



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



JUNE 2023

MONTHLY RESEARCH HIGHLIGHTS

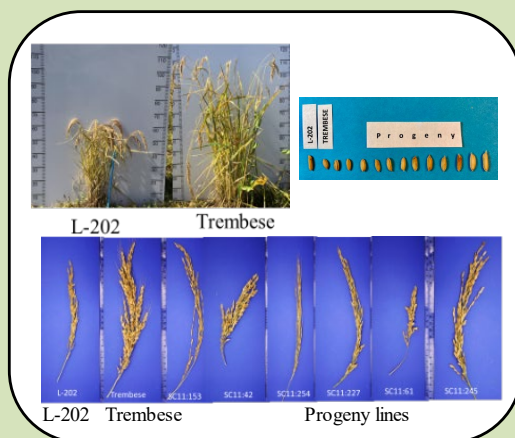
For More Information: Dr. Yulin Jia, Acting Research Leader/Center Director
yulin.jia@usda.gov

- **Recent Scientific Publications**

This addresses USDA-ARS Research Goal: Development of well characterized genetic mapping populations for trait discovery.

Eizenga, G. C., Rice, A. D., Huggins, T. D., Shakiba, E., Edwards, J. D., Jackson, A. K., Jia, M. H., & Ali, M. L. (2023). Yield component QTLs identified by genome-wide association mapping validated in a diverse tropical japonica × tropical japonica rice biparental mapping population. *Crop Science*, 1–22. <https://doi.org/10.1002/csc2.20999>

Rice is the staple food for over half of the world's 7.6 billion people and population growth is predicted to reach 8.6 billion in 2030 and 9.8 billion in 2050. To meet this growing demand for food, it is essential to understand the plant processes that control grain yield, thus expediting breeding efforts to produce more pounds of rice per acre. Rice yield is determined by several factors including number of panicles per plant, number of panicle branches per panicle, number of seeds per panicle, seed size (length and width) and seed weight. To better understand the biological processes controlling these traits, a global collection of 400 diverse rice varieties was phenotyped for these yield-related traits and mapped with DNA markers to identify the genes controlling these traits. To validate these results, two diverse rice varieties from this collection, L-202, a short statured plant with a long grain originating from California, USA and Trembese, a tall plant with a medium grain originating from Indonesia, were selected as parents for population development. The population was advanced eight generations and evaluated for the same yield-related traits as the parents. Using DNA markers, we identified 37 chromosome regions across both studies where genes controlling yield-related traits are located. Most significant was a genomic region on chromosome 7 which affects the number of seeds per panicle, panicle branching, seed length and seed weight. These results will be used to develop user friendly DNA markers associated with these yield-related traits that can be used by rice breeders to accelerate selection for the desired panicle architecture, seed size and seed weight; ultimately improving rice yield.



Plant, panicle and seed images of the parents, L-202 and Trembese, and selected recombinant inbred line progeny illustrating the variation in seed, plant and panicle architecture.

- **Technology Transfer**

- ✓ **Interactions with the Research Community**

Research by Drs. Ming Chen (now retired), Shannon Pinson, Jeremy Edwards and Aaron Jackson is a featured story on the AgriPlex Genomics News website, available at <https://www.agriplexgenomics.com/news>. This team of DB NRRC scientists identified novel genes and gene combinations that increase the content of health-beneficial pigmented antioxidant compounds (i.e., anthocyanin and proanthocyanidin) in whole grain rice having purple or red colored brans using genome-wide SNP marker data contracted through AgriPlex.

On June 14, 2023, the Stuttgart and Little Rock location hosted a diversity day celebration where scientists and staff members from different regions of the globe presented their culture with a wide range of authentic cuisines and a display table of items. Three employees presented talks about their heritage. Dr. Trevis Huggins presented on Batik artwork from St. Kitts, Ms. Melissa Jia presented on Knoxville Tennessee highlighting nearby Leconte Lodge in the Smokey Mountains, and Dr. Yulin Jia presented on Xichang, China. A total of 60 employees, friends and family members attended the event. The event was highlighted by celebrating Dr. Anna McClung's retirement when several scientists from university, ARS, and Arkansas farmer Chris Isbell expressed their gratitude for her contribution for rice industry and science.





✓ **Rice Germplasm Distributed**

During the month of June, 931 rice genetic stocks were shipped to researchers in the United States.

Dr. Anna McClung and the breeding staff provided seed of specialty varieties to several stakeholders this month. 1 variety to Jubilee Justice, Alexandria, LA; 6 varieties to Purple Mountain Organics, Takoma Park, MD; 14 varieties to SFR, Newport, AR; and 1 variety to a grower in Humnoke, AR.

