RESEARCH HIGHLIGHTS
(FY2022)

Dale Bumpers National Rice Research Center, Stuttgart, Arkansas

USDA Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE

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Summary of Major DB NRRC Outcomes During FY22

By Dr. Yulin Jia, Acting Research Leader/Center Director- yulin.jia@usda.gov

DB NRRC Mission Statement: To enhance the sustainability of U.S. rice production by delivering improved germplasm for use in breeding programs by combining novel genes for stress tolerance, productivity, enhanced nutrition, and processing quality.

- Distributed 5,115 rice genetic stocks, germplasm and varieties to the stakeholders in the USA, 86% of which had been developed by DB NRRC scientists.
- 2,000 global rice accessions were accurately characterized phenotypically and molecularly, rejuvenated, and made available for distribution through the USDA National Plant Germplasm System.
- More than 10 rice varieties developed by DB NRRC are currently in commercial production.
- New genetic markers and genetic stocks were developed for controlling two major rice fungal diseases - rice blast and sheath blight. These make the desired genes/resistance available to breeders for easier incorporation into new varieties.
- New rice production management methods including alternate wetting and drying, and reduced fertilizer application were evaluated to sustain rice yield and nutritional quality and reduce greenhouse gas emissions
- Methods were developed to evaluate rice grain quality characteristics (including resistant starch) as well as crop abiotic stress tolerance and climate resilience.
- Rice was demonstrated to be a flavorful and nutritional ingredient for new food and beverage products.

OCTOBER 2021

Scientific Publications

This addresses USDA-ARS Research Goal: Develop technologies and practices producers can readily use to improve management of soil and water resources, reduce impact on air resources, efficiently use inputs, and contribute to ecosystems services.

Runkle, B.R.K., Seyfferth, A.L., Reid, M.C., Limmer, M.A., Moreno-García, B., Reavis, C.W., Peña, J., Reba, M.L., Adviento-Borbe, M.A.A., **Pinson, S.R.M.**, and Isbell, C. Hypothesis and Theory: Co-implementing rice husk amendment and alternate wetting and drying irrigation for sustainable rice production. Frontiers in Agronomy, Oct. 22, 2021.
DOI:
https://doi.org/10.3389/fagro.2021.741557

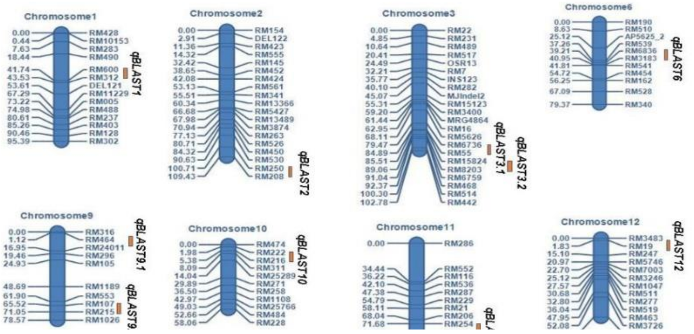
Rice is a staple food and primary source of calories and mineral nutrients for much of the world. However, rice can be a dietary source of toxic metal(loid)s like arsenic and cadmium, and its production in traditional flooded paddies requires significant water resources and can result in emission of the greenhouse gasses responsible for global warming. We therefore propose a modification to the rice production system that combines silicon management via incorporation of milled rice husks into the soil with growing rice under unflooded conditions for all or part of the growing season (alternate wetting and drying) to conserve water resources. Present research shows the promise of both strategies independently. This review paper presents how combining the two strategies could be expected to provide additional benefit. For example, reduced flooding periods and addition of silicon from rice husks have both been shown to independently decrease accumulation of arsenic in rice grains. Because silicon has also been shown to improve rice drought tolerance, combining the two strategies could allow the use of even longer dry periods during rice production, which could further decrease grain arsenic concentrations, water costs, and greenhouse gas emissions. Thus, these practices may be more effective together to counter the accumulation of toxic metal(loid)s, manage water usage and lower climate impacts separately. The production system we propose would take advantage of rice husks which are an underutilized byproduct of milled rice. The wide availability of rice husks, with ~10% silicon content, and their physical proximity to commercial rice fields offer an opportunity for application to paddy soils as a silicon amendment. Rice husk application could, alongside alternate wetting and drying or furrow irrigation management, help resolve multiple sustainability challenges in rice production: (1) limit toxic metal(loid) accumulation in rice; (2) minimize greenhouse gas emissions from rice production; (3) reduce irrigation water use; (4) improve nutrient use efficiency; (5) utilize a waste product of rice processing; and (6) maintain plant-accessible soil Si levels. This review presents how such a shift in rice production practices could operate, identifies challenges, opportunities, and synergies to its implementation, and highlights remaining research issues. This review also suggests how farmers and millers would implement this practice together. This paper's purpose is to advocate for a changed rice production method for consideration by community stakeholders, including producers, millers, breeders, extension specialists, supply chain organizations, and consumers, while highlighting remaining research questions.

Moving rice husk waste at a rice mill by bulldozer.

NOVEMBER 2021

This addresses USDA-ARS Research Goal: Crop plants with resistance or tolerance to diseases and pests.
Jia, Y., **Jia, M.H**., Yan, Z. 2021. Mapping blast resistance genes in rice varieties 'Minghui 63' and 'M-202'. Plant Disease. Published online Nov. 13, 2021. **DOI:** https://doi.org/10.1094/PDIS-09-21-2095-RE.

Rice blast disease is one of the most lethal diseases for sustainable rice production worldwide, and major disease resistance genes are often broken down shortly after deployment. Minor blast resistance genes are more durable than major blast resistance genes. We evaluated disease reactions of two rice breeding parents 'Minghui 63' and 'M-202' with eleven common US blast races: IA45, IB1, IB45, IB49, IB54, IC1, IC17, ID1, IE1, IG1, and IH1 to find minor blast resistance genes. A recombinant inbred line (RIL) population derived from a cross of these parents was evaluated with the same blast races and analyzed with 156 simple sequence repeat (SSR) and insertion and deletion (Indel) genetic markers distributed on all 12 rice chromosomes. Eight resistance QTLs from 'Minghui 63' and two resistance QTLs from 'M-202' were mapped, and 16 blast resistant lines were identified as genetic stocks. One resistance QTL, *qBLAST2*, on rice chromosome 2, was identified providing resistance to seven blast races. The remaining resistance QTLs were mapped on rice chromosomes 1, 3, 6, 9, 10, 11, and 12. These findings supply useful genetic markers and resources for marker assisted selection in rice breeding programs.



A map showing chromosomal locations of genetic markers for newly identified blast resistance genes.

DECEMBER 2021

This addresses USDA-ARS Research Goal: Genetic mapping populations, mutant lines, and other germplasm designed for trait discovery, analysis, and increasing genetic diversity in crop plants.

