



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



**OCTOBER 2018**

**MONTHLY RESEARCH HIGHLIGHTS**

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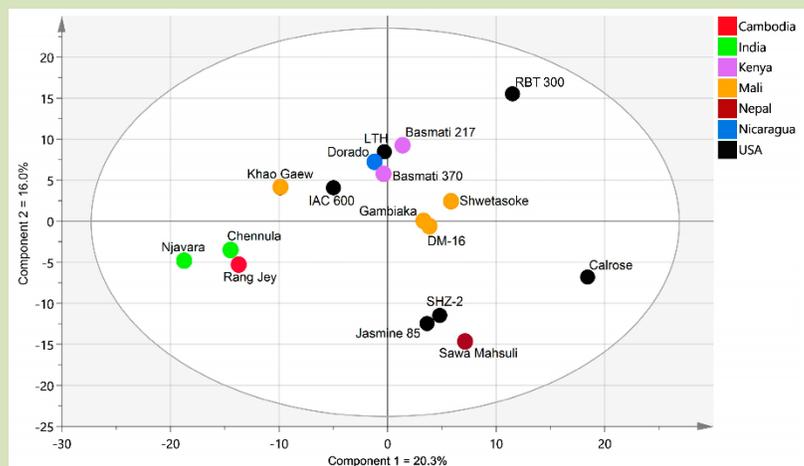
● **Recent Scientific Publications**

*This addresses USDA-ARS Research Goal: Development of crop plants with enhanced nutritional quality*

Zarei, I., Luna, E., Leach, J.E., **McClung, A.M.**, Vilchez, S., Ousmane, K., Ryan, E.P. 2018.  
**Comparative rice bran metabolomics across diverse cultivars and functional rice gene-bran metabolite relationships.** <https://doi:10.3390/metabo8040063>. Metabolites

During the rice milling process, the bran is removed to produce whole milled rice. Although some bran is used to produce rice bran oil, most bran is sold as inexpensive animal feed. Recent research has demonstrated that rice bran contains a number of nutritional compounds, namely bioactive metabolites, that are of benefit to human and animal health. Dietary consumption of rice bran has been shown to increase key nutrients and fiber intakes and provide health promoting properties in the

prevention and control of major chronic diseases, such as diabetes, chronic inflammation, cardiovascular disease, as well as cancers of colon, liver, prostate, and breast. There is limited information on how much variation exists among global rice cultivars for these bioactive compounds. The objective of this study was to investigate variation in the rice bran metabolome of 17 diverse cultivars and to identify genes and physiological pathways relevant to the nutritional and medicinal quality



of rice bran. The total number of metabolites identified ranged from 378 for the variety Njavara produced in India to 430 for the variety Gambiaka grown in Mali. Of the US developed varieties, Calrose medium grain rice, produced in California, had the highest total number of metabolites (421). Among the total number of compounds observed, 71 were found to differ in relative abundance among the 17 rice cultivars. Metabolites that are associated with lipids accounted for about 40% of the total metabolites. Rice bran is known to be a good source of the lipid soluble vitamin E which is an important antioxidant and free-radical scavenger that contributes to the bioactivity of rice bran. These results indicate that there is genetic variability for rice bran metabolites, many of which are associated with health beneficial properties, which affords the possibility of developing new rice

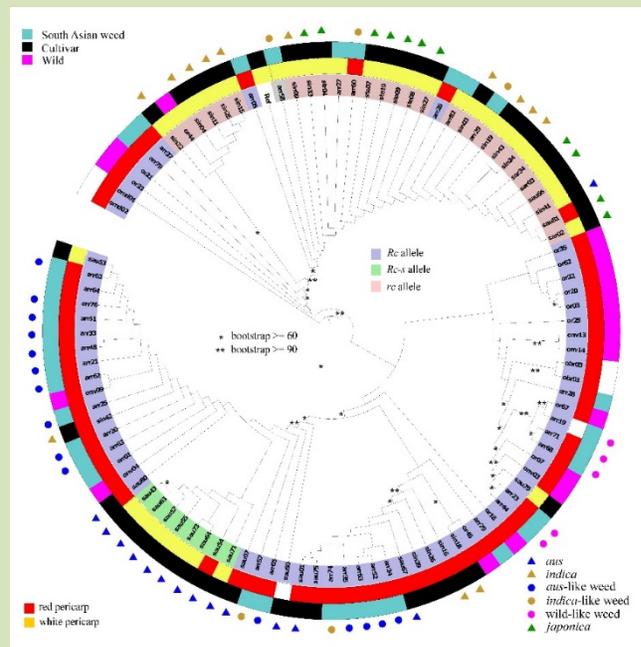
cultivars with enhanced nutritional value. (Pictures shows clustering of global rice varieties for different metabolite compounds found in rice bran)

*This addresses USDA-ARS Research Goal:* Enhanced knowledge of existing diversity in crop plant interactions with biotic environmental factors at the molecular, whole genome, and systems levels

Huang, Z., Kelly, S., Matsuo, R., Li, L.-F., Li, Y., Olsen, K., **Jia, Y.**, Caicedo, A. 2018. **The role of standing variation in the evolution of weedy rice (*Oryza spp.*)**. G3, Genes/Genomes/Genetics. Early online October 1, 2018; <https://doi.org/10.1534/g3.118.200605>.

