



TEXAS TECH UNIVERSITY

Institute of Genomics for
Crop Abiotic Stress Tolerance

IGCAST ANNUAL REPORT

2023

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MESSAGE FROM THE IGCAS T DIRECTOR

When facing a problem affecting food production or health, people often say, “Scientists must be doing something to solve the problem,” especially concerning significant issues like climate change. We have been doing it at the Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAST). IGCAST was created in 2018 with the support of a grant from the program Governor’s University Research Initiative (GURI) of the State of Texas. The primary research mission of IGCAST is to study the genetic, genomic, metabolomic, and physiological mechanisms that allow plants to tolerate, avoid, or escape detrimental environmental conditions, such as drought, high temperatures, salinity, and other factors that contribute to soil degradation. We are exploring functional genomics, metabolomics, computational biology, and synthetic biology approaches to understand abiotic stress responses in photosynthetic organisms and use the obtained knowledge to design strategies for crop improvement.

When it was established in 2018, IGCAST had only two faculty and two students. Five years later, the IGCAST team grew to 7 faculty, 10 undergraduate students, 40 graduate students, and 10 postdoctoral fellows by the end of 2023. IGCAST currently has seven research teams led by Drs. Damar López-Arredondo, Yinping Jiao, Gunvant Patil, Son Tran, Degao Liu, Madhusudhana Janga, and Luis Herrera-Estrella, who regularly publish in the most prestigious international scientific research journals. As part of the strategic program to promote research excellence at Texas Tech, IGCAST expects to have three additional faculty by the end of 2024.

The rapid growth of IGCAST’s publications in peer-reviewed journals (from two in 2019 to a total of 122 by the end of 2023) and funding (which climbed sharply from \$100,000 in 2019 to \$4.56 million in 2023 with more than 60% coming from federal agencies) illustrate the successful development of our institute.

Our research program has grown to cover a diverse set of important topics for crop improvement, including:

- Molecular basis of disease resistance in cotton and soybean.
- Molecular physiology of plant nutrition and nitrogen fixation.
- Genome sequencing projects of different species, including cotton, sorghum, resurrection plant species, chia, and several microalgae species.
- Signaling molecules and gene regulatory and metabolic networks that govern responses and tolerance of *Arabidopsis* and important crops, including cotton, soybean, sorghum, and common bean, to drought, heat, salinity, and their combined stress conditions.
- Strategies for carbon sequestration in plants and microalgae.
- Development of tissue culture-independent gene editing strategies.
- Improve gene transfer protocols for important crops such as cotton, sorghum, maize and soybean.

With the committed and diligent work of all IGCAST members and the constant support from our colleagues, the department chair of PSS, and particularly the central administration, we will continue our contributions to plant biology and crop improvement. We welcome you to learn more about our work and scholarly pursuits by reading the IGCAST newsletter.

Every year, we summarize in this newsletter our research highlights the number of papers published, the funding received by our faculty from federal agencies, industry groups, for-profit businesses, and philanthropic organizations, and the honors and awards that students, postdocs, and faculty have received.

HERRERA-ESTRELLA LAB



The genomic and metabolic networks that control plant response to abiotic stress. Every year, crops face the challenging environmental conditions of abiotic stress. This leads to decreased productivity and economic losses for farmers. Environmental factors, including the availability of water and nutrients, temperatures, salinity, and soil physical properties, heavily influence crop yields. In the past two decades, abiotic stresses have become increasingly prevalent due to climate change and the excessive mechanization and grassing of land. Understanding how these environmental factors interact with a crop's genetic makeup is essential for optimizing yield potential and developing successful agricultural strategies. Our research program aims to solve these problems by providing an advanced analysis of the genomic and metabolic networks that control the response of plants to abiotic stress.

Research subjects

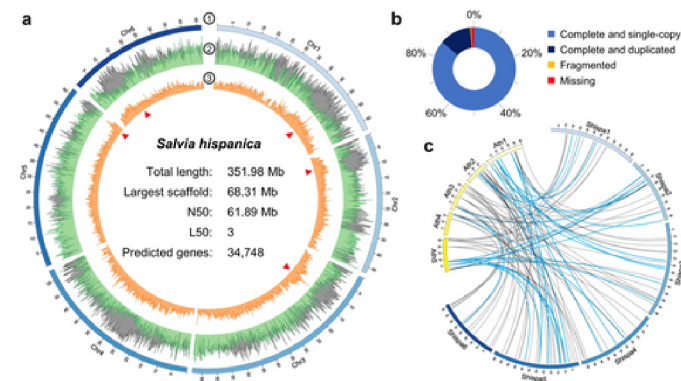
Identifying and characterizing gene regulatory and metabolic networks involved in plant desiccation tolerance. Identifying the sensors and signaling pathways that activate plants' systemic and local responses to phosphate deprivation. Genomics of plant species with nutraceutical or medicinal properties. Development of genetic and genomic strategies to modulate root architecture to enhance plant carbon sequestration.

Major discoveries/ achievements

- Development of a high throughput, non-destructive method to measure photosynthetic activity in plants subjected to drought.
- Chromosome level genome sequence of two *Selaginella* species, one tolerant and one susceptible to desiccation.
- Chromosome level genome sequence of *Salvia hispanica* and metabolomic analysis of the chia seed.
- Characterization of changes in chromatin accessibility in the adaptation of plants to low phosphate availability.

