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: Well-characterized genetic mapping populations and associated molecular markers designed for trait discovery, analysis, and breeding diverse crops.

Eizenga, G.C., Edwards, J.D., Jackson, A.K., Huggins, T.D. 2024. Substitution mapping of yield-related traits utilizing three Cybonnet rice x wild introgression libraries. Crop Science, 1-17. https:\\doi.org\10.1002/csc2.21264

Improving rice yields is a major objective of breeding programs worldwide. The *Oryza rufipogon* species complex (*ORSC*) which includes the rice ancestral species, *O. rufipogon* and *O. nivara*, is an underutilized resource. Using three phenotypically and genotypically diverse *ORSC* accessions identified as OrA, OrB and OrC, three Cybonnet x *ORSC* chromosome segment substitution line (CSSL) libraries were developed to make this genepool more accessible to breeders. The objective was to characterize the 212 CSSLs in these libraries for 20 yield-related traits to discover genes not currently deployed for rice improvement. Across the three libraries, 62 CSSLs were found to be significantly different from Cybonnet for one or more traits. To ascertain the chromosome region and underlying candidate gene(s) causing these differences, substitution mapping was performed utilizing both trait data and genotypes. Mapping with the CSSLs which had delayed heading under long days, revealed five known genes associated with rice flowering time pathways. The *OsMADS50*, *RFT1*, *HD3A*, *SE1* and *GHD7* genes were mapped in the Cybonnet x OrB and Cybonnet x OrC libraries but only *OsMADS50* mapped in the Cybonnet x OrA library. (Substitution mapping of the *RFT1*, *HD3A* and *SE1* genes is illustrated in the figure.) Employing this approach for the other 19 traits revealed 28 total candidate genes. Twelve of these genes are currently not deployed for yield enhancement. The introgressed *ORSC* regions associated with these genes are potential sources of novel variation for rice improvement.

