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QTL mapping of resistance to *Pseudomonas syringae* pv. *glycinea* in soybean by using the high density SNP genetic map

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Bacterial leaf blight (BLB) caused by *Pseudomonas syringae* pv. *glycinea* has been reported as one of the common diseases in main soybean producing regions worldwide. It is also a serious leaf disease in Northeast and Yangtze-Huai river valleys of China. Some germplasm accessions with resistance to BLB have been identified and four resistant genes, *Rpg1-Rpg4*, were reported. Among them, the positional cloning of the resistant *Rpg1-b* gene containing a complex NBS – LRR was reported in 2004 by Tom Ashfield. *Rpg4* is roughly positioned in the N linkage group (Chromosome 3), while *Rpg2*, *Rpg3* still have no further reports. To reveal the genetic base of the Chinese resistant sources, we performed QTL linkage mapping of disease resistance response to BLB using a NJZM6 recombinant inbred line population. The NJZM6 linkage map contains 2600 BIN markers with the total length of 2630.22 cM and the average distance of 1.01 cM/bin. According to the results by using QTL analysis software Win QTL Cartographer 2.5 and composite interval mapping method, two QTLs (*qRpg_17_1*, *qRpg_19_1*) were repeatedly detected in years 2014 and 2015, and located near 33.8 cM and 0 cM positions on chromosome 17 and 19 respectively. Their average phenotypic contribution rates were 9.70% and 7.01%, and total 16 and 43 candidate genes were identified in the QTL region respectively. Another QTL *qRpg_13_1* which overlapped with the region of a previously reported *Rpg1-b* gene on chromosome 13 was found in 2016, indicating *Rpg1* gene was also the major controller for resistance to Chinese BLB strain. At least three QTL were involved in genetic control of resistance to BLB in Chinese soybeans. Our results may lay a good foundation for fine mapping and cloning of the major resistant QTL for further disease resistance breeding in soybean.