Jia, Y., Singh, V., **Gealy, D.R**., Liu, Y., Ma, J., Thurber, C.S., Roma-Burgos, N., Olsen, K.M., and Caicedo, A.L. 2021. Registration of two rice mapping populations using weedy rice ecotypes as a novel germplasm resource. Journal of Plant Registrations. Published Dec. 7, 2021. **DOI:** https://doi.org/10.1002/plr2.20174

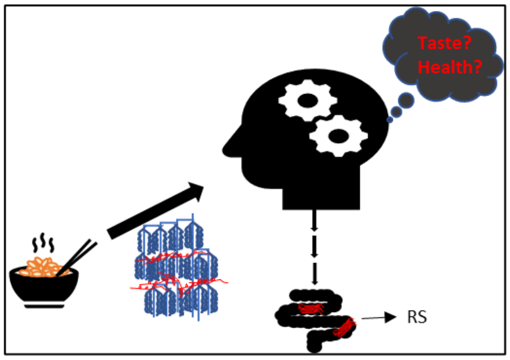
Weedy rice, competing with cultivated rice, is a major agricultural pest worldwide. Knowledge of the competitiveness of weedy rice can benefit the development of improved rice varieties and improve weedy rice control. We developed two mapping populations from crosses of the Asian indica rice variety 'Dee Geo Woo Gen,' (DGWG) with two weedy rice ecotypes, an early-flowering straw hull (SH) type 'AR-2000-1135-01' from Arkansas and a late-flowering black hull (BHA) type 'MS-1996-9' from Mississippi. The progeny from these weed and mapping populations have been used to identify genomic regions associated with weedy traits, as well as resistance to sheath blight and rice blast diseases. The mapping population consists of 186 (DGWG/SH) and 236 (BHA/DGWG) F_8 progeny, of which 175 (DGWG/SH) and 224 (BHA/DGWG) were used to construct two linkage maps using single nucleotide polymorphic markers (SNPs) to identify weedy traits, sheath blight and blast resistance loci. These mapping populations and related datasets represent a valuable resource for basic rice evolutionary genomic research and applied marker-assisted breeding efforts in disease resistance.

Seeds of weedy red rice and domesticated Asian rice, panicles of mapping parents and enhanced blast resistance, and a commercial field infected with red rice.

JANUARY 2022

This addresses USDA-ARS Research Goal: Germplasm with enhanced nutritional quality for consumers, rice producers and the food industry.

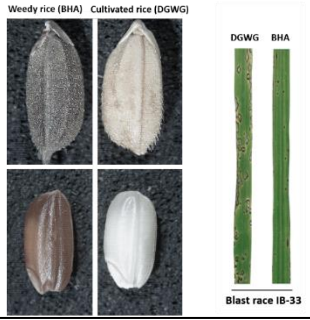
Chen, M.-H., Bett-Garber, K., Lea, J., McClung, A.M., Bergman, C.J. 2022. High resistant starch rice: Variation in starch related SNPs and functional and sensory properties. Foods. **DOI:** https://doi.org/10.3390/foods11010094.



Human diets containing greater dietary fiber are associated with superior glycemic control and preventing chronic diseases. Resistant starch (RS) is the primary form of dietary fiber in cooked milled rice. Although high amylose rice has higher RS than lower amylose content varieties, sensory and processing properties associated with RS have not been evaluated. We evaluated the processing properties and sensory quality of cooked rice of eight global varieties that were identified as having the highest RS in a previous study. For comparison, two representative US high amylose varieties were included. Trained panelists using descriptive sensory analysis determined that only two of 14 cooked rice texture attributes were different between the high RS group of varieties and other high amylose US varieties. Roughness was the only texture attribute associated with RS content; while protein content influenced roughness and stickiness between grains. Moreover, in an evaluation of the functional properties, few differences were found between the high RS varieties and US varieties that have similar parboiling quality. These results demonstrate the potential for increasing RS in US rice varieties that enhances the health benefits of consuming rice while having minimum impact on cooked rice texture or processing quality.

This addresses USDA-ARS Research Goal: New methods to effectively recombine genomes and introgress useful alleles and novel diversity.

Haijun Zhao, Yan Liu, **Melissa H Jia**, and **Yulin Jia**. An Allelic Variant of the Broad-Spectrum Blast Resistance Gene *Ptr* in Weedy Rice is Associated with Resistance to the Most Virulent Blast Race IB-33. Plant Disease, Published Online: Dec. 28, 2021. **DOI:** https://doi.org/10.1094/PDIS-09-21-2043-RE



Seeds and blast reactions of weedy and cultivated rice after inoculation with blast race IB-33.

Rice resistance (*R*) genes have been effectively deployed to prevent blast disease caused by the fungus *Magnaporthe oryzae*, one of the most serious threats for stable rice production worldwide. Weedy rice, competing with cultivated rice, may carry novel or lost *R* genes. In the present study, we examine the resistance mechanism of weedy rice to *M. oryzae* using machine learning. The *Ptr* gene in rice encodes a predicted protein with four armadillo repeats and confers a broad spectrum of blast resistance except for race IB33. A blast resistance QTL *qBR12.3b* was previously mapped at the *Ptr* locus in a black hulled awned weedy strain using a weed-crop mapping population under greenhouse conditions. A gene-specific marker was developed from *Ptr* to distinguish alleles in weed and crop. The existence of the *Ptr* gene in 207 individuals of the same mapping population was examined using this gene-specific marker. Disease reactions of 207 individuals and their parents to IB33 were evaluated. The resistant individuals had the *Ptr* whereas the susceptible individuals did not. Sequence analysis of the *Ptr* gene from weedy rice, Ptr^{BHA}, identified a unique amino acid glutamine (Gln) at protein position 874. **Using machine learning** minor changes of protein structure of the *Ptr*^{BHA} gene were identified. These findings are useful to determine pathogen recognition specificity of the *Ptr*^{BHA} gene mediated disease resistance signaling pathways and incorporate weedy allele *Ptr*^{BHA} into rice breeding programs for enhanced blast resistance using marker assisted selection.

MARCH 2022

This addresses USDA-ARS Research Goal: Germplasm with enhanced nutritional quality for consumers, rice producers and the food industry.

