

# Application of genomics into rice breeding

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## Abstract

By the progress of genome sequencing, infrastructures for marker-assisted breeding (MAB) of rice came to be established. Fine mapping and gene isolation have been conducted using the breeding materials derived from natural variations and artificial mutants. Such genetic analysis by the genome-wide dense markers provided us the knowledge about the many genes controlling important traits. We identified several genes or quantitative trait loci (QTL) for heading date, blast resistance, eating quality, high-temperature stress tolerance, and so on. NILs of each gene controlling heading date contribute to elongate the rice harvest period. Determination of precise gene location of blast resistance gene *pi21*, allowed us to overcome linkage drag, co-introduction of undesirable eating quality. We could also breed the first practical rice cultivar in Japan with a brown planthopper resistance gene *bph11* in the genetic back-ground of an elite cultivar. Discovery of major and minor QTLs for good eating quality allowed us to fine-tune of eating quality according to the rice planting area or usage of rice grain. Many rice cultivars have bred efficiently by MAB for several traits, or by marker-assisted backcross breeding through chromosome segment substitution lines (CSSLs) using genetically diverse accessions. We are also systematically supporting the crop breeding of other sectors by MAB or by providing resources such as CSSLs. It is possible to pyramid many genes for important traits by using MAB, but is still difficult to improve the yielding ability. We are performing a Genomic Selection (GS) for improvement of rice biomass and grain yield. We are also trying to apply the genome editing technology for high yield rice breeding.

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