



TEXAS TECH UNIVERSITY

Institute of Genomics for  
Crop Abiotic Stress Tolerance™

20  
22

NEWS  
LETTER



Texas Tech University, Institute of Genomics for Crop Abiotic Stress Tolerance.  
1006 Canton Ave, Lubbock, TX 79409



806.742.3417



IGCAST.info@ttu.edu



[www.depts.ttu.edu/IGCAST/](http://www.depts.ttu.edu/IGCAST/)



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## Message from the IGCAT Director

### Dr. Luis Herrera-Estrella

Often when facing a problem affecting food production or health, people say “scientists must be doing something to solve the problem”, especially when it comes to big issues like climate change. At the Institute of Genomics for Crop Abiotic Stress Tolerance (IGCAT), we have been doing it. IGCAT 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 main research mission of IGCAT is to study the genetic and physiological mechanisms that allow plants to tolerate, avoid and/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, IGCAT had only two faculty and two students. Four years later, the IGCAT team grew to 5 faculty, 10 undergraduate students, 25 graduate students, and 10 postdoctoral fellows by the end of 2022. IGCAT currently has five research teams, led by Drs. Damar López-Arredondo, Yinping Jiao, Gunvant Patil, Son Tran, and Luis Herrera-Estrella, regularly publish in the most prestigious international scientific research journals. As part of the strategic program to promote research excellence at Texas Tech, we expect to have three additional faculty in 2023.

The rapid growth of IGCAT’s publications in peer-reviewed journals (from two in 2019 to 42 in 2022) and funding (which climbed sharply from \$100,000 in 2019 to \$2.56 million in 2022 with more than 60% coming from federal agencies) illustrate the successful development of our institute. Moreover, in the first three months of 2023, we already secured funding totaling more than \$3 million.

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 microalgae such as *Chlorella* sp.
- Signaling molecules and gene regulatory and metabolic networks governing responses and tolerance of *Arabidopsis thaliana* and important crops, including cotton, soybean, sorghum, and common bean to drought, heat, and salinity, as well as their combined stress conditions.
- Strategies for carbon sequestration in plants and microalgae.

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

Every year, we will summarize 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, as well as the honors and awards that students, postdocs, and faculty have received.





## Herrera-Estrella Lab 2022

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. Crop yields are heavily influenced by environmental factors, including the availability of water and nutrients, temperatures, salinity, and soil physical properties. 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 at offering a solution to this problem by providing an advanced analysis of the genomic and metabolic networks that control the response of plants to abiotic stress. By combining our computational insights with experimental data, we gain a deeper understanding of plant biology to develop new strategies for crop improvement. Our team is using molecular and evolutionary approaches to investigate the physiology and genomic basis of drought tolerance as well as nutrient uptake and assimilation capacity in plants.



### Research subjects

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

### Major discoveries

- Development of an in vitro system to assess root penetration capacity in plants and the discovery of QTL associated with high root penetration capacity.
- Development of methods and markers to study desiccation tolerance in plants and their use to study the transcriptomic response of *Selaginella* species to dehydration.
- Characterization of changes in chromatin accessibility in the adaptation of plants to low phosphate availability.

### Most relevant publications

- Alejo-Jacuinde, et al. (2022). Viability markers for determination of desiccation tolerance and critical stages during dehydration in *Selaginella* species. *Journal of Experimental Botany* 73:3898–3912.
- Bello, et al. (2022). *ROOT PENETRATION INDEX 3*, a major quantitative trait locus associated with root system penetrability in *Arabidopsis*. *Journal of Experimental Botany* 73:4716–4732.
- Zhang, et al. (2022). High-temperature adaptation of an *OsNRT2.3* allele is thermoregulated by small RNAs. *Science Advances* 8:47.