Relevant publications

- Rico-Cambron, T.Y., Bello-Bello, E., Martinez, O., Herrera-Estrella L. (2023). **A non-invasive method to predict drought survival in Arabidopsis using quantum yield under light conditions.** Plant Methods 19, 127.
- Alejo-Jacuinde, G., Nájera-González, H.R., Chávez Montes, R.A.,... Herrera-Estrella L. (2023). **Multi-omic analyses reveal the unique properties of chia (*Salvia hispanica*) seed metabolism.** Commun Biol 6, 820.
- Flores Tinoco V., Herrera-Estrella, L., Lopez-Arredondo, D.(2023). **Back to primary endosymbiosis: from plastids to artificial photosynthetic life-forms.** Trends in Plant Science. Vol. 28, Issue 7.



Features and metrics of chia genome assembly. a) Track 1 depicts chromosome number and their length (Mb), track 2 shows gene density (green) and repetitive elements (gray), and track 3 methylation patterns. Red triangles indicate the approximate locations of centromeres. b) Genome completeness indicated by conserved embryophyte orthologs. c) Synteny with lines representing homologous genes for mucilage production between *A. thaliana* (Ath) and *S. hispanica* (Shispa). Blue lines highlight the expansion of mucilage synthesis genes in the chia genome.

TRAN LAB



The world population has been rapidly increasing, setting food security one of the major issues in many countries. In addition, climate change also puts a great burden on food production. Environmental stresses, such as drought, extreme temperatures, high salinity, nutrient deficiency, soil erosion, and pollutants are factors affecting yield and stability of crop production, thereby threatening sustainable agriculture. Our research group has interests in (i) studying the roles of signaling molecules and their interactions in plant responses to environmental stresses, as well as (ii) translational genomics aiming to enhance crop productivity under adverse environmental stress conditions.

Research subjects

Molecular elucidation of hormonal regulatory networks in plant responses to environmental stresses. Roles of signaling molecules in environmental stress adaptation. Functional genomics of food crops for improvement of crop productivity in adverse conditions.

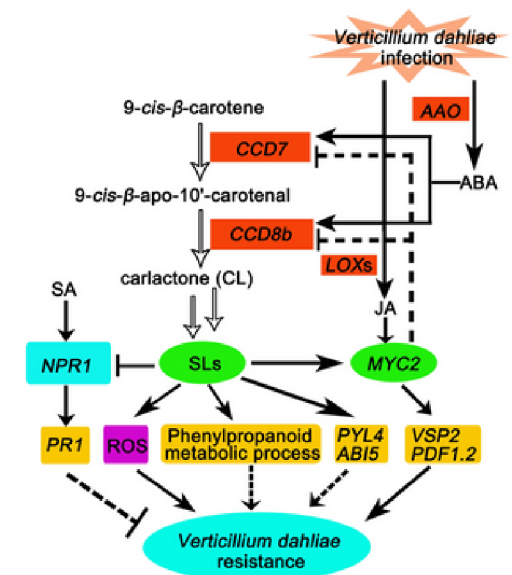
Major discoveries/ achievements

- We found that the Zn application improves cotton drought tolerance by improving the plant's water status and antioxidant capacity.
- We provided evidence that acetic acid enhances drought tolerance of common bean by maintaining ROS homeostasis and improving photosynthetic performance.
- We demonstrated that strigolactones positively regulate cotton resistance to *Verticillium* wilt through crosstalk with abscisic acid, jasmonic acid and, salicylic acid hormones.

Relevant publications

- Anik, T.R., Mostofa, M.G., Rahman, M.M., ...Tran, L.-S. P. (2023). **Zn Supplementation Mitigates Drought Effects on Cotton by Improving Photosynthetic Performance and Antioxidant Defense Mechanisms.** *Antioxidants*, 12, 854.
- Nguyen, H.M., Ha, C.V., Le, V.P., ...Tran, L.-S. P. (2023). **Improvement of Photosynthetic Performance by Acetic Acid to Enhance Drought Tolerance in Common Bean (*Phaseolus vulgaris*).** *J Plant Growth Regul.* 42:7116-28.
- Yi, F., An, G., Song, A., ...Cai, Y. (2023). **Strigolactones positively regulate *Verticillium* wilt resistance in cotton via crosstalk with other hormones.** *Plant Physiology, Plant Physiol* 192:945-66.

Model for the role of strigolactones (SLs) in improving cotton resistance to *Verticillium dahliae* through the crosstalk with abscisic acid-, jasmonic acid- and salicylic acid-signaling pathways, and promoting phenylpropanoid metabolism and reactive oxygen species (ROS) accumulation.





LOPEZ-ARREDONDO LAB

Unraveling regulatory networks behind biotic and abiotic stresses in plants and microalgae: the driving force of domestication and trait improvement. Our research group is interested in studying plants and microalgae responses to environmental stressors and fluctuating growing conditions, e.g., phosphorus and nitrogen starvation, and pathogens. We use molecular biology, metabolomics, lipidomics, transcriptomics, and genomics, to unravel the mechanisms behind those responses and gain insights into their regulation. But we do not stop there; our major goal is to go beyond by taking advantage of this knowledge to design strategies to solve real-world problems. We study the regulatory networks controlling *Fusarium* and root-knot nematode resistance in cotton to identify genes that can be used to speed up breeding programs to improve resistance to these pathogens. Similarly, in microalgae, we study the metabolic and regulatory networks controlling biosynthesis of lipids and novel molecules with potential herbicidal and nematocidal activities, and design strategies to enhance their production via synthetic biology strategies.

Research subjects

Understanding plants and algae responses to environmental stresses and identifying associated signaling pathways. Identifying and characterizing metabolic and gene regulatory networks that govern neutral lipid biosynthesis in microalgae. Identifying novel molecules and metabolic pathways in microalgae that lead to new biopesticides. Identifying and characterizing gene regulatory networks that control *Fusarium* and root-knot nematode resistance. Genomics of plants and microalgae with potential for biofuels and bioproducts.

