



Identification of QTLs for resistant starch and total alkaloid content in brown and polished rice

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ABSTRACT. An F_3 population consisting of 117 $F_{2,3}$ families derived from a cross between two varieties of rice, Gongmi No. 3 and Diantun 502, with a large difference in their resistant starch and total alkaloid content, was used for quantitative trait locus (QTL) mapping. Two QTLs of resistant starch for rice (*qRS7-1*, *qRS7-2*) were identified in a linkage group on chromosome 7, which could explain phenotypic variance from 7.6 to 17.3%, due to additive effects for resistant starch from Gongmi No. 3 or over-dominance effects for *qRS7-2* of the

marker interval (RM3404-RM478) on chromosome 7 from Gongmi No. 3, accounting for 13.8-17.3% of the phenotypic variance. Two QTLs of total alkaloids for brown rice (*qALb7-1*, *qALb7-2*) were identified in the same linkage group, which could explain phenotypic variance from 7.7 and 19.3%, respectively, due to dominance or over-dominance effects for total alkaloids on chromosome 7 from Diantun 502. To our knowledge, these are the first QTLs to be identified, which are related to resistant starch and total alkaloid content in rice. These results are beneficial for understanding the genetic basis of, as well as for developing markers linked with, resistant starch and total alkaloids of functional components for marker-assisted selection breeding in rice.

Key words: Resistant starch; Total alkaloids; Quantitative trait locus; Brown and polished rice