Dale Bumpers National Rice Research Center
USDA-ARS
Stuttgart, Arkansas

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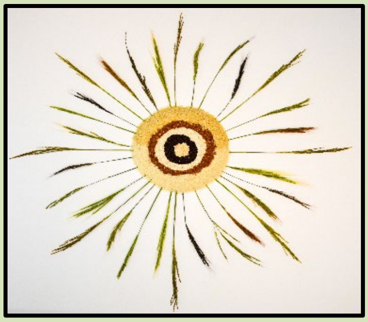

MONTHLY RESEARCH HIGHLIGHTS

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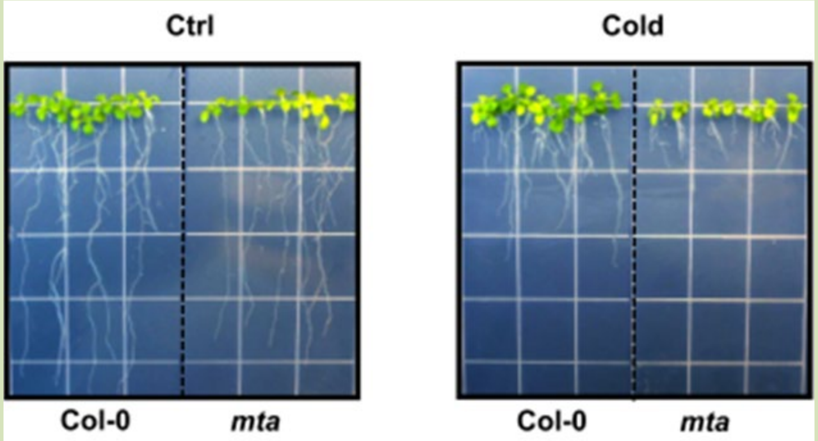
- **Recent Scientific Publications**

This addresses USDA-ARS Research Goal: Developing crop plants with enhanced tolerance to extreme temperatures.

Govindan, G.; Sharma, B.; Li, Y.; Armstrong, C. D.; Merum, P.; **Rohila, J. S.;** Gregory, B. D.; and Sunkar, R. 2022. mRNA N^6-methyladenosine is critical for cold tolerance in Arabidopsis. The Plant Journal. https://doi.org/10.1111/tpj.15872.

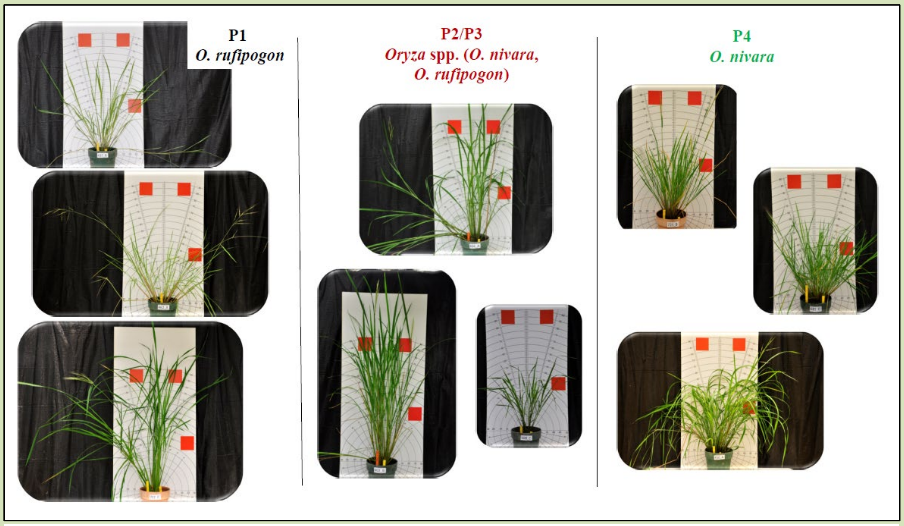
Through decades of research, it has been established that gaining abiotic stress tolerance in plants are highly complex in nature and often DNA alone was not able to explain many of the stress tolerance mechanisms fully. Recently, it was discovered that stress tolerance may not be as simple as just reading the DNA blueprints. It could involve one more layer of regulation in the form of biochemical markers, such as methylation, on specific RNA molecules and provides finer control on stress tolerance mechanisms. This phenomenon is known as epitranscriptional regulation. In this study, role of epitranscriptional regulation was studied during cold stress using a model plant *Arabidopsis*. The study revealed a large-scale shift in mRNA methylation in response to cold stress treatment of the plants. Further, we found that under cold stress the abundance of m^{6}A-containing transcripts had increased significantly and also these methylated mRNA had increased ribosome occupancy for the translation (process of protein synthesis from RNA) events. The results were validated using a mutant line of *Arabidopsis*, called *mta* mutant, which has a known defect for the m^{6}A methylation of mRNA. When the wild type (non-mutant) and the *mta* mutant of Arabidopsis were exposed to cold stress it was found that the *mta* mutant plants were highly susceptible to cold stress, had poor growth and development, and exhibited significant differences in gene expression levels of previously known cold-tolerance genes such as CBF and COR genes. This research concludes that the m^{6}A methylation of mRNA may play a critical role for cold tolerance trait in crop plants. Overall, mRNA modifications provide new avenues to scientists for increasing abiotic stress tolerance and climate resiliency in crop plants.