Major discoveries/ achievements

- Strains of the *Chlamydomonas* and *Chlorella* genera that produce bioactive compounds with pesticide activities.
- The mechanisms underlying root-knot nematode resistance in NemX cotton are constitutive while avoiding a fitness penalty, and that phenylpropanoid metabolism determines *Fusarium* wilt race 4 resistance in Pima-S6 cotton.

- Transcription factors that orchestrate cell growth and neutral lipid biosynthesis/accumulation in green algae.
- Chromosome level genome sequence of Pima-S6 (*G. barbadense*) cotton, resistant to FOV4.

Relevant publications

- Ojeda-Rivera J., Ulloa M., Pérez-Zavala F., ... Lopez-Arredondo D. (2024). **Enhanced phenylpropanoid metabolism underlies resistance to *Fusarium oxysporum* f. sp. vasinfectum race 4 infection in the cotton cultivar Pima-S6** (*Gossypium barbadense* L.) *Front. Genet.* 14:1271200.
- Brito-Bello, A. A., Lopez-Arredondo D. (2023). **Bioactive Compounds with Pesticide Activities Derived from Aged Cultures of Green Microalgae.** *Biology* 12, no. 8: 1149.
- Chávez Montes, R. A., Ulloa, M., Biniashvili, T., ... Herrera-Estrella, L. (2023). **Assembly and annotation of the *Gossypium barbadense* L. “Pima-S6” genome raise questions about the chromosome structure and gene content of *Gossypium barbadense* genomes.** *BMC Genomics*, Vol.24.





JIAO LAB

The research in Jiao lab is devoted to gaining a deeper understanding of the genetic diversity and regulatory mechanism of important agronomic traits in crops, with the ultimate aim of advancing breeding. The specific focus of my research program is to identify the beneficial genes and alleles to enhance sorghum grain quality and abiotic stress tolerance, aligning with diverse market requirements.

Research subjects

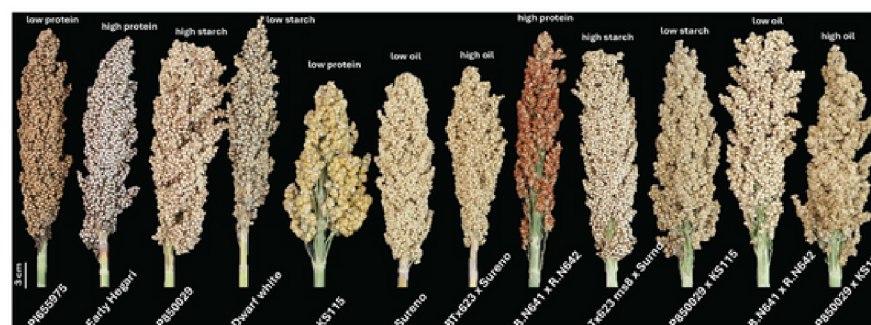
- Identify key genes and alleles to improve the sorghum grain nutrition.
- Construct gene regulatory networks related to sorghum drought tolerance.
- Establish sorghum mutant populations to support the functional genomics research.

Major discoveries/ achievements

- The release of the sequenced indexed sorghum mutant population covering 98% of sorghum genes.
- The first transcriptomic and metabolomic landscapes of sorghum seed development.
- The identification of four new genes controlling sorghum cuticular wax and root development.
- The second sorghum mutant population in the genetic background of a breeding variety is established for new traits discovery to meet the need of sorghum breeding.

Relevant publications

- Jiao, Y., Nigam, D., Barry, K., ... Xi Z. (2023). **A large sequenced mutant library - valuable reverse genetic resource that covers 98% of sorghum genes.** The Plant Journal, Volume 116, Issue 6, 1365-1313X.
- Khan, A., Khan, N.A., Bean, S.R., ... Jiao, Y. (2023). **Variations in Total Protein and Amino Acids in the Sequenced Sorghum Mutant Library.** Plants, 12, 1662.
- Xin, Z., Jiao, Y., Burow, G., ... Ware, D. (2023). **Registration of 252 sequenced sorghum mutants as a community reverse genetic resource.** Journal of Plant Registration. 1. 17, 599-604.



The high diversity of the sorghum MAGIC population for the study the grain quality.



PATIL LAB

Unlocking the potential of genome engineering holds the key to revolutionary advancements in crop improvement. With this groundbreaking technology, we gain the power to precisely activate, deactivate, or fine-tune the expression of specific genes, thereby enhancing desired traits and optimizing plant fitness. Despite this promise, the genetic transformation process remains a bottleneck in crop improvement, often limited to a handful of genotypes per species, resulting in suboptimal agronomic performance. To overcome these challenges, my focus is on pioneering a platform for 'genotype-independent' genetic transformations and refining genome editing systems across major crop species, including legumes, fiber, and energy crops. Furthermore, my research endeavors to unravel the intricacies of 'Targeted Quantitative Variations' induced in plant genomes using genome editing technologies. This exploration aims to decode the molecular mechanisms governing abiotic stress tolerances and disease resistance traits in crops, paving the way for resilient and high-performing agricultural ecosystems.

Research subjects

- Discover novel traits to improve disease resistance, nutrient uptake, and seed composition.
- Develop high-throughput technologies to improve genetic transformation and gene-editing platforms in recalcitrant crop species.

Major discoveries/ achievements

- We uncovered the novel accessions, haplotypes, allelic diversity, and the potential candidate genes underpinning the mineral nutrient accumulation in soybean.
- Develop novel methods to induced transgenic and gene-edited de novo shoots without tissue culture.
- Develop a platform to isolate high-quality nuclei from various tissue types for single cell genomics platform.

