



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



**JANUARY 2020**

**MONTHLY RESEARCH HIGHLIGHTS**

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- **Recent Scientific Publications**

*This addresses USDA-ARS Research Goal: Developing crop plants with enhanced water use efficiencies*

McClung, A.M., Rohila, J.S., Henry, C.G., and Lorence, A. 2020. Response of U.S. Rice Cultivars Grown under Non-Flooded Irrigation Management. *Agronomy* 10 (1): 55. doi:10.3390/agronomy10010055

The sustainability of conventional season-long flood irrigation in rice is a concern among rice growers in the USA because some irrigation resources are being depleted. Using reduced irrigation practices, such as alternate wetting and drying (AWD) or furrow irrigation, in rice cultivation are new methods being adopted by growers as a means of making more efficient use of available water resources. However, because all current US rice varieties were developed for production under season-long flooded paddies, it is important to identify genetic materials and agronomic traits that are important for production using AWD. A three-year study was conducted evaluating 15 cultivars under four soil moisture levels using a subsurface drip irrigation system. The study identified rice varieties that were tolerant to water stress conditions and six agronomic traits that accounted for over 35% of the variation in grain productivity over the different irrigation treatments. This information will guide breeders in developing new rice cultivars that have high yield potential when grown under water saving cultural practices.

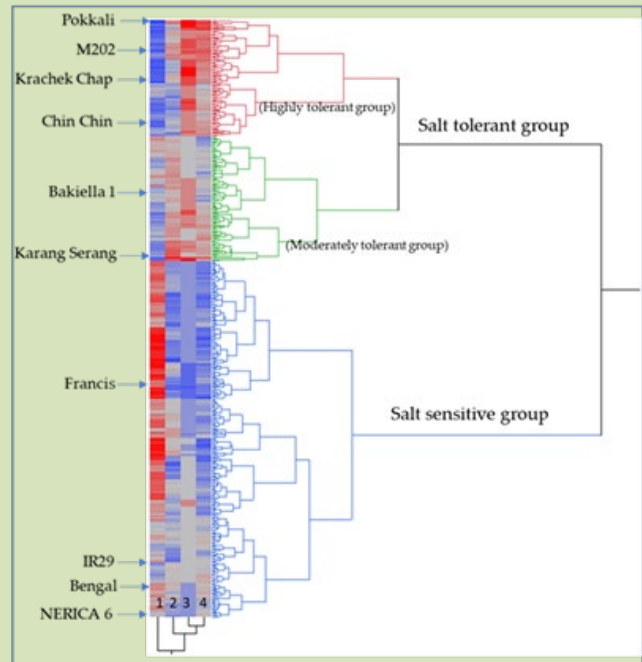


Field study with different rice varieties being evaluated under four irrigation regimes that vary in soil volumetric water content (VWC).

*This addresses USDA-ARS Research Goal: Crop plants tolerant to environmental extremes*

Rohila, J.S., Edwards, J.D., Tran, G.D., Jackson, A.K., and McClung, A.M. 2019. Identification of superior alleles for seedling stage salt tolerance in the USDA rice mini-core collection. *Plants*, 8(11), 472; <https://doi.org/10.3390/plants8110472>.

In some rice production systems, exposure to saline conditions can occur due to salt water intrusion in irrigation resources. Most rice varieties are very sensitive to saline conditions at the seedling stage. Identifying genetic resources possessing novel genes/alleles for seedling stage salt tolerance is needed to develop new varieties that can withstand these unfavorable production conditions. In this study, a panel of 162 rice accessions from around the world were screened for tolerance of salt stress using a hydroponic system. We identified nine genomic regions associated with salt tolerance that were mapped to five different chromosomes. Of these, none were in the region known to possess the “Saltol” gene, suggesting new probable genes and mechanisms responsible for salt tolerance. Several rice accessions performed better than varieties developed in a salt tolerance rice breeding program in Vietnam, indicating that there is the opportunity to pyramid diverse alleles to make further genetic gains in salt tolerance. Ten highly salt-tolerant accessions, six novel loci, and 16 candidate genes in their vicinity were identified that may be useful in breeding for salt stress tolerance. This information will be useful for improving salt tolerance in modern US rice varieties that will mitigate salt affected soils and increase profitability for rice production in the USA.



Dendrogram showing clustering of 162 global rice cultivars according to tolerance to salt stress at the seedling stage.