This addresses USDA-ARS Research Goal: Well-characterized germplasm designed for trait discovery and increasing genetic diversity in crop plants

Eizenga GC, Kim HJ, Jung JKH, Greenberg AJ, **Edwards JD**, Naredo MEB, Banaticla-Hilario MCN, Harrington SE, Shi Y, Kimball JA, Harper LA, McNally KL and McCouch SR (2022) Phenotypic Variation and the Impact of Admixture in the *Oryza rufipogon* Species Complex (*ORSC*). Frontiers Plant Science 13:787703. https://doi.org/10.3389/fpls.2022.787703

Crop wild relatives represent valuable reservoirs of useful characteristics for breeding including tolerance to extremes in climate and plant pests that were lost during domestication. Unfortunately, populations of crop wild relatives are threatened in natural habitats, are sparsely represented in genebanks, and most are poorly characterized. The focus of this study was the *Oryza rufipogon* species complex (*ORSC*), wild progenitor of Asian rice (*Oryza sativa*). The *ORSC* comprises perennial, annual and intermediate forms which are designated as *O. rufipogon, O. nivara*, and *Oryza* species in genebanks. "*Oryza* species" refers to an annual form of mixed ancestry including traits which characterize *O. rufipogon, O. nivara* and *O. sativa*. Understanding the relationships between these *ORSC* accessions collected from diverse locations and environments enables rice geneticists and breeders to make selections among the diverse *ORSC* accessions in genebanks for domestication studies and for introgressing novel genes into new cultivated rice varieties. To this end a "statistical tool" named a "Mixture Model" was developed to group the wild *Oryza* species accessions having similar phenotypes (traits) together. Subsequently, the Mixture Model was tested with a collection of 222 *ORSC* accessions which were previously grouped by genotypes. This model ascertained three phenotypic groups which were largely consistent with genebank species designations (*O. rufipogon*, *O. nivara*, *Oryza* species) and were similar to groups based on genotype, thus validating that the Mixture Model can group these ancestral *ORSC* accessions based on phenotypic traits. Having both the genotypic and phenotypic groups allows genebank managers to determine if accessions are misclassified, thus having the incorrect species name. In summary, one phenotypic group (P1) contained predominantly *O. rufipogon* accessions characterized as perennial and largely out-crossing and a second group (P4) contained predominantly *O. nivara* accessions characterized as annual and largely inbreeding. The third group (P2/P3), comprising 20% of our collection, had the most accessions identified as *Oryza* species (51.2%) and levels of *O. sativa* accounting for >50% of the genome. This third group is potentially useful as a "pre-breeding" pool for breeders attempting to incorporate novel variation into elite breeding lines.