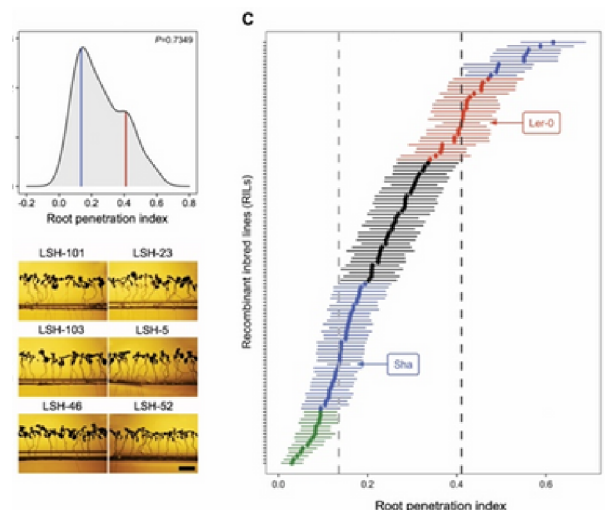


Figure: Distribution of the root penetration indexes (RPIs) in the Ler-0 × Sha population.

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

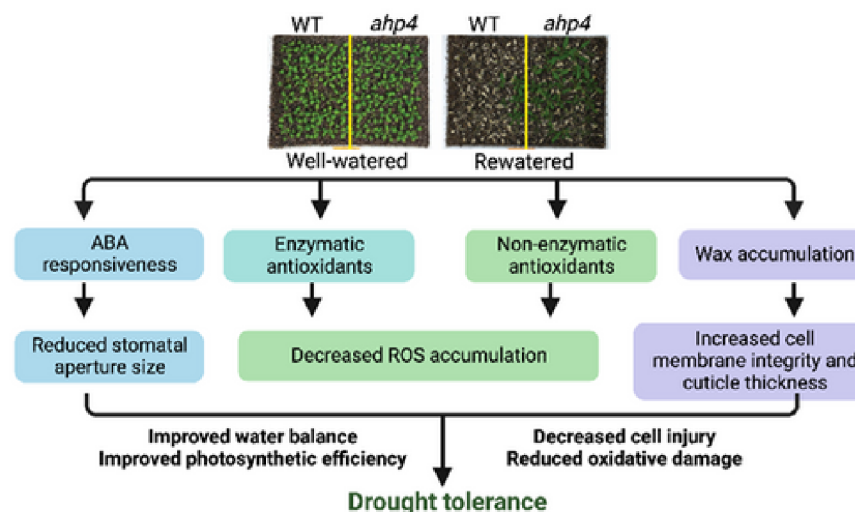
- Molecular elucidation of hormonal regulatory networks in plant responses to environmental stresses.
- Roles of signaling molecules in environmental stress adaptation.
- Functional genomics of food crops for improvement of crop productivity in adverse conditions.

### Major discoveries

- We found that the cytokinin HISTIDINE PHOSPHOTRANSFER AHP4 plays an important role in plant drought adaptation as a negative regulator.
- We provided evidence that simultaneous deficiency of phosphate and nitrate generated a unique profile of metabolic changes.
- We demonstrated that the KARRIKIN UPREGULATED F-BOX 1 KUF1 acts as a regulator of drought response.

### Most relevant publications

- Ha, et al. (2022). The histidine phosphotransfer AHP4 plays a negative role in *Arabidopsis* plant response to drought. *Plant J* 111:1732-52.
- Nasr Esfahani, et al. (2022). Differential metabolic rearrangements in the roots and leaves of *Cicer arietinum* caused by single or double nitrate and/or phosphate deficiencies. *Plant J* 111:1643-59.
- Tian, et al. (2022). KARRIKIN UPREGULATED F-BOX 1 negatively regulates drought tolerance in *Arabidopsis*. *Plant Physiol* 190:2671-87.



Roles of AHP4 in response of *Arabidopsis thaliana* to drought. Under drought, the expression of AHP4 is repressed, affecting the action of the cytokinin signaling. Downregulation of AHP4 results in changes in various physiological and biochemical processes, thereby improved drought tolerance.

## Lopez-Arredondo Lab 2022

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 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 effect, and design strategies to enhance their production via synthetic biology strategies.



### Research subjects

- Study of plant and microalgae responses to abiotic and biotic stresses.
- Elucidation and rewiring of regulatory networks controlling stress responses.
- Plant and microalgae molecular improvement.
- Discovery of microalgae metabolites with herbicidal and nematocidal effects.
- Domestication of microalgae to optimize production of biofuels and bioproducts.