Weedy rice is a problematic weed of cultivated rice around the world. Recent studies suggest that there may be multiple, but independent, evolutionary origins of weedy rice which raises questions about which traits and genes are necessary for its successful evolution. South Asia has the most diverse weedy rice populations that can be traced

to at least three origins, two from the de-domestication of rice cultivars and one from local wild rice. A set of traits advantageous to weedy rice were analyzed to determine the similarities, both genetically and morphologically, between the three weedy groups. Three traits were common among all suggesting that easy seed shattering, red pericarp color, and compact plant architecture are important for weedy rice success in the South Asian environment. Black hull color was common among weeds with wild ancestors and weeds that evolved from cultivated rice group "aus". Two different known candidate genes are likely expressed for weed seed pericarp color and hull color. The characterization of weedy rice groups in South Asia and the associated candidate genes contributes to a better understanding of weedy rice evolution and the role of ancestral variation of cultivated and wild rice. (Picture shows genetic relatedness of cultivated and weedy rice biotypes.)



- **Technology Transfer**

- ✓ **Interactions with the Research Community**

On October 10, 2018, Dr. Dong-Hong Wu, rice geneticist with TARI in Taiwan, presented a seminar Title: "Biology and Diversity of Weedy Red Rice and the Use of Phylogeographical Clustering to Understand and Control its Seed-mediated Contamination in Taiwan: an Update of Results". Dr. Wu was a visiting scientist with us at DBNRRC in 2016 and has made some very interesting discoveries about the weedy red rice problems in Taiwan.



Drs. Jinyoung Barnaby, Georgia Eizenga, Shannon Pinson and Jai Rohila attended the 5<sup>th</sup> International Rice Genetics Congress (5IRC) held October 15 through 17, 2018 in Singapore. The 5IRC, was held in conjunction with the 8<sup>th</sup> International Rice Genetics Symposium, with close to 1,500 scientists and specialists from 40 countries attending. The Congress featured over 300 research posters as well as 400 research presentations including invited oral presentations by Dr. Barnaby entitled “Profiles of Rhizosphere Soil Microbial Composition Affecting Methane Emissions”, Dr. Eizenga entitled “Identifying Panicle Architecture Traits for Rice Improvement: A Treasure Hunt from Genome-wide Association Studies to QTL Validation, Marker Development and Germplasm Release”, Dr. Pinson entitled “Genes and Physiological Factors Associated with Natural Variation in Rice Arsenic Concentrations”, and a poster presentation by Dr. Rohila entitled “Identification of Genetic Diversity in the USDA-Mini-core and Among Selected Vietnamese Rice Accessions for Seedling Stage Salt Tolerance”. The congress covered a broad range of topics of interest to DBNRRC scientists including climate change and environmental sustainability; human health and nutrition including grain quality; physiology of plants including roots; and crop, water and weed management. Topics focused on rice genetics included high throughput technologies for genotyping, phenotyping and omics; hybrid rice updates; utilizing genome and gene editing; and genetic improvement for yield, and both abiotic and biotic stress tolerance.



Dr. Shannon Pinson presenting her research



USDA-ARS Arkansas attendees (L-R): Drs. Georgia Eizenga, Jin Barnaby, Shannon Pinson, Arlene Adviento-Borbe (Jonesboro, AR) and Jai Rohila

## ✓ Rice Germplasm Distributed

During October, 2,213 rice accessions from the Genetics Stocks *Oryza* (GSOR) collection were distributed to researchers in the United States, Austria and United Kingdom.

### • Stakeholder Interactions

The DBNRRC provided a genomic assessment of off types found in a registered seed field to a grower in Texas. The information can be used to determine the source of seed impurities to assure production of true to type certified seed.

On October 31<sup>st</sup>, Dr. Jinyoung Barnaby (DBNRRC) hosted four research officers from the Division of Planning and Coordination, Rural Development Administration (RDA), South Korea: Drs. Kyongho Kim (National Institute of Crop Science), Yunchan Huh (National Institute of Horticultural and Herbal Science), Siyoung Lee (National Institute of Agricultural Sciences), and Dongjo Yu (National Institute of Animal Science). Dr. Barnaby introduced DBNRRC research activities and scientists as well as the status of her current USDA-RDA OIRP grant research project. The meeting was followed by research facility tour at the Alternative Cropping Systems Lab in Beltsville, MD where Dr. Barnaby is currently located.



### • Education and Outreach

On October 9<sup>th</sup>, Dr. Anna McClung provided historical information about the establishment of the rice industry, originally in the Carolinas, and its movement to the south-central USA where it is today to PBS Digital Studios with Louisiana Public Broadcasting. The information will be used as background for a story on the resurgence of heirloom varieties, like Carolina Gold rice.

On October 10-11, Anthony Suau (New York) visited the DBNRRC as part of a documentary film he is making on organic crop production. He toured the rice research fields and learned about genetic diversity and rice management systems that save water with Dr. Anna McClung. Visiting with Dr. Ming Chen he learned about improving nutritional quality of rice. Dr. Yulin Jia discussed rice fungal disease control and showed examples of fungal spores under the microscope along with how to make crosses for mapping genes and plant breeding.

Ms. Tristan Johnson (Left) and Mr. Joshua Lewis (Right) from Oxon Hill High School started their 1-yr research internship with Dr. Jinyoung Barnaby (in Beltsville). They will be working on understanding the impact of genotype x environment (CO<sub>2</sub> and heat stress) interactions on rice grain chalk formation.