Pinson, S.R.M., Heuschele, D.J., **Edwards, J.D., Jackson, A.K., Sharma, S., Barnaby, J.Y**. Relationships among arsenic-related traits, including grain arsenic concentration and rice straighthead resistance, as revealed by genome-wide association. Front. Genet. 12:787767. **DOI:** https://doi.org/10.3389/fgene.2021.787767

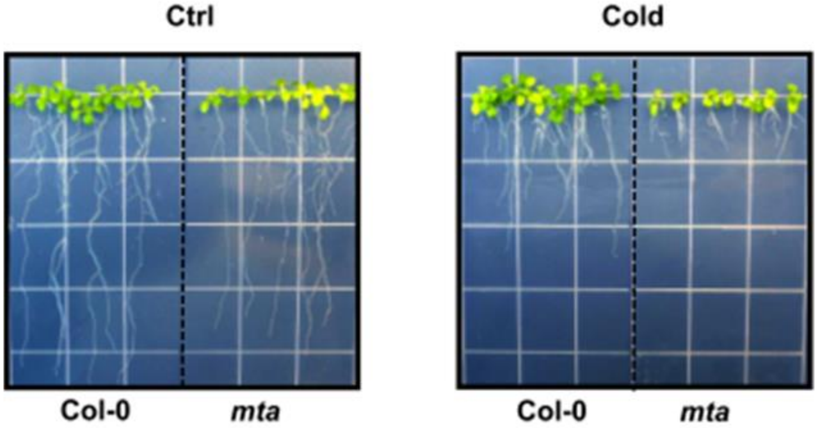
There is concern that rice grains and foods can contain harmful amounts of arsenic (As), motivating rice breeders around the world to produce cultivars that restrict As accumulation in grains to protect human health. Arsenic enters roots through phosphorus (P) and silica (Si) transporters, As-detoxification involves S, and cell signaling to tolerate abiotic stress is impacted by Si, Ca, and Cu. Arsenic is also toxic to plants, with straighthead disorder (StHD) reducing yields by causing panicle sterility, resulting in upright or straight grain heads. Genetic variation in StHD resistance suggests that plants have evolved mechanisms that reduce As toxicity, possibly via regulation of As uptake, transport, or detoxification/sequestration. Because these mechanisms could also be causing the wide differences in grain As concentrations (grain-As) observed among diverse rice genotypes, it was hypothesized that some genes reduce both grain-As and StHD susceptibility. Detection of QTLs for both traits at the same chromosomal location would be indicative of a single gene affecting both traits. To test this hypothesis, we mapped genes for both grain-As, StHD and Si, P, S, Ca, and Cu in the USDA Rice Minicore Collection (RMC) using genome wide association study (GWAS). Response to arsenic-induced StHD was rated over two years in the Stuttgart, AR straighthead nursery. Grain element data were determined using ICP-MS of grains grown over two years in Beaumont, TX, and hull silica data were from two years of grains harvested in both AR and TX. Multiple QTLs (from 9 to 33) were identified for each of the investigated As-associated traits. The StHD and Si QTLs identified by this study were the first to be identified using high-density mapping, resulting in their being more precisely mapped to genomic regions of shorter Mb lengths than previously reported QTLs.

JUNE 2022

This addresses USDA-ARS Research Goal: *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. **DOI:** 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^6A-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^6A 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^6A methylation of mRNA

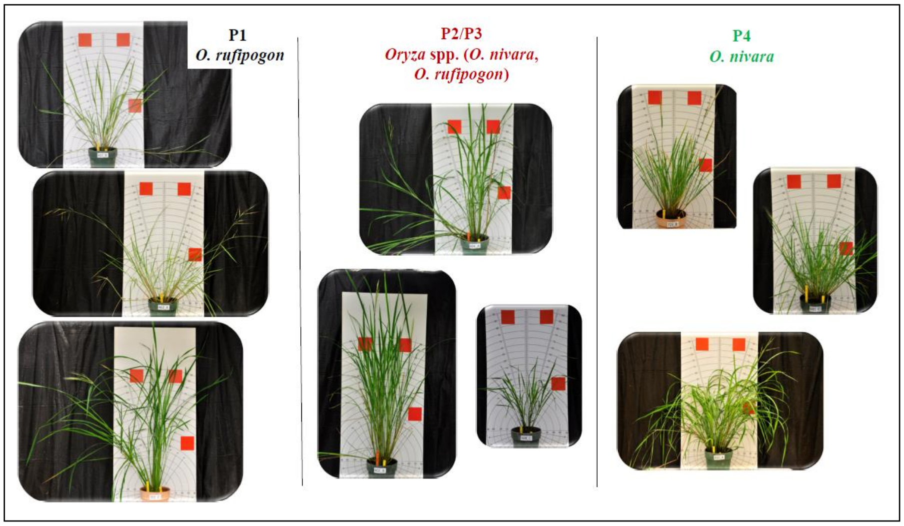


may play a critical role for cold tolerance trait in crop plants. Overall, mRNA modifications provide new avenues to scientists for increasing abiotic stress tolerance and climate resiliency in crop plants.

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



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".

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.

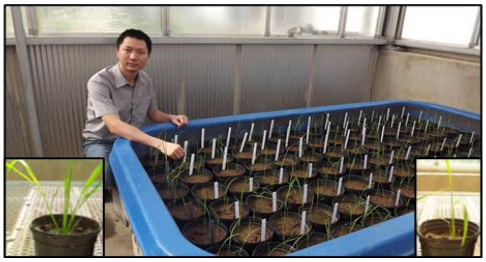
This addresses USDA-ARS Research Goal: Well-characterized genetic mapping populations for trait discovery and increasing genetic diversity in crop plant

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. **DOI:** 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 rates the RDP1 cultivars for sheath blight in Arkansas with a susceptible accession in the lower left corner.

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



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

JULY 2022

This addresses USDA-ARS Research Goal: New uses for current crops.

Beaulieu, J.C., Grimm, C.C., Obando-Ulloa, J.M. and **McClung, A.M**. 2022. Volatiles recovered in novel, diverse and uncharacterized rice varieties. Cereal Chemistry. **DOI:** https://doi.org/10.1002/cche.10579

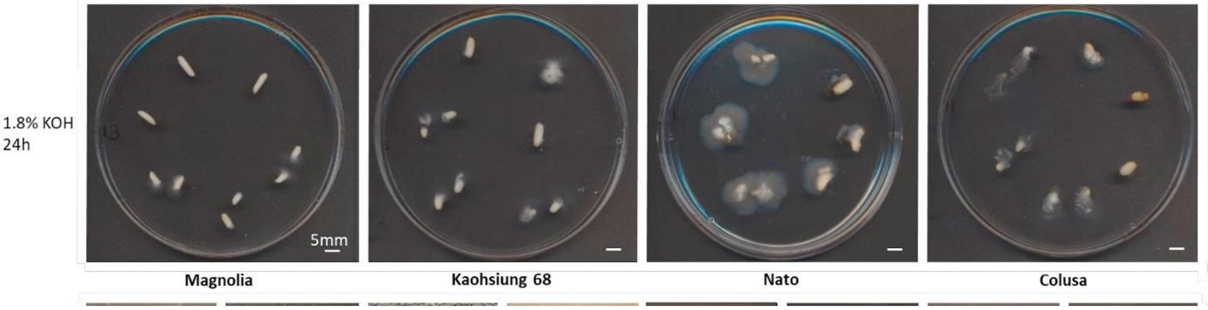
GCMS instrument used to detect rice volatiles

The nutritional beverage market is a rapidly growing industry and some of the products use milled or brown rice as the core ingredient. However, sprouted grains are known to possess a wide variety of compounds that are associated with health beneficial properties, suggesting that sprouted rice may serve as a nutritionally enhanced ingredient for plant-based beverages. In a collaborative study between ARS researchers in Stuttgart, Arkansas and the Southern Regional Research Center in New Orleans, Louisiana, five diverse rice varieties were evaluated for 19 volatile compounds that may affect flavor to identify a rice variety that provides the best combination of sensory traits and nutritional compounds. A purple bran aromatic variety was identified as having the highest levels of favorable volatiles as well as being high in natural anti- oxidant compounds. This research demonstrates expanded opportunities for using rice as a flavorful and nutritional ingredient for new food and beverage products.