Selected images of *Oryza rufipogon* Species Complex accessions in the three phenotypic groups. The group P1 is predominately O. rufipogon accessions, P4 is predominately *O. nivara* accessions and P2/P3 includes accessions designated as Oryza species with more than 50% O. sativa, thus useful as for "pre-breeding".

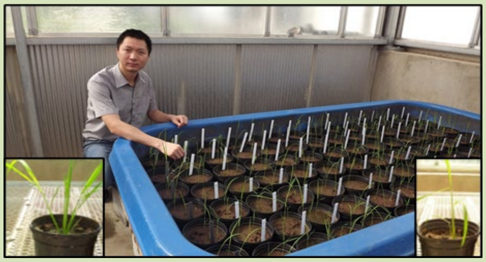
This addresses USDA-ARS Research Goal: Well-characterized genetic mapping populations for trait discovery and increasing genetic diversity in crop plant

Li, D., Zhang, F., **Pinson, S.R.M**., **Edwards, J.D., Jackson, A.K.,** Xia, X., and **Eizenga, G.C.** (2022) Assessment of Rice Sheath Blight Resistance Including Associations with Plant Architecture, as Revealed by Genome-Wide Association Studies. Rice 15:31. https://doi.org/10.1186/s12284-022-00574-4

Sheath blight disease is one of the most economically damaging rice diseases worldwide. It occurs in all areas where rice is grown, reducing grain yields up to 50%. Sheath blight is caused by a soil-borne fungus, *Rhizoctonia solani*, that spreads by filaments ("hairs" produced by the fungus, *R. solani*) creating new lesions along the plant stems that results in a loss of grain development. Recently *R. solani* fungal isolates were discovered that were tolerant to one of the main fungicides in the USA currently used to control sheath blight. This is a problem because there are no known major resistance genes, thus there is a need to discover additional genes that can be incorporated into modern rice cultivars to improve natural resistance to sheath blight disease. Unfortunately, many of the sheath blight resistance genes currently reported are associated with traits detrimental to grain yields such as tall plant height, late maturity, spreading tillers, or reduced tiller number. In this study we evaluated a set of 424 rice cultivars known as the Rice Diversity Panel-1 (RDP1) and discovered 18 potential genes for sheath blight resistance that were not associated with tall height or late maturity. As part of this study, 19 cultivars were highly tolerant to sheath blight tolerant in both the Arkansas and Nanning, China field studies. These cultivars are not adapted to the US growing conditions and have most of the 18 sheath blight resistance genes reported in this study, illustrating the need to have several resistance genes to achieve useful levels of sheath blight resistance. Rice breeders can potentially incorporate these genes for sheath blight resistance into U.S. adapted cultivars, thus reducing the need for fungicide applications. We also noted that four different sheath blight resistance genes were near genes for producing more panicles, thus these genes could potentially also be used to improve grain yield.

Dr. Danting Li, visiting scientist rating the RDP1 cultivars for sheath blight in Arkansas with a susceptible accession in the lower left corner.

The RDP1 cultivars being transplanted in Nanning, China for sheath blight evaluation.



Dr. Fantao Zhang, visiting scientist evaluating the RDP1 cultivars for tiller number. The Chinese cultivar Zhe733 (left) produces many tillers and the U.S cultivar Lemont (right) produces few tillers.

- **Technology Transfer**

  ✓ **Interactions with the Research Community**

  On June 2nd, Dr. Shannon Pinson provided information to Dr. Debasis Golui at North Dakota State University, Fargo, ND, regarding commercial potting soil and fertilization methods for growing potted rice plants for research purpose.

  ✓ **Rice Germplasm Distributed**

  During the month of June, 22 rice genetic stocks were shipped to researchers in Costa Rice, Canada, and the United States.