- **Technology Transfer**

- ✓ **Interactions with the Research Community**

January 11<sup>th</sup> – 15<sup>th</sup>, three DBNRRC scientists attended the 28th Plant and Animal Genome Conference (PAG) in San Diego, CA which brought together 2951 researchers representing 62 countries. Four oral DBNRRC presentations were made including: “Ricebase: A Breedbase Implementation for Rice with Tools for Gene Discovery and Marker Development” by Dr.



Jeremy Edwards, “SNP Markers for Panicle Architecture and Grain Traits Developed from GWA-QTL and Available for Japonica Rice Improvement” by Dr. Georgia Eizenga, and “Co-Evolutionary Mechanisms of the *Oryza sativa* and *Magnaporthe oryzae* Pathosystem” and “Identification of Critical Amino Acid Residues in Ptr mediated Plant Innate Immunity” by Dr. Yulin Jia. Poster presentations included “Overexpression of the Candidate Pi-ta2 Gene in Rice (*Oryza sativa* L. japonica cv. Katy) for Resistance Against Blast Fungus (*Magnaporthe oryzae*)” by collaborator Dr. Muthusamy Manoharan (Univ. of Arkansas-Pine Bluff, an 1890 Land Grant institution) and Dr. Jia, and “Rice Seedling Cold Stress QTL Revealed By Genome-Wide Association Mapping and Biparental Mapping” by Dr. Eizenga and collaborator Dr. Michael Schläppi (Marquette University). In addition, Dr. Jia co-organized the “Rice Functional Genomics” workshop and Dr. Edwards organized the “Allele Mining” workshop.

On January 22<sup>nd</sup>, Drs. Anna McClung and Ming-Hsuan Chen attended the annual breeders’ meeting held at Texas A&M AgriLife Research Center in Beaumont, TX. Dr. McClung presented the molecular marker data for the Uniform Regional Rice Nursery for predicting grain quality traits and blast resistance genes and Dr. Chen presented the comparison of two imaging systems for determining milled rice chalkiness and grain shape traits.

On January 24<sup>th</sup> Dr. Ming-Hsuan Chen provided advice to a graduate student at Texas A&M University on protocol modification for using the WinSeedle imaging system for determining milled rice chalkiness in a study.

On January 29<sup>th</sup>, Dr. Ming-Hsuan Chen provided the protocol for the WinSeedle imaging system, which was established by the DBNRRC for determining chalkiness in milled rice, to the Missouri breeding program.

#### ✓ **Rice Germplasm Distributed**

During the month of January, 17 rice accessions from the Genetics Stocks *Oryza* (GSOR) collection were distributed to researchers in the United States and Belgium. At the request of a state foundation seed program, 140 lbs of headrow seed was provided of the USDA-ARS developed variety “Sierra”.

#### • **Stakeholder Interactions**

On January 15<sup>th</sup>, Dr. Anna McClung provided seed of eight global rice varieties for growing at the Montreal Botanical Garden in Quebec.

Dr. Jeremy Edwards on January 27<sup>th</sup> provided information to a private seed company regarding using genetic markers to fingerprint new rice varieties.

#### • **Education and Outreach**

On January 28<sup>th</sup>, a story ‘Brown Rice Variety Packs Antioxidant Punch’ was posted on ARS’ News and Events page regarding research conducted by Drs. Ming-Hsuan Chen, Anna McClung and Casey Grimm with ARS and Christine Bergman with University Nevada-Las Vegas that demonstrated the enhanced nutritional quality of brown rice from a rice variety that has a giant embryo and its potential use by the food industry.

<https://www.ars.usda.gov/news-events/news/research-news/2020/brown-rice-variety-packs-antioxidant-punch/>

- **International Research Collaborations**

Dr. Yulin Jia, as mentor, and Dr. Jai Rohila, as co-mentor, Dr. Annapurna Devi Allu, an Assistant Professor in the Department of Biology at the Indian Institute of Science Education and Research, one of major federal research institutes in India. Dr. Allu’s visit is funded by the Borlaug International Agricultural Science and Technology Fellowship Program (Borlaug Fellowship Program) and the USDA-FAS Office of Capacity Building and Development. Dr. Allu attended the 28<sup>th</sup> Plant and Animal Genome conference. On January 16, 2020 she initiated her research project entitled "Identification of miRNA’s Involvement with the Presence of the Blast Resistance gene *Ptr* Under Water Stress Conditions" at the DBNRRC. She will work at DBNRRC for three months and complete the entire project by January 2022.

