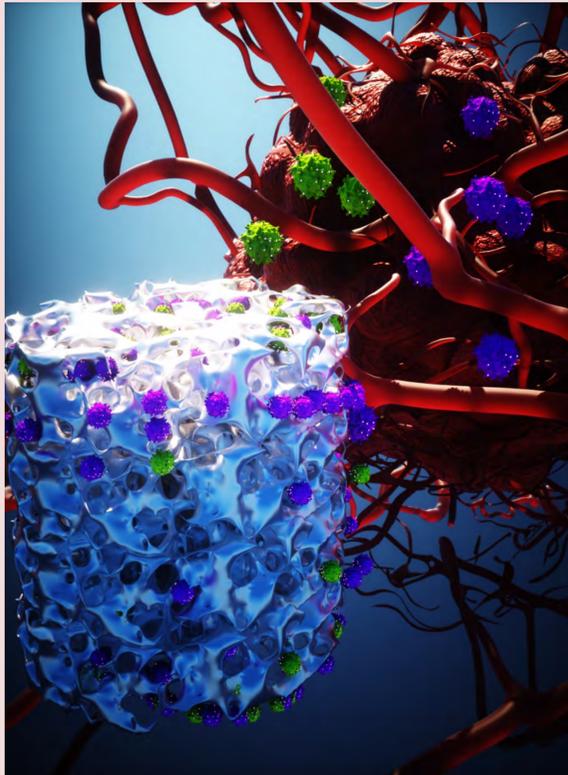
- I cook the best Italian food in town
- I am a very social person and my hobbies rely on organizing networking events.
- All my lab members get an Arabidopsis vase when they move on in their careers





Reimagining CAR-T Cell Therapy

...we will not cure cancer at \$500,000 per dose!



Genetically modified cells are:

- **Transformative:** A game changer in cancer therapy.
- **Effective:** Lead to durable and long lasting cancer remission.
- **Broadly Applicable:** Could treat solid tumors, heart attacks, and HIV.

Cell manufacturing is:

- **Laborious:** Require clean room facilities
- **Time-Intensive:** 4-8 weeks patients wait, and die, for manufacturing
- **Expensive:** \$250,00-400,000 per dose.

We are developing technologies to change how genetically altered cells are manufacturing, drastically speeding up production times and reducing costs.

Central to this effort are bioinstructive biomaterial scaffolds that enable same-day generation of CAR-T cells.



Learn More

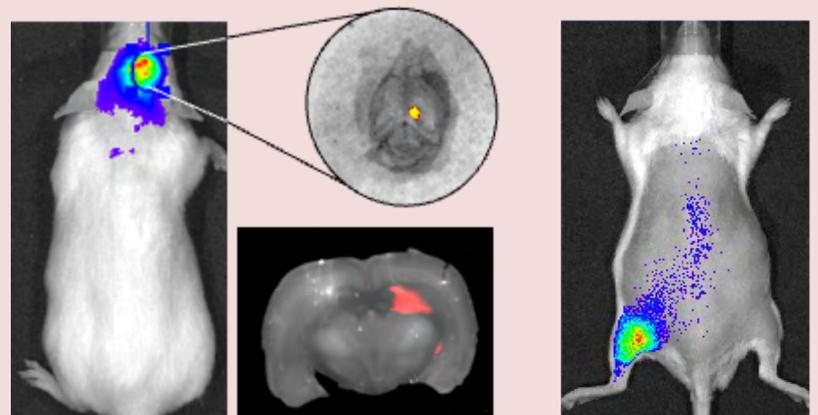
Ultra-Targeting of Therapeutics

...targeting the tumor, only the tumor, and nothing but the tumor...



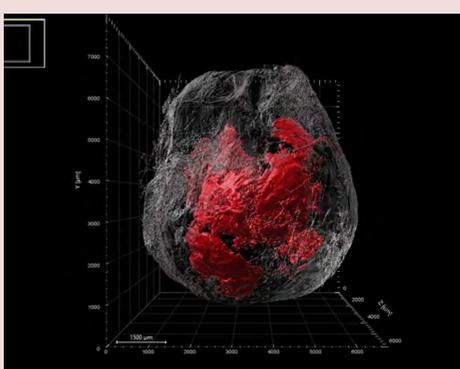
LEARN MORE

We are developing strategies for ultra-specific drug targeting. This means we can get a drug to just one part of area of the brain or only one muscle in the body. To enable this, we use cutting edge chemistry and materials science to perform reactions in the body.



