

200,000 rice mutants available worldwide for scientific investigation

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Scientists across the world are building an extensive repository of genetically modified rice plants in the hope of understanding the function of the approximately 57,000 genes that make up the genome of *Oryza sativa*. The International Rice Functional Genomics Consortium recently announced the public availability of more than 200,000 rice mutant lines, which represent mutations in about half of the known functional genes mapped for rice to date.

Researchers have estimated the number of different rice mutants needed to have a mutant for every gene as somewhere between 180,698 and 460,000. Two hundred thousand rice mutants are now available and have been mapped by the insertion of what are known as flanking sequence tags - small pieces of DNA or molecular tags that integrate into the rice genome. This approach is useful because it allows scientists to link a physical location on the genome to a specific gene and its visible feature or phenotype.

Arjun Krishnan, first author on the paper and a graduate student in Andy Pereira's laboratory at the Virginia Bioinformatics Institute, stated: "Bioinformatics is making it possible to visualize the vast amounts of sequence information available to researchers. The resources described in this paper, which are the combined output of many leading international rice research laboratories, mean that researchers can see and explore on their computers the precise positions of mutations in the rice genome sequence, for each rice mutant plant. About 50 percent of the protein-coding genes have knockout mutations, which probably abolish their expression and can provide valuable information on the genes by virtue of their loss of function. This is a significant milestone for the project and the availability of these rice plants represents a powerful resource for the rice genomics community."

More than 2 million rice mutants were generated in

this project and the diversity of the available plants suits many of the experimental objectives of researchers looking at rice and other commercially important grasses. Mapping of the remaining genes from this population will be required to complete the resource. Many of them will be smaller genes less amenable to mutation that will pose significant challenges for researchers as they continue their work.

Dr. Andy Pereira, Professor at the Virginia Bioinformatics Institute, stated: "The *Oryza sativa* genome was sequenced in 2002 and researchers have come a long way since. Advances in technologies such as high-throughput sequencing and RNA interference gene silencing methods should help to accelerate the process of identifying the functions of the remaining genes in the rice genome." He added: "The availability of the rice mutant resource is already helping researchers in their quest to gain insights into the biology of this commercially important crop. These efforts are critical to understand gene function and, ultimately, the many biological processes that take place in rice and other grasses, including maize and wheat, which collectively produce our staple food."

More information: Krishnan A, Guiderdoni E, An G, Hsing YI, Han CD, Lee MC, Yu SM, Upadhyaya N, Ramachandran S, Zhang Q, Sundaresan V, Hirochika H, Leung H, Pereira A (2009) *Plant Physiology* 149(1): 165-170.

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