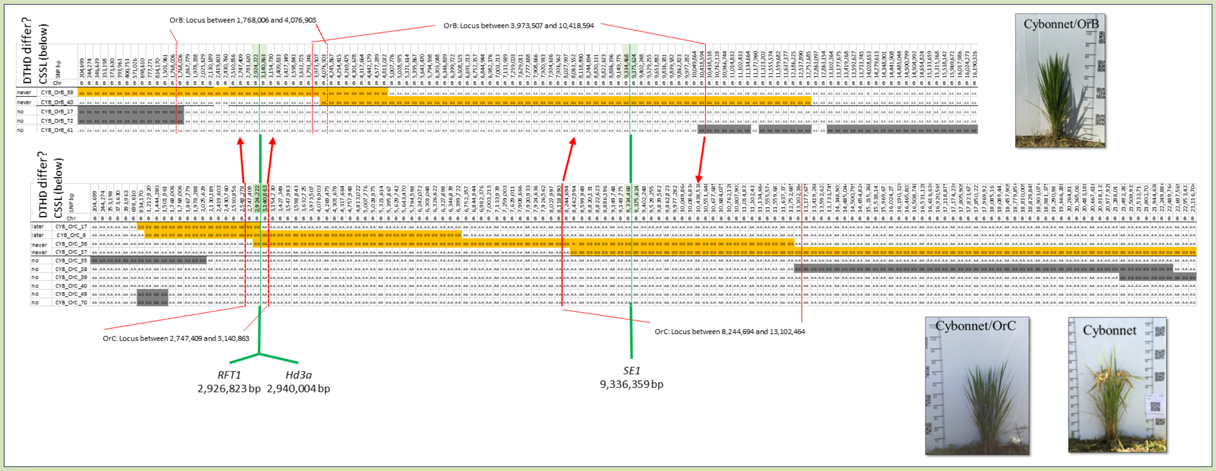
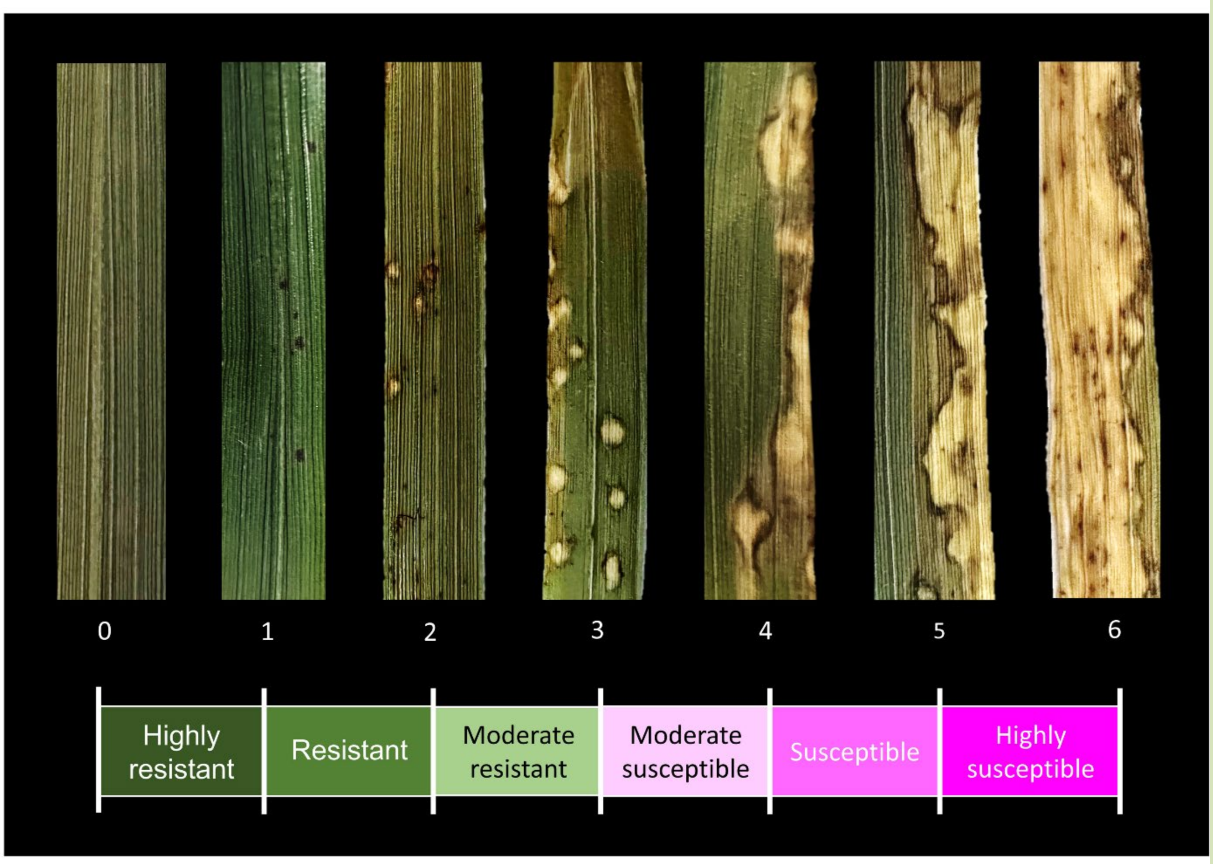


Illustration of substitution mapping on chromosome 6 for the days to 50% heading (DTHD) trait using the CSSLs in the Cybonnet (CYB) x OrB and CYB x OrC libraries which had ORSC introgressions in this region. The ORSC introgressions of the CSSLs which never headed or headed later than Cybonnet in the field season, are highlighted in gold, and the CSSLs which did not exhibit delayed heading are highlighted in gray. Substitution mapping identified the RICE FLOWERING LOCUS T 1 (RFT1) and HEADING DATE 3A (HD3A) genes (2.7-3.1 Mb) and the PHOTOSENSITIVITY 1 (SE1) gene (8.2-10.4 Mb).

This addresses USDA-ARS Research Goal: Crop plants with resistance or tolerance to diseases and pests.

Ely Oliveira-Garcia, Bernard Orense Budot, Jennifer Manangki, Felipe Dala Lana, Brijesh Angira, Adam Famoso and **Yulin Jia**. 2024. An Efficient Method for Screening Rice Breeding Lines Against Races of *Magnaporthe oryzae*. Published Online: Plant Disease. May 2, 2024, 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.

