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: Enhanced knowledge of existing diversity in crop plant interactions with biotic factors at the molecular level

Upinder S. Gill, Seonghee Lee, **Yulin Jia** and Kirankumar S. Mysore. (2018) Exploring natural variation for rice sheath blight resistance in *Brachypodium distachyon*. Plant Signaling & Behavior. Published on line December 12, 2018. DOI: 10.1080/15592324.2018.1546527S

Sheath blight caused by the soil borne fungus *Rhizoctonia solani* is a major disease of rice in the world. Developing genetic resistance in rice against this disease has not been very successful so far. We explored potential novel sources of durable resistance in a related model species, *Brachypodium distachyon*. Screening of *Brachypodium* accessions identified a few lines which showed a resistant response against the pathogen. We also quantified defense plant hormones in resistant, moderately susceptible, and susceptible *Brachypodium* lines and found a link between hormone concentration, especially jasmonic acid, and disease resistance. Our results provide a new foundation to explore this area for more durable resistance against sheath blight disease of rice.
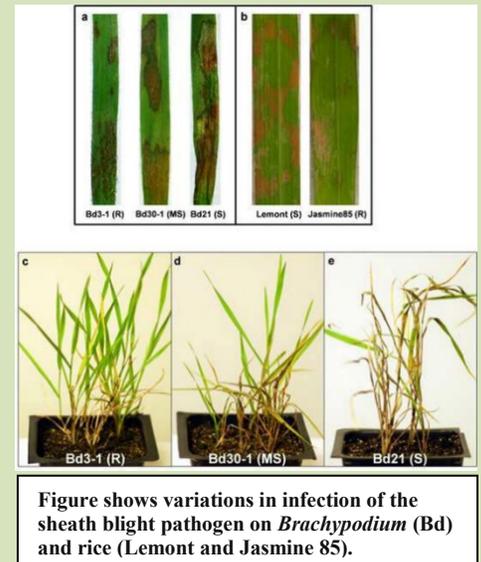
Figure shows variations in infection of the sheath blight pathogen on *Brachypodium* (Bd) and rice (Lemont and Jasmine 85).

This addresses USDA-ARS Research Goal: Development of crop plants with superior grain quality for consumers.

Chen, M.-H., Bergman, C.J., and **McClung, A.M**. 2019. Hydrolytic rancidity and its association with phenolics in rice brans. Food Chemistry.
https://doi.org/10.1016/j.foodchem.2019.01.139

Whole grain rice, which has the bran layer intact, contains more nutrients and health beneficial compounds than milled rice (bran moved) and its consumption is associated with a

reduction of several chronic diseases. However, the bran layer is also where most lipids are deposited along with lipid degrading enzymes, lipase and lipoxygenase, which shorten the shelf life of whole grain rice. A set of diverse rice varieties differing in bran color from the USDA-ARS world collection were evaluated for the lipase induced hydrolytic rancidity levels (HR) in the bran and more than 15-fold variation in HR was found. Among the varieties, those with red or brown bran had lower HR than the purple, light brown and white brans. Within the light brown bran color class, the bran color typical of U.S. cultivars, varieties having lower lipase activity than U.S. cultivars were found and could be used as breeding materials to improve storage stability of U.S. brown rice.
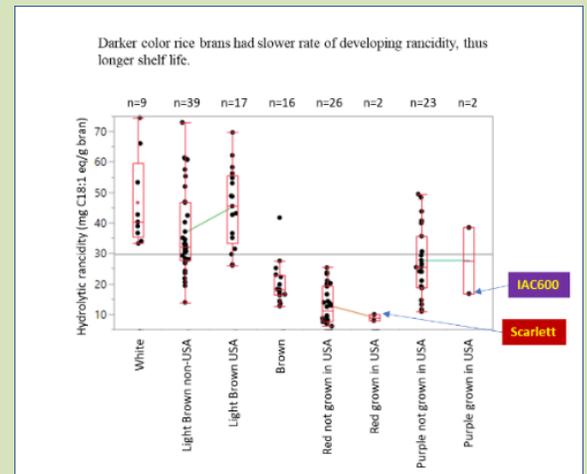
This addresses USDA-ARS Research Goal: Crop plants with resistance or tolerance to diseases.

