



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



MARCH 2021

MONTHLY RESEARCH HIGHLIGHTS

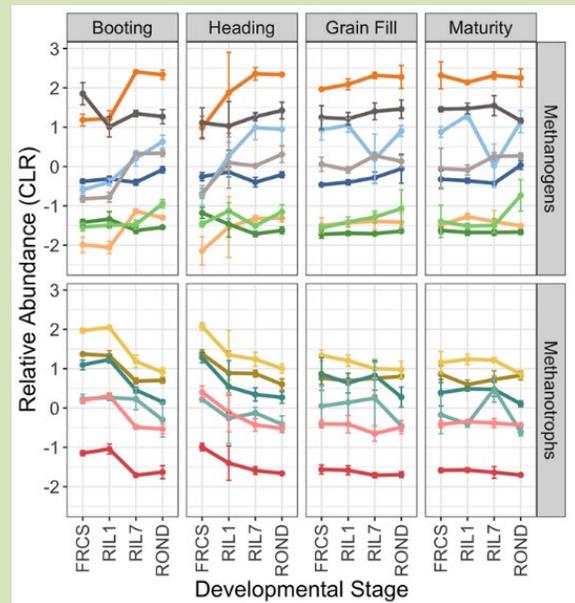
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• Recent Scientific Publications

This addresses USDA-ARS Research Goal: Enhanced knowledge of how plant microbiomes influence crop performance at the genetic, molecular and physiological levels

Fernandez-Baca, C.P., Rivers, A.R., Kim, W.J, Iwata, R., **McClung, A.M.**, Roberts, D.P., Reddy, V.R., and **Barnaby, J.Y.*** Changes in rhizosphere soil microbial communities across plant stages of high and low methane emitting rice genotypes. *Soil Biology and Biochemistry*. 108233. 2021. <http://doi.org/10.1016/j.soilbio.2021.108233>

Rice production is an important source of methane accounting for 11% of global anthropogenic emissions. Methane emissions can be effectively reduced by management practices and cultivar selection. Our results show that rice genotypes and plant developmental stage are associated with different soil microbial community structures. Additionally, rice genotype impacts methane-cycling populations and the observed methane emissions to a greater extent during the reproductive phases (i.e., booting and heading) as compared to the ripening phases (i.e., grain fill and maturity). Low methane emitting genotypes had an increase in overall methanogen abundance over time as compared to methanotrophs or iron and sulfate reducing populations. However, high methane emitting genotypes had similar methanogen abundances across all stages. Future breeding efforts should focus on mitigating methane emissions during the rice reproductive phase by selecting cultivars that modulate the methane-cycling community during this critical period.

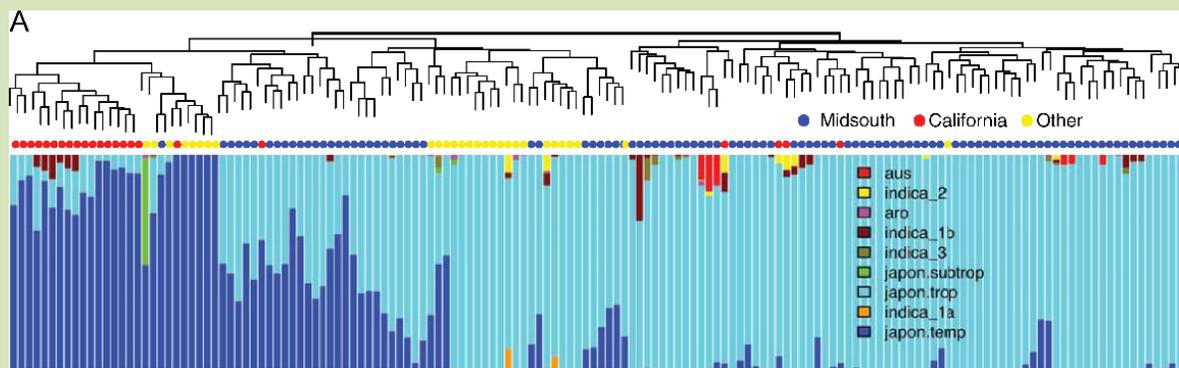


Comparison of two cultivars, Francis and Rondo, and two offspring (RILs) at four growth stages. Colored lines represent the relative abundance of different species of methane producing and methane consuming soil microorganisms.

