



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



**OCTOBER 2023**

## **MONTHLY RESEARCH HIGHLIGHTS**

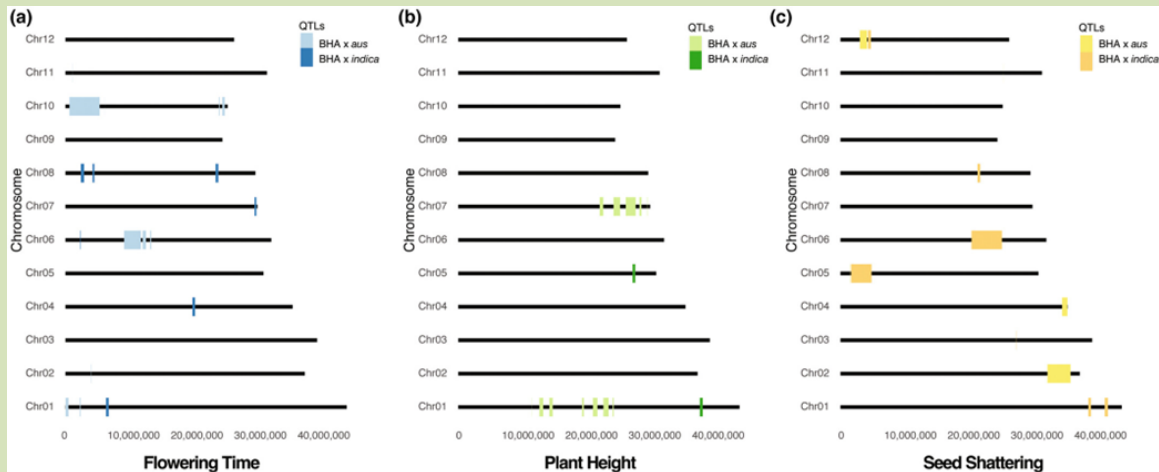
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- **Recent Scientific Publications**

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

Li, X., Zhang, S., Lowey, D., Hissam, C., Clevenger, J., **Jia, Y.**, Caicedo, A.L. 2023. A weed x ancestral cultivar cross identifies evolutionarily relevant weediness QTLs. *Molecular Ecology*. Published online: October 20. DOI: <https://doi.org/10.1111/mec.17172>

Weedy rice is a weedy relative of cultivated rice that poses a significant threat to crop production by competing with crops and causes considerable yield loss. The annual yield loss in the United States alone due to weedy rice infestations could feed approximately 12 million people. Weedy rice has evolved independently from various cultivated rice groups through a process of de-domestication, during which it has evolved a suite of traits collectively known as the "agricultural weed syndrome." These traits include rapid growth, high nutrient use efficiency, seed dormancy, seed dispersal, and herbicide resistance. However, the genetic basis underlying these weediness traits remains to be fully elucidated. To address this knowledge gap, we developed a novel mapping population through a cross between BHA weedy rice and aus cultivars to explore the genetic mechanisms underpinning three key weedy traits: flowering time, plant height, and seed shattering. A significant novelty of this study is that we took into consideration the phylogenetic relationships between the parents of the cross. We leveraged population genomic data to identify regions under selection and overlapping these selective sweeps with quantitative trait loci (QTLs) could enable us to identify the QTLs that contribute to the evolution of weediness traits. We performed QTL mapping using a combination of bulked segregant analysis and high-throughput whole-genome re-sequencing, resulting in a more time-efficient and accurate method. The loci and candidate genes identified not only provide insights into the genetic basis of evolutionary mechanisms of these traits but also have the potential to inform weed management strategies and help identify rice varieties that are more likely to produce weedy descendants.

