



A fast neutron mutant population in model rice variety KitaakeX and its use to facilitate forward and reverse genetics

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Abstract:

The Kitaake variety (*ssp. japonica*), has emerged as a model for rice research. It is an extremely early flowering rice cultivar, easy to propagate, with good yield potential and eating quality. Here, we report the de novo genome sequencing and analysis of KitaakeX, a Kitaake variety carrying the XA21 immune receptor. Our KitaakeX sequence assembly contains 377.6 Mb, consisting of 33 scaffolds (476 contigs) with a contig N50 of 1.4 Mb. The assembly is complemented with detailed gene annotations of 35,594 protein coding genes. We identified 331,335 variations between KitaakeX and the reference genome Nipponbare (*ssp. japonica*), and 2,785,991 variations between KitaakeX and Zhenshan97 (*ssp. indica*).

Biography:

Rashmi Jain is currently working as an associate scientist at Department of Plant Pathology and the Genome Center, University of California, Davis, CA 95616, USA



Recent Publications:

1. Jain R et. al.(2019). Genome sequence of the model rice variety KitaakeX.
2. Jain R et. al.Mutants in the Model Rice Variety Kitaake Facilitate Rapid Functional Genomic Studies.
3. Jain R et. al. (2016). Mol. Plant.