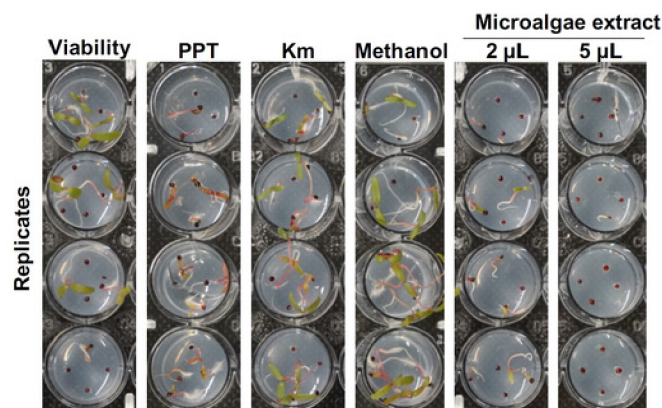
### Major discoveries

- Genes with the potential to improve *Fusarium* and nematode resistance in cotton were identified.
- Genome sequencing and annotation of Pima-S6, a *Fusarium* race 4-resistant cotton genotype.
- Gene regulatory networks of lipid production in response to nitrogen and phosphorus starvation in microalgae *Chlorella* were identified.
- Microalgae metabolites with herbicidal and nematocidal effects were identified.

### Most relevant publications

- Ojeda-Rivera, et al. (2022). Root-Knot Nematode resistance in *Gossypium hirsutum* determined by a constitutive defense-response transcriptional program avoiding a fitness penalty. *Front Plant Sci* 13:858313.
- Han, et al. (2022). Genome-wide chromatin accessibility analysis unveils open chromatin convergent evolution during polyploidization in cotton *PNAS* 119:44.

Herbicidal effect of microalgae extracts on a glyphosate-resistant Palmer amaranth ecotype. Controls: PPT, phosphinotricin (15 mg/L); Km, kanamycin (50 µg/mL); methanol (5 µL).







## Jiao Lab 2022

Identify key genetic alleles for improving sorghum grain nutrition. Sorghum is a highly drought and heat-tolerant ancient grain and gluten-free crop having food, feed, forage, fuel, sugar, and alcoholic beverage end uses. It is a key subsistence food and feed crop in dryland agriculture throughout the semi-arid tropics of Asia, Africa, and South America where it is cultivated in areas with limited water availability that are not suitable for maize. However, despite these intrinsic benefits, grain sorghum utilization is limited by several aspects of its grain quality, including low levels of lysine, low protein content and/or low protein digestibility, low starch digestibility, and small grain size. Improving grain quality is a major goal for sorghum breeding. Genetic knowledge is the foundation for applying molecular technologies to accelerate breeding. Currently, there is a knowledge gap in the genetics regulating the synthesis of high-value, nutritional biomolecules in sorghum.



### Research subjects

- Understand the sorghum seed development on transcriptomic and metabolomic levels.
- Identify key genes involved in the biosynthesis of starch, protein, and oil in sorghum seed.
- Develop molecular markers to facilitate sorghum grain quality breeding.

### Major discoveries

- The transcriptome profiling of the sorghum seed development under high temperatures demonstrated that heat stress at early seed development stages could cause server damage to sorghum production.
- User-friendly molecular markers were developed to facilitate waxy sorghum breeding.
- New mutant germplasms with high protein and lysine content have been identified for molecular genetics study and breeding.
- 1,000 sorghum mutants were sequenced for gene function studies.

### Most relevant publications

- Gladman, et al. (2022). SorghumBase: a web-based portal for sorghum genetic information and community advancement. *Planta* 255: 35.



Top: The process of sorghum seed development; Below left: A mutant line with reduced amylose content and increase total protein; Below right: Impact of HS on seed size and panicle architecture. After successful pollination, plants were exposed to HS after 2,3,4,7,10,14,18,22 dpa and maintained for 3 days.





## Patil Lab 2022

### Molecular crop Improvement.

Genome engineering has tremendous potential in crop improvement; and, using this technology, we can precisely turn ON, turn OFF or fine-tune the expression of targeted gene/s and improve desirable traits and plant fitness. Our lab at IGCAS, TTU integrates genome engineering and genomics tools to (1) discover novel traits to improve disease resistance, nutrient uptake, and seed composition and (2) develop high-throughput technologies to improve genetic transformation and gene-editing platforms in recalcitrant crop species.



### Research subjects

- Understanding nutrient uptake and molecular interaction between roots and beneficial microorganisms.
- Development of a robust regeneration and transformation system in crops.
- Next generation soybeans with durable resistance to multiple soybean cyst. nematode (SCN) races through genome engineering.