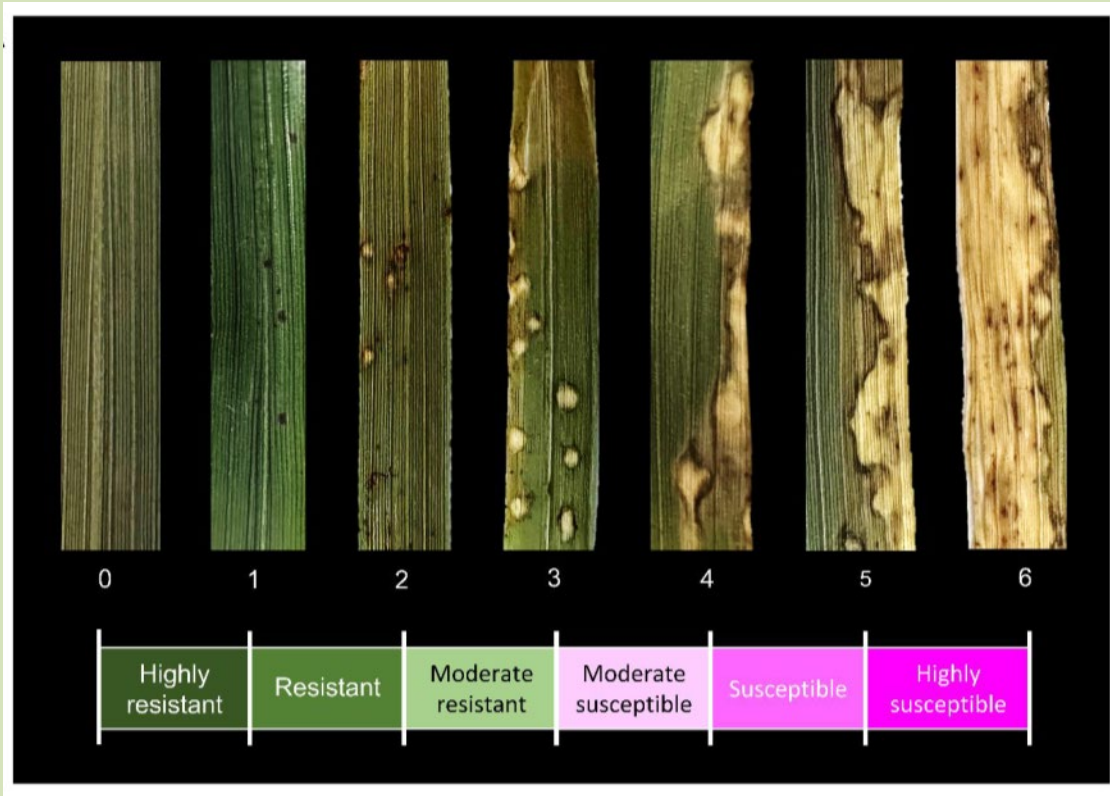


Distributions of the Quantitative Trait Loci (QTLs) identified in the crosses of BHA  $\times$  aus and BHA  $\times$  indica for the three weedy traits, flowering time, plant height and seed shattering along the chromosomes. (a) Flowering time; (b) plant height and (c) seed shattering. The colored rectangles represent the QTLs along the chromosome.

*This addresses USDA-ARS Research Goal:* Improved plant breeding techniques that apply knowledge from genetic interaction with environment and management factors and interactions with economically important pests of crops.

Oliveira-Garcia., Ely, Budot, Bernard Orense, Manangkil., Jennifer, Lana, Felipe Dala, Angira, Brijesh, Famoso, Adam, and **Jia, Yulin**. 2023. An efficient method for screening rice breeding lines against races of *Magnaporthe oryzae*. Plant Disease. Published online: October 8. <https://doi.org/10.1094/PDIS-05-23-0922-RE>

