

Fully sequenced rice genome could accelerate biofuel research

Rice is a staple food for over half of the world's population and a model for studies of candidate bioenergy grasses such as sorghum, switchgrass, and Miscanthus. To optimize crops for biofuel production, scientists are seeking to identify genes that control key traits such as yield, resistance to disease, and water use efficiency.

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In a paper published in *The Plant Cell*, a team led by Pamela Ronald, a professor in the Genome Center and the Department of Plant Pathology at UC Davis ... reported the first whole-genome-sequenced, fast-neutron-induced mutant population of Kitaake, a model rice variety with a short life cycle.

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This novel collection will accelerate functional genetic research in rice and other monocots, a type of flowering plant species that includes grasses.

[Read the full [study](#) (behind paywall)]

fast neutron induced mutations in the Kitaake rice Icon circos courtesy Guotian Li x
Genome-wide distribution of fast-neutron-induced mutations in the
Kitaake rice mutant population (green). The genome-wide distribution of
mutations indicates a non-biased saturation of the genome. Colored
lines (center) represent translocations of DNA fragments from one
chromosome to another. (Credit: Guotian Li and Rashmi Jain/Berkeley
Lab)

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [A whole-genome sequenced rice mutant resource for the study of biofuel feedstocks](#)