This addresses USDA-ARS Research Goal: New phenotyping approaches for quantitative trait analysis.

Armstrong, P.R., Maghirang, E.B., **Chen, M.H**., **McClung, A.M**., Yaptenco, K.F., Brabec, D. and Wu, T., Predicting Single Kernel and Bulk Milled Rice Alkali Spreading Value and Gelatinization Temperature Class Using NIR Spectroscopy. *Cereal Chemistry*. 2022 **DOI: https://doi.org/10.1002/cche.10587**

Rice cooking and processing quality is largely determined by the amount of starch and the temperature of its gelatinization when cooked. Most rice varieties developed in the USA have uniform cooking quality but imported rice or hybrid rice may have variable cooking properties. A SKNIR instrument was developed by ARS scientists at Manhattan, Kansas that can rapidly scan individual raw kernels of milled rice using near-infrared wavelengths. In a previous collaborative study with researchers at DB NRRC, this method was shown to be able to predict the chalkiness of a single grain and, in the current study, shown that it can also predict the gelatinization temperature of rice when it is cooked. These results demonstrate that such instrumentation can be used to scan raw rice and determine its ultimate cooking properties. This technology may be used to rapidly segregate mixed samples of rice without the use of harsh chemical assays as a means to assure uniformity in cooking and processing quality which is important to the processing industry that produces parboiled, instantized, and canned rice.



From Griebel, et al. 2019. Alkali spreading value test using potassium hydroxide as a predictor of gelatinization temperature.

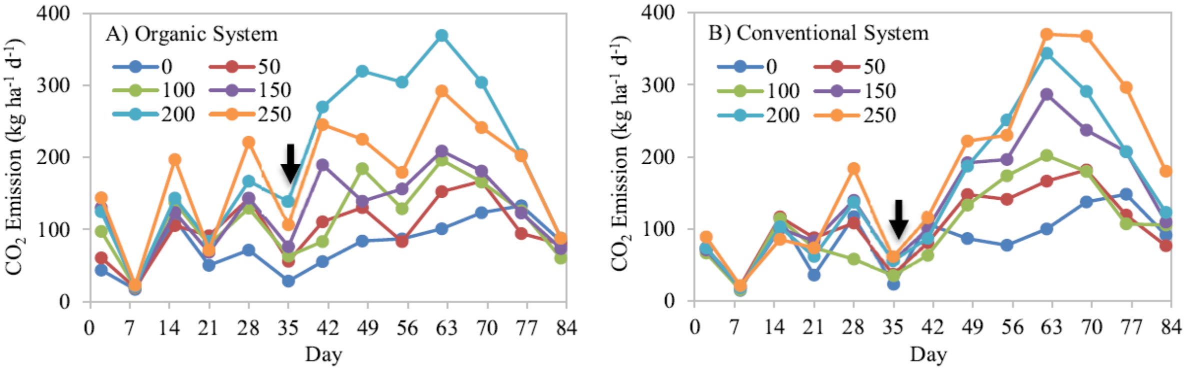
AUGUST 2022

This addresses USDA-ARS Research Goal: Enhanced knowledge of crop plant interactions with abiotic and biotic environmental factors at the systems level.

Li, X., Jiang, J., Guo, J., **McClung, A.M.,** Chen, K., Velarca, M., Torbert Iii, H.A., Dou, F. 2022. Effect of nitrogen application rate under organic and conventional systems on rice

(*Oryza sativa* L.) growth, grain yield, soil properties, and greenhouse gas emissions. Journal of Plant Nutrition. **DOI:** https://doi.org/10.1080/01904167.2022.2093746.

The market for organically produced rice continues to increase with demand outpacing production. Although nutrient availability is critical for crop productivity, organic production prohibits the use of synthetic agricultural chemicals and thus, the yield potential of organically produced rice is generally lower than in conventional systems. In addition, rice produced in flooded fields is an important source of methane emissions, a major contributor to global warming, and thus, it is important to develop an organic management system that optimizes productivity while minimizing greenhouse gas emissions (GHGE). This greenhouse study was conducted to determine the optimum fertilizer rates for rice production under organic management along with the impact on GHGE. Six rates of nitrogen (N) were applied using an organic certified soil amendment and compared with the same rates using urea. Because organic fertilizer is released slowly, the entire rate was applied prior to planting whereas the urea was applied as a three-way split. Results demonstrated that the organic fertilizer resulted in greater tiller production with increasing N rate whereas the synthetic fertilizer resulted in greater plant height. Although the timing of fertilizer application differed between the two systems, GHGE (present as CO2 equivalents) peaked during the reproductive growth phase (arrow indicates onset of flowering in graphs) for both. In addition, grain yield and total GHGE did not differ between the two management systems. This study indicates that careful management of fertilizer application can result in organic rice yields comparable to conventional production. In addition, under moderate N input levels, rice yields are optimized and GHGE are minimized.



This addresses USDA-ARS Research Goal: Expanded knowledge of how growth and development of crop plants are controlled at the genetic level.

Barnaby, J.Y., McClung, A.M., Edwards, J.D., Pinson, S.R.M. 2022. Identification of quantitative trait loci for tillering, root, and shoot biomass at the maximum tillering stage in rice. *Scientific Reports* 12:13304. **DOI:** https://doi.org/10.1038/s41598-022-17109-y

Rice root and shoot biomass have been shown to influence soil microbiome structure influencing nutrient uptake, plant health, and methane emissions. Exploring the interrelationship of tillering, shoot biomass and root biomass is integral to understanding productivity in rice as well as the interaction of the rice plant with the environment. This study identified 11 QTLs affecting tiller number, root biomass and shoot biomass in an *indica* × tropical *japonica* mapping population at the early vegetative stage as well as at harvest maturity. Furthermore, the positive additive effects of these QTLs were associated with alleles from the *indica* parent demonstrating the importance of this gene pool as a source of genetic improvement in the predominantly tropical *japonica* germplasm that is used in the USA. In this study, a number of candidate genes that are linked with plant growth and root development were identified. This knowledge of the QTLs, associated markers, candidate genes, and germplasm resources is of value to rice cultivar improvement programs.