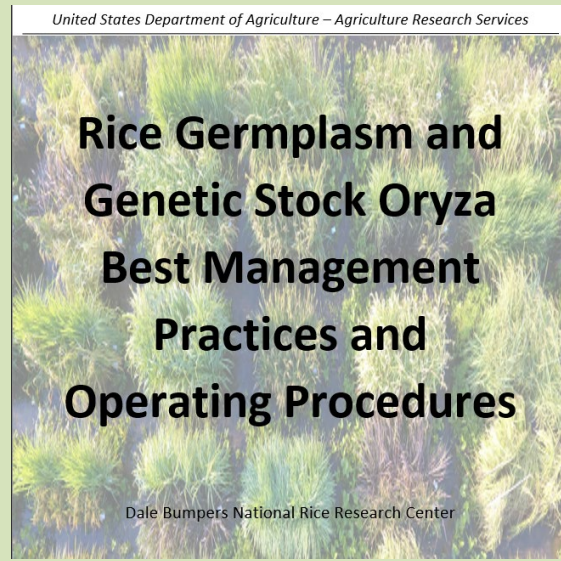
Blast disease of rice caused by the fungus *Magnaporthe oryzae* is one of the most lethal diseases of rice worldwide. Traditionally the 0-5 scale rating has reached limited success to evaluate disease reactions of breeding lines and rice varieties for breeding and genetic studies. In the present study, we developed a 0-6 scale for blast disease that allowed assignment of rice breeding lines and varieties into six resistance levels (highly resistant, resistant, moderate resistant, moderate susceptible, susceptible, and highly susceptible) by using 40 common rice varieties with known disease reactions under field conditions and tested them against four major blast races (IB1, IB17, IB49, and IE1-K) under greenhouse conditions. Disease reactions using 0-6 rating system verified field observations of rice varieties with blast resistance genes. Varieties carrying the *Pi-ta* gene were either highly resistant, resistant, or moderate resistant to IB17. The IE1-K race was able to break *Pi-ta*-mediate resistance of the rice varieties. The *Piz* gene conferred resistance to the IB17 and IE1-K races. The varieties M201, Cheniere, and Frontier were highly susceptible (score 6; 100% disease) to the race IE1-K. Moreover, varieties that were resistant or susceptible to all four blast races also showed similar levels of resistance/susceptibility to blast disease in the field. Taken together, our data proved that the 0-6 blast scale can efficiently determine the resistance levels of rice varieties against major blast races. This new method will assist rice breeding programs to incorporate durable resistance against major and emerging blast races.



**Trevis Huggins and Yulin Jia. 2023.** Rice Germplasm and Genetic Stock Oryza Operating Procedures and Best Management Practices.  
[https://www.ars.usda.gov/ARUserFiles/60280500/GSOR/Rice%20Germplasm%20SOP/Rice\\_germplasm\\_SOP\\_v7web.pdf](https://www.ars.usda.gov/ARUserFiles/60280500/GSOR/Rice%20Germplasm%20SOP/Rice_germplasm_SOP_v7web.pdf)

Genebanks are an essential part of the effort to conserve worldwide crop genetic diversity and wild species. Curators play an important role in providing valuable information that can be used by plant breeders to improve agricultural productivity and nutritional quality. Rice germplasm collections are challenged by multiple issues such as seed mixtures, misidentification of accessions, accession redundancy, lack of phenotypic and genotypic characterization, and poor seed viability. To address these issues, Drs. Huggins and Yulin Jia wrote a handbook that extensively outlines the key steps in the rejuvenation and characterization process of rice germplasm from start to finish. This document includes methods to identify common rice diseases, rice blast, sheath blight, false smut, kernel smut, Brown spot, Narrow Brown Leaf Spot and a new emerging rice disease, bacterial leaf blight caused by *Pantoea ananatis*. The document is the first of its kind for the curation of rice germplasm in the U.S. and facilitates the effective and efficient curation of the NSGC and GSOR rice germplasm collections. The document includes a flow chart that summarizes the rejuvenation and characterization process of the rice germplasm and includes imaging of seeds received from NSGC, comparison of seed to data in GRIN-Global, IRRI GRIN and Ted Johnson field books, germination of seeds to test viability, leaf tissue collection for DNA and genotyping, imaging of panicles at flowering and maturity and resolving true-to-type