### Major discoveries

- We identified novel soybean germplasm with improved resistance to soybean cyst nematodes.
- We discovered and characterized novel nutrient transport genes involved in water stress tolerance in soybean using advanced gene-editing technology.
- We developed and improved methods for protoplast isolation and gene-editing.

### Most relevant publications

- Patil, et al. Protoplast isolation, transfection, and gene editing for soybean (*Glycine max*). Protoplast technology: methods and protocols. (2022). New York, NY: Springer US. 173-186.
- Bhardwaj, et al. Advances and applicability of genotyping technologies in cotton improvement. (2022). Genotyping by Sequencing for Crop Improvement. 20:250-69.
- Bayer, et al. Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. (2022). The Plant genome 15:e20109.

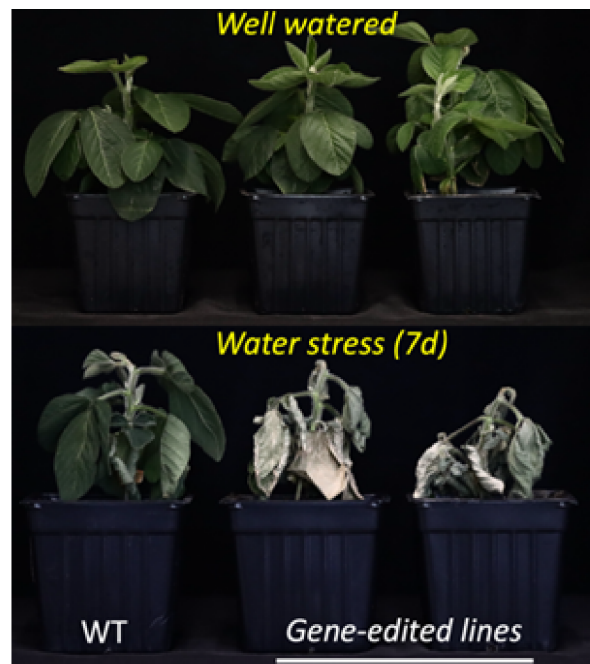


Figure: CRISPR/Cas9 gene-editing of a key gene involved in nutrient/water uptake

## Publications in Peer-reviewed Journals

Our publications are the best way to communicate our discoveries and technological developments to the scientists and public at the national and international levels. High-quality research reported in publications is the magic key to opening doors for collaborations to enhance our contribution to scientific development and offer solutions to societal problems.

We are proud to announce that our productivity increased from 2 publications in 2019 to 42 in 2022, and a total of 89 publications in the past three years. In 2022, we doubled the number of articles published in prestigious magazines, such as PNAS (Proceedings of the National Academy of Science of the United States of America), Science Advances, Plant Physiology, Plant Journal, Environmental Pollution, Journal of Experimental Botany, Plant & Cell Physiology, Environmental and Experimental Botany, Trends in Plants Science among others.

## Honors and Distinctions

The dedicated work of the faculty, students, and staff is reflected in the distinction that Dr. Luis Herrera-Estrella and Dr. Son Tran received in 2022 as members of the 0.1% most highly cited scientists in the world according to SCOPUS. We invite you to review all the articles published to date by IGCAT members at our website:

<https://www.depts.ttu.edu/igcast/Research/Publications.php>



Congratulations on the awards  
**Highly Cited Researchers**  
top 1% most highly cited researchers in the world  
by Clarivate Analytics