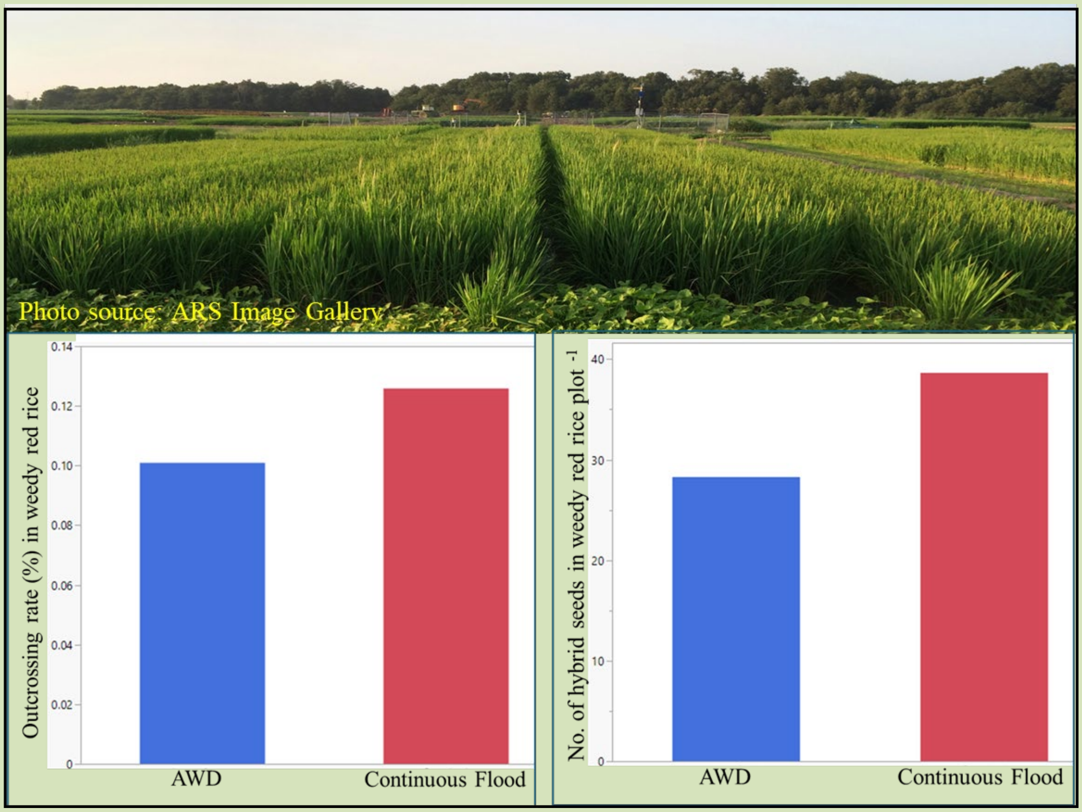


A new disease rating system for blast representing rice response to blast under field conditions.

This addresses USDA-ARS Research Goal: Climate resilient crop plants tolerant to limited water and environmental changes or extremes.

Rohila, JS., Gealy, DR., Jackson, AK., Ziska, LH. 2024. Assessment of outcrossing potential between cultivated and weedy rice under alternate wetting and drying irrigation management. Agronomy Journal. http://doi.org/10.1002/agj2.21594

Weedy red rice reduces the value of the rice crop and causes a high milling penalty for farmers. Since weedy red rice is essentially "rice" controlling it with herbicide requires rice growers to grow cultivated rice varieties that contain herbicide resistance. Rice growers routinely use Clearfield and Provisia varieties with herbicide resistance. Naturally occurring crosses between herbicide resistant (HR) varieties and weedy red rice can lead to herbicide resistant red rice genotypes, which can severely limit the efficacy of herbicide use for controlling red rice. To increase the understanding of outcrossing potential between rice and weedy red rice under water deficit irrigation systems such as AWD, a two-year replicated randomized field study was conducted. Outcrossing frequencies between two HR rice varieties (a long grain cv. CL142AR and medium grain cv. CL261), and two major weedy rice genotypes (blackhull and strawhull) were measured after growing together in plots irrigated with either conventional season-long flood or AWD irrigation. The study found that overall, AWD reduced outcrossing rates and the number of cross-hybrid seeds produced in weedy red rice. Specifically, outcrossing rates were significantly lower in medium grain than for the long grain rice cultivar, and the AWD irrigation management reduced outcrossing rates with the strawhull red rice, but not with the blackhull genotype. Further, the investigation explored potential explanations for these differences and found that higher outcrossing rates were associated with increased synchrony of flowering times and closer vertical proximity of panicles of weedy red rice to a rice variety. This study is the first of its kind to demonstrate that water conservation irrigation systems such as AWD have the potential to provide the additional benefit of reducing outcrossing between rice and weedy rice. The knowledge gained from this study will help in finding better solutions for long-term weedy rice control measures in commercial rice production by adding cultural management practices along with genetic improvement.



