

Research identifies wild ancestor genes for crop improvement

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Using the genetic variation found in wild and exotic rice species, researchers are providing breeders with genomics tools and knowledge to develop higher yielding, stress-tolerant varieties, a Cornell researcher reported Feb. 19 at the annual American Association for the Advancement of Science meeting in Washington, D.C.

"Using genomics, we are discovering cryptic forms of natural genetic variation hidden in low-yielding wild and exotic strains and demonstrating that these genetic resources can be used to enhance the performance of the world's most productive cultivars," said Susan McCouch, professor of plant breeding and genetics, who presented her research, "Discovery of Genes for Crop Improvement From Wild Ancestor Plants," at the meeting.

For example, when selected alleles (gene variants) from a low-yielding wild ancestor of Asian rice (*O. rufipogon*) were bred into local high-yielding rice cultivars in China, Indonesia, Brazil, Korea, Sierra Leone and the United States, the results led every time to selected offspring with 15-20 percent higher yields than their cultivated parent, said McCouch.

To create novel varieties, plant breeders typically cross the best performing lines with each other, but the rules of genetics say that crosses between genetically dissimilar plants are more likely to generate something new, McCouch said. It's not about whether the genes come from a wild or cultivated plant, but rather whether those genes come



from different gene pools, meaning they have evolved separately. Wild rice offers an obvious source of untapped genetic variation that has evolved separately from domesticated rice for thousands of years.

Today's gene banks hold seeds from hundreds of thousands of wild and cultivated forms of plants whose DNA could lead to new crop varieties, but the genes contained in these seeds are largely uncharacterized, McCouch said. Recently, genomics-based tools have opened the door to investigating these genetic resources. Large-scale genomics experiments are helping to identify genes and sequences of DNA from wild and exotic plants, understand their functions and develop predictive models about how to unlock the genetic potential of these underutilized plants for crop improvement, McCouch said.

"These discoveries are catalyzing new interest in underutilized exotic germplasm [strains] and are helping to transform the field of <u>plant</u> <u>breeding</u> from black box experimentation to predictive science," she added.

Provided by Cornell University

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