- **Education and Outreach**

  On June 24, Dr. Yulin Jia and staff members hosted Dr. Jianzhong Su, Professor and Chair of Department of Mathematics of the University of Texas at Arlington (UTA) along with of UTA graduate/undergraduate students (Ashley Alfred, Jonathan Andres, Logan Marshall, Angela Avila, Jordan Rodriguez, Lisvet Ortiz). The meeting of DB NRRC staff members with visitors was taken place in hybrid- virtually and on site. Dr. Jia welcomed the visitors with an introductory talk showing all scientific projects and impact, and led visitors to tour the lab, greenhouse and field and his team member Dr. Jeremy Edwards presented an update on machine learning. UTA visitors, Angela Avila shared progress on machine learning for leaf area index data for predicting planting dates. Johnathan Andres shared working on cattle acoustic data, Ashley Alfred and Jordan Rodriguez shared hyperspectral imaging data for foodborne pathogens identification, respectively. Ideas on plant sensor, plant abiotic stress, pathogen detection and root imaging and irrigation systems were discussed for future collaboration.

Picture was taken in a greenhouse at DB NRRC. From left to right, Su, Orbiz, Avila, Andres, Marshall, Rodriguez and Alfred.

On June 24, 2022, Drs. Shannon Pinson, Yulin Jia, Jai Rohila, and Georgia Eizenga, along with Mr. Jonathan Moser and Ms. Melissa Jia took turns hosting Ms. Megan Bristol, undergraduate at University of Arkansas, Fayetteville. Ms. Bristol is in Stuttgart, AR this summer working with Dr. Yeshi Wamishe, research and extension pathologist, UAR Rice Research and Extension Center. She asked to spend one day job shadowing at the DBNRRC in order to learn more about the USDA ARS research mission and career opportunities. In the fall, Ms. Bristol will return to the UAR to complete her B.S. degree in Agri Business Management and Marketing with a minor in Crop Science.

Jeremy Edwards is a Research Molecular Geneticist at the DBNRRC. He grew up in Bradenton FL where he spent much of his free time exploring the mangrove swamps of the Braden River tidal estuary by canoe and small pontoon boat. His first introduction to agricultural research came in High School when he applied for a summer internship at the local University of Florida Gulf Coast Research and Extension center (GCREC). He was ultimately not selected for the internship, but instead of giving up, he applied and was hired to work on the GCREC field crew where he spent the summer harvesting research plots of tomatoes and peppers. The subsequent summer he was hired to work for Dr. Jay Scott, a GCREC tomato breeder, who discovered Jeremy's computer programming talent. While attending the University of Florida as an undergraduate Jeremy continued working for the tomato breeding program each summer where he programmed a database to track seeds and crosses and help manage the breeding program. This experience led Jeremy to major in Horticultural Science, and ultimately to pursue his Ph.D. in plant breeding and genetics at Cornell University.

At Cornell Jeremy studied under Dr. Susan McCouch where he researched genetic diversity in the wild ancestors of cultivated rice and its potential use in improving modern rice varieties. After completing his Ph.D., Jeremy accepted a postdoc position at the University of Arizona with Dr. David Galbraith on a project that developed microarray-based genomics tools for rice. After the postdoc, Jeremy returned to CGREC as an Assistant Professor/tomato breeder where he established a molecular marker lab and participated in the first discovery of a gene to control the Tomato Yellow Leaf Curl Virus (TYLCV).

In 2012 Jeremy felt a calling to pursue his early interest in creating software to improve plant breeding programs and took a position at the Boyce Thompson Institute (BTI) in Ithaca, NY as Assistant Director of the Solanaceae Genomics Network led by Dr. Lukas Mueller. At BTI Jeremy developed the plant breeding functionality of the free and open-source breeding platform (Cassavabase) aimed at accelerating cassava breeding worldwide, and he traveled to visit cassava breeding programs in Nigeria, Uganda, and Kenya to provide training and collect feedback from local breeders who use the database. This platform has now been extended under the name Breedbase and is used by dozens of different crops including banana, sweet potato, yam, rice, wheat, oat, kelp, potato, and maize, and a manuscript describing the Breedbase system was published this year. Jeremy notes that it's very satisfying to see the journey he began almost 30 years ago writing software as a student intern grow into a software project with international impact on global food security.