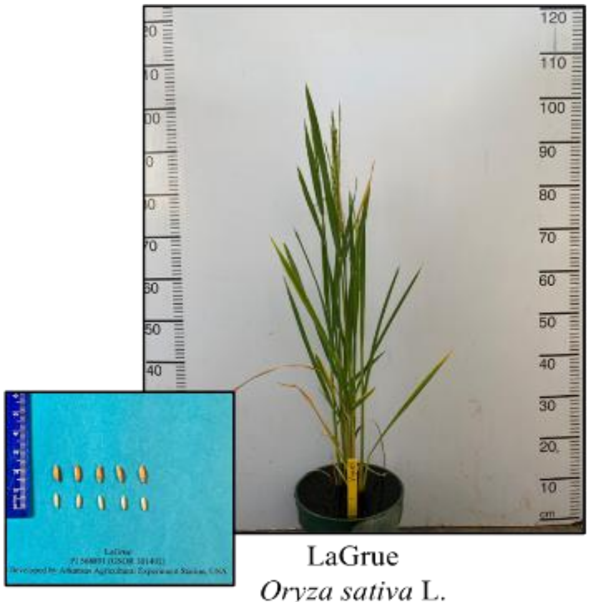
SEPTEMBER 2022

This addresses USDA-ARS Research Goal: Well-characterized genetic mapping populations and associated molecular markers designed for trait discovery, analysis, and breeding crops

Eizenga, G.E., Li, D., **Jia, M.H., Huggins, T.D., Jackson, A.K.** 2022. Identification of sheath blight QTL in a LaGrue x *Oryza nivara* rice advanced backcross population. Euphytica https://doi.org/10.1007/s10681-022-03101-0

Sheath blight disease, caused by the *Rhizoctonia solani* fungus, is one of the most prevalent fungal diseases of cultivated rice and results in significant economic damage to rice production worldwide. No source of complete resistance to sheath blight disease has been identified in cultivated rice (Oryza sativa). The wild *Oryza* species, which are closely related to cultivated rice, are a potential source of important traits including new resistance genes to fight pests like sheath blight disease. *O. nivara* is a wild ancestral species that can be successfully crossed with cultivated rice. The objective of this study was to identify the chromosomal location(s) of possible sheath blight resistance gene (s) in an *O. nivara* accession that previously demonstrated moderate resistance to sheath blight disease in greenhouse studies. The goal of this study was to identify these potential resistance genes and transfer them into the popular southern U.S. long grain variety, LaGrue, which is susceptible to sheath blight disease. One major chromosomal region on the distal region of chromosome 9 was associated with the sheath blight resistance contributed from the *O. nivara* parent. This region was previously identified in cultivated rice but the *O. nivara* species may have a novel resistance gene which can be used in the development of elite rice varieties that will decrease crop vulnerability to this important disease.

Rice sheath blight disease in an Arkansas field



LaGrue
Oryza sativa L.
Developed by Arkansas
Agricultural Experiment Station

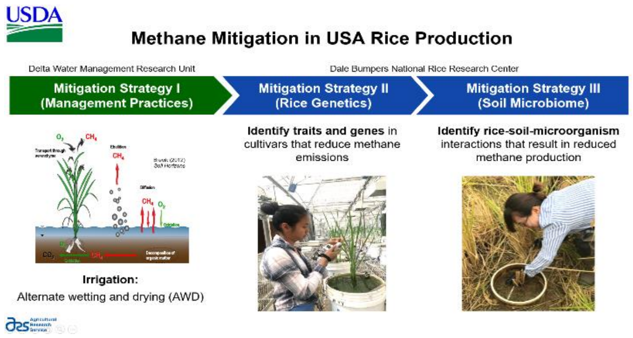
Oryza nivara Sharma et Shastry
Collected in Phitsanulok, Thailand

Interactions with Rice Research Community

OCTOBER 2021

On October 6, 2021, Drs. Anna McClung and Ming-Hsuan Chen were interviewed by Brownfield AgNews Service about the recent announcement of the first export of long grain rice produced in the southern USA entering in the China market. The rice varieties that were included in the shipment were produced in Arkansas and were developed by USDA-ARS. They included aromatics and pigmented bran cultivars. Information was provided regarding the unique cooking, sensory, and health beneficial properties associated with the rice varieties which served as the basis of interest by the buyers in China.

On October 14, 2021, Drs. Anna McClung and Jinyoung Barnaby were invited by National Program Leader, Dr. Jack Okamuro, to participate in the USDA – Japan Ministry of Agriculture, Forestry and Fisheries (MAFF) meeting on greenhouse gas mitigation strategies for paddy rice and livestock production. Both organizations presented overviews of recent research



Methane Mitigation in USA Rice Production

Delta Water Management Research Unit

Dale Bumpers National Rice Research Center

Mitigation Strategy I (Management Practices)

Mitigation Strategy II (Rice Genetics)

Mitigation Strategy III (Soil Microbiome)

Identify traits and genes in cultivars that reduce methane emissions

Identify rice-soil-microorganism interactions that result in reduced methane production

Irrigation:

Alternate wetting and drying (AWD)

NOVEMBER- DECEMBER 2021

On November 2, 2021, Dr. Shannon Pinson provided information to Dr. Blanco and Ms. Ester at the University of Bayreuth, Germany regarding selecting and obtaining seed of rice varieties for their planned studies to determine relationships between concentrations of methylated-arsenic in seed and vegetative tissues with resistance to straight head disorder.

On November 7-10, 2021, the Crop Science Society of America held their annual meeting in Salt Lake City. “Unraveling the Relationship between Phenotype Based Classification of the *Oryza rufipogon* Species Complex and Genotypic Subpopulations” was prepared by Dr. Georgia Eizenga, DB NRRC, for presentation in the Exploration, Conservation, and Characterization of Plant Genetic Resources Using Phenomics and Genomics symposium. This was collaborative research with Dr. Jeremy Edwards (DB NRRC), Cornell University, the International Rice Research Institute and Bayesic Research. Also, Dr. Eizenga contributed “Evaluation of Seedling Cold Stress in the Krasnodarskij 3352 x Carolino 164 Recombinant

Inbred Line Population" as both 5-minute oral and poster presentations. This was collaborative research with Dr. Michael Schläppi (Marquette University) and Dr. Edwards.

On November 22, 2021, Drs. Yulin Jia, Jeremy Edwards, and Jai Rohila attended a meeting hosted by Dr. Alton Johnson and staff members of University of Arkansas Rice Research and Extension Center on how artificial intelligence can help to maintain sustainability of rice production in Arkansas with scientists from University of Arkansas (UA)-Fayetteville. Subsequently, Drs. Jia and Rohila led a walking tour of DB NRRC for 7 visitors from UA-Fayetteville.

From November 26 to December 7, 2021, Dr. Yulin Jia assisted Dr. Brian Staskawicz, Professor of Department of Plant and Microbial Biology of University of California at Berkeley to seek rice germplasm with blast resistance genes.

