



May 2015
Highlights from the Dale Bumpers National Rice Research Center
Stuttgart, AR

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1. Recently accepted Publications

ARS Anticipated Product: Genetically and phenotypically characterized germplasm designed for elucidating gene function and/or developing superior cultivars.

Georgia C. Eizenga and Gurdev S. Khush. 2015. Registration of twenty-four 'IR36' rice trisomic lines. *Journal of Plant Registrations*. doi:10.3198/jpr2014.11.0079crgs (Available on-line at: <https://dl.sciencesocieties.org/publications/jpr/articles/0/0/jpr2014.11.0079crgs>)

Rice is a diploid species having 12 different chromosomes, or 24 total chromosomes. Rice plants with an additional chromosome, thus three copies of a particular chromosome rather than two, have 25 total chromosomes and are called trisomic plants. In many cases, the presence of the additional chromosome changes the growth and development of the rice plant and these trisomic plants can be used in genetic mapping studies to identify the location of a particular trait or gene on a chromosome. A set of these trisomic lines was developed using the rice variety IR36 which was developed at the International Rice Research Institute in the Philippines and 24 of these IR36 trisomic lines were brought through the U.S. quarantine process, re-selected based on morphology, validated by microscopic observation, and made available to the rice research community through the Genetic Stocks-*Oryza* collection.

ARS Anticipated Product: Plants tolerant to environmental changes or extremes.

Qi, X., Liu, Y., Vigueira, C., Young, N., Caicedo, A., Jia, Y., Gealy, D., and Olsen, K. 2015. More than one way to evolve a weed: parallel evolution of U.S. weedy rice through independent genetic mechanisms. *Molecular Ecology* (published on line June 1, DOI: 10.1111/mec.13256).

Weedy red rice, a variant of cultivated rice (*Oryza sativa*) is one of the most challenging agricultural weeds in rice production. It is known that genes have been lost in rice through its domestication from ancient wild species. Little is known regarding if weedy red rice has also gone through a genetic bottleneck. In the present study, we performed comparative quantitative trait loci (QTL) mapping of weediness traits using two recombinant inbred line populations derived from crosses between an indica rice variety and representatives of each of the two major weedy rice strains found in U.S. rice fields, strawhull (S) and blackhull awned (B). Candidate genes for some weediness traits (awn length and grain pigmentation) were identified within QTL mapped regions and were associated with single genes. However, for more complex quantitative traits (heading date, panicle length, and seed shattering) we





found multiple QTL, with little evidence of shared genetic bases between the S and B populations or across previous studies of weedy rice. Together these findings demonstrated that despite the genetic bottleneck that occurred during rice domestication, there is ample genetic variation in rice to allow agricultural weed evolution through multiple genetic mechanisms. Understanding the genetic variability of weedy rice demonstrates the ability of this weed to evolve with changing environments, resulting in challenges for weed control.

2. New Significant research collaborations

International

USA

3. New awarded grants

4. Technology Transfer

a. Formal Events:

To Non-research stakeholders

During May 21-22, 2015, Dr. Rolfe Bryant, participated in the Industry Alliance meeting hosted Dr. Terry Siebenmorgen, Rice Processing Program Director, University of Arkansas, Fayetteville.

To Research Community

On May 7, 2015, Computational Biologist, Dr. Angela Baldo participated in the South East Area Big Data Meeting for Undersecretary Simon Liu, presenting an overview of the high-throughput computational research ongoing at DBNRRC.

b. Informal Contacts:

On May 11, 2015 Dr. Zaiquan Cheng contacted Dr. Yulin Jia for an intended visit of ARS by three rice scientists from Yunnan Academies of Agricultural Sciences, Kunming from September 26 to 29. Dr. Cheng will give a seminar titled: “Constructing introgression lines of wild rice species into *Oryza sativa* cultivars by different approaches”.

c. New MTAs

d. Germplasm Exchanged:

During May 2015, 2,189 rice accessions from the Genetics Stocks *Oryza* (GSOR) collection were distributed to researchers in the US, Belgium, South Korea, and the United Kingdom. Some of the recipients of GSOR seed stocks have acknowledged





the source of these materials in publications that have resulted from their research use. An example of these journal articles is (online) 2015 *Molecular Plant-Microbe Interactions* 28(5):519-533.

5. Educational Outreach

On May 14, 2015, Drs. Georgia Eizenga and David Gealy served as judges for science projects done by students at Meekins Middle School in Stuttgart, Arkansas

On May 4, 2015, Drs. Baldo, Pinson, and Edwards participated in the Future Scientist program, a program supported by USDA/Hispanic Serving Institutions, Texas A&M University, and the Arkansas Farm Bureau. They served on a scientist Question and Answer Panel and awarded local K-12 students and their educators' certificates for participating in the program. The program was followed by a tour of the DBNRRC facility with hands-on interactions with project staff in plant pathology (Jia), plant physiology (Gealy) and cereal chemistry (Bryant and Chen). The event was featured in the local newspaper and in *ARS and You*.

(<http://www.stuttgartdailyleader.com/article/20150513/NEWS/150519855>)

6. Awards/Honors

