Distributing Nipponbare Around The World

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The Dale Bumpers National Rice Research Center's Genetic Stocks Oryza (GSOR) Collection established in 2003 provides genetic tools to researchers worldwide.

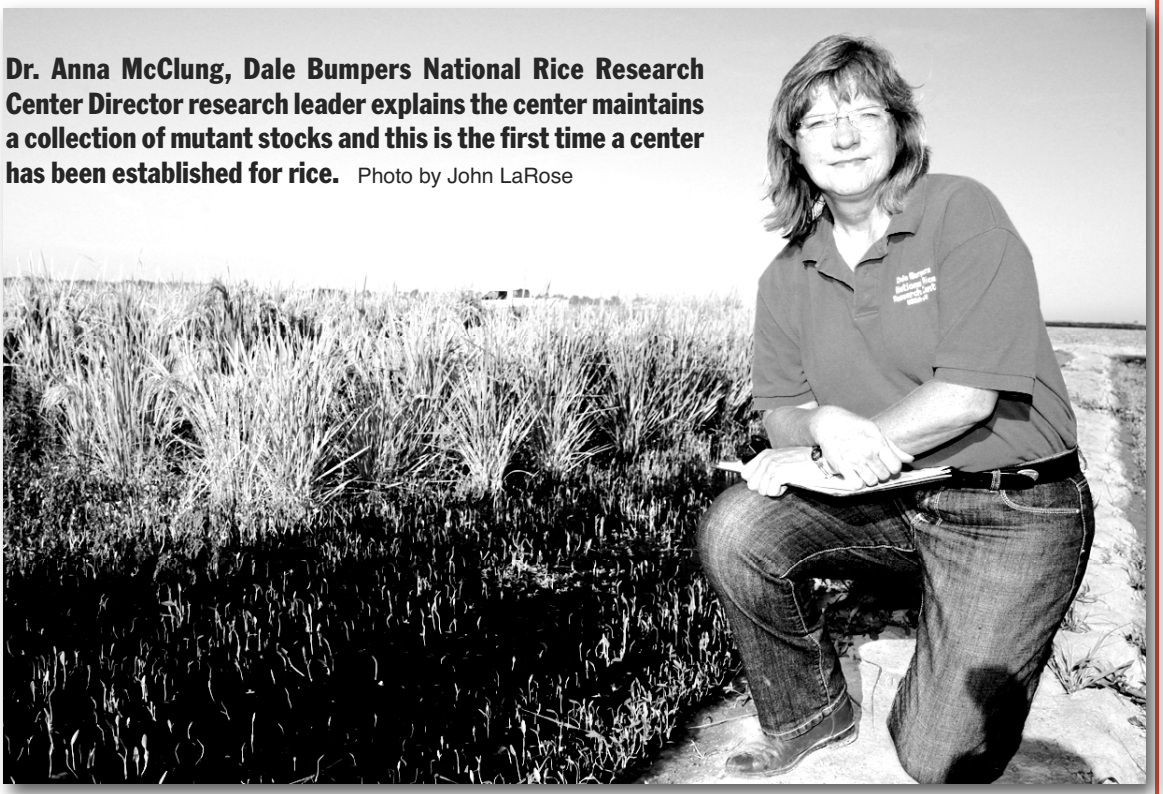
Dr. Anna McClung, center director research leader, explains, "This is a collection of mutant stocks that are maintained here at the Dale Bumpers National Rice Research Center."

This is the first time a center has been established for rice, "to store these materials and make that as a means of distribution to the research community," said McClung.

This is what we call genetic tools. They are tools that geneticists are going to use to actually relate DNA sequence changes with changes in actual traits that are important to the U.S. rice industry."

McClung goes further to explain, "in this collection we have materials that say for example, have a lot of kernels on the panicle that has been induced by a very simple change in the DNA sequence. The researchers will be involved with actually understanding that change in sequence and what that does in terms of the physiology of the plant to result in more kernels per panicle."

McClung said, "what we would hope to do is be able to come up with a genetic marker that would be associated with that trait, that marker would then be handed off to breeders."



Dr. Anna McClung, Dale Bumpers National Rice Research Center Director research leader explains the center maintains a collection of mutant stocks and this is the first time a center has been established for rice. Photo by John LaRose

Breeders could use this genetic marker to develop improved cultivars. The collection currently contains about 1000 accessions, which are available to researchers worldwide.

One of the most important accessions the Dale Bumpers National Rice Research Center distributes is a variety called Nipponbare.

Nipponbare is the first rice variety that was sequenced as part of the first International Rice Gene Sequencing Project. It is the first rice cultivar to have the complete genetic sequence determined. "By knowing that genetic road map of that one cultivar, we are then going to be able to compare that to any other cultivar, look for the differences between the two and track down genes associated with traits," said McClung. Δ