As part of the Second Workshop on "The Nature of Reproductive Barriers in Rice" held December 9, 2021, in Kunming, P.R. China, Dr. Georgia Eizenga made an invited virtual presentation entitled "Phenotypic Data Augments Interpretation of Population Structure in the *Oryza rufipogon* Species Complex" based on the co-authored research article submitted to the *Frontiers in Plant Science* special issue entitled "Reproductive Barriers and Gene Introgression in Rice Species -Volume II". The conference was organized by co-editor of the special issue, Dayun Tao (Yunnan Academy of Agricultural Sciences), along with Yaoguang Liu (South China Agricultural University), Yidan Ouyang (Huazhong Agricultural University) and Zhigang Zhao (Nanjing Agricultural University).

JANUARY 2022

DB NRRC scientists, Drs. Yulin Jia, Anna McClung and Georgia Eizenga participated in the Plant and Animal Genome Conference XXIX held January 8-12, 2022, which was changed to a virtual conference due to rising covid cases on January 5, 2022. As part of the conference Anna presented *Utilization of the USDA-ARS Germplasm Collection in US Rice Breeding Programs* in the "Rice as a Model for Genetics, Genomics and Breeding" workshop which had 42 participants. This workshop was organized and chaired by Dr. Jia. Georgia was scheduled to present *Exploring Relationships Between Phenotypic Groups and Genotypic Subpopulations in Ancestral Rice, the Oryza rufipogon Species Complex (ORSC)* in the "Genomics of Genebanks" workshop but due to technical difficulties, the workshop organizers decided to postpone the workshop until 2023.

Speakers in the Rice as a Model for Genetics, Genomics and Breeding workshop organized by Dr. Yulin Jia.

Value of Using USDA Rice Germplasm Resources in Breeding

- Traits/genes are not present in the narrow US genepool- sterility restorers
- Capture new grain qualities for high value markets: basmati, jasmine, risotto, Japanese premium quality, high amylose, resistant starch, protein
- New threats: new pests, new biotypes of existing pests, impacts of climate extremes
- New production systems: alternate wetting and drying, upland, organic
- *Most of the germplasm is not restricted by IP*

The value of the USDA-ARS Rice Germplasm Collection (Dr. Anna McClung)

On January 19, 2022, Dr. Trevis Huggins shared updates about the National Small Grains Center (NSGC) rice germplasm and Genetic Stocks Oryza (GSOR) germplasm at the Rice Breeder's meeting. The updates included information about addressing redundancy and true-to-type issues in the NSGC collection. The breeders were also informed of the six new phenotypic traits that have been added to GRIN and the genotyping of the low inventory and redundant by name accessions. The attendees were also informed of the two new sources of genetic diversity that will be added to the collection in the next two years.

FEBRUARY 2022

On February 15, 2022, Dr. Yulin Jia gave an overview of research opportunities at Dale Bumpers National Rice Research Center to 30 faculty members of 1890 land grant universities who are interested in applying for faculty research sabbatical program at USDA ARS. The meeting was organized by Dr. Nina Lyon Bennett, Assistant Dean for Academics, School of Agriculture, Fisheries & Human Sciences, University of Arkansas at Pine Bluff.

On February 16, 2022, Dr. Shannon Pinson provided to Dr. Lew Ziska at Columbia University, New York, NY, seed harvested over an eight-year period for the purpose of studying the effect of annual differences in field temperatures on the concentration of arsenic in rice grains.

On February 22, 2022, Dr. Shannon Pinson provided information to Dr. Debasis Golui at North Dakota State University, Fargo, ND, regarding selection of rice accessions for use in studies on arsenic uptake by rice plants.

As part of a collaboration between Dr. Georgia Eizenga (DB NRRC), and Dr. Diane Wang (Purdue University), Master's student Racheal Imel (Purdue University) evaluated water-deficit responses in wild-by-cultivated rice introgression lines in a high throughput phenotyping facility at Purdue University. Aaron Jackson and Dr. Jeremy Edwards shared the merged gene annotation files they developed from on-line databases for identifying candidate genes with Rachel so she could identify the underlying candidate genes associated with tolerance to reduced water

On February 25, 2022, Dr. Yulin Jia provided information to a faculty member from Texas Tech University, Lubbock and assisted to establish a research project with University of Arkansas- Pine Bluff and Dale Bumpers National Rice Research Center on genetic and molecular regulation of plant immunity.

MARCH 2022

On March 17, 2022, Dr. Shannon Pinson provided information to Dr. Debasis Golui at North Dakota State University, Fargo, ND, regarding selection of rice germplasm for use in studies on arsenic uptake by rice plants.

APRIL 2022

On April 4, 2022, Dr. Shannon Pinson was invited, as an expert on genes and mechanisms for reducing rice grain arsenic concentrations, to participate in a USDA NIFA workshop (virtual) designed to share knowledge and identify knowledge gaps related to toxic elements in food crops and their products.

On April 12, 2022, Dr. Anna McClung provided small, packaged samples of Riceland rice for use on an event on April 26, 2022. This was part of the University of Arkansas for Medical Sciences (UAMS) program on culinary medicine that was conducted by Ms. Alyssa Frisby. On April 26, 2022, Ms. Frisby and other UAMS staff prepared a grain-based salad for forty students as a demonstration of a healthy food at the J.A. Fair K8 Preparatory School, a magnet school, located in Little Rock which opened in August 2021. The small samples of milled rice from Riceland along with homemade trail mix were provided to the students to take home as part of an effort to demonstrate rice as part of a healthy balanced diet to these young people.

On April 27, 2022, Dr. Shannon Pinson provided information to Dr. Sarah Beebout, National Program Leader of USDA National Program 216 - Sustainable Agricultural Systems, regarding rice grain elements grown flooded and unflooded.

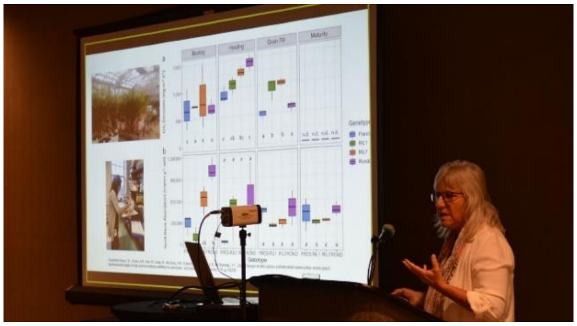
On April 27, 2022, Drs. Anna McClung and Shannon Pinson were invited speakers for the joint USDA and US FDA all day public meeting entitled “Closer to Zero”, an initiative to lower exposure of infants and toddlers to toxic elements like arsenic, lead, mercury, and cadmium in food. Dr. McClung presented “Mitigating Arsenic in Rice, A Path Forward”, and Dr. Pinson presented “Plant Genes and Mechanisms that Regulate Arsenic Uptake, Transport, and Accumulation in Rice Grains”. The meeting had more than 900 registrants and was attended by nearly 400 industry representatives and crop researchers.

JUNE 2022

On June 2, 2022, 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 purposes.