2022

*Category Cross-field*  
**Dr. Luis Herrera-Estrella**

*Category Plant and Animal Science*  
**Dr. Tran Lam-Son Phan**

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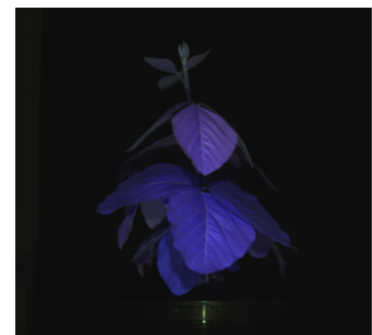
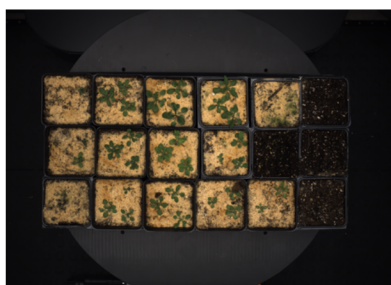
In the winter of 2021, a new phenotyping cabinet was installed in the Phytotron. The PhenoAlxpert HTC is a custom-made imaging system designed and installed by LemnaTec. It boasts five sensors allowing our researchers to collect detailed data on up to 216 small plants in a single run. Two sensors collect hyperspectral images, two sensors collect RGB images and the fifth sensor collects PAM fluorescent images. Hyperspectral and RGB images can be taken from both the top and side view of the plant. The system also allows for degree by degree rotation of the plant resulting in RGB and hyperspectral 3D imaging. Current methods of analyzing RGB and hyperspectral imaging provides pixel by pixel comparisons between plants' size, color, shapes, and reflectance. The images collected by the PAM sensor can be used to compare photosynthetic activities. This information can help researchers differentiate between plant traits, or phenotypes, at finer scale than is possible with the human eye. Imaging analysis can detect early responses to stresses such as drought and disease. Furthermore, unlike traditional chemical analyses, this method of phenotyping does not harm the plant; and, researchers can continue growing the selected plants to collect seeds.

Coming soon in the winter of 2023-spring of 2024, a second phenotyping system will be installed in a Phytotron greenhouse. This new custom LemnaTec system will include the sensors used in the PhenoAlxpert HTC, plus multispectral imaging capabilities. This state-of-the-art system will carry up to 18,000 small plants on a conveyor system which will automatically move from the greenhouse through the imaging cabinet. Research plants will also be moved throughout the greenhouse to automated weighing, fertilizing, and watering stations. This new design will allow continuous imaging of a large number of experiments. It will also accommodate larger plants than the current cabinet style imaging system. Both systems will improve and value to current and future research at the IGCAS Phytotron.

Plant imaging options  
 RGB format  
 Hyperspectral  
 PAM Fluorescence



PhenoAlxpert HTC





## IGCAST Symposium

On December 7th, the first IGCAST Symposium was held with the participation of invited speakers from the Plant and Soil Science and Biological Sciences Departments of TTU. Our guest speakers presented an overview of their work:

- Dr. Hong Zhang presented an exciting talk about different strategies to enhance abiotic stress tolerance entitled “Aiming at doubling crop yield for West Texas”.
- Dr. Jyotsna Sharma gave a wonderful overview of the interaction between microbes and plants under the title “Ecological niches of rare plants: heterogeneity and specificity across geographic scales”.
- Dr. Zhixin Xie, presented an overview of the fascinating world of small RNAs in plants at our symposium with an interesting talk entitled “the birth, death, and evolutionary dynamic features of plant miRNAs”
- Dr. Benildo de los Reyes talked about the mysterious world of epigenetics and the effects of epigenetic changes on plant performance with a talk entitled “Adaptive phenotypic novelties in plants: does the epigenome matter?”

In addition to the invited speakers to the IGCAST symposium, 7 graduate students and postdoctoral researchers made oral presentations highlighting their research progress, and 27 graduate students presented the advances of their research project in a lively poster session in the lobby of the ESBII. At the end of the symposium, a fruitful session to discuss possible avenues to strengthen inter- and intra-departmental collaborations was held. Given the success of the IGCAST symposium, it was decided to hold it as a yearly event with invited guest speakers from other universities.



**Symposium participants 2022**





## Graduate Students Poster Competitions

The Graduate Student Research Poster Competition of the Davis College of Agricultural Sciences & Natural Resources took place on September 29th, 2022. The jury was integrated by people from the industry, government representatives, and students from the Lubbock area. Posters presented by several IGCAS students were selected among the top three positions in different categories:

### Powering Our Future Category

- First Place. Matteo Tosoni: (DPSS Ph.D. student), from Lopez-Arredondo's group presented the poster "An integrated approach for developing a sustainable source of lipids using green microalgae".
- Third place. Jessica Kennedy: Windhoek, Namibia (DPSS B.Sc. student), Patil's group presented the poster "Understanding the role of secondary metabolites in root nodule development in soybean".