In 2014 Jeremy returned to rice research and joined DBNRRC. He oversees the genomics core facility, currently staffed by Aaron Jackson and Melissa Jia (Geneticists), Brenda Lawrence (Biological Science Technician), and John Mitchell (summer intern). At DBNRRC Jeremy has supervised two postdocs, Dr. Trevis Huggins (now a permanent scientist at DBNRRC) and most recently Dr. Santosh Sharma who accepted a new position with the USPTO in June, and Jeremy is currently recruiting a new postdoc to work on artificial intelligence and 3D protein structure prediction aimed at finding new sources of resistance to rice diseases.

In his time off, Jeremy enjoys fishing, kayaking, hiking, and exploring the diverse natural environments of Arkansas.

Santosh Sharma worked as a Computational Biologist (Post Doctorate) at Dale Bumpers National Rice Research center (DBNRRC) from 2019 until June 2022. At DBNRRC he conducted research on developing computational resources for genomic prediction, machine learning and deep learning for important traits in rice including root system architectures, grain arsenic concentration, grain yield and blast disease.

Santosh was born in western Nepal on a small rice and vegetable farm. He explains his childhood memory as full of small farm activities where his parents had an upland farm for vegetables, rapeseeds and corn, and lowland farm for rice. Most of the farm produce were consumed in-house seasonally. He liked the look and smell of rice farm while in tillering and smell of corn field while flowering. Rice cultivation and farming was their livelihood in western Nepal. Most of the festivals in Nepal are around rice cultivation and harvesting time. Hence, the special food like "Sel Roti", "Puwa", "Kheer", "Fini", "Latte" in different festival is made from rice and he still makes and enjoys them in special occasions and gatherings with friends and family.

Santosh earned his B.S. in Agriculture sciences from Tribhuvan University. Upon completion of his undergraduate, he worked as a research assistant in Nepal Agriculture Research Council in corn breeding for a year to improve local hill corn varieties.

He came to US for his graduate study in Plant Sciences in 2008 as research assistant in corn breeding and genetics in North Dakota State University (NDSU) with Dr. Marcelo Carena. His M.S. work was on a genetic incorporation of exotic germplasm from early corn in North Dakota to develop varieties with high grain quality, early maturity and yield. His Ph. D was in understanding the quantitative genetics of drought tolerance in early corn of North Dakota. He liked lab work, crop pollinations, planting, harvesting and research site visits across North Dakota. He thinks communication in science is key to understanding and forwarding science. He developed an interest in science communication during his time at NDSU and participated in symposium talks, innovation challenges and science writing.

Santosh wanted to join the military after completing his undergraduate degree, however he delayed it to further his study. When he got that chance after his graduate education, he opted for it. He was interested to learn about leadership, resiliency and importance of a national defense for our country. This led him to join US Army after his graduate degree. He had great opportunity of training and working as an active-duty soldier in Fort Leonard Wood, MO, Fort Jackson, SC, Fort Shafter HI, and Schofield Barracks, HI during his service. He explains this was his very proud and joyful experience, to learn about resiliency, the nation, leadership and also budgeting and finance.

While in Nepal, he liked to work with rice pollination, genetic mutants and their cytogenetics. His experience and interest in rice along with statistical computing and quantitative genetics led him to connect to Dr. Jeremy Edwards at DBNRRC and he joined DBNRRC as a post doctorate in Computational Biology. At DBNRRC he developed and used computational tools to solve important agricultural problems faced by rice farmers and consumers. He enjoyed greenhouse and growth chamber studies of roots and their image analysis. He enjoyed every second working alongside the great staff at DBNRRC. He thinks USDA is a great place with tremendous infrastructure like the SCINet high-performance computing clusters that he used in Bayesian Networks, machine learning, deep learning and exploring genomic predictions and selections in rice.

In June, Santosh accepted a job at USPTO where he will promote innovators and innovations in biological sciences by identifying and safeguarding their intellectual property.

Santosh likes visiting new places and enjoying their local foods. He volunteers as peer reviewer for several journals and likes to take new courses in Coursera. Santosh is married to Durga, and they have a son Shrey. In his personal time, he enjoys reading, cooking, talking with people, hiking, running, working in the garden, and spending time with his son.