Relevant publications

- Dhingra A., Shinde S., D'Agostino L., Devkar V., Shinde H., Patil G.B. (2024). **Identification of Novel Germplasm and Genetic Loci for Enhancing Mineral Element Uptake in Soybean.** Environmental and Experimental Botany. Vol. 219, 105643.
- Nwoko L., Ojha A.K., Devkar V., Patil G.B. (2023). **An Improved Method for Protoplast Isolation and Gene-Editing from Soybean Root, Callus and Transgenic Hairy-Roots.** J Plant Biol Crop Res.; 6(2): 1088.
- D'Agostino L.W., Yong-Villalobos L., Herrera-Estrella L., Patil G.B. (2023). **Development of High-Quality Nuclei Isolation to Study Plant Root-Microbe Interaction for Single-Nuclei Transcriptomic Sequencing in Soybean.** Plants. 2023 12(13):2466.
- Ojha, A., Zhang, F., Patil, G. B. (2023). **Genome editing and chromosome engineering in plants.** The Plant Genome, 16(2) e20352.



OPENING OF TWO NEW LABORATORIES

IGCAST is proud to have two world-renowned researchers joining the team, bringing their expertise to contribute to our cutting-edge research.

LIU LAB

Global climate change, caused mainly by the rising CO₂ concentration in the Earth's atmosphere, presents challenges to agricultural production systems. Plants are linchpins in global carbon cycling, with a unique capacity to capture CO₂ via photosynthesis.



Application of gene-editing for crop improvement has been slow, due to inefficient methods of reagent delivery and the reliance on tissue culture to create gene-edited plants. Our research program is dedicated to advancing high-throughput genome editing and synthetic biology technologies. By leveraging these innovative approaches, we aim to redesign photosynthesis to contribute to the sustainable fulfillment of global food, fiber, bioenergy, and carbon sequestration needs in response to the climate crisis.

Research subjects

- Development of cutting-edge genome editing and synthetic biology technologies.
- Establishment of transgene-free, tissue culture-independent genome editing methods in crop plants.
- Engineering photosynthesis for improving water use efficiency and abiotic stress tolerances in plants.
- Investigation into the molecular and cellular mechanisms that underlie plant responses to abiotic stresses.

JANGA LAB

Our primary focus is on investigating gene functions to gain a deeper understanding of their underlying mechanisms. I intend to apply this knowledge to enhance crop plants by boosting their tolerance to both abiotic and biotic stressors, increasing overall yields, and improving nutritional value. Within my research program, I plan to leverage advanced genomics and swift gene characterization methods, such as developing stable transgenic plants through *Agrobacterium* or biolistic-mediated transformation for gene overexpression. Simultaneously, I will utilize genome editing techniques such as CRISPR/Cas9, base editing, or prime editing to create knockout lines and achieve precise modifications. Additionally, I aim to apply developmental regulatory genes to enhance crop transformation frequencies in various crops, including cotton, sorghum, soybean, maize and, peanut. The bottleneck issue of plant transformation poses a significant challenge in crop genetic research. To address this, I am keen on offering collaborative plant transformation services. This collaborative effort aims to produce stable transgenic lines, contributing to an enhanced understanding of crop genetics and the progression of crop improvement programs.

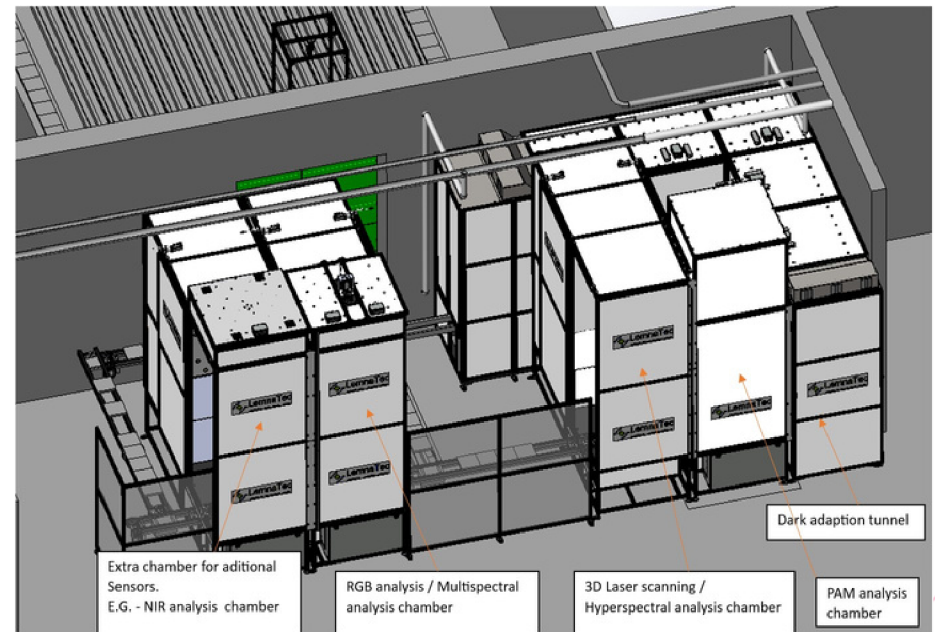


PHYTOTRON NEWS

The second phenotyping system recently acquired for the Phytotron facility is currently being received in installments. The new, customized LemnaTec system will revolutionize crop abiotic stress tolerance research at Texas Tech. While a date has not been set, installation of the new equipment is expected to begin in 2024. In anticipation of the pending installation of the new phenotyping system, greenhouse number 3 has been dismantled, and the benches removed. The door to greenhouse number 3 will be demolished, and a larger opening will be added to the space between the greenhouse and the headhouse. A high-speed, automatic door will replace the old door. The new imaging cabinet will be installed inside the headhouse, and conveyors with pot holders will be installed inside the greenhouse. New experiments can then be loaded into the system from inside the headhouse, and plants sent into the greenhouse along the conveyor system.