Materials- Free Drug Depots

...unshackled from the yoke of materials...



Traditional controlled-release drug delivery systems use materials to hold drugs in place. We are developing material-free drug-eluting technologies that penetrate deeper into tissues for better drug presentation at disease sites.



Our Website

Zack Brown

Department of Agricultural
and Resource Economics



Areas of Expertise:

Bioeconomics, resource economics

Current Research

We work on the economic optimization of biomathematical models, as well as on the empirical analysis of feedbacks between economic and biological systems. Previous examples include the economics of pesticide resistance, consumer effects of agricultural gene drives, public goods effects of pest control on farmer decision-making, effects of biofuels policies on biotech patenting, optimization of release programs for Wolbachia-infected mosquitoes, as well as farm-level optimization of cover crop usage over time.

Ideas

I am interested in expanding work on **economic and decision analysis for benefits and risks of gene drive insect releases in agriculture and public health**. I am also interested in **modeling effects of plant genetic improvements in NUE on farmers' economically optimal fertilizer decisions**.

Collaborations

Biomathematicians, gene drive developers, soil scientists, agronomists
(STEPS affiliates)



Training for a 40 mile trail run in February! (Gulp.)



NC STATE
UNIVERSITY

Khara Grieger

- Department of Applied Ecology
- Executive Committee member of Genetic Engineering and Society (GES) Center
- Plant Science Initiative
- NC State Extension



Areas of Expertise:

Risk analysis of emerging technologies, Risk governance, Stakeholder engagement, Science-and-society interactions

Current Research

- *Interdisciplinary Approaches to Evaluate Societal Implications and Foster Sustainability of Genetic Engineering and Nanotechnology in Food and Agriculture*; USDA/NIFA-funded grant (2022-2026; PI = Grieger; Co-PI=Kuzma)
 - Project 1. Benefit-risk evaluations of genetic engineering and nanotech in food/ag
 - Project 2. Stakeholder engagement for sustainable agrifood futures
 - Project 3. Interdisciplinary education and training on societal implications of genetic engineering and nanotech in food/ag

Ideas

- NC State-hosted workshops and seminars to train next-generation of students and researchers on:
 - Benefit-risk evaluations of new agrifood technologies
 - Role of genetic engineering and nanotech in sustainable agrifood futures
 - Engaging stakeholders in food and agriculture systems
 - Best practices in science and risk communication
 - Engaging stakeholders using online (virtual) platforms
 - Best practices for conducting interdisciplinary research in food and agriculture
 - Responsible innovation of genetic engineering and nanotech in food/ag

Collaborations

- Researchers and experts in evaluating potential risks and benefits of genetic engineering used in food/ag systems
- Researchers, students, postdocs, and others interested in leading, co-leading or participating in workshops and seminars focused on improving sustainability and responsible innovation of new technologies in food/agriculture
- Researchers, students, postdocs, and others interested in conducting interdisciplinary investigations of the role of new technologies to create sustainable futures

<https://risksciences.wordpress.ncsu.edu/>



Research Team



Hobbies

- Running
- Swimming
- Parenting



NC STATE
UNIVERSITY

Benjamin Callahan



Dept. of Population Health and Pathobiology
Bioinformatics Research Center

Areas of Expertise:

Microbiomes, Amplicon sequencing and metagenomics,
Computational biology, Bioinformatics

Current Research

- **Quantitative metagenomics** by modeling and correcting bias in metagenomic measurements of microbial communities
- **Predicting preterm birth** from the vaginal microbiome: A meta-analysis of published studies
- **The diversity of *Gardnerella*** and its ecology in the vaginal microbiome of pregnant women
- **Serovar-level identification of foodborne pathogens** from 16S sequencing data
- **Software integration** of the decontam and dada2 R packages into the QIIME2 microbiome data science platform
- **Microbial strain sharing** between pets and their owners

Ideas

- Wet+dry lab methods development for better measurements of microbial communities using metagenomics or other high-throughput methods.
- Great science and applications, probably involving microbes and/or quantitative measurements in some way.

Collaborations

Life scientists, or quantitative scientists interested in biological questions.

