

NEWS RELEASE

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Gene Clustering Boosts Rice Plant Defenses Against Pathogens

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When a plant's resistance genes – or genes that recognize and decide how to fight a disease or pathogen – cluster together, it gives those genes the best chance to successfully repel the pathogen.

Clustering apparently allows resistance genes to recombine in order to face the ever-evolving attacks of pathogens, says North Carolina State University's Dr. Ralph Dean, professor of plant pathology, director of the Center for Integrated Fungal Research and co-author of a new research paper that describes the sequencing of the rice genome's chromosome 10. The paper appears in the June 6 issue of the journal *Science*.

Learning more about a plant's defense mechanisms – how it recognizes and fights the mutating pathogens – can help save crops like rice, the major food staple for about half the world's population, from pathogen attack.

Dean and an NC State colleague, Hua-Qin Pan, senior bioinformatics scientist, searched for and characterized resistance genes and downstream pathways likely involved in the resistance response.

Dean and Pan found 43 different resistance genes on chromosome 10, which contains a total of 3,471 genes, according to the *Science* paper.

“We found a variety of different types of resistance genes; some were novel and some were well known,” Dean says. “The most interesting thing was that most were grouped in three major clusters that were quite similar.”

Dean believes this clustering helps rice improve its specificity of resistance to pathogens. In other words, resistance genes form clusters and then recombine forces in order to repel specific harmful advances from pathogens.

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Dean says finding out more about these resistance genes' functions will aid the rice plant's battle to defend itself.

“Identifying and characterizing these resistance genes – particularly these clusters – will give us a very good idea of how they change their specificities to different pathogens, specifically rice blast.”

Rice blast, an important and powerful rice disease, is a major focus of Dean's lab. Dean and colleagues from the Whitehead Institute/MIT Center for Genome Research sequenced the rice blast genome last summer.

Dean calls the ever-evolving battle between rice and pathogens “a constant arms race.”

“Pathogens mutate to bypass resistance mechanisms, while the host, rice, recombines various components in resistance genes so it can again recognize pathogens. These resistance genes are like generals in a battle who recognize what's going on with the enemy and then tell the troops downstream to fight the pathogen.”

A consortium of eight different groups – the rice chromosome 10 sequencing consortium – representing various universities and institutes worked together to sequence and characterize chromosome 10. The *Science* paper chronicles a high degree of collinearity between rice and two other major cereal crops – sorghum and maize – providing further evidence that rice can be a model for cereal crop research.

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Editor's note: A copy of the *Science* paper is available before 2 p.m. June 5 by calling *Science* at 202/326-6440. An abstract of the paper follows.

“In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10”

Authors: The Rice Chromosome 10 Sequencing Consortium, including lead author Rod A. Wing, University of Arizona; and Ralph A. Dean and Hua-Qin Pan, North Carolina State University

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Abstract: Rice is the world's most important food crop and a model for cereal research. At 430 megabases in size, its genome is the most compact of the cereals. We report the sequence of chromosome 10, the smallest of the 12 rice chromosomes (22.4 megabases), which contained 3,471 genes. Chromosome 10 contained considerable heterochromatin with an enrichment of repetitive elements on 10S and an enrichment of expressed genes on 10L. Multiple insertions from organellar genomes were detected. Collinearity was apparent between rice chromosome 10 and sorghum and maize. Comparison between the draft and finished sequence demonstrated the importance of the finished sequence.