Hundreds of large crop plants, such as maize and cotton, or tens of thousands of small plants, such as *Arabidopsis thaliana* or winter wheat, will be automatically scheduled for watering, weighing, and imaging. The new system is also designed to eliminate noise in data caused by microclimates within the greenhouse. Plants will be rotated in each position within the greenhouse so that each plant experiences similar microclimates throughout the experiment.

Phenotyping using the new and improved system will allow researchers to evaluate stress responses, non-destructively, in a continuous, seamless workflow. Imaging data will be collected using multispectral, hyperspectral, fluorescent, and RGB sensors. Automated watering, weighing, and imaging will also reduce accidental inconsistencies due to user errors. Using the data collected by the imaging system, fine differences among genotypes may be detected early in the experiment.





IGCAST SYMPOSIUM

The second annual symposium hosted by the IGCAST was a resounding success, with notable growth in all areas. The Dairy Barn provided a stunning backdrop for the event, which boasted a larger audience and the attendance of three esteemed guests, including Dr. James Umen, Joseph Varner Distinguished Investigator at the Donald Danforth Plant Science Center in St. Louis, Missouri, and a member of the Enterprise Rent-a-Car Institute for Renewable Fuels. Dr. Umen presented his groundbreaking research using *Chlamydomonas* algae to identify stress and growth-related genes in the green lineage. His presentation was received with great interest from the symposium attendees.

We were pleased to have Dr. Gloria Burow as a special guest at our event. She is a research geneticist who leads the Sorghum Genetics and Translational Genomics (GTG) group at USDA-ARS Lubbock. Dr. Burow is also a member of the Sorghum CRIS project at the Plant Stress and Germplasm Development Unit, Cropping Systems Research Laboratory, USDA. Her research is closely linked with the work carried out at the IGCAST to improve crops in Texas. She shared insightful findings of her research group during her presentation titled, "New Insights into Signaling Mechanisms in Sorghum."

We were also privileged to host Dr. Huazhong Shi's presentation, a Texas Tech University's Department of Chemistry & Biochemistry professor, who shared his insights on "Membrane Transporters in Plant Response to Salt and Heat Stress." Dr. Shi's presentation was instrumental in enhancing the interdisciplinary knowledge at IGCAST.

During the symposium, researchers from five laboratories at IGCAST shared their latest work. Dr. Abdelrahman Mostafa from the Tran Lab presented on "Unveiling Resilience: Integrative Analysis of Transcriptomes and Metabolomes for Enhancing Crop Stress Tolerance." Dr. Deepti Singh from the Jiao Lab spoke about "Metabolome-Scale Genome-Wide Association Studies Reveal Chemical Diversity and Genetic Control of Specialized Metabolites in Sorghum Grain." M.S. Alethia Brito, a Ph.D. student from the Lopez-Arredondo Lab, presented on "Bioactive Compounds with Pesticide Activities Derived from Aged Cultures of Green Microalgae."



IGCAST SYMPOSIUM



Later in the afternoon, M.S. Arjun Ojha Patil, a Ph.D. student from the Patil Lab, presented "Shoot At Site: An improved method for inducing de novo shoots without tissue culture." The final presentation was given by M.S. Moises Frausto, a Ph.D. student from the Herrera-Estrella Lab, on "Reprogramming plant root development and metabolism: Dealing with phosphorus starvation."

The symposium ended with a scientific poster exhibition and contest session, with winners announced in three categories: postdoctoral, doctoral students, and master's students.

Master student category

Touhidur Rahman Anik, First place.
Nasir Khan, Second place.
Paulina Martinez Irastorza, Third place.

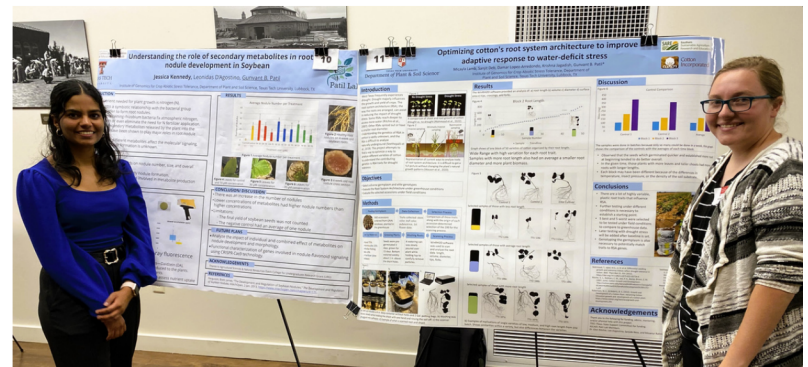
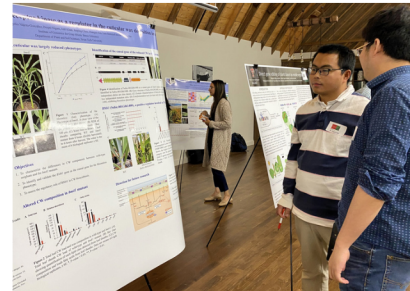
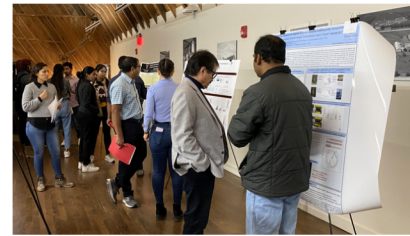
Ph.D. student category

Rogelio Najera-Gonzalez, First place.
Benjamin Perez, Second place.
Tania Kean Galeno and Pallavi, Third place.

