

Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length

2018

Posted by : webmaster

Posted on : 2018/2/2 11:00:35

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Euphytica

February 2018, 214:41

<https://doi.org/10.1007/s10681-018-2119-1>

Abstract

Grain weight and grain length are the most stable components of rice yield and important indicators of consumer preference. Considering the potentials of wild rice and to enhance the rice yields to meet the increasing demands, 185 Backcross Inbred Lines (BILs) in the background of *O. sativa* ssp. *indica* cv. PR114, including 63 rufi-BILs derived from *O. rufipogon* IRGC104433 and 122 glumae-BILs from *O. glumaepatula* IRGC104387 were evaluated for mapping QTLs for yield and yield component traits using Genotyping by Sequencing (GBS). Phenotypic evaluation of BILs in three seasons spanning two locations revealed significant differences compared with recurrent parent. BILs which did not show significant differences for any trait under investigation, or similar based on pedigree, were excluded from GBS. Some glumae-BILs had to be excluded from mapping QTLs due to less sequence information. A custom designed approach for GBS data analysis identified 3322 informative SNPs in 55 rufi-BILs and 3437 informative SNPs in 79 glumae-BILs. QTL mapping identified one QTL for thousand grain weight (qtgw5.1), two for grain width (qgw5.1, qgw5.2) and one for grain length (qgl7.1) in rufi-BILs. In the glumae-BILs, three QTL for thousand grain weight (qtgw2.1, qtgw3.1, qtgw6.1) and two for grain length (qgl3.1, qgl7.1) were identified. Most of the grain weight and width QTL showed positive additive effect contributed by wild species allele, whereas the grain length QTL showed positive additive effect contributed by recurrent parent allele. Based on their physical position, none of the QTLs were found similar to previously cloned QTLs. QTLs for grain traits identified from low yielding wild relatives of rice reveals their significance in improving further the rice yields and widen the genetic base of cultivated rice.