• **Stakeholder Interactions**

On June 1- 2, 2023, Drs. Yulin Jia, Laxmi Yeruva, Michael Deshotel, Adam Fuller from Stuttgart and Little Rock attended the reception and the 88th annual meeting of Delta Council. Delta Council is an area organization representing the 19 Delta and part-Delta counties of Northwest Mississippi since 1935. Delta Council now leads the effort to solve common problems and promote research and development focusing on catfish, cotton, rice, and soybean programs in the Mississippi Delta in partnership with USDA- ARS.



The President of Delta Council Bubba Simmons (middle), next to the area director Mr. Tucker with all other ARS acting and Research Leaders in Arkansas. Photo credit: Laxmi Yeruva

- **Education and Outreach**

Dr. Anna McClung retired on June 30, 2023, after more than 31 years as a Research Geneticist with USDA ARS at the Rice Research Unit (RRU), Beaumont, Texas, and the Dale Bumpers National Rice Research Center (DBNRRC), Stuttgart, AR. The ARS mission at both RRU and DBNRRC is to conduct research in classical, quantitative, and molecular genetics along with plant physiology, metabolomics, cereal chemistry, plant pathology, and weed physiology that will bring greater value and sustainability to the US rice industry. Dr. McClung also served as the Research Leader/Center Director for these two locations from 1996-2021.

Dr. McClung received a B.S. in Agronomy (1977) and a MS in Plant Breeding (1980) from Texas A&M University, and a Ph. D in Plant Breeding (1984) from North Dakota State University. After completing her Ph. D, she took a position as a Senior Plant Geneticist with Allied Corp., Syracuse, NY for two years and was a Principal Scientist with Enimont America in Monmouth Junction, NJ for five years. During that time, she conducted genetic research for the development of nitrogen use efficient corn varieties. Dr. McClung joined USDA ARS as a Research Geneticist at RRU, Beaumont, Texas in 1991, and served as Research Leader from 1996-2005. She served as the Research Leader for both the RRU and DBNRRC for six years at which time the units were consolidated in Stuttgart. Dr. McClung directed a multidisciplinary research program of nine scientists that addresses research issues relevant to National Program 301, Plant Genetic Resources, Genomics, and Genetic Improvement. During her career she was awarded with over \$32 M in competitive grant funds and developed and released four conventional and 24 specialty rice cultivars (combined, these have been grown on over 810,000 ac with 12 currently in commercial production), 26 germplasm lines, three diversity panels, and one mapping population. Dr. McClung has authored/co-authored 153 peer reviewed publications and five book chapters. USDA-ARS recognized her success in developing conventional and specialty rice cultivars and developing genetic markers to enhance rice breeding by presenting her with the Technology Transfer Award for the Southern Plains in 2000 and in 2009, as well as a Federal Lab Consortium Award for Excellence in Technology Transfer in 2010. She was selected as ARS Senior Scientist of the Year for the Southern Plains in 2009. The USA rice research community presented her with the Distinguished Rice Research and Education award in 2012 (individual) and in 2020 (team). She was elected as Crop Science Society Fellow in 2022.



- **International Research Collaborations**

Research by Drs. Ming Chen (now retired), Shannon Pinson, Jeremy Edwards and Aaron Jackson is a featured story on the AgriPlex Genomics News website, available at <https://www.agriplexgenomics.com/news>. This team of DB NRRC scientists identified novel genes and gene combinations that increase the content of health-beneficial pigmented antioxidant compounds (i.e., anthocyanin and proanthocyanidin) in whole grain rice having purple or red colored brans using genome-wide SNP marker data contracted through AgriPlex.



- **New Research Grants**

NIFA-AFRI (Physiology of Agricultural Plants): Mechanisms of Cold Stress Tolerance Responses in Rice; with Michael Schläppi, PI (Marquette Univ., Milwaukee, WI), Georgia Eizenga and Jeremy Edwards, CoPIs (USDA-ARS Dale Bumpers National Rice Research Center); \$137,063, 4 years.

The main object of this research is to gain a better understanding of physiological mechanisms and underlying genes affecting cold tolerance at germination and the seedling growth stages in rice. To conduct these studies several mapping populations were developed to identify cold tolerance genes. From this, cold-tolerant-parent-specific gene co-expression modules and their central hub genes will be ascertained, and the modules and hub genes associated to previously mapped quantitative trait loci for cold tolerance at germination and the seedling stages distinguished. Once identified, selected genes will be fine mapped and validated with CRISPR/Cas9 and overexpression systems at Marquette University. Subsequently, introgression lines developed by backcrossing the desired genes into an adapted background will be used as the basis for gene discovery and identification of cold-associated DNA markers. Ultimately, these lines will be released as rice germplasm with improved seedling vigor for use in cultivar development programs.



From left to right: Drs. Jeremy Edwards, Georgia Eizenga and Michael Schläppi

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/>