Postdoc category

Ran Tian, First place.
Gabriela Cabrales Orona, Second place.
Kaushik Ghose, Third place.

The work accomplished by IGCAST was disseminated to the Texas Tech University community as well as to diverse businesses and institutions to seek collaborative efforts in support of agricultural production. This approach of sharing research discoveries presents a remarkable opening to cultivate pioneering initiatives that can optimize the agricultural industry and enhance our research endeavors.



Congratulation M.S. Category
TO THE WINNERS

Second place



Nasir Khan

First place



Touhidur Rahman Anik

third places



Paulina Martinez

IGCAST Symposium
 November 14th, 2023
 TEXAS TECH UNIVERSITY
 Institute of Genomics for
 Crop Abiotic Stress Tolerance



Congratulation Ph.D. Category
TO THE WINNERS

Second place



Benjamin Perez

First place



Rogelio Najera-Gonzalez

Two third places



Tania Kean Galeno
and Pallavi

IGCAST Symposium
 November 14th, 2023
 TEXAS TECH UNIVERSITY
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Congratulation Postdoc Category
TO THE WINNERS

Second place



Gabriela Cabrales

First place



Ran Tian

third places



Kaushik Ghose

IGCAST Symposium
 November 14th, 2023
 TEXAS TECH UNIVERSITY
 Institute of Genomics for
 Crop Abiotic Stress Tolerance



FUNDING

\$689,070 USD

Herrera-Estrella Lab Grants

- USDA-NIFA
- NSF
- Cotton Incorporated
- United Sorghum Checkoff

Lopez-Arredondo Lab Grants

- Texas Tech Start-up
- USDA-NIFA
- United Soybean Board
- Texas State Support Committee
- Cotton Incorporated
- USDA-ARS
- United Sorghum Checkoff
- TSCC

Jiao Lab Grants

- Texas Tech Start-up
- USDA-ARS
- USDA NIFA
- United Sorghum Checkoff

Patil Lab Grants

- United Soybean Board
- USDA-NIFA
- FFAR
- BASF-TTU Project Revolution
- Southern Soybean Research Program
- Texas State Support Committee

Tran Lab Grants

- Texas Tech Start-up
- BASF-TTU Project Revolution
- United Soybean Board
- The Texas State Support Committee
- Cotton Incorporated
- United Arab Emirates University Program for Advanced Research

2023

USDA-NIFA

2023

Cotton Inc.

2023

United
Soybean
Board

2023

Texas State
Support
Committee

2024

USDA-NIFA

2024

Cotton Inc.

2024

USDA-ARS

2024

United
Soybean
Board

2024

BASF

2024

National
Science
Foundation

2024

United
Sorghum
Checkoff
Program

2024

Southern
Soybean
Research
Program

*Fiscal year report



PUBLICATIONS IN PEER-REVIEWED JOURNALS

From 2019 to date, IGCAS has published more than 100 articles in scientific journals of international prestige. Each article is put under scrutiny so that together (institutions, journals, and researchers), we generate new knowledge that in the future will be instrumental in understanding different topics. It is a constant work that, in many cases, takes years to achieve a publication.

In 2023, IGCAS managed to have 29 publications and collaborate with different Institutes and Universities from different countries, such as China, India, Israel, Mexico, Thailand, and Vietnam. These articles were published in recognized scientific journals such as BMC Genomics, Communications Biology, Biology, Plants, Plant Methods, Plant Physiology and Biochemistry, and Plant Biotechnology, among others.

Thanks to those efforts, Dr. Son Tran and Herrera-Estrella have been recognized as Highly Cited Researchers for the year 2023 by Clarivate. They are being recognized for their high-quality scientific research achievements and outstanding contributions to their professional fields. Tran has been tapped for the list for six consecutive years between 2018-2023 and 2016, while Herrera-Estrella has been recognized in 2022 and 2023. Their impactful papers are among the top 1 percent in the citation distribution of one or more of the 21 fields analyzed in the "Essential Science Indicators", distinguishing them as hugely influential among their peers.



RECOGNITIONS

Lam-Son Phan Tran

The Texas Tech Parents Association's Barney E. Rushing, Jr., Faculty Distinguished Research Award – STEM, 2023.

Elected Fellow of The National Academy of Sciences, India (effective 01-January-2023).



Gunvant Patil

2023- Global Exchange Research Seed Award, TTU International Affairs.

International Award for Environmental Botany - Eurasian Academy of Environmental Sciences (EAES).

Chien Ha

Crops are of immense importance not just in Texas but worldwide, given the many challenges they face. The IGCAS, as part of the effort Texas Tech is making on that topic, has expanded this year, with three professors being named members. In March, Dr. Chien Ha, an internationally recognized expert in biotechnology, was appointed as a research assistant professor at Son Trans Lab.



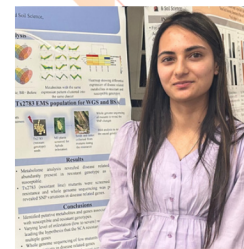
Mylea Lovell

Mylea IGCAS Phytotron Manager was named Standout faculty and staff member honored for service and support of Texas Tech University's Davis College of Agricultural Sciences & Natural Resources.



Pallavi

Ph.D. A Student, from Jiao Lab, won third place in the Davis College graduate research poster contest, with the topic "Understanding the Molecular Mechanism of Sugarcane Aphid Resistance in Sorghum."



Lois Nwoko

Lois won third in the Graduate Students Oral Presentation in the 2023 Plant & Soil Science Student Research Symposium.