Weedy red rice (taller yellowish-green plants in the picture within rice rows) have potential for outcrossing with cultivated rice in commercial fields. The resulting cross-hybrid seeds could become herbicide tolerant and have economic impact by reducing quality of rice crop in the southern rice belt. Water conserving irrigation schemes such as AWD and furrow irrigation are good for sustainability and are being accepted among rice growers, but very little is known about the outcrossing risk between rice cultivars and weedy red rice, in such water conserving irrigation systems.

Technology Transfer

- ✓ **Interactions with the Research Community**

  On May 7, 2024, **Dr. Yulin Jia** and **Heather Dunlap (Box)** visited and offered a tour to museum curator, Curtis Smith. Smith is with the Arkansas Department of Parks, Heritage, and Tourism and he curates at the Plantation Agricultural Museum in Scott, AR. There they preserve Arkansas' farming history. The park is highly interactive and houses live exhibits. September through November 2024 the museum will showcase an exhibit named the "The History of Rice." We hope to showcase our work over the last 25+ years as a part of this history. Discussions with Smith were also centered around exploring outreach aspects, as they have an education building on site and would love to showcase some actual rice growing at the museum someday. We are grateful to have made this contact and hope to better connect with this area of Arkansas in the future.

  On May 22 – 23, 2024, **Mr. Jace Everette** attended the Rice Quality and Evaluation Short Course presented by Rice Processing Program Faculty, within the University of Arkansas Food Science Department, Fayetteville, AR. During this two-day training course, Mr. Everette interacted with members of the rice industry as well as Univ. of AR graduate students as they learned about how specific grain attributes impact the processing and end-use qualities of importance to the US rice industry and gained hands-on experience with various rice processing and evaluation equipment and methods available for use at the Univ. of AR Food Science Department. Mr. Everette gained specific knowledge on their use of NIR measurements for determining the degree of milling on rice samples based on their surface lipid contents. He also connected with multiple Rice Industry Partners during this training and arranged for future interaction and sharing of information with DBNRRC Scientists.

  On May 30, 2024, **Dr. Shannon Pinson** shared information with Mr. Max Hardish, Quality Food Scientist III at Post Consumer Brands, Lakeville, MN, on how the accumulation of elements in rice grains affected by genes, and by field irrigation management during crop production. This virtual meeting for informational sharing was a result of the above-mentioned participation by Mr. Everette in the May 22 & 23 Rice Quality and Evaluation Short Course.

- ✓ **Rice Germplasm Distributed**

  During the month of May, 17 rice genetic stocks were shipped to researchers in Canada and the United States.

- **Stakeholder Interactions**

  On May 21, 2024, **Dr. Yulin Jia**, **Dr. Shannon Pinson**, and **Mr. Jace Everette** attended the annual Rice Industry Alliance Meeting in Fayetteville, AR. This meeting was hosted by the Rice Processing Program within the University of Arkansas Food Science Department.

Nearly 100 attendees representing all aspects of the US Rice Industry, including farmers, millers, food processors such as Kellogg's and Anheuser Busch, and international marketers, as well as public and private breeders and researchers came together to share methodology and ideas for enhancing the food and processing quality of rice grains and rice-based foods.

- **New Research Grants**

Dr. Yulin Jia received an award entitled 'Risk assessment of emerging diseases caused by *Pantoea* spp. on rice, peanut, and corn in the USA' from the Office of National Programs. This is the second year of a team investigation of emerging crop diseases with scientists in ARS and Universities in the southern USA.

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/