

Public rice genomic resources are boon for breeders

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Credit: Earth100/Wikipedia

A Cornell-led international team of researchers has launched a set of open-access genomic resources that will greatly accelerate the ability of geneticists and breeders to link genes to important traits in rice.

This publicly available research platform – including seeds of diverse

rice varieties, genomic diversity data, analysis tools and visualization resources – represents a major milestone in advancing the ability to breed new rice varieties to feed a growing population, while also addressing the challenges of growing crops in a changing climate.

The team has published two companion papers in the Feb. 5 issue of *Nature Communications*.

The first paper describes the launch of the platform that will facilitate genome-wide association mapping in rice, a staple crop that feeds 3 billion people. Genome-wide association mapping looks at many different versions, or variants, of a gene to determine if any of them are linked to specific traits, which is useful information for breeders.

The platform includes a panel of 1,568 diverse rice varieties; a dataset featuring 700,000 [single nucleotide polymorphisms](#) (SNPs), or genetic variants; and a suite of tools for analyzing and evaluating traits. The platform is the culmination of a \$7 million National Science Foundation grant to Principal Investigator Susan McCouch, professor of plant breeding and genetics in Cornell's School of Integrative Plant Sciences.

"There are dozens of groups around the world already using these resources to study their favorite traits, and their papers will be published shortly now that ours is out," said McCouch, lead author of the paper describing the platform.

The genomic tools are helping other researchers describe links between genes and traits, including disease and insect resistance, photosynthetic and nitrogen use efficiency, starch quality, salt, heat and cold tolerance.

"This is a global initiative," McCouch added. "The technology and information we are releasing are very catalytic and will impact breeding in many parts of the world."

Rice genetics poses unusual challenges because rice has deep cultural roots tied to national identities and has been inbred for certain characteristics in each location. There are thousands of different rice varieties, selected for growth in diverse environments, and for distinctive grain qualities that match culinary preferences.

Unlike maize and wheat, which are often transformed into flours or pastes or made into beer, rice is eaten as a whole grain, and people in different countries have strong preferences for grain size, texture, color and smell, so its marketable features must be maintained. This is a challenge because many genes are involved, and changing one trait can change others as well.

"As the climate changes, we need new adaptive traits but we have to keep the diversity of quality traits," McCouch said. "This work is designed to help us mine the wealth of natural variation available in rice to accelerate plant breeding and create strains of rice that are adapted to new climate conditions."

The team's second paper utilized the genomic resources reported in the first paper, to examine panicle structure, the branched stalks that hold clusters of developing [rice grains](#). Led by Samuel Crowell, a former graduate student in McCouch's lab, the study discovered extensive variation for panicle architecture in [rice](#), yet showed that the highest yielding varieties had intermediate sized panicles.

"If you try to make a panicle longer and think, therefore, you are going to get more yield, the plant typically compensates by making it less branched or filling fewer seeds," McCouch said.

The work suggests that in some cases, this is due to the action of several genes that are so closely linked along the chromosomes that they have never been separated. Using the resources described in these papers,

breeders now have the opportunity to selectively recombine these linked arrays of genes, offering exciting new possibilities to optimize the relationship between panicle architecture, yield and grain quality.

More information: Samuel Crowell et al. Genome-wide association and high-resolution phenotyping link *Oryza sativa* panicle traits to numerous trait-specific QTL clusters, *Nature Communications* (2016). [DOI: 10.1038/ncomms10527](https://doi.org/10.1038/ncomms10527)

Susan R. McCouch et al. Open access resources for genome-wide association mapping in rice, *Nature Communications* (2016). [DOI: 10.1038/ncomms10532](https://doi.org/10.1038/ncomms10532)

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