Micayla Lamb

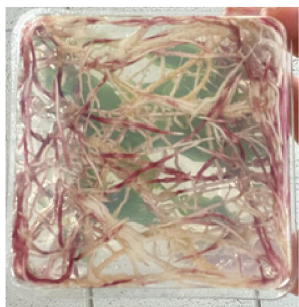
Graduate Student, from Patil Lab received the Sustainable Agriculture Research and Education (SARE) Graduate Student Grant' for the project, "Development of active root system architecture of upland cotton for improved sub-surface water uptake during drought conditions."



RECOGNITIONS

Arjun Ojha Kshetry from Patil Lab, and Benjamin Pérez Sánchez from Herrera-Estrella Lab receiving the NSF Workshop scholarship to attend the Plant Transformation and Gene Editing workshop at the Crop Innovation Center (University of Wisconsin).

Arjun shares his experience at the workshop. "It was an amazing opportunity to be awarded a fellowship from the National Science Foundation (NSF) to attend a workshop on "Fundamentals & Practice of Agrobacterium-mediated Plant Transformation" at the Wisconsin Crop Innovation Center, University of Wisconsin-Madison in August 2023. The lectures from experts hands-on training, and demonstrations were very informative. I was fortunate to get hands-on training from Dr. Stanton B. Gelvin (Purdue University), who has been working with Agrobacterium for more than 45 years. His lecture was very insightful and informative. I have learned a lot. This workshop was truly empowering and has changed my perception of how important the basics of biology and *Agrobacterium*-mediated plant transformation are. I have learned that, while we are planning for an ambitious project, careful attention must be taken to the basics, for instance, proper handling of the plant material and or the *Agrobacterium* that minimizes the failures in research. I have had the opportunity to meet and connect people with diverse interests and positions with a common goal of improving crops with the application of modern plant biotechnology tools. It is an amazing experience that everyone should attend."



VISITING PROFESSOR DR. HENRY T. NGUYEN

As part of the different collaborations that Texas Tech and IGCAT have in place, we had the opportunity to have Dr. Henry T. Nguyen Distinguished Professor of Plant Genetics.

Founding Director, of the National Center for Soybean Biotechnology, University of Missouri, as a visiting professor in May. He gave the talk "The Greenest Revolution: A Reflection and Future Perspective." He also shared his experiences and knowledge with students and professors. It was a great opportunity to learn more about the work that Dr. Nguyen does.





2023 PLANT & SOIL SCIENCE STUDENT RESEARCH SYMPOSIUM

The 2023 Plant & Soil Science Student Research Symposium was held on April 19th with the participation of IGCAST members in the poster session and oral presentations. This annual symposium provides a valuable platform for students at all stages of their programs to showcase their research and receive constructive feedback from peers, faculty, and staff. In this edition, nine IGCAST researchers presented their work through posters, which was a commendable effort on their part. Overall, the symposium was a great opportunity for the participants to gain insights and recognition for their research work.

Adil Khan, Ph.D. student

Transcriptome analysis of high-temperature stress in sorghum seed development.

Alethia Brito-Bello, Ph.D. student

Green microalgae as a source of biopesticides to improve agricultural practices.

Arjun Ojha Kshetry, Ph.D. student

Tissue-culture-free genetic transformation and gene-editing in plants
Deciphering the dynamics of sugarcane aphid resistance mechanism in sorghum.

Pallavi, Ph.D. student

Development of a chemical switch to improve phosphorus assimilation and usage efficiency in plants.

Hector-Rogelio Najera-Gonzalez, Ph.D. student

Development of a chemical switch to improve phosphorus assimilation and usage efficiency in plants.

Leonidas D'Agostino, Ph.D. student

Developing single nucleus transcriptome technology for the study of soybean root nodulation.

Sanjida Keya, Ph.D. student

Exogenous salicylic acid helps to mitigate saline stress in cotton.

Zhiyuan Liu, Ph.D. student

Develop PACE markers for waxy-sorghum Marker-Assisted Selection.

Mylea Lovell, Ph.D. student

Synthetic tetraploidization as a strategy to face abiotic stresses in crops.

Likewise, **Lois Nwoko** got third place at the 2023 Plant & Soil Science Student Research Symposium with her research "An improved method for protoplast isolation and gene-editing from soybean root, callus, and transgenic hairy-roots" with an oral presentation.



ENGAGEMENT AND OUTREACH PROGRAMS

Our efforts have been extended over the past year to align with Texas Tech's engagement and outreach programs. We have also participated in the International Day of Women and Girls in Science on February 11th aimed at encouraging women to pursue scientific careers. As a research organization, IGCAST is proud to have many female collaborators who have expressed their passion and concerns regarding science, and we are committed to promoting gender equity in STEM.

As they have been doing for the last three years, the Lopez-Arredondo lab visited Lubbock Copper Central Elementary in Lubbock to have experimental sessions with 23 kids from the first grade of the Dual Language Program (English-Spanish) offered by the school, of which half were of Hispanic origin. The demonstrations aimed to show kids photosynthetic organisms (plants and microalgae), how they grow, what they need to grow, and that they are composed of units we call cells. Kids were amazed to observe roots, root hairs, onion cells, and swimming *Chlamydomonas* cells under a microscope.

Also, we have produced more research videos to share with students and researchers about the protocols, equipment, and strategies we use to approach different biological questions.

In 2023, the first Scientific Image Competition was held at IGCAST. The M.S. Rogelio Najera obtained first place, Benjamin Perez second place, and Carlos Barragan third place. With these images, a collaboration project is being carried out with the Faculty of Arts and Design of the Autonomous University of Mexico to link art and science as a means of disseminating the research carried out at IGCAST.

