

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Germplasm Enhancement
Keyword 2	: Genomics-assisted breeding
Keyword 3	: Marker-assisted selection
Title of Entry	: Genome-wide association study on twelve agronomic traits of temperate japonica rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Temperate japonica rice is widely cultivated and plays a very important role in food security. Understanding the genetics of important agronomic traits is essential for developing high yield varieties. In this study, we selected 191 temperate japonica accessions from the three thousand rice genome project (3K-RGP), and planted in two sites (Yuanjiang and Fumin) in Yunnan province of China. Twelve agronomic traits including plant height, number of effective tillers per plant, panicle length, number of grains per panicle, grain density, spikelet fertility, awn length, grain length, grain width, grain length and width ratio, grain thickness and thousand-grain weight were measured. The results showed wide range of variations for the measured traits. Most of the accessions are short, three accessions have big panicles, seven accessions have big grains were identified and could be used in future breeding programs. Sixty-two quantitative traits loci (QTLs) were identified for 12 measured traits by genome-wide association analysis. Among them, twenty-one QTLs were identified in both experiments, and 41 QTLs were identified only in one site. Some of the known genes are located in the QTL regions identified in our study, for example, An-3 is located in QTL qAL8.2, GS3 is located in QTL qGL3.1, GL3.1 is located in qGW3.2, GW5 is located in qGW5.1 and qGT5.1, GL7/GW7 is located in qTGW2.2. SNP markers for grain size were identified and could be efficiently used for breeding selection. This study provided useful information for future

gene validation and marker assisted selection for some important agronomic traits of temperate japonica rice.

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