discrepancies. The document includes seven new trait descriptors, apiculus color, awn color, presence of long sterile lemma, leaf blade pubescence, photoperiod/daylength sensitivity, seed shattering and leaf blade color to improve characterization and phenotyping. These descriptors were added to the rice characterization descriptors on GRIN-Global. All rejuvenated NSGC rice accessions are genotyped with 24 molecular markers for traits of interest to U.S. rice breeders is standard practice. The document also addresses accession redundancy, redundant by name (RBN) accessions are planted side-by-side in the field and evaluated for phenotypic traits. The RBN accessions are also genotyped with 24 molecular markers to create a genetic profile. The phenotypic and genotypic data collected was used to create a system to characterize whether they are similar or different genotypically and phenotypically. These efforts have enhanced the value and utilization of the germplasm, especially for economically important traits to U.S. rice breeders. Stakeholders will be assured of true-to-type germplasm with good viability and genotypic characterization. Identified RBN accessions that were phenotypically and genotypically similar were removed from active distribution, thus freeing space for additional genetically diverse germplasm.



- **Technology Transfer**

- ✓ **Interactions with the Research Community**

On October 7, 2023, Dr. Jeremy Edwards gave an invited talk for a symposium at the Boyce Thompson Institute in Ithaca NY, honoring the retirement of Dr. Susan McCouch. Dr. McCouch is the Barbara McClintock Professor of Plant Breeding and Genetics at Cornell University and a member of the National Academy of Sciences. Dr. Edwards, a former Ph.D. student of Dr. McCouch, presented an overview of his current research program, his history of working in the McCouch lab, and how Dr. McCouch has influenced his research and approach to mentoring new scientists. Dr. McCouch has been a long-time collaborator and supporter of the DB



NRRC, and DB NRRC researchers have served as co-investigators with Dr. McCouch on a series of grants from the National Science Foundation. As a result of these grants, many genetic stocks were generated, and these stocks are now distributed through the Genetic Stocks-*Oryza* collection located at the DB NRRC. One of these genetic stocks was developed and released in partnership with former DB NRRC Center Director Dr. Anna McClung as a commercially successful specialty rice variety named “Scarlett”, which has a nutty and rich flavor with high levels of antioxidants and flavonoids. Dr. McCouch has been a powerful force in building a strong and interconnected community of rice researchers and stakeholders in the US and around the globe. DB NRRC thanks Dr. Susan McCouch for her outstanding scientific contributions, leadership, and vision throughout her career, and wishes her a fulfilling and happy retirement.

✓ **Rice Germplasm Distributed**

During the month of October, 1 rice genetic stock was shipped to researchers in the United States.

● **Education and Outreach**

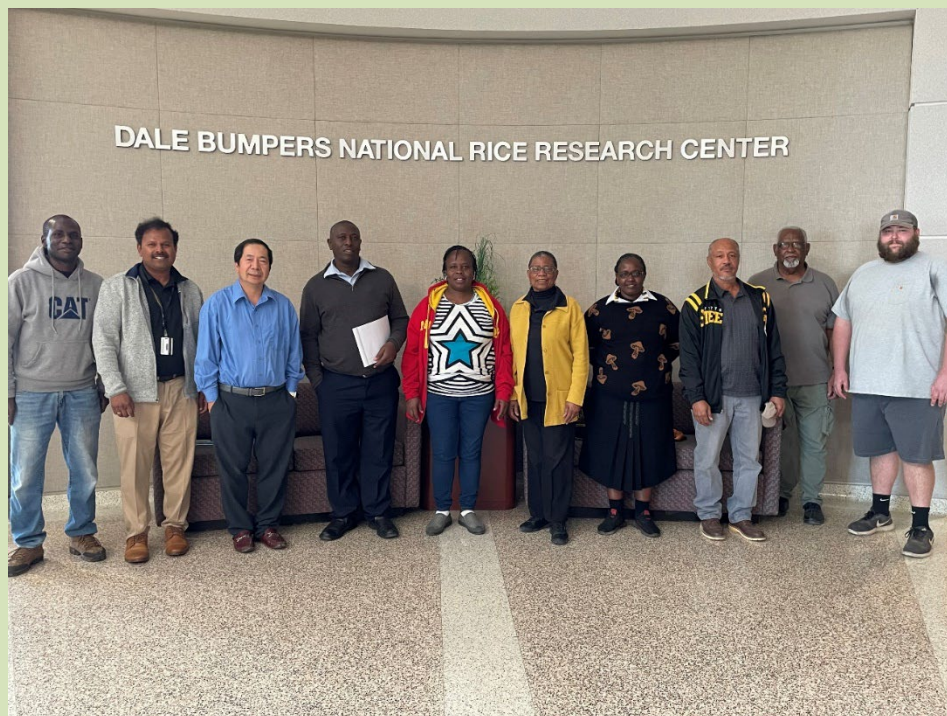
On October 26, 2023, DBNRRC celebrated our end of the year rice harvest with a harvest day celebration. Members of the committee to plan the celebration were Jackie Hughes, Quynh Grunden, Melissa Jia, and Yulin Jia. There we had hamburgers and hot dogs with all the trimmings and many potluck items. We played games and had a costume contest. Prizes were awarded to the winners of the competitions. We enjoyed good food and good fellowship.