During the recent Family STEM night at TTU, which was held on November 13th, we had the pleasure of sharing our knowledge with families regarding the mechanisms of water transportation in plants. Through hands-on activities, we conveyed the diligent efforts that plants make in this process and the significance of multidisciplinary agriculture topics. This experience allowed us to educate attendees on the complexities of plant biology and to inspire a deeper understanding of the interdependence of various scientific disciplines.



IGCAST MEMBERS 2023



Herrera-Estrella Lab

Luis Herrera-Estrella (Professor)
Rozalynne Samira (Assistant Professor)
Gerardo Alejo Jacuinde (Postdoc)
Carlos Barragan Rosillo (Postdoc)
Gabriela Cabrales Orona (Postdoc)
Dolores Gutierrez-Alanis (Postdoc)
Shumayla (Postdoc)
Lenin Yong-Villalobos (Postdoc)
Moises Frausto (Ph.D. Student)
Tania Kean Galeno (Ph.D. Student)
Hector Najera Gonzales (Ph.D. Student)
Lois Nwoko (Ph.D. student)
Benjamin Perez-Sanchez (Ph.D. Student)
Pablo Silva Villatoro (Ph.D. Student)

Patil Lab

Gunvant Patil (Assistant Professor)
Vikas Devkar (Research Scientist)
Kaushik Gosh (Research Scientist)
Malleshm Bulle (Postdoc)
Anuradha Dhingra (Postdoc)
Gaurav Raturi (Postdoc)
Leonidas D'Agostino (Ph.D. student)
Arjun Ojha (Ph.D. student)
Pallavi (Ph.D. Student)
Durgeshwari Prabhakar Gadpayale (Research Intern)
Vaishnavi Deshmukh (Student assistant)
Rangoli Dhatrak (Student assistant)
Lee Fischel (Student assistant)
Patil Gourav (Student assistant)
Ethan Myers (Student assistant)
Johnathan Salter (Student assistant)
Jessica Kennedy (Student)

Tran Lab

Lam-Son Phan Tran (Professor)
Chien Ha (Research Assistant Professor)
Mostafa Abdelrahman (Research Scientist)
Aarti Gupta (Research Scientist)
Arifur Khan (Research Scientist)
Huong Nguyen (Visiting Scientist)
Vy P Le (Ph.D. student)
Md Mezanur Rahman (Ph.D. student)
Sanjida Sultana Keya (Ph.D. student)
Touhidur Rahman Anik (Graduate Research Assistant)
Mai Dao (Student assistant)
Anket Sharma (Student)

Jiao Lab

Yinping Jiao (Assistant Professor)
Deepti Singh (Postdoc)
Ran Tian (Postdoc)
Adil Khan (Ph.D. student)
Zhiyuan Liu (Ph.D. student)
Pallavi (Ph.D. student)
Shejal Soumen (Ph.D. student)
Nasir Khan (M.S. student)
Kuljeet Kaur (Student assistant)

Lopez-Arredondo Lab

Damar Lopez-Arredondo (Assistant Professor)
Ricardo Chavez Montes (Postdoc)
Jonathan Ojeda-Rivera (Postdoc)
Francisco Perez-Zavala (Postdoc)
Alethia Alejandra Brito Bello (Ph.D. Student)
Claudio Barrera Duarte (Ph.D. Student)
Valeria Flores Tinoco (Ph.D. Student)
Vy Le Phuong (Ph.D. Student)
Matteo Tosoni (Ph.D. Student)
Himanshu Yadav (Ph.D. Student)
Paulina Martinez Irastorza (M.S. Student)
Singh Gagan Deep (Student assistant)
Patel Hetvi Alpeshkumar (Student assistant)
Gourav Patil (Student assistant)
Ashish Ramani (Student assistant)

Janga Lab

Madhusudhana Janga (Professor)
Sachin (Research Aide)

Staff

Lori Walraven (Business Manager)
Deanna Galvan (Lead Administrator)
Gabriela Castillo-Estrada (Lab Manager LHE/DLLA)
Gabriela Prieto Soriano (Multimedia Specialists)
Mylea Lovell (Phytotron Manager)
Ava Hale (Phytotron Student Assistant)

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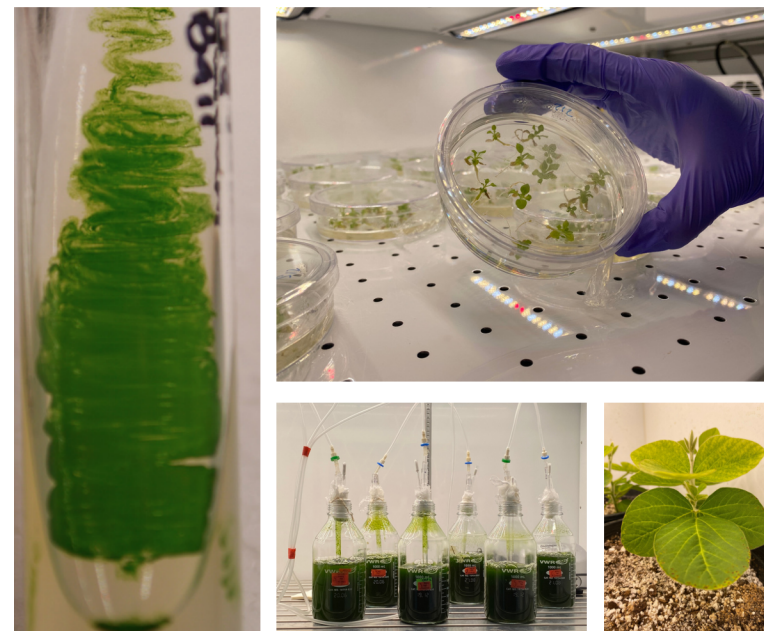
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