John Mitchell is a Biological Science Aid with the Dale Bumpers National Rice Research Center, Stuttgart, AR. He is a recent graduate of University of Arkansas at Pine Bluff with a bachelor’s degree in Agriculture Business. He will assist Drs. Edwards and Rohila in their research on abiotic stresses such as drought resistance in rice.

John is from Fordyce, Arkansas. As a child he began his agricultural path by working for a small Farmer near his town. At the age of 12, he picked watermelons from the surrounding fields and harvested many other vegetables for the produce store. By the end of that summer, he was offered a job at the Fordyce greenhouses. The Fordyce greenhouses had been a career path for his uncle who had worked there as a boy as well. John’s love for horticulture began at the greenhouses just as his uncle before him. John’s uncle, Dr. Randy Woodson, was a major role model in his life. Dr. Woodson is a renowned plant physiologist who earned his M.S. and Ph.D. at Cornell University and is the current chancellor of North Carolina State University. John worked for the Fordyce greenhouses for several years before the business shut down due to the owner retiring. After high school, John attended South Arkansas Community College. During this time, he worked construction remodeling houses in El Dorado in between school. In 2019 he transferred to University of Arkansas at Pine Bluff to earn his B.S.

After interning at DBNRRC, John plans to return to UAPB and earn his master's degree in Agriculture Regulations, specialized in plant breeding/genetics under his mentor Dr. Sathish Ponniah. John is overwhelmed with joy to be part of the DBNRRC team and excited to see what the future holds for him.

Passing of Dr. Charles N. Bollich

Dr. Charlie Bollich, Research Agronomist, passed away on June 16, 2022, in Beaumont, TX at the age of 95. He was born on September 9, 1926, in Mowata, Louisiana, and he served in the United States Navy during World War II.

His entire career was with the USDA-ARS in rice breeding which began in Crowley, LA, but over 25 years were spent as the Research Leader at the Rice Research Unit, in Beaumont. He was the developer of 20 rice varieties that were grown extensively along the Texas and Louisiana Gulf Coast. Bluebelle rice, released in 1965, was considered the standard for grain quality for many years and is still considered so in South America. Labelle, released in 1972, was an early maturing variety that was presented as a short-term transition variety, but was grown for over 15 years. Newrex (1979) was the first rice variety developed for the parboiling industry. Rice varieties were also developed for the medium grain and aromatic markets. He is best known for the development of "Lemont" in 1983, a semidwarf variety that transformed rice production in the Southern USA. This short statured variety allowed higher nitrogen rates to be applied which increased yields some 20% and also provided "biological insurance" from lodging, a common concern along the hurricane vulnerable Gulf Coast. From that point forward, essentially all the rice varieties that were developed for that region were semidwarf in height with many having Lemont in their parentage. Over the course of his career, he received many prestigious awards including: the USDA-ARS Award for Superior Service (1983); Fellow of the American Society of Agronomy (1985); Fellow of the Crop Science Society of America (1986); the 1986 Distinguished Research and Education Team Award from the Rice Technical Working Group; the ASA Agronomic Achievement Award in Crops (1991); Distinguished Service Award from RTWG (1992); the USDA-ARS Hall of Fame (1994); the C.N. Bollich Endowment Program by Texas A&M University (1994); and the Louisiana State University Alumni Hall of Distinction (1995). In addition to this high impact career, he still had time for his "first love in science" – archeology – and he served as president of the Texas Archeological Society and as a member of the Louisiana Archeological Society. He was considered an expert on the pottery of Southeast Texas and Louisiana. The Museum of the Gulf Coast in Port Arthur is home to some select pieces of his archeological findings. He is fondly remembered as a man of short stature, who cast a long shadow.

Dr. Charlie Bollich standing in a field of Lemont rice at Beaumont, Tx (ca. 1985).

See the web version of all DBNRRC research highlights at: https://www.ars.usda.gov/southeast-area/stuttgart-ar/dale-bumpers-national-rice-research-center/docs/monthly-research-highlights/