Wenqi Li, **Yulin Jia**, Fengquan Liu, Fangquan Wang, Fangjun Fan, Jun Wang, Jinyan Zhu, Yang Xu, Weigong Zhong and Jie Yang. 2019. Integration analysis of small RNA and degradome sequencing reveals microRNAs responsive to *Dickeya zeae* in resistant rice. Published on January 8. International Journal of Molecular Sciences 20, 222, doi:10.3390/ijms20010222.

Rice foot rot disease caused by the pathogen *Dickeya zeae* is a newly emerging bacterial disease of rice. Plant microRNA, osa-miR396f, was reported to fight against the rice blast pathogen, *Magnaporthe oryzae* by degrading the target rice gene transcript. However, it is unknown if osa-miR396f or any other miRNAs are involved in resisting infection by *D. zeae*. In this study, using RNA sequencing, we identified 652 miRNAs including osa-miR396f from rice. We determined that there were 79 miRNAs including osa-miR396f whose expressions were different upon pathogen infection. Using degradome sequencing, we identified 799 target rice genes that can be degraded by 168 identified miRNAs. Among them, 29 differentially expressed miRNA and target gene pairs including miRNA396f-*OsGRFs* were determined by co-expression analysis. We then produced abundant transcripts of osa-miR396f in a susceptible rice variety and demonstrated that the susceptible rice with overexpressed miRNA396 has an enhanced resistance to *D. zeae*. Taken together, we showed miR396f plays an important role in rice disease resistance and this knowledge will aid the development of novel strategies to control rice diseases.

Expression of rice miRNA at different time points after pathogen inoculation
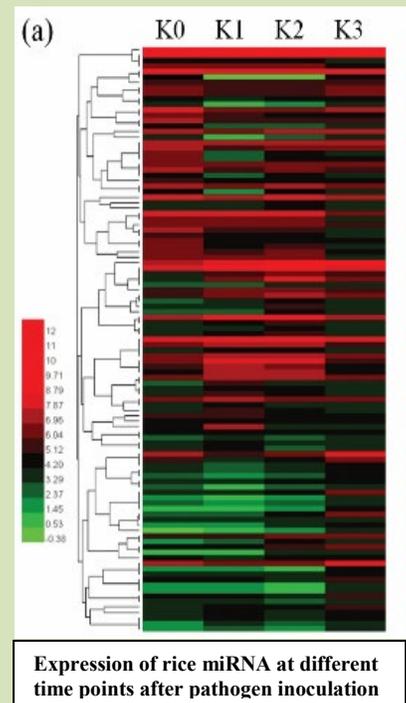
This addresses USDA-ARS Research Goal: Crop plants with enhanced nutritional quality

Chen, M.-H. and **McClung, A.M.** 2018. Genotypic diversity of bran weight of whole grain rice and its relationship with grain physical traits. Cereal Chemistry DOI:10.1002/cche.10117.

Rice bran, the outer most layer of the whole grain, is the primary site of deposition of most nutrients, minerals and bioactive compounds, however, rice bran accounts for a very small portion of the whole grain by weight. Increasing the proportion of the bran to whole grain weight will enhance whole grain (brown) rice nutritional value. Using 134 diverse rice cultivars from the USDA-ARS world collection, more than 2.3- and 2.5-fold variation in total bran weight and bran weight per surface area (BWS), respectively, of the whole grain was found. Purple bran genotypes had the highest BWS, followed by red, white, light brown and brown. This report showed high bran weight genotypes can be selected for in a breeding program to improve whole grain nutritional quality.

