



Verification and evaluation of grain QTLs using RILs from TD70 x Kasalath in rice

Y.D. Zhang^{1,2}, J. Zheng², Z.K. Liang³, Y.L. Liang¹, Z.H. Peng³ and C.L. Wang^{1,2}

¹College of Agriculture, Nanjing Agricultural University, Nanjing, China

²Institute of Food Crops, Jiangsu Academy of Agricultural Sciences, Nanjing, China

³Department of Biochemistry, Molecular Biology, Plant Pathology and Entomology, Mississippi State University, Starkville, MS, USA

Corresponding author: C.L. Wang

E-mail: cailin_wang@sina.com

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ABSTRACT. Grain size is an important trait that directly influences the yield of rice. Validation and evaluation of grain genes is important in rice genetic studies and for breeding. In a population of 240 recombinant inbred lines (RILs) derived from a cross between an extra-large grain *japonica* variety TD70 and a small grain *indica* variety Kasalath, we mapped 19 QTLs controlling grain traits. These QTLs included six cloned grain genes, namely, *GW2*, *GS3*, *qSW5*, *qGL3*, *GS5*, and *GW8*. All of the alleles with the optimal effects on grain size came from TD70, the variety with extra-large grains. To verify these gene loci, we cloned and sequenced *GW2*, *GS3*, *GW5* (*qSW5*), *qGL3*, *GS5*, *GW8*, and *TGW6* in TD70 and Kasalath, and found several functional polymorphisms in the sequences of the genes. New functional markers for the cloned genes were designed to identify parents and RILs. The contributions of these polymorphisms to the improvement in rice grain size traits were evaluated. Our results indicate that at least six functional polymorphisms have additive effects on grain shape and that one non-functional polymorphism in *TGW6* affects grain shape in TD70. The newly designed markers will be useful in further studies to identify

functional grain genes. Our findings provide insight into the control of grain size in rice, and they will be of value for improving rice grain yield.

Key words: Rice; Grain gene; Molecular markers; Verification; Effect evaluation