- **International Research Collaboration**

On October 16, 2023, after visiting Harry K. Dupree Stuttgart National Aquaculture Research center three scientists from Kenya, Drs. Rebecca Jepkorir Yegon, Geoffrey Kingori Gathungu, Mildred Pauline Nawiri visited DB NRRC organized by Dean Dr. Pamela Moore and Professor Dr. Satish Ponniah of University of Arkansas at Pine Bluff, School of Agriculture, Fisheries and Human Sciences. These scholars were visiting for a professional development program exploring topics associated with global food security, the food value chain and small farmer resiliency in an unpredictable global context. Dr. Yulin Jia, Acting Research Leader/Center Director welcomed visitors and presented an overview of the research program at DB NRRC. Mr. John Mitchell, graduate student who is conducting research at DB NRRC led a walking tour of DB NRRC facility.



October 25-28, 2023, Dr. Yulin Jia, Acting Research Leader and Center Director of DB NRRC with Dr. Alton Johnson, Director of University of Arkansas Rice Research and Extension Center (UA RREC) hosted a US-Japan Climate Change Workshop in a hybrid format (on site and virtual via MS Team) to present the progress and discuss challenges of the ongoing collaborative project between the USDA-ARS and National Agricultural and Food Research Organization (NARO), Japan. The workshop was attended by all scientists and staff at DBNRRC. Presentations were made by Dr. Yulin Jia and Dr. Shannon Pinson, DBNRRC, Dr. Sarah Beebout, NPL, National Resources and Sustainable Agricultural Systems (virtually), Dr. Noriko Yamaguchi and Dr. Koji Ito, National Agricultural and Food Research Organization (NARO), Japan, Dr. Michele Reba, Dr. Arlene Adviento-Borbe, Dr. Joe Massey, Delta Water Management Research Unit (DWMRU), and Dr. Alton Johnson, University of Arkansas (RREC). The presentation session was followed by a round table

discussion among all the DB NRRC and visiting scientists. Few other highlights of the workshop were participation of visitors in the Fall harvesting party with staff of DB NRRC, visit to UA RREC and DB NRRC facilities, field experimental site, visit to Museum of the Arkansas Grand Prairie, and presentations by Derek Thor Cary, John Shekailo from International Affairs, USDA-ARS explaining International Affairs roles in international collaborations, and Dr. Suntay Choi, USDA-RDA (South Korea) project coordinator providing ongoing collaborative projects in the US and opportunities to collaborate with RDA, South Korea.



*Project scientists visiting to field experimental site. From left to right: Koji Ito (NARO), Yulin Jia (DB NRRC), Noriko Yamaguchi (NARO), Jai Rohila (DBNRRC), Shannon Pinson (DBNRRC).*





*Visitors with Dr. Jia at the Fall harvest party. From left to right: Alton Johnson (RREC), Yulin Jia (DB NRRC), Michele Reba (DWMRU), Noriko Yamaguchi (NARO), Koji Ito (NARO), Joe Massey (DWMRU), Arlene Adviento-Borbe (DWMRU).*

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/>