This addresses USDA-ARS Research Goal: Improved methodology for predictive analyses

Vaughn, J.N., Korani, W., Stein, J.C., **Edwards, J.D.**, Peterson, D.G., Simpson, S.A., Youngblood, R.C., Grimwood, J., Chougule, K., Ware, D.H. and **McClung, A.M.**, 2021. Gene disruption by structural mutations drives selection in US rice breeding over the last century. *PLoS genetics*, 17(3), p.e1009389.

Some crop varieties have superior performance across years and environments. This vigor is often observed in hybrids and is thought to be related to the fact that many harmful mutations (or “deleterious alleles”) in one parent are being masked by functional (“desirable”) alleles in the other parent. Unfortunately, these alleles are very difficult to identify precisely because, individually, they only have a small effect; thus, the role of these hidden mutations as a mechanism responsible for vigor remains unclear. In this study, we use long-read genomic sequencing to characterize the entire mutational spectrum between two rice varieties. Long-read sequencing differs from other sequencing methods in that it can detect large structural mutations in the DNA sequence such as insertions and deletions. We then tracked these mutations through the last century of rice breeding by evaluating the DNA sequence of over 100 US rice cultivars. We showed that large deletions occurring in genes are eliminated through the selection imposed by breeding at a faster rate than those occurring in other parts of the genome that do not code for genes and are not directly selected for by breeders. These findings suggest that gradual purging of deleterious alleles from the gene pool is a component of the progress made through historical breeding efforts and will guide attempts to predict variety vigor based solely on genomic information.



Dendrogram showing relationship among US cultivars developed over the last century from the Mid-South and California, as well as imported cultivars used in breeding. Colored bars indicate the proportion of the genome of each cultivar derived from different rice genetic populations. Ex. Most of the cultivars from California (red dots, far left) are medium grains with DNA primarily derived from japonica genetic resources.

This addresses USDA-ARS Research Goal: Enhanced knowledge of how plant microbiomes influence crop performance at the genetic, molecular and physiological levels

Fernandez-Baca, C.P., Rivers, A.R., Maul, J.E., Kim, W.J, **McClung, A.M.**, Roberts, D.P., Reddy, V.R., and **Barnaby, J.Y.*** Rice Plant-Soil Microbiome Interactions Driven by Differential Root and Shoot Biomass. *Diversity*. 13 (3): 125. 2021.
<https://doi.org/10.3390/d13030125>

Plant-soil microbe interactions are important in determining plant uptake of soil minerals, plant health, and methane emissions. We examined to what extent plant growth and development influences soil microbial species and their function. The rice varieties, Francis and Rondo, and nine of their inbred offspring, all known to differ for root and shoot biomass, were grown in a greenhouse study and the



composition of the rhizosphere microbial community was determined at two growth stages, heading and maturity. Results indicated changes in root and shoot biomass throughout the plant growth cycle play an important role in driving the microbial community structure. The identified species included those involved in nitrogen cycling and methane production, as well as known endophytes. Many of the microbial community functions and genes observed during the heading stage were representative of cell growth, while functions correlated with physiological maturity were indicative of cell decay. We also found that shoot biomass may be used as a surrogate for predicting root biomass growth which would be advantageous in a breeding program, as root biomass quantification is time consuming and prone to error, while shoot biomass quantification is more efficient and accurate. Our study underscores the potential of exploiting rice phenotypic variation in plant breeding to promote beneficial plant-soil microbiome interactions.

- **Technology Transfer**

- ✓ **Interactions with the Research Community**

On March 23, Dr. Jinyoung Barnaby, Research Plant Physiologist, co-hosted the 2021 Korean American Women in Science and Engineering (KWise) Eco- and Data-Science forum in the US and South Korea as the KWise Washington D.C. Chapter president and as a forum organizing committee. Prof. Meeyoung Cha at the Institute for Basic Science, Korea Advanced Institute of Science and Technology (KAIST), presented a talk on “Unveiling North Korea’s Local Economic Development via Human-Machine Collaboration”.

On March 25, Dr. Jinyoung Barnaby, Research Plant Physiologist, co-hosted the 2021 Korean American Women in Science and Engineering (KWise) forum on *New Technologies in COVID-19 Diagnostics* in the US and South Korea as the KWise Washington D.C. Chapter president and as a COVID forum organizing committee. Two internationally recognized experts on biotechnology, Dr. Clare Fasching at Mammoth Biosciences, United States, and Prof. Tae Seok Seo at Kyung Hee University, South Korea, gave talks. Dr. Fasching presented “Rapid Development of a SARS-COV-2 CRISPR Diagnostic”- an overview of how to adapt CRISPR/Cas9 a gene editing technology to develop a simple, rapid and inexpensive diagnostic assay for SARS Coronavirus-2. Prof. Seo at Kyung Hee University presented “Point-of care genetic diagnostic platform for COVID-19 identification” regarding a portable gene analyzer to deploy in field hospitals that can automatically analyze ten samples per hour for Covid19 testing.