JULY 2022

Dr. Anna McClung was an invited speaker at the 5th Global Research Alliance Paddy Rice Research America Sub-group meeting that was hosted by the ARS Delta Water Management Research Unit, in Jonesboro, AR on July 12-13, 2022. The event was attended in person and virtually by 50 participants from USA, Europe, India, and numerous countries in Central and South America. The purpose of the meeting was to discuss the latest research findings and the opportunities to reduce greenhouse gas emissions associated with sustainable rice production. Dr. McClung presented a talk "The Role of Rice Genotypes in Mitigation of Methane Emissions" which highlighted research findings from collaborative work conducted at DB NRRC, much of which was led by Dr. Jinyoung Barnaby, former Plant Physiologist with the unit. After the formal presentations, breakout groups discussed various approaches for future research. Dr. McClung led the discussion regarding biological mitigation efforts.



On July 15, 2022, Dr. Yulin Jia provided disease evaluation for rice farmers in southeast of New York. This was performed based on disease pictures in consultation with Dr. Yeshi Wamishe, an extension plant pathologist of University of Arkansas Rice Research and Extension Center.

On July 27, 2022, Dr. Shannon Pinson provided information to Jane Houlihan, Director of Research for the non-profit Healthy Babies Bright Futures (hbbf.org), regarding the accumulation of mineral elements in rice grains.

On July 27, 2022, Drs. Anna McClung and Shannon Pinson provided information to Pamela Starke-Reed, USDA ARS Deputy Administrator for Nutrition, Food Safety and Product Quality/New Uses, regarding factors that can reduce accumulation of toxic elements in rice grains.

AUGUST 2022

On August 17, 2022, Drs. Yulin Jia, Shannon Pinson and Jai Rohila virtually met with Dr. Mario Ferruzzi, Professor and Chief of the Section of Developmental Nutrition in the Department of Pediatrics at the University of Arkansas for Medical Sciences, to discuss how the content of nutritional and detrimental minerals, starches, and antioxidant compounds in rice grains are affected by genetics, production system, and environment.

On October 3, 2022, Dr. Yulin Jia led a field tour to Dr. Samuel Gnanamanickam, Agricultural Consultant/Plant Pathologist & PGPR Pioneering Scientist, Fort Worth, Texas. Subsequently they discussed research on rice diseases with Dr. Yeshi Wamishe, Extension Plant Pathologist of University of Arkansas Rice Research and Extension Center (UA RREC).

L to R: Drs. Wamishe, Jia and Gnanamanickam. Picture taken at UA RREC

On October 7, 2022, Dr. Yulin Jia introduced DB NRRC research program and led a field tour of DB NRRC research to Dr. Karen Mencl, Professor of the Ohio State University, and Dr. Larry Antosch, Senior Director of Ohio Farm Bureau, Columbus, OH.

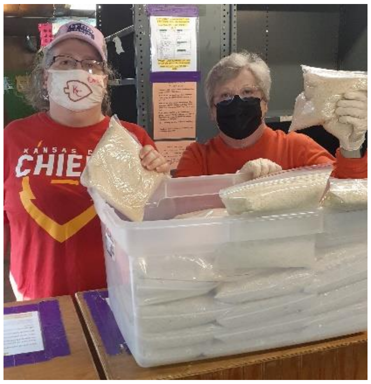
On October 7 – 18, 2022, Drs. Yulin Jia, Shannon Pinson, and Anna McClung communicated in-person and via email with Dr. Scott Lafontaine, Food Science Department, University of Arkansas, Fayetteville, to provide advice on selection of rice germplasm for evaluating effects of rice grain starch, antioxidant, and aroma qualities as ingredients for various beverage markets. ARS scientists provided Dr. Lafontaine with grain samples of nine rice varieties.

On October 31, 2022, Dr. Yulin Jia provided two blast cultures to Dr. Satish Ponniah of University of Arkansas at Pine Bluff (UAPB), and Heather Box, Biological Science Lab Technician showed Dr. Ponniah’s graduate students Rehhan Mutethia and Bishnu Prasad Joshl how to collect blast from oatmeal plates. This is ongoing collaborative research between DB NRRC and UAPB on the development of novel strategies to control rice blast disease.

Education, Outreach and Interactions with Rice Industry Stakeholders

The research article entitled "Enhancing the Searchability, Breeding Utility and Efficient Management of Germplasm Accessions in the USDA-ARS Rice Collection", published in *Crop Science*, was selected as one of two 2021 Outstanding Papers in the Plant Genetic Resources division (C8) of the Crop Science Society of America (CSSA). The award was announced at the C8 Division business meeting on November 10. The article was selected based on scientific merit, innovation, and discovery of novel or new approaches in the field of plant genetic resources. The publication was authored by DB NRRC scientists, Anna McClung, Jeremy Edwards, Melissa Jia, Trevis Huggins, and Georgia Eizenga, and curator of the rice germplasm collection, Harold Bockelman. The article can be found at: https://doi.org/10.1002/csc2.20256.

On January 14, 2022, DBNRRC donated 64lbs of milled rice to the Stuttgart, AR. Food bank



On February 4, 2022, Dr. Yulin Jia attended a brainstorming virtual meeting with faculty members of University of Arkansas, Rice Research and Extension Center, Stuttgart, UA-Pine Bluff, and ARS- Delta Water Management Research Unit, Arkansas State University, Jonesboro. The discussion was focused on ideas to provide STEM students with hands-on experience in agricultural research that address a range of issues from rice physiology, genetics to irrigation and/or climate change.

On February 18, 2022, Dr. Trevis Huggins virtually participated in the Former Lions In Research and Technology (FLIRT) symposium. Dr. Huggins spoke with undergraduate students in the Natural Science department about careers in plant science. He also shared his experiences as a graduate student and spoke about study habits, and life habits that are essential to be a successful graduate student.

On March 23, 2022, Dr. Trevis Huggins was invited to speak at the Center for Computational Systems Biology Biweekly virtual seminar at Prairie View A&M University in Texas. The title of Dr. Huggins's seminar was "Curating the USDA-ARS National Small Grains Rice World Collection and the Genetic Stocks Oryza Collection". The seminar was organized by Dr. Tesfamicheal Kebrom, a research associate at Prairie View A&M, and a former colleague at Dr. Dirk Hays Lab at Texas A&M University. The seminar participants included undergraduate students and professors.

Staff with the Dale Bumpers National Rice Research Center recently participated in a mentorship with the Arkansas Children's Nutrition Center in Little Rock, AR. Jacqueline Hughes, Office Automation and Glen Beedle, Program Support Assistant mentored Tobi Smith a recently hired Program Support Assistant. Jackie and Glen assisted Tobi for 3 days explaining how WebTA, ARIS entries, travel, purchasing, annual reports and other ARS procedures are processed. Thanks to their efforts, Tobi will be familiar with the daily operations of her center.

On May 17, 2022, Dr. Yulin Jia welcomed two undergraduate students Mr. John Mitchell and Mr. Isaiah Young from the University of Arkansas at Pine Bluff, an 1890 historically black University and their faculty advisor Dr. Sathish Ponniah at Dale Bumpers National Rice Research Center, Stuttgart, AR. The students discussed their research interests and potential projects for the summer of 2022 with Dr. Jeremy Edwards and Dr. Jai Rohila. After the discussion the visitors had a tour of greenhouses and labs.