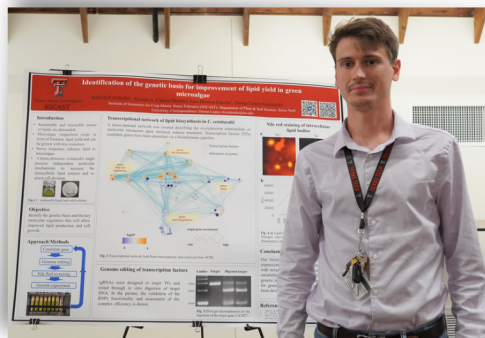
### Climate Resilience Category

- Second Place. Benjamin Perez Sanchez: Leon, Mexico (DPSS Ph.D. student), from Herrera-Estrella's group presented the poster "Direct gene editing of plants based on mobile vectors".

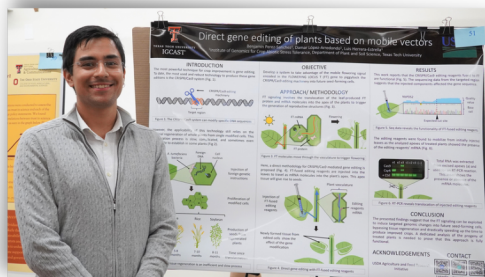
The 2022 Plant & Soil Science Student Research Symposium was held on April 18. This annual symposium provides an opportunity for students at all stages of their graduate programs to present their research and receive feedback from peers, faculty, staff, and external experts.

IGCAST students participated and were awarded as follows:

- Second Place. Oral Session, M.Sc. students Leonidas D'Agostino from the Patil and Herrera-Estrella's group presented the work entitled "Understanding the dynamics of soybean root nodule development using single-cell transcriptome technology".
- First Place. Poster presentation, M.Sc. student Chidinma Lois Nwoko from Dr. Patil's group presented the work entitled "Developing an efficient method for protoplast isolation, transfection, and gene editing from soybean roots".



**Matteo Tosoni**



**Benjamin Perez Sanchez**



**Judges**



## Congressmen Visit IGCAS

In 2022, IGCAS had several distinguished visitors. We want to make a special mention of the visit of Mr. John Boozman, Arkansas's senior U.S. senator, and Mr. Mike Thompson, representative of California's 5th Congressional District on September 23rd. During their visit to IGCAS, our distinguished visitors toured our research and greenhouse facilities. Dr. Luis Herrera-Estrella made a brief presentation on IGCAS research aimed at developing crops more resilient to adverse environmental conditions and their potential to contribute to more sustainable agriculture. Dr. Son Tran, Dr. Damar López-Arredondo, and Phytotron Manager Mylea C. Lovell showed the greenhouse, phenotyping, and plant transformation facilities to our distinguished visitors.





## The 2022 Plant & Soil Science Student Research Symposium

The 2022 Plant & Soil Science Student Research Symposium was held on April 18th. The annual symposium provides an opportunity for students at all stages of their programs to present their research and receive feedback from peers, faculty, staff, and external experts. ICGAST students participated and were awarded as follows:

- Second Place. Oral Session, Graduate Students Leonidas D'Agostino, MS student, Plant, and Soil Science. Title: Understanding the Dynamics of Soybean Root Nodule Development Using Single Cell Transcriptome Technology. Leonidas D'Agostino, Lenin Yong-Villalobos, Luis Herrera-Estrella and Gunvant B. Patil.
- First Place. Poster presentation Student/presenter: Chidinma Lois Nwoko, MS student, Plant, and Soil Science. Title: Development of an efficient method for protoplast isolation, transfection, and gene editing from soybean roots. Chidinma Lois Nwoko, Arjun Ojha, Vikas Devkar, Gunvant B. Patil.

## Funding

Since the creation of ICGAST, it has been possible to carry out multiple projects thanks to the support from different government agencies, institutions, companies, and universities. From 2018 to February 2023, ICGAST obtained a total of \$8.2 million in grant support. We thank the State of Texas, the National Science Foundation, Cotton Inc., NIFA, USDA/ARS, United Soybean Board, Kentucky Soybean Board, Southern Illinois, University of Missouri, Southern Soybean, University of Minnesota, SmithBucklin for joining the ICGAST and Texas Tech commitment to developing an internationally competitive research program to contribute to more sustainable agriculture in Texas and nationwide.