- **Technology Transfer**

  ✓ **Interactions with the Research Community**

  On Dec. 4th, Dr. McClung provided 2kg of rice straw for a research group evaluating its potential for use in purification of waste water.

  On Dec. 10th, Dr. McClung provided several pounds of rice grain for each of 22 diverse rice varieties for a researcher in Arkansas studying grain quality traits.

  ✓ **Rice Germplasm Distributed**

  During December and January, 348 rice accessions from the Genetics Stocks *Oryza* (GSOR) collection were distributed to researchers in the United States. 2018 marked the 14th year since the GSOR collection was established. During this time 105,678 genetic stocks have been distributed globally with 20,125 being sent out in 2018 alone. This demonstrates the increasing value of the materials in the collection to the rice research community.

  Forty-one new weedy red rice accessions were submitted to the USDA-ARS National Small Grains Collection for public distribution. The project was led by Dr. Dave Gealy and staff and included providing plant and grain trait data. This increases the number of diverse southern U.S. weedy red rice accessions available from the NSGC collection to a total of 69. The accessions were collected from Arkansas, Louisiana, Mississippi, and Missouri in 2000, prior to the extensive use of non-selective herbicides being used in rice production that is seen today. Thus, these accessions are a sampling of weedy red rice genetic diversity in the southern rice growing region. A number of these have been deposited at the Svalbard Global Seed Vault in Norway which houses a collection of over 1 million seed accessions representing some 6000 plant species. Svalbard Global Seed

Vault serves as a backup for critical portions of collections from world germplasm centers like USDA-NSGC.

- **Stakeholder Interactions**

On Dec. 1st, Dr. Anna McClung provide seed of 8 rice varieties for field testing in South Carolina for potential commercialization for niche markets.

On Dec. 13th, Dr. McClung provided seed rice of a specialty variety for production in the northeastern USA.

On Jan. 30th, Dr. McClung provided milled rice samples for sensory testing and future potential rice production in the mid-Atlantic area of the USA.

On Jan. 30th, Dr. Shannon Pinson provided advice to Dr. Manisha Barthwal, a scientist with the private rice breeding company Bayer BioScience Pvt. Ltd in India. Dr. Barthwal sought advice on using a grain fissure resistance evaluation method developed by Dr. Pinson as a breeding selection tool to develop improved rice varieties.

- **Education and Outreach**

On Dec. 11th, Dr. Anna McClung provided background information on rice production practices to optimize rice yield and grain nutritional quality to staff from the Canadian Broadcast Company and facilitated them meeting Arkansas rice growers on Dec. 19th for further information for a news story.

On Dec. 12th, Dr. McClung provided milled rice samples of ARS variety Carolina Gold Select to the ARS Information Staff for a news media story.

Evie Jackson is a 10th grade student at Stuttgart High School that was mentored by Dr. Trevis Huggins and Aaron Jackson at DBNRRC for a science fair project. Evie's project involved association mapping of 50 U.S. soybean lines for salt tolerance. Her project allowed her to advance from the local competition, to an opportunity to compete at the regional level. The project was conducted with modest supply costs, using publicly available data bases along with ARS facilities and resources. The genomic SNP information for the 50 soybeans was gleaned from public databases (ncbi.nln.nih.gov and figshare.com) and seed was provided by the USDA-ARS NPGS. The software used for the association mapping analysis, TASSEL, was developed by ARS researcher Dr. Ed Buckler in collaboration with Cornell University. Much of the basic statistics, spreadsheets, and word processing software came from the open source package, Apache Open Office. Evie found approximately 160 SNPs associated with salt tolerance, with 43 of these occurring at or near known salt tolerant genes. The remaining 100+ SNP's indicate potential regions where new salt tolerant genes reside. Evie's project highlights the importance of having public resources available to encourage STEM students and advance science. These resources provide opportunity for laboratories on limited budgets throughout the world to not only take advantage of the treasure trove of genetic information that exists, but also integrate it into breeding programs for crop improvement.