From left to right: Dr. Yulin Jia, Dr. Jeremy Edwards, Mr. John Mitchell, Mr. Isaiah Young, Dr. Jai Rohila and Dr. Sathish Ponniah.

On May 20, 2022, Dr. Yulin Jia was named as **Mentor of the Year** for 2021 cohort for career development program (CDP) of Federal Asian Pacific American Council (FAPAC, https://fapac.org/) during 2021 graduation and opening ceremony for 2022 class. Dr. Jia

has been a mentor for CDP since 2016 and was also named as a mentor of year for 2020 class. The CDP is six-month mentoring opportunity for all federal, military and the District of Columbia employees with permanent career status at all levels. The CDP mentors and mentees must be able to participate in all program components including orientation, mutually scheduled one-on-one mentoring sessions, professional development workshops, a mid-term progress review, leadership projects, and graduation. The role of a mentor is to foster caring and supportive professional relationships, encourage mentees to develop to their full potential, provide resources to strengthen personal goals and career planning, and prepare participants for career advancement opportunities.
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On June 24, 2022, 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.

From left to right: Su, Orbiz, Avila, Audres, Marshall, Rodrigues and Alfred in a greenhouse at DBNRRC.

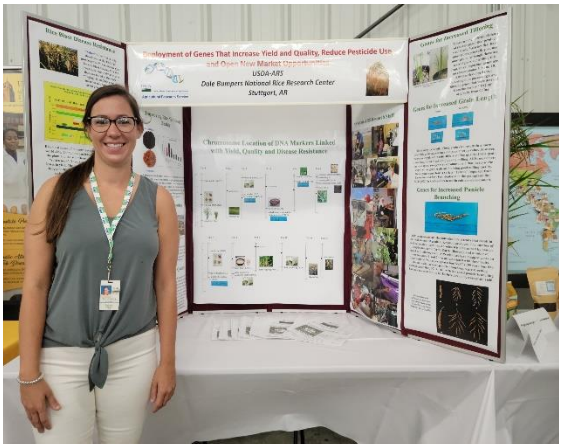
On June 24, 2022, Drs. Shannon Pinson, Yulin Jia, Jai Rohila, and Georgia Eizenga, along with Mr. Jonathan Moser and Ms. Melissa Jia took turns hosting Ms. Megan Bristol, undergraduate at University of Arkansas, Fayetteville. Ms. Bristol is in Stuttgart, AR this summer working with Dr. Yeshi Wamishe, research and extension pathologist, UAR Rice Research and Extension Center. She asked to spend one day job shadowing at the DB NRRC 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.

On July 27, 2022, Dr. Shannon Pinson was job-shadowed by a young man who will be starting his High School career this fall at Stuttgart High School, interested in a future career in Genetics. Dr. Pinson demonstrated the daily use of math, chemistry, engineering, and economics as well as biology in her career as a crop plant geneticist.

On August 3, 2022, Drs. Anna McClung and Trevis Huggins were visited by Mr. Don Quattlebaum of historic White House Farms located in Georgetown County, South Carolina where they produce Charleston Gold rice. He was accompanied by Dr. Brian Ward, Assistant Professor with Clemson University, and they were seeking information on establishing operations in South Carolina to produce pure seed of Carolina Gold derived varieties. Although, these specialty varieties are grown on very limited acreage, they offer high value market opportunities for small independent growers.

On August 5, 2022, DB NRRC scientists, staff and National Program leader Dr. Jack Okamuro attended the Rice Research and Extension Field Day held by the University of Arkansas Rice Research & Extension Center (UA RREC) in Stuttgart, AR. At the field day luncheon, Dr. Okamuro delivered remarks on the importance of the US rice industry and rice research. DB NRRC scientists and staff presented three posters at the field day. The posters showcased the USDA's rice collections and how DB NRRC scientists are utilizing this material to identify lines that are resistant to biotic and abiotic stress and have superior quality to share with the rice community. There was also a selection of rice products from local farms that have utilized germplasm that DB NRRC scientists selected and improved from the collections. Drs. Jeremy Edwards, Anna McClung, Georgia Eizenga, Trevis Huggins, Ms. Heather Box and Ms. Melissa Jia were available to interact with attendees and answer questions about the posters.

Dr. Jack Okamuro



Bio Science Tech Ms. Heather Box.

Geneticist Ms. Melissa Jia.

On August 18, 2022, Glenn Roberts from Anson Mills, Columbia, SC visited with Drs. Anna McClung and Trevis Huggins, and Mr. Adam Rice to view seed increase operations for the USDA ARS rice collection as well as for new specialty rice varieties released from the DB NRRC research program. Pictured here is the nursery for seed increases from the *Oryza glaberrima* collection, a rice species indigenous to Africa.

Left to right: Glen Roberts, Adam Rice and Dr. Trevis Huggins

On August 19, 2022, Drs. Yulin Jia, Anna McClung, Shannon Pinson, Jai Rohila, Georgia Eizenga, and Jeremy Edwards along with Ms. Melissa Jia and Mr. Aaron Jackson virtually met with Pete Vegas and Danny Baxter with Sage V Foods to share information about the virtually cooking and processing quality needs of the US rice industry and how these qualities might be provided met through improved genetics of US rice varieties.

On October 19, 2022, Dr. Jeremy Edwards and Dr. Jai Rohila traveled to the University of Arkansas at Pine Bluff (UAPB, an 1890 Land-Grant Institution) as invited guests to attend the USDA-ARS student internship final presentations. This is a new summer internship program that was established this year by UAPB and USDA-ARS to give undergraduates hands-on research experience that will help them apply what they've learned in the classroom to real-world situations. After the interns' presentations, Dr. Edwards and Dr. Rohila spoke about their enthusiasm for the program and future opportunities for internships at the DB NRRC. John Mitchell, an intern co-mentored by Dr. Edwards and Dr. Rohila, and advised by Dr. Sathish Ponniah (UAPB), presented his summer research project on identification of genetic factors that help rice grow with less water. For more details, see the article on John's internship in the *Stuttgart Daily Leader*: https://www.stuttgartdailyleader.com/agricultural-research-service-internship-leads-to-uapb-student-being-employed/

From left to right: Dr. Jeremy Edwards, John Mitchell, Erikton Goodloe, Trent Wills, Kur'an Suluki, Madison Purifoy, and Dr. Jai Rohila

On October 19, 2022, Chris Isbell, a rice farmer in Arkansas (a multi-generational family rice farm located in Central Arkansas with a focus on the sustainable production of quality rice) visited Dr. Yulin Jia (Research Plant Pathologist/acting Center Director /Research Leader) and plant pathology team (Heather Box, Paul Braithwaite) to examine disease resistant premium medium grain improvement program at DB NRRC.

From left to right: Mr. Isbell, Dr. Jia and Mr. Braithwaite

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/