<https://callahanlab.cvm.ncsu.edu/>
bcallah@ncsu.edu
Twitter @bjecal



Hobbies

Always up for a round of disc golf

Rafael Guerrero

Department of Biological Sciences &
Bioinformatics Research Center



Areas of Expertise:

Computational evolutionary biology, theoretical population genetics, genomic data analysis

Current Research

- Evolution of chromosome polymorphism
- Sex determination and sex chromosomes in dioecious plants
- Hybrid incompatibilities in a gene network framework
- Genetic conflict in human pregnancy

Ideas

Fine mapping of causal loci inside chromosome inversions (for any phenotype of interest). I would be interested in analyzing data from QTL approach + sequencing populations. I'd provide a computational prediction of causal loci inside inversion.

Collaborations

- Genetics of plant reproduction, floral development.
- Functional validation of computational predictions.

<https://twitter.com/guerruhroh>
<http://www.rguerrer.org>



PROPOSAL DEVELOPMENT UNIT

The **Proposal Development Unit (PDU)**, apart of the Office of Research and Innovation, supports faculty and teams from all colleges and offices across NC State on large interdisciplinary proposals. Our team helps with many elements of proposal development including:

PDU Events

Register at the homepage using the QR code below!

**NIH@NC State Grant
Writing Series
RePORTER Tips and Tricks**

Thursday, 11/10/2022, 12 pm

**PDU@Lunch
Get to Know the Centers,
Institutes and Academies**

Wednesday, 1/25/2023, 12pm

NSF CAREER Workshop

Wednesday, 3/22/2023, 1-4pm



Amanda Krentzel has joint appointments with the PDU and the GGA to work specifically with GGA members on their proposal ideas and needs. GGA members can work with Amanda on proposals with both big and small budgets and ranging a wide scope of topics, including research, education, and outreach. Some services include but are not limited to:



- Consultations about specific funding mechanisms
- Assistance in identifying NC State collaborators for your proposals
- Scheduling and moderating team meetings for proposals
- Hosting seminars on topics of interest



- Finding funding announcements for your ideas
- Assistance in writing strong abstracts, aims, or introductory pages
- Feedback on scientific rigor and responsiveness to funding announcements
- Drafting of non-technical sections



- Assistance with budgets
- Assistance with formatting and agency-specific forms
- Assistance with NC State submission processes

Depending on your needs, services can be à la carte or full proposal assistance.



Email Amanda Krentzel (aakrentz@ncsu.edu) to schedule a consultation. Submit requests for full services at <https://go.ncsu.edu/rdo-pdu>.

Jennifer Baltzegar

Genetic Engineering & Society Center



Areas of Expertise:

Population Genomics, Applied Evolution, Genetic Engineering & Society (GES), Insecticide Resistance, *Aedes aegypti*

Current Research

- Evolution of insecticide resistance in *Aedes aegypti*.
- Identifying the contributions to pyrethroid resistance by specific SNPs in the Voltage-Gated Sodium Channel gene.
- Population structure of *Aedes aegypti* in Iquitos, Peru.

Ideas

- Population Genomics of insecticide resistance in *Aedes aegypti*.
- Molecular genetics/gene editing of *Aedes aegypti* to investigate polymorphisms of interest.

Collaborations

- Scientists with expertise in sequencing low-quality DNA.
- Mathematical modelers.
- Scientists with gene editing expertise.
- Anthropologists who could help close the human-mosquito interaction loop.

Email: jfbaltze@ncsu.edu



Hobbies

- Mushroom foraging
- Stained glass
- House plants



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The Phylodynamics Research Group

PI David Rasmussen, Shi Cen,
Fangfang Guo, Lenora Kepler, May Wang

Entomology and Plant Pathology
Bioinformatics Research Center



Areas of Expertise:

Genomic Epidemiology / Viral Evolution / Phylogenetics

Current Research

- Evolution of generalist plant-infecting RNA viruses and the fitness tradeoffs that determine their host range
- Learning what selection pressures shape the fitness of microbial pathogens in real-world environments
- Recombination-aware phylogenetic methods for demographic inference from genomic data
- Designing optimal sampling strategies for pathogen genomic surveillance

Ideas

- Experimental evolution of microbial survival/persistence strategies in extreme, fluctuating environments.
- Co-evolutionary dynamics between plant viruses and their host's antiviral RNA interference systems
- The future of agricultural pests and pathogens in artificial environments like indoor farms.