### Funding Support

#### Herrera-Estrella Lab Grants

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

#### Tran Lab Grants

- United Soybean Board
- Cotton Incorporated
- Project Revolution-TTU-BASF

#### Lopez-Arredondo Lab Grants

- USDA-AFRI
- Cotton Incorporated
- United Soybean Board
- USA-NIFA

#### Jiao Lab Grants

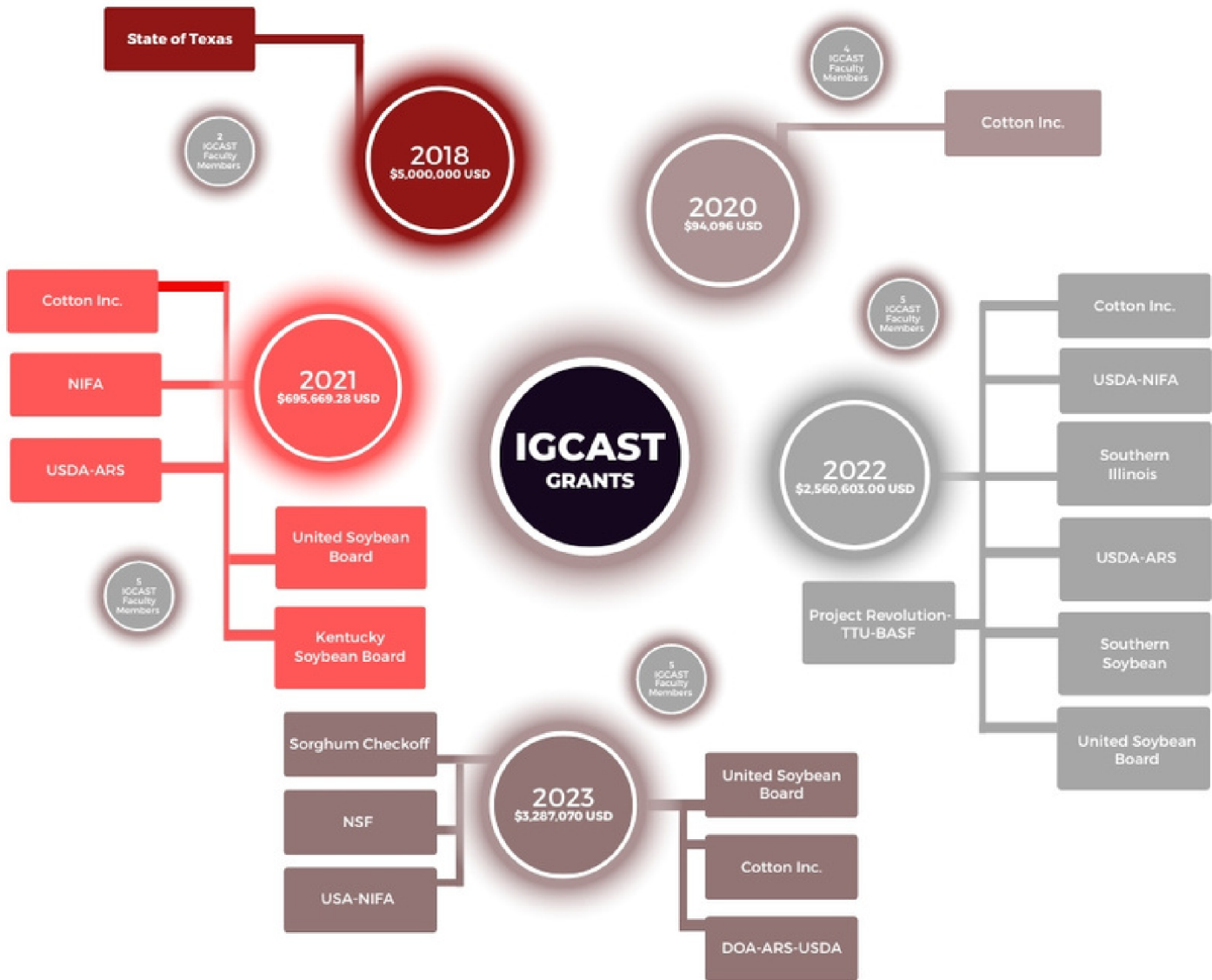
- USDA-ARS
- USDA-NIFA

#### Patil Lab Grants

- USDA-NIFA
- United Soybean Board
- FFAR-USB
- Southern Soybean Research Program
- Cotton Incorporated
- Project Revolution-TTU-BASF