✓ **Rice Germplasm Distributed**

Seed of ARS developed rice varieties Carolina Gold Select, Santee Gold, Scarlett, Tiara, IAC600, Sierra, Dixiebelle, Jasmine 85, and Presidio were distributed to growers and seed companies in Texas, South Carolina, North Carolina, Pennsylvania, Arkansas, Maryland, and Indiana during this month.

During the month of March, 268 rice genetic stocks were shipped to researchers in the United States, Belgium, Italy and Suriname from the Genetic Stocks *Oryza* (GSOR) collection.

Recent publications by the research community using germplasm provided by GSOR:

Fernandez-Baca, C.P., McClung, A.M., Edward, J.D., Codling, E.E. Reddy, V.R., and Barnaby, J.Y. * 2021. Genotype and water management impacts on mitigation of inorganic arsenic in rice. *Frontiers in Plant Sciences*. 11: 2284.
<https://doi.org/10.3389/fpls.2020.612054> (TeQing into Lemont TILs)

Liu, H, Long S-X, Pinson SRM, Tang Z, Guerinot ML, Salt DE, Zhao F, Huang X-Y. 2021. Univariate and multivariate QTL analyses reveal covariance among mineral elements in the rice ionome. *Frontiers in Genetics*, <https://doi.org/10.3389/fgene.2021.638555> (Lemont/TeQing RILs)

Pokhrel, S., S.K. Ponniah, Y. Jia, O. Yu, and M. Manoharan. 2021. Transgenic rice expressing isoflavone synthase gene from soybean shows resistance against blast fungus (*Magnaporthe oryzae*). *Pl. Dis.* DOI: [10.1094/PDIS-08-20-1777-RE](https://doi.org/10.1094/PDIS-08-20-1777-RE) (Nipponbare)

Singh, R.R., et al. 2020. Ascorbate oxidation activates systemic defence against root-knot nematode *Meloidogyne graminicola* in rice. *J. Exp. Bot.* DOI: [10.1093/jxb/eraa171](https://doi.org/10.1093/jxb/eraa171) (Nipponbare)

- **Stakeholder Interactions**

On March 9th, Drs. Anna McClung, Jeremy Edwards, Trevis Huggins, Yulin Jia, and Jai Rohila participated in a virtual meeting with researchers from ViSUS <https://visus.org/> about the potential for use of UAV imaging for rice research and crop production.

March 15th, Dr. Trevis Huggins, Geneticist and Curator of the Genetic Stocks *Oryza* (GSOR) Collection, provided information to a researcher at the University of Nebraska-Lincoln, regarding utilizing rice accessions that are photoperiod sensitive. These require a shorter interval of daylight to trigger the plant to flower and set seed.

On March 24th, Dr. Yulin Jia, Molecular Plant Pathologist, provided information on insect vectors and distribution of rice viruses to assist a scientist from APHIS for a project related rice quarantine.

On March 26th, Dr. Anna McClung, Research Geneticist, was interviewed by a journalist from Science Line regarding women in science.

March 29th, Ms. Lorie Bernhardt, Computer Assistant for the Genetic Stocks *Oryza* (GSOR) Collection, provided information to a researcher at Mississippi State University regarding specific rice accessions in the USDA Collection, providing availability, identifier information, how to create an account, and place an order on [GRIN-Global \(ars-grin.gov\)](http://ars-grin.gov)

March 29th, Dr. Trevis Huggins, Geneticist and Curator of the Genetic Stocks *Oryza* (GSOR) Collection, provided information to a researcher at the University of Manitoba, Canada regarding fertilizer application to rice accessions growing under greenhouse conditions.

- **Education and Outreach**

In the book, *Rice - Germplasm, Genetics and Improvement*, the chapter titled “Current Advances on Genetic Resistance to Rice Blast Disease” authored by Wang, X., Lee, S., Wang, J., Ma, J., **Bianco, T.A., Jia, Y.** (2014. DOI: 10.5772/56824) has been downloaded 4000 times by readers in USA, China, India, Vietnam, Indonesia, Germany, and Sri Lanka.

See the web version of all DBNRRRC research highlights at:

<https://www.ars.usda.gov/southeast-area/stuttgart-ar/dale-bumpers-national-rice-research-center/docs/monthly-research-highlights/>