Collaborations

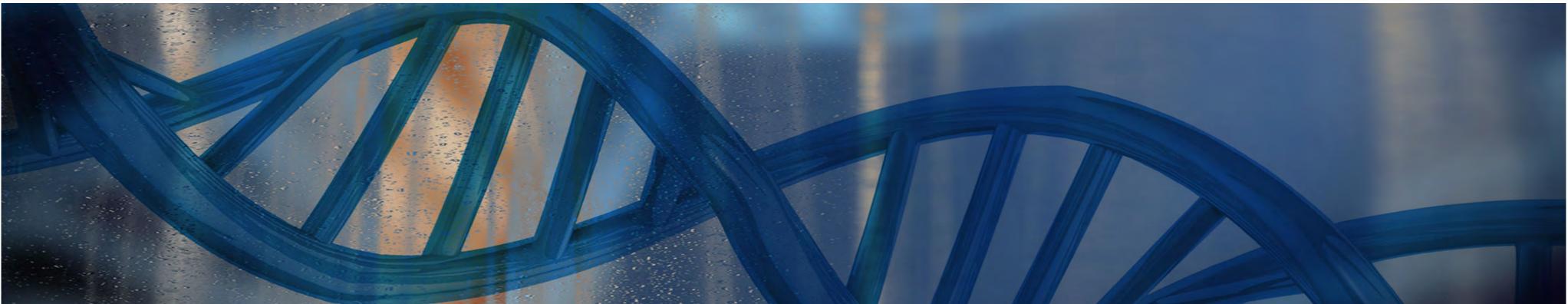
- Other evolutionary and population geneticists
- Virologists and microbiologists
- Molecular biologists working on genetic barcoding
- Engineers working on controlled environments

<https://phylodynamics.wordpress.ncsu.edu/>
drasmus@ncsu.edu



SCAN ME

“Specialization leads the individual, if (s)he follows it unreservedly, into bypaths still further off the highway where men, struggling together, develop strength”
-John Dewey (1902)



NC State University Genomic Sciences Laboratory

About Us

The Genomic Sciences Laboratory (GSL) is a Shared Research (Core) Facility of NC State University, operated under the direction of the Office of Research and Innovation. Staffed by a Director, an Assistant Director, and seven Research Specialists, the GSL provides Sanger and Next Generation DNA sequencing services to over 200 laboratories at NC State and the broader Research Triangle community. The GSL also maintains shared instrumentation and equipment that faculty, staff and students can use directly in their research.



Illumina NovaSeq 6000
Sequencer



Illumina MiSeq
Sequencer



Oktopure DNA extraction
system



Thermo Kingfisher Flex
DNA extraction



BioRad CFX
Opus qPCR



Applied Bio 3730xl
Capillary Sequencer



EpMotion 5075 Liquid
Handling Robot



Spex 2010 Genogrinder

Location

The GSL facility is located in Thomas Hall on the main NC State campus. In 2022, the GSL opened a second facility, the PSB Genotyping Laboratory, in the Plant Sciences Building on Centennial campus.



GSL Facility

2518 Thomas Hall
Central Campus
112 Derieux Place



PSB Genotyping Laboratory (GSL)

2364 Plant Sciences Bldg.
Centennial Campus
840 Oval Drive

Contact Us



Dr. David (Andy) Baltzegar
GSL Director

Phone: (919) 513-0738
Email: dabaltze@ncsu.edu



Kelly Sides
Asst. GSL Director

Phone: (919) 513-2012
Email: kafridey@ncsu.edu



Heike Sederoff, PhD Megan Franklin, PhD cand.



Department of Plant & Microbial Biology

Areas of Expertise:

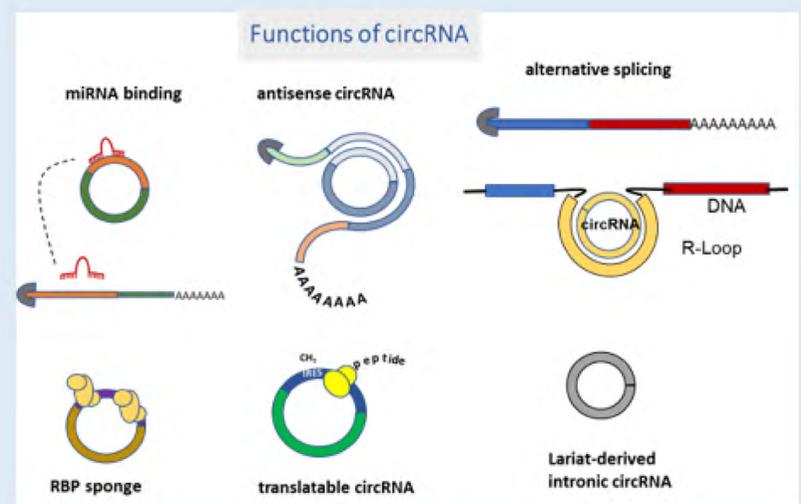
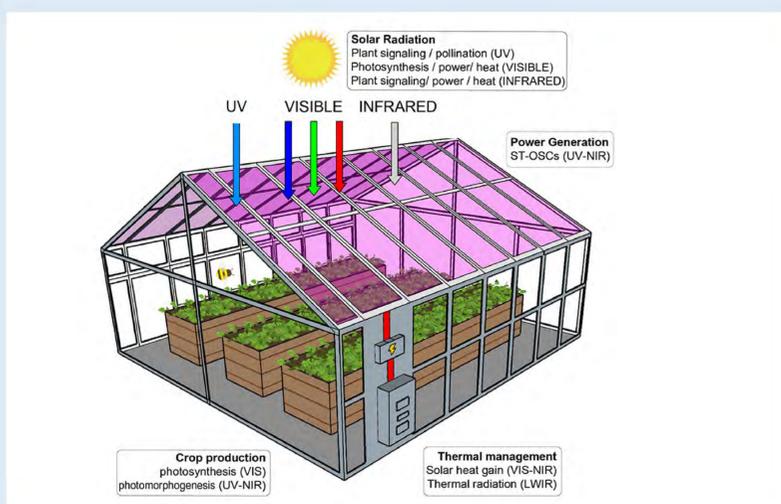
Plant Molecular Engineering, Systems and Synthetic Biology

Current Research

- Systemic signaling in plants in response to different microbes
- Function of circular RNA in plant symbiotic signaling
- Re-engineering lost symbiotic host trait genes into Brassicaceae
- GreenERhouses - crop production in net-zero energy greenhouses using semitransparent organic photovoltaics

Ideas and Collaborations

- Engineering circular RNA for protein production in plants and microbes.
- High-throughput methods for (circ)RNA:protein interactions



Genetics & Genomics and Bioinformatics Graduate Programs

Students & Faculty in:

CALS/CNR/COE/COS/CVM



Reade Roberts (Bio Sci)
Director
Genetics & Genomics

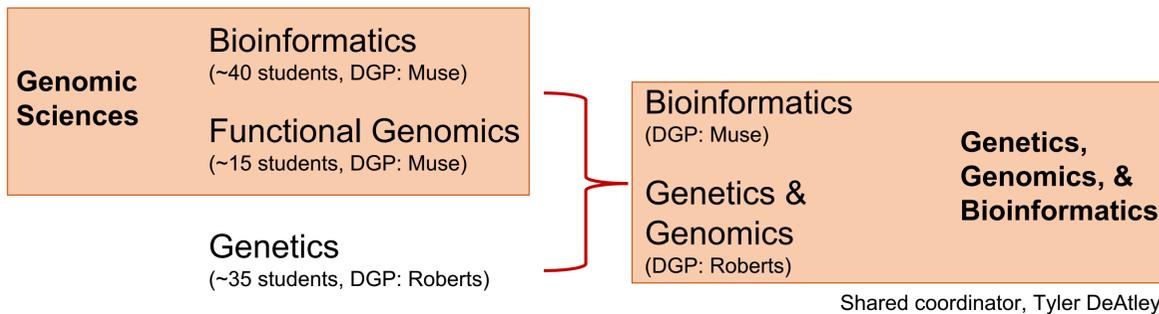


Spencer Muse (Stats)
Director
Bioinformatics



Tyler DeAtley
Coordinator
G&G and Bioinformatics

Merging three programs into two:



Three degrees

- PhD
- MS (thesis)
- MR (non-thesis)

Shared core curriculum (G&G)