## Funding

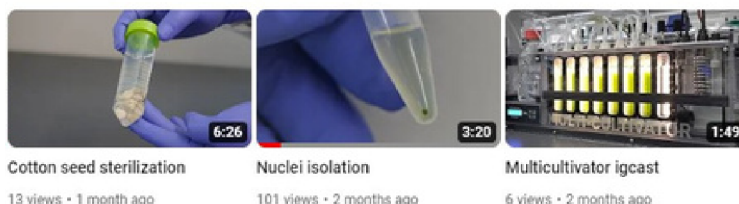






## IGCAST Public Engagement

As part of IGCAST's social commitment, scientific dissemination began through videos shared on the IGCAST YouTube channel, in which protocols and techniques are demonstrated with a detailed description of each step to facilitate other researchers implementing these protocols in their laboratories. We also produced a couple of videos to promote the study of science and sensitize future students about the increasing problems of environmental stresses in the era of climate change.



## IGCAST Members 2022

### Herrera-Estrella Lab

Luis Herrera-Estrella (Professor)  
Rozalynne Samira (Assistant Professor)  
Gerardo Alejo Jacuinde (Postdoc)  
Carlos Barragan Rosillo (Postdoc)  
Dolores Gutierrez-Alanis (Postdoc)  
Jonathan Ojeda Rivera (Postdoc)  
Lenin Yong-Villalobos (Postdoc)  
Moises Frausto (Ph.D. Student)  
Tania Kean Galeno (Ph.D. Student)  
Hector Najera Gonzales (Ph.D. Student)  
Benjamin Perez-Sanchez (Ph.D. Student)  
Paulina Martinez Irastorza (M.S. Student)

### Tran Lab

Lam-Son Phan Tran (Professor)  
Chien Ha (Research Scientist)  
Mohammad Mostofa (Research Scientist)  
Huong Nguyen (Postdoc)  
Ning Yuan (Postdoc)  
Md Mezanur Rahman (Ph.D. student)  
Sanjida Sultana Keya (Ph.D. student)  
Vy P Le (Ph.D. student)  
Touhidur Rahman Anik (M.S. student)

### Lopez-Arredondo Lab

Damar Lopez-Arredondo (Assistant Professor)  
Ricardo Chavez Montes (Postdoc)  
Claudio Barrera Duarte (Research Aide)  
Alethia Alejandra Brito Bello (Ph.D. Student)  
Vy Le Phuong (Ph.D. Student)  
Valeria Flores Tinoco (Ph.D. Student)  
Matteo Tosoni (Ph.D. Student)  
Himanshu Yadav (Ph.D. Student)

### Jiao Lab

Yinping Jiao (Assistant Professor)  
Ran Tian (Postdoc)  
Deepti Singh (Postdoc)  
Adil Khan (Ph.D. student)  
Zhiyuan Liu (Ph.D. student)  
Pallavi Fn (Ph.D. student)  
Nasir Khan (M.S. student)  
Inosha Wijewardene (Technician)

### Patil Lab

Gurvant Patil (Assistant Professor)  
Vikas Devkar (Research Scientist)  
Anuradha Dhingra (Postdoc)  
Mallesh Bulle (Postdoc)  
Kaushik Gosh (Research Scientist)  
Arjun Ojha (Ph.D. student)  
Leonidas D'Agostino (PhD student)  
Lois Nwoko (M.S. student)  
Pallavi (Ph.D. Student)

### Staff

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



## IGCAST Publication List 2022

- Abdelrahman, M., Mostofa, M. G., Tran, C. D., El-sayed, M., Li, W., Sulieman, S., Tanaka, M., Seki, M., & Tran, L.-S. P. (2022). The Karrikin receptor Karrikin Insensitive2 positively regulates heat stress tolerance in *Arabidopsis thaliana*. *Plant and Cell Physiology*. Vol.63, pages 1914–1926. <https://doi.org/10.1093/PCP/PCAC112>.
- Alejo-Jacuinde, G., & Herrera-Estrella, L. (2022). Exploring the high variability of vegetative desiccation tolerance in *Pteridophytes*. *Plants* 2022. Vol. 11, page 1222. <https://doi.org/10.3390/PLANTS11091222>.
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