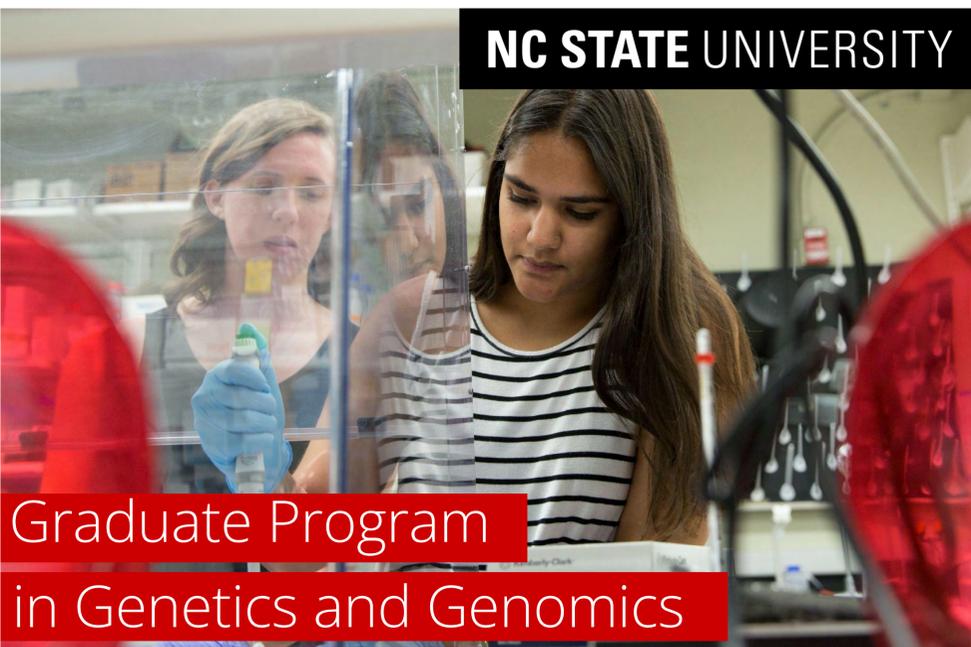
- GN 701 Molecular Genetics
 - GN 703 Pop & Quant Genetics
 - GN 702 Cell & Dev Genetics or GN 735 Functional Genomics
 - ST 511 Stats for Researchers I
 - Genetic/Genomic Data Analysis (multiple options)
 - Research Ethics (multiple options)
 - GN 810 G&G Journal Club (taken twice)
- Core total: 18-20 credits**

Merger goals

- Combine existing resources
- Maintain support and expectations for current students
- Stability and flexibility
- Unified admissions and other activities
- Shared, updated curriculum
- Rebranding to improve and simplify recruitment
- Critical mass of students for training grants and other opportunities
- A larger, more interactive community of students and faculty

Ongoing objectives

- Formal and informal affiliations to improve and individualize graduate training
- Opportunities and partnerships for student funding and professional development
- Inclusive recruitment of excellent applicants with diverse histories
- Solutions and structures for university-wide programs
- Instruction for program courses
- Increase and improve Master's degree training
- Core community building



The **NC State University Graduate Program in Genetics and Genomics** combines the strengths of classic and modern genetics, providing training in **cutting edge genetics and genomics research** on a strong foundation of **comprehensive training in genetics concepts**. The Genetics and Genomics Program community is truly interdisciplinary, with a network of over **100 faculty** from **14 departments** and **6 colleges**.

RESEARCH & TRAINING

- Diverse basic and applied research programs impacting **agriculture, human health**, and our **understanding of life** on this planet
- **Robust curriculum** trains experts in the fundamental topics in genetics
- Opportunities for **laboratory rotations**
- Workshops and symposia through the **Genetics & Genomics Academy**
- **World-class seminar series**

COMMUNITY & SUPPORT

- Genetics and Genomics PhD students are provided **competitive fellowships**, including **stipend, tuition, and benefits**
- Training and support for students through **Genetics & Genomics Scholars**, and **AgBioFEWS**
- Diverse career support via network of **industry partners** and programs in **education and policy**
- Located in the vibrant city of Raleigh, in the heart of North Carolina's Research Triangle
- **Vibrant student community and collaboration** with **Bioinformatics** sibling graduate program



Contact us at genetics@ncsu.edu today! Or scan the QR code to visit our homepage!



The **NC State University Graduate Program in Bioinformatics** responds to the urgent need for big data analytics in genomic science, providing training in **cutting edge computational research** on a strong foundation of **training in genetics and genomics concepts**. The Bioinformatic program community is truly interdisciplinary, with a network of over **100 faculty